



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 04:04 AM EDT

PDB ID : 1VQO / pdb_00001vqo
Title : The structure of CCPMN bound to the large ribosomal subunit 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

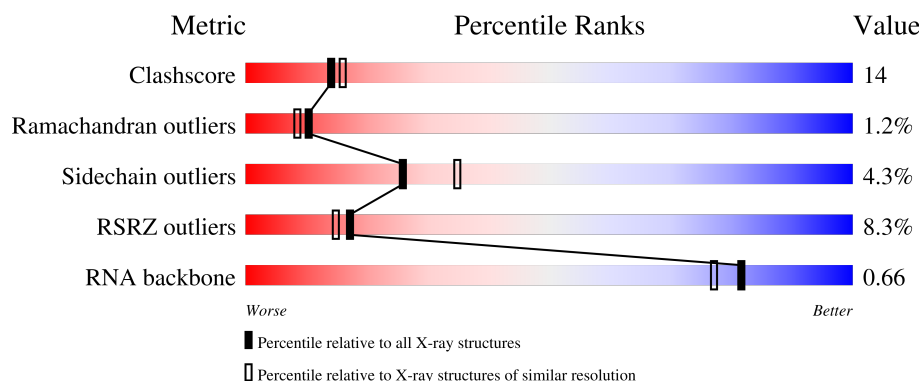
1 Overall quality at a glance i

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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)
RNA backbone	3983	1052 (2.50-1.90)

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

Mol	Chain	Length	Quality of chain
1	0	2922	3% 65% 25% 6%
2	9	122	7% 60% 30% 9%
3	4	3	33% 33% 33%
4	A	240	9% 56% 37% 6%
5	B	338	3% 57% 37% 6%

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Mol	Chain	Length	Quality of chain
6	C	246	
7	D	177	
8	E	178	
9	F	120	
10	G	348	
11	H	171	
12	J	145	
13	K	132	
14	L	165	
15	M	195	
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	

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Mol	Chain	Length	Quality of chain
31	3	92	
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	8040	-	-	-	X
33	MG	0	8082	-	-	-	X
34	K	0	9001	-	-	-	X
35	NA	0	9122	-	-	-	X
35	NA	0	9152	-	-	-	X

2 Entry composition

There are 39 unique types of molecules in this entry. The entry contains 99040 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			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	628	1MA	A	modified residue	GB 3377779
0	2587	OMU	U	modified residue	GB 3377779
0	2588	OMG	G	modified residue	GB 3377779
0	2619	UR3	U	modified residue	GB 3377779
0	2621	PSU	U	modified residue	GB 3377779

- 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*(PPU))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	4	3	Total	C	N	O	P	0	0	0
			74	40	13	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	S	0	0	0
			1118	670	222	226				

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 34 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 35 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	0	64	Total Na 64 64	0	0
35	9	1	Total Na 1 1	0	0
35	B	1	Total Na 1 1	0	0
35	C	1	Total Na 1 1	0	0
35	D	1	Total Na 1 1	0	0
35	J	1	Total Na 1 1	0	0
35	M	1	Total Na 1 1	0	0
35	Q	1	Total Na 1 1	0	0
35	R	3	Total Na 3 3	0	0
35	S	1	Total Na 1 1	0	0

- Molecule 36 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	0	9	Total Cl 9 9	0	0
36	A	1	Total Cl 1 1	0	0
36	B	1	Total Cl 1 1	0	0
36	J	3	Total Cl 3 3	0	0
36	K	1	Total Cl 1 1	0	0
36	L	1	Total Cl 1 1	0	0
36	M	1	Total Cl 1 1	0	0
36	N	1	Total Cl 1 1	0	0
36	O	1	Total Cl 1 1	0	0
36	R	1	Total Cl 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	Y	1	Total 1	Cl 1	0	0
36	3	1	Total 1	Cl 1	0	0

- Molecule 37 is STRONTIUM ION (CCD ID: SR) (formula: Sr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	0	98	Total 98	Sr 98	0	0
37	9	3	Total 3	Sr 3	0	0
37	A	3	Total 3	Sr 3	0	0
37	B	2	Total 2	Sr 2	0	0
37	F	1	Total 1	Sr 1	0	0
37	H	1	Total 1	Sr 1	0	0
37	L	1	Total 1	Sr 1	0	0
37	R	1	Total 1	Sr 1	0	0
37	S	1	Total 1	Sr 1	0	0
37	1	2	Total 2	Sr 2	0	0
37	3	1	Total 1	Sr 1	0	0

- Molecule 38 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	O	1	Total 1	Cd 1	0	0
38	U	1	Total 1	Cd 1	0	0
38	Z	1	Total 1	Cd 1	0	0
38	1	1	Total 1	Cd 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	3	1	Total	Cd	0	0
			1	1		

- Molecule 39 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
39	0	5780	Total	O	0	0
			5780	5780		
39	9	136	Total	O	0	0
			136	136		
39	4	4	Total	O	0	0
			4	4		
39	A	124	Total	O	0	0
			124	124		
39	B	141	Total	O	0	0
			141	141		
39	C	177	Total	O	0	0
			177	177		
39	D	46	Total	O	0	0
			46	46		
39	E	43	Total	O	0	0
			43	43		
39	F	25	Total	O	0	0
			25	25		
39	G	16	Total	O	0	0
			16	16		
39	H	71	Total	O	0	0
			71	71		
39	J	58	Total	O	0	0
			58	58		
39	K	60	Total	O	0	0
			60	60		
39	L	82	Total	O	0	0
			82	82		
39	M	125	Total	O	0	0
			125	125		
39	N	62	Total	O	0	0
			62	62		
39	O	40	Total	O	0	0
			40	40		
39	P	60	Total	O	0	0
			60	60		

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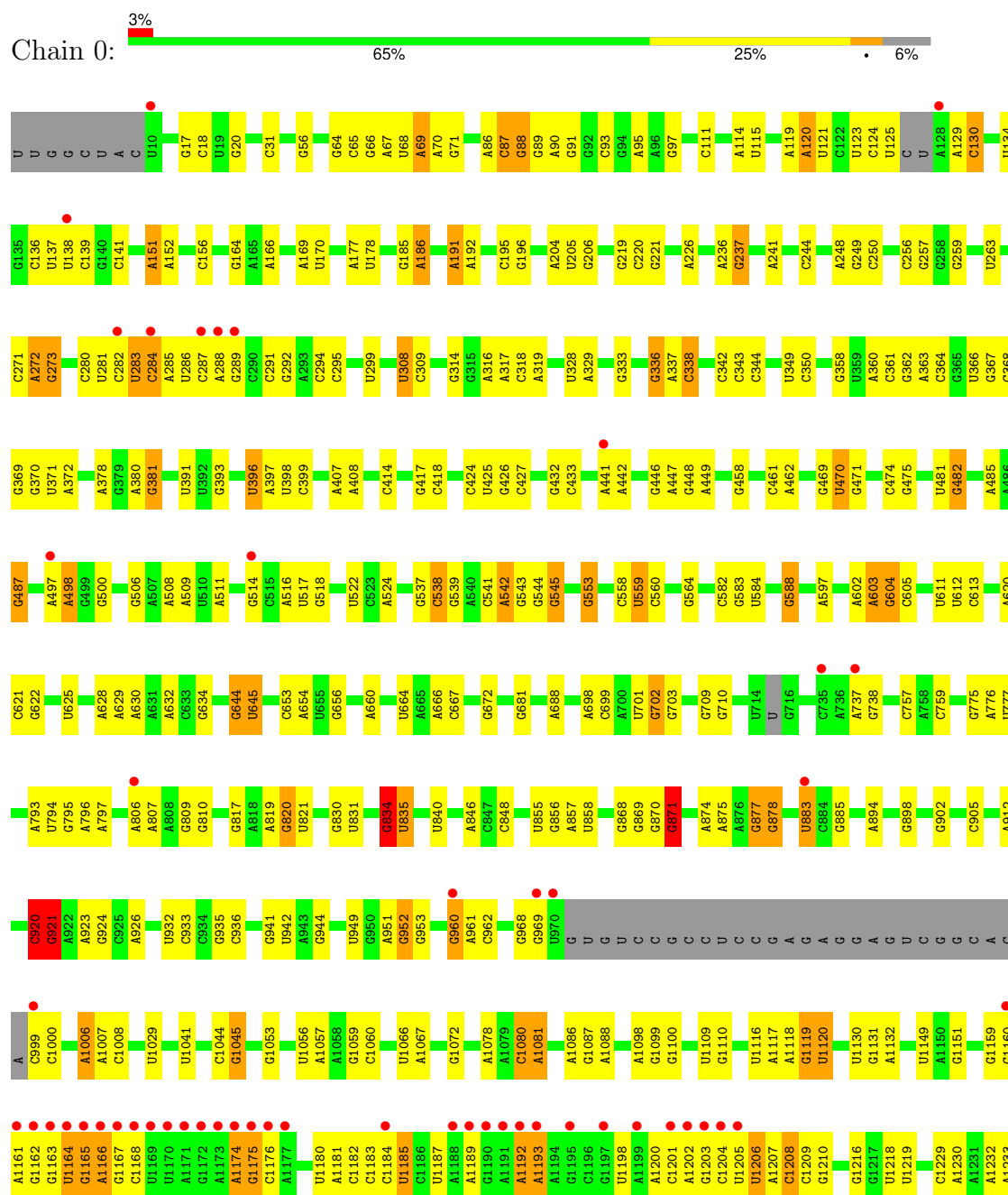
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
39	Q	49	Total 49	O 49	0	0
39	R	83	Total 83	O 83	0	0
39	S	30	Total 30	O 30	0	0
39	T	36	Total 36	O 36	0	0
39	U	28	Total 28	O 28	0	0
39	V	12	Total 12	O 12	0	0
39	W	68	Total 68	O 68	0	0
39	X	26	Total 26	O 26	0	0
39	Y	93	Total 93	O 93	0	0
39	Z	29	Total 29	O 29	0	0
39	1	52	Total 52	O 52	0	0
39	2	40	Total 40	O 40	0	0
39	3	66	Total 66	O 66	0	0
39	I	8	Total 8	O 8	0	0

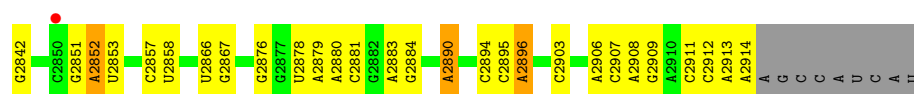
3 Residue-property plots [i](#)

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

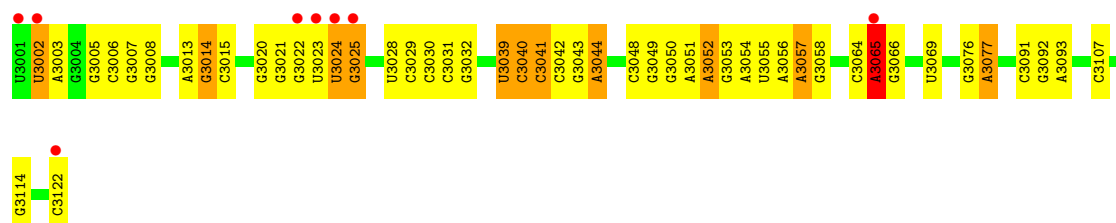
- Molecule 1: 23S ribosomal rna



G2748	A2633	G2595	G2420	C2313	U	U	A1919	U1766	C1666	U1503	U1234
G2749	G2634	C2526	G2421	G2313	G	G	G1926	A1767	A1667	A1504	G1235
G2750	A2635	U2531	U2422	C2317	A	A	G1926	C1768	U1668	U1505	A1236
C2636	C2636	A2532	G2426	A	A	A	A1927	U1769	A1669	U1506	U1237
G2754	A2637	C2533	U2426	U2320	A	C	G1928	C1770	G1670	C1523	C1238
G2755	C2644	C2534	U2435	A2321	U	C	G1929	U1771	C1675	G1523	G1239
A2761	U2645	U2535	U2435	A2321	C	A	C1940	G1773	C1675	U1524	A1242
C2762	A2649	C2536	C2443	G2324	U	U	A1941	A1778	G1681	U1525	C1243
A2649	C2537	G2537	G2453	C2329	A	G	A1942	A1778	A1682	A1526	C1243
C2765	U2650	U2538	G2453	U2330	C	U	C1943	A1779	G1683	A1527	U1244
C2651	U2651	U2539	A2456	U2330	C	U	U2054	C1787	A1684	A1528	G1245
U2652	U2652	C2540	U2457	G2337	C	A	C1946	C1787	A1685	G1529	A1246
C2769	U2661	U2541	U2457	G2337	G	U	C1946	U1788	C1686	U1532	A1247
G2770	G2662	C2549	G2462	G2338	U	G	G1951	U1788	C1687	G1552	C1250
U2663	U2663	C2552	G2462	A	C	A	U	C1798	G1692	G1555	C1251
A2664	A	A2553	A2465	C	G	A	A	A1829	A1693	U1559	A1252
U	U	G	A2467	G	U	C	A	U1817	C1700	U	C1253
G2782	G2667	U2563	A2467	G2344	C	C	U	C1818	A1701	U1561	A1261
A2783	A2668	C2564	A2469	A2345	C	U	A	G1819	A1702	C1562	C1268
A2784	G2670	C2565	C2472	C2346	U	A	U	G1820	U1702	G1563	A1268
C2785	U2671	C2566	C2472	C2347	A	C	G	C1826	C1705	C1564	C1400
G2786	C2676	A2568	C2476	C2348	C	A	A	G1827	C1705	U1573	A1278
U2791	G2679	C2578	G2480	A2353	G	C	C	A1829	C1714	C1574	U1279
A2792	C2679	G2578	G2481	A2354	A	C	C	U1835	C1715	A1407	A1287
C2795	A2680	U2586	G2482	A2355	G	G	U1964	U1835	A1716	G1409	U1288
U2796	A2681	U2587	U2483	A2356	U	U	C1965	U1838	A1717	C1593	C1289
C2682	C2682	U2588	U2484	G2357	A	A	U1967	U1839	U1722	C1594	A1291
A2800	A2694	G2589	A2485	A2361	C	C	U	A1840	G1723	U1596	A1294
U2807	A2697	U2590	A2485	A2362	C	C	G1971	A1840	U1724	A1603	G1295
A2811	C2698	C2591	A2490	A2363	C	C	U1972	A1845	C1725	G1430	A1294
A2812	A2699	G2592	G2491	A2364	C	G	A1973	U1845	G1726	G1604	G1295
A2813	G2700	U2492	U2492	A2365	C	C	U2100	U1846	G1730	G1605	U1298
A2814	C2704	A2600	C2493	A2366	G	C	C2104	A1847	C1731	A1606	G1299
G2815	U2705	G2602	U2499	A2369	U	U	U1980	C1853	U1731	A1607	U1304
A2816	U2711	U2607	G2500	A2374	A	G	U1981	C1856	C1734	A1615	U1304
G2817	G2712	C2608	G2501	G2375	C	C	U1992	U1863	C1735	C1451	U1306
C2821	G2715	G2611	G2502	U2377	G	G	U1996	C1864	A1736	G1452	U1306
C2824	G2716	A2612	A2503	U2378	G	C	U2003	G1867	U1741	A1458	U1314
G2825	C2717	G2613	A2504	U2378	C	C	U2004	G1868	G1744	C1462	G1327
A2827	A2718	G2618	G2505	G2379	A	A	G2005	G1868	G1745	A1630	A1328
G2828	U2719	U2619	A2506	G2379	C	C	C2006	U1877	U1748	A1463	A1331
C2831	U2721	U2620	A2507	G2388	C	C	U2007	U1878	U1749	G1634	G1332
C2832	U2724	U2621	C2508	A2401	C	C	U2008	G1879	C1750	A1470	C1333
C2833	G2725	C2626	A2510	A2402	C	G	A2011	U1880	G1751	U1473	C1334
U2837	U2726	G2627	A2511	A2403	A	U	G2012	C1881	C1474	C1474	G1340
A2838	U2735	G2630	C2515	U2406	G	C	G2013	C1882	G1752	G1475	G1340
C2839	U2735	U2631	A2516	U2406	U	U	G2014	A1754	A1476	A1476	A1341
A2840	C2747	U2632	G2522	A2414	C	C	A2015	G1902	C1477	C1342	A1341
A2841	C2747	U2632	G2524	G2416	A	A	U2016	U1903	A1656	A1482	C1343
C2843	U2747	U2632	U2523	G2416	C	C	U2017	A1657	G1756	C1483	U1350
C2844	U2747	U2632	U2524	U2419	C	C	A2018	A1909	A1759	G1484	A1351
C2845	U2747	U2632	U2524	U2419	C	C	A2019	A1909	A1759	A1658	A1352



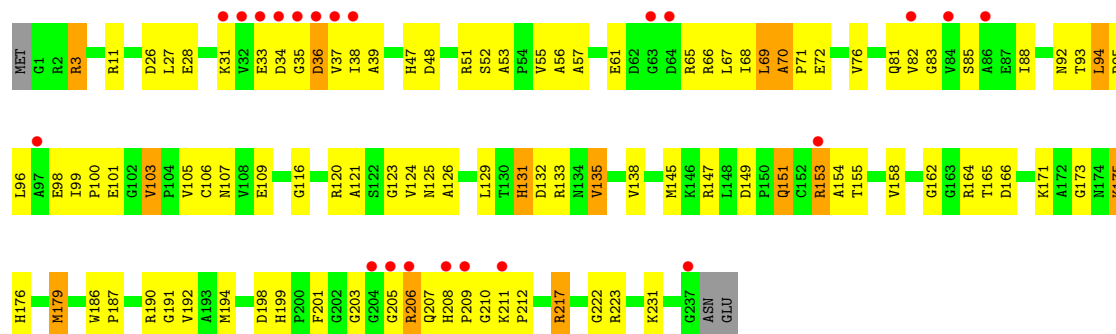
• Molecule 2: 5S ribosomal RNA



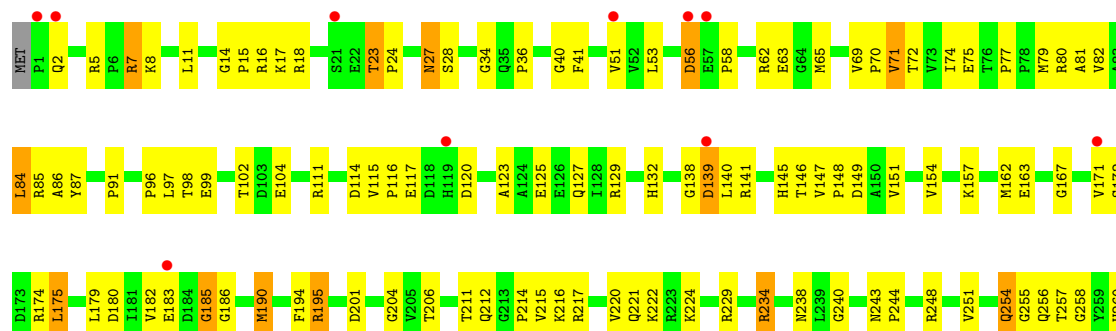
• Molecule 3: 5'-R(*CP*CP*(PPU))-3'



• Molecule 4: 50S ribosomal protein L2P

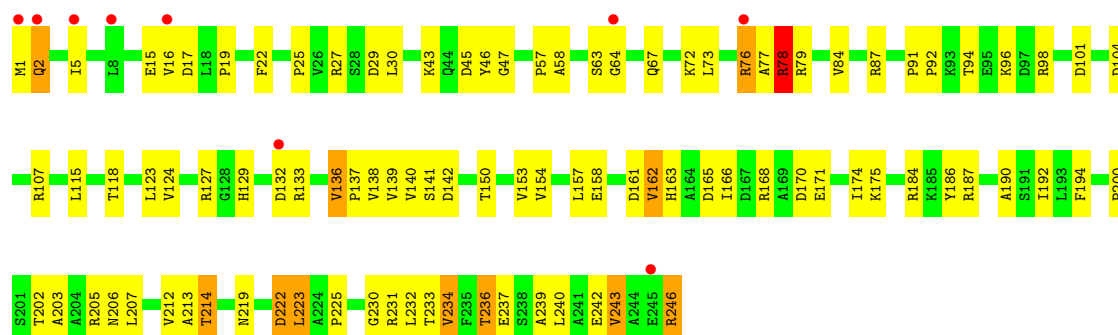


• Molecule 5: 50S ribosomal protein L3P

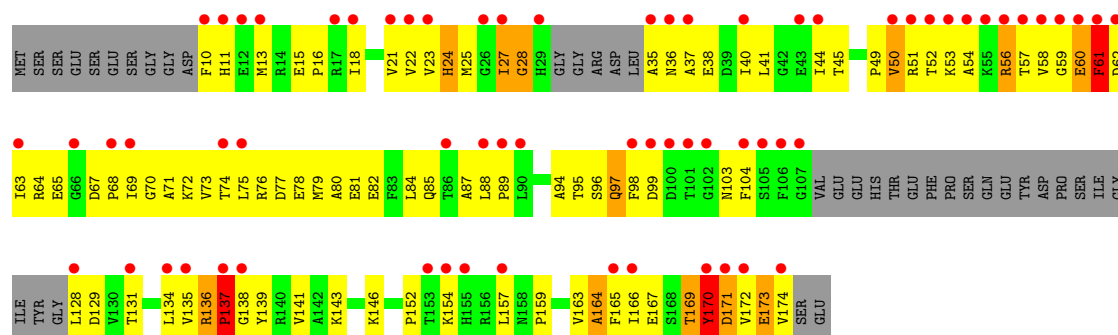




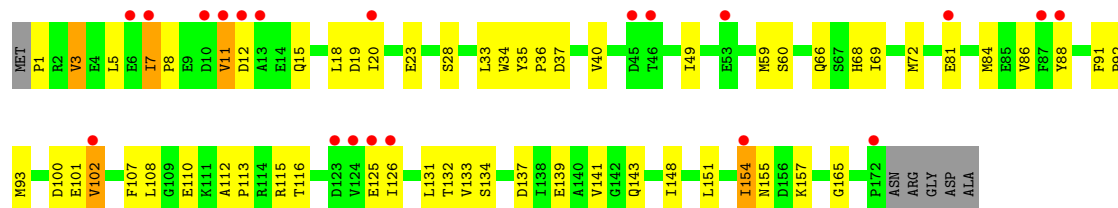
• Molecule 6: 50S ribosomal protein L4E



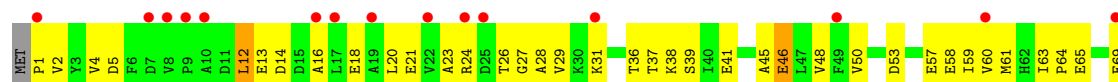
• Molecule 7: 50S ribosomal protein L5P

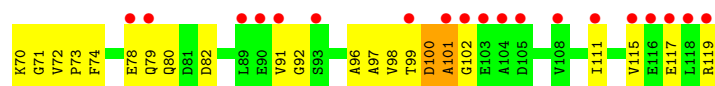


• Molecule 8: 50S ribosomal protein L6P

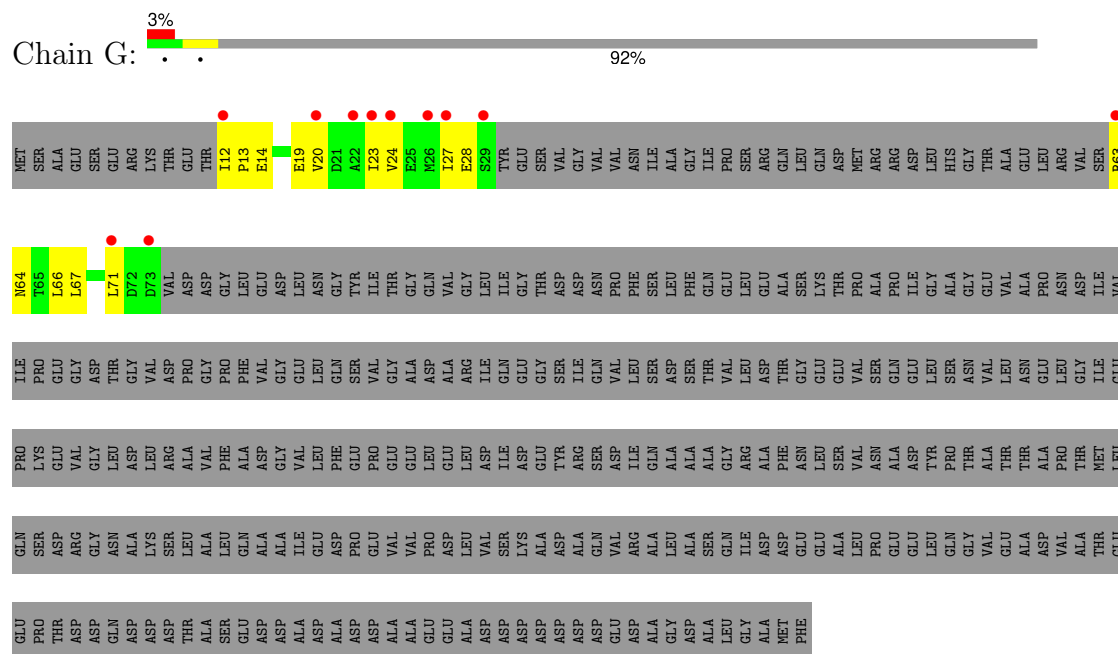


• Molecule 9: 50S ribosomal protein L7AE

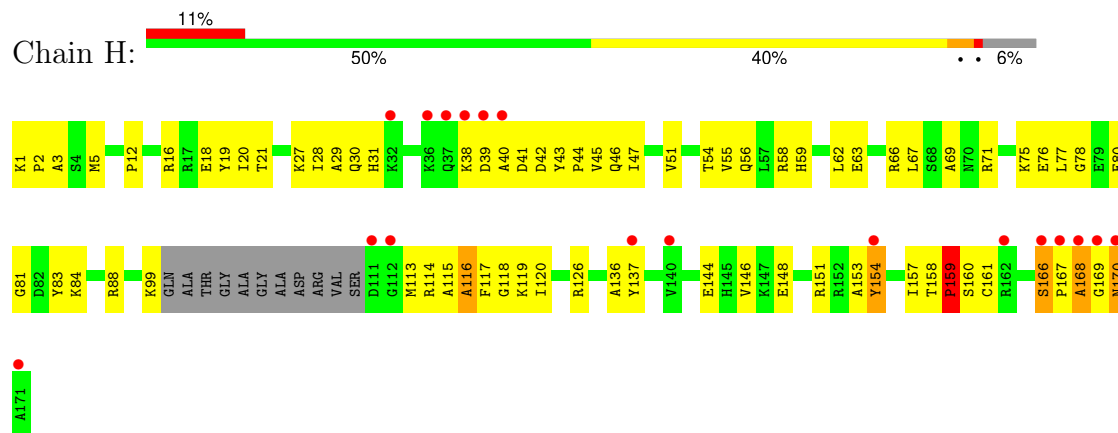




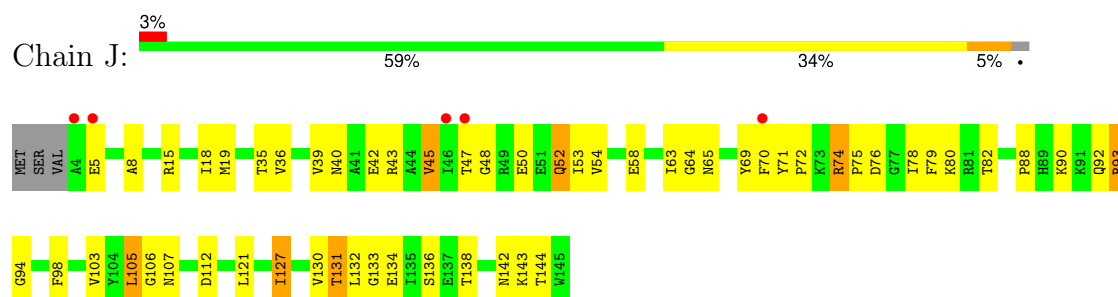
• Molecule 10: ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG



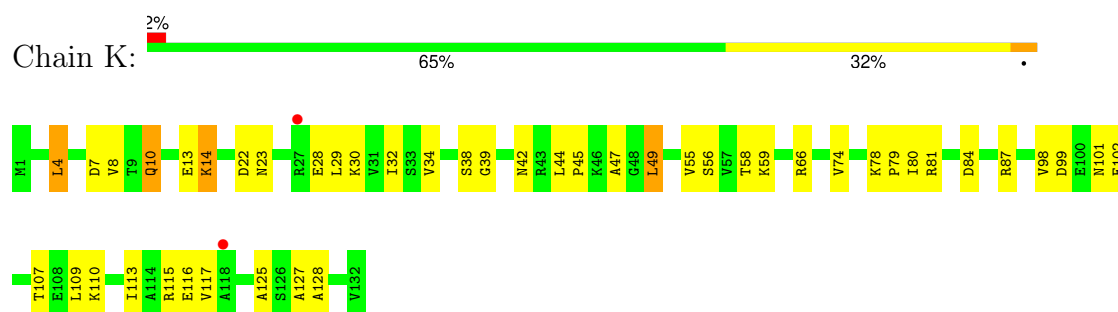
• Molecule 11: 50S RIBOSOMAL PROTEIN L10E



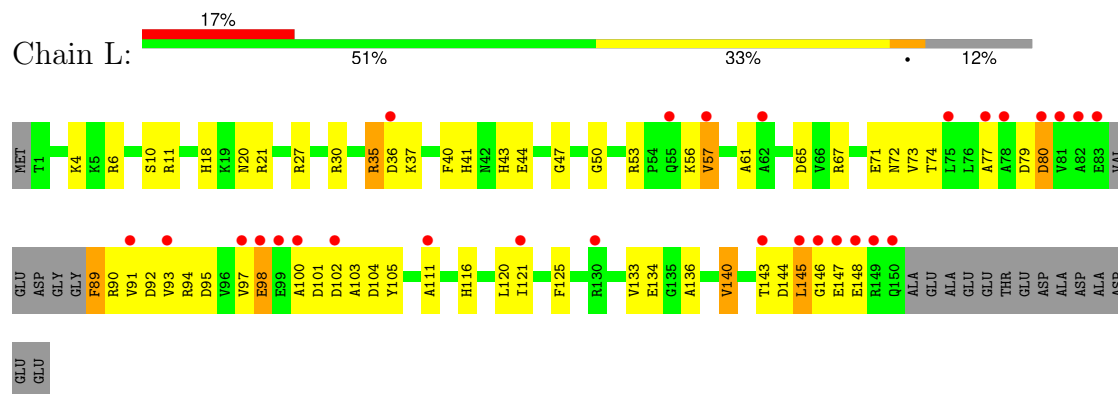
• Molecule 12: 50S ribosomal protein L13P



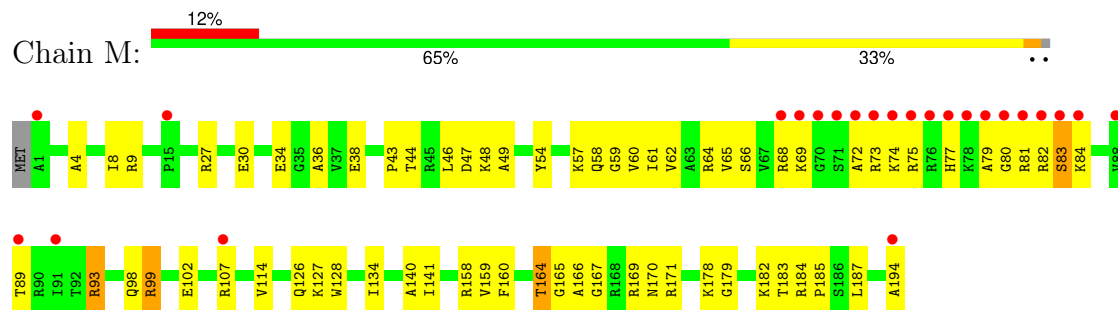
• Molecule 13: 50S ribosomal protein L14P



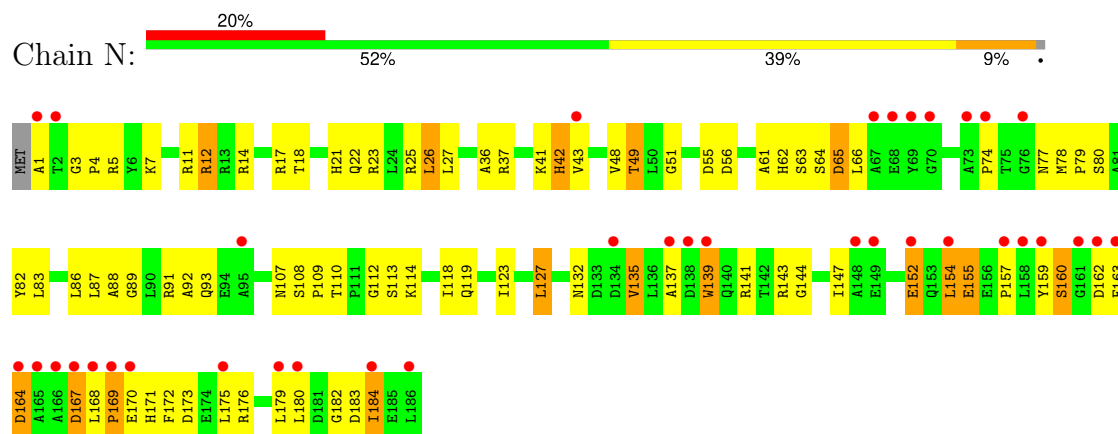
- Molecule 14: 50S ribosomal protein L15P



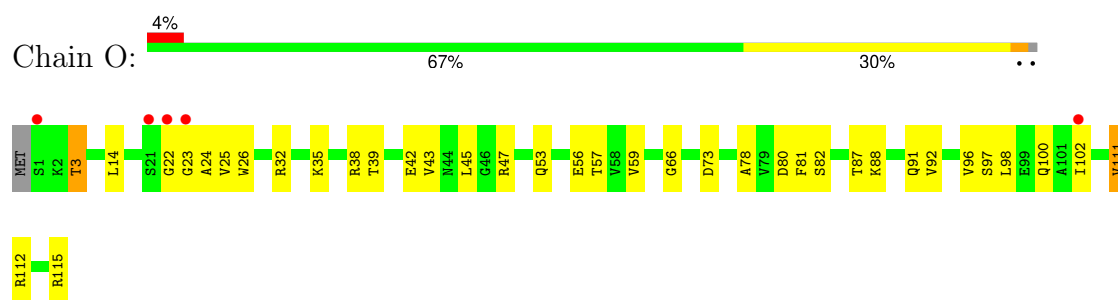
- Molecule 15: 50S Ribosomal Protein L15E



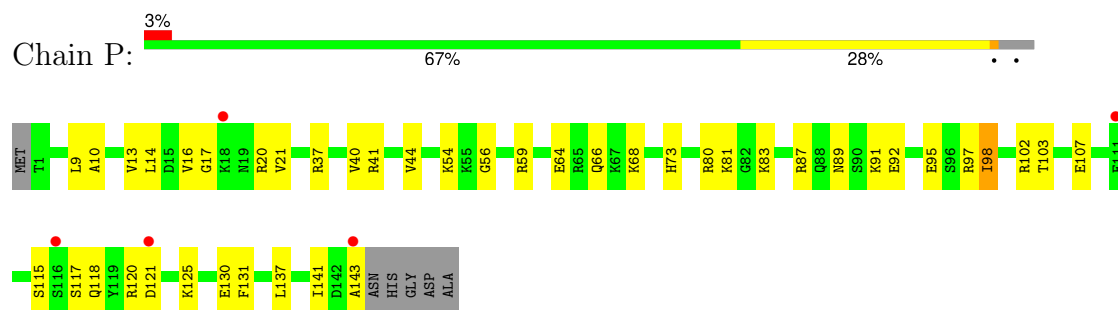
- Molecule 16: 50S ribosomal protein L18P



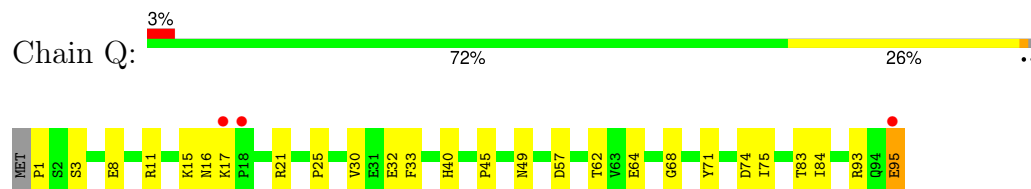
- Molecule 17: 50S ribosomal protein L18e



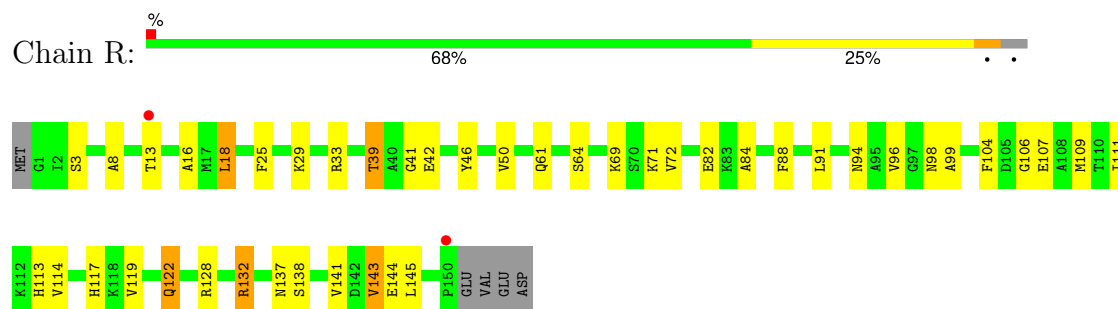
- Molecule 18: 50S ribosomal protein L19E



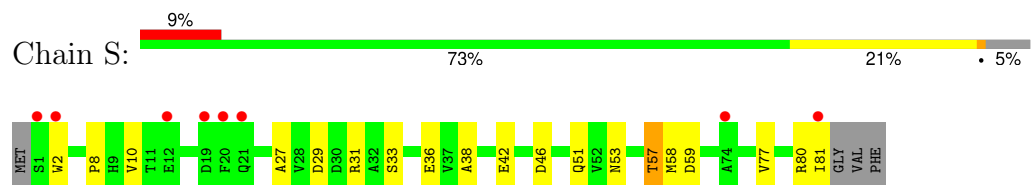
- Molecule 19: 50S ribosomal protein L21e



- Molecule 20: 50S ribosomal protein L22P

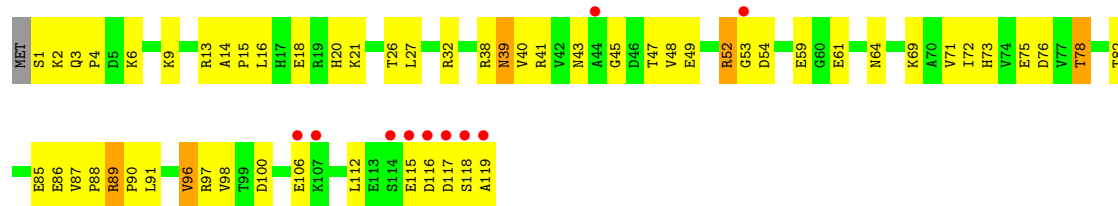


- Molecule 21: 50S ribosomal protein L23P



- Molecule 22: 50S ribosomal protein L24P

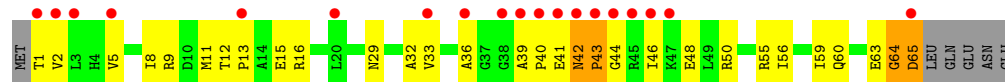




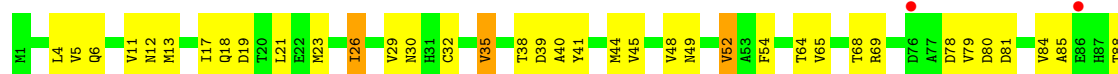
- Molecule 23: 50S ribosomal protein L24E



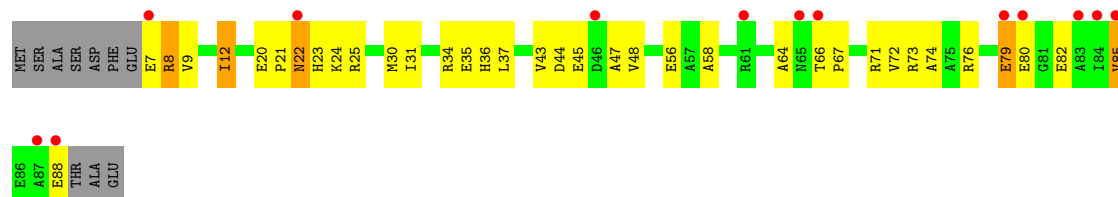
- Molecule 24: 50S ribosomal protein L29P



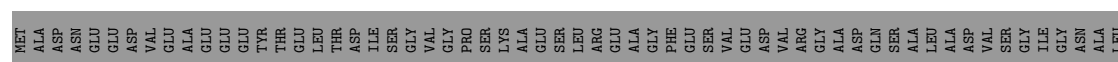
- Molecule 25: 50S ribosomal protein L30P

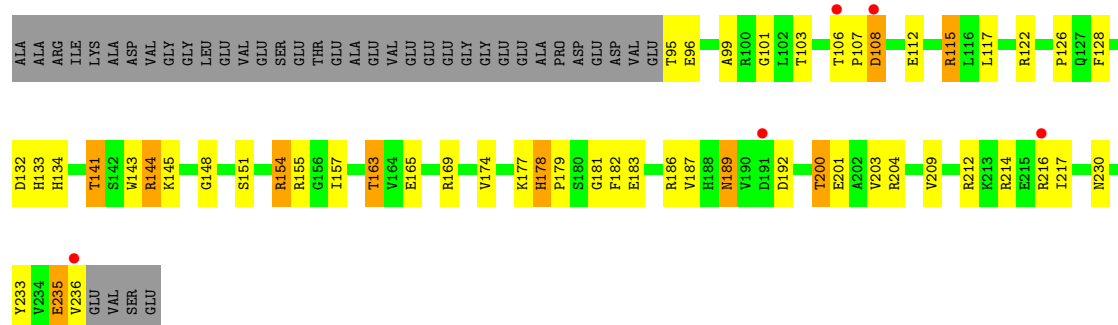


- Molecule 26: 50S ribosomal protein L31e

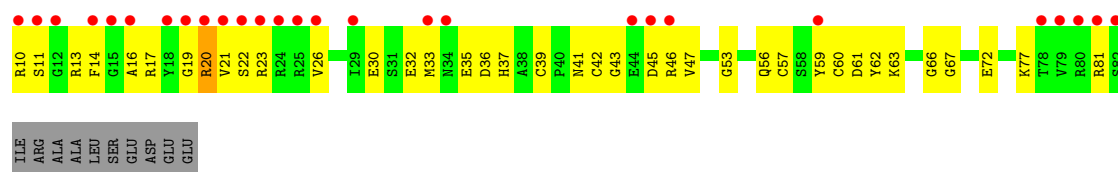


- Molecule 27: 50S ribosomal protein L32E





• Molecule 28: 50S ribosomal protein L37Ae



• Molecule 29: 50S ribosomal protein L37e



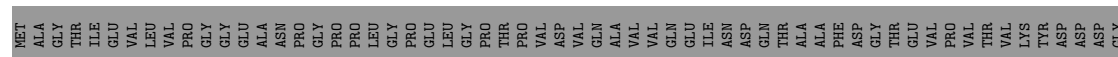
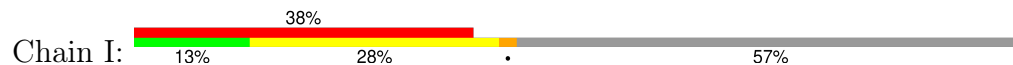
• Molecule 30: 50S ribosomal protein L39e

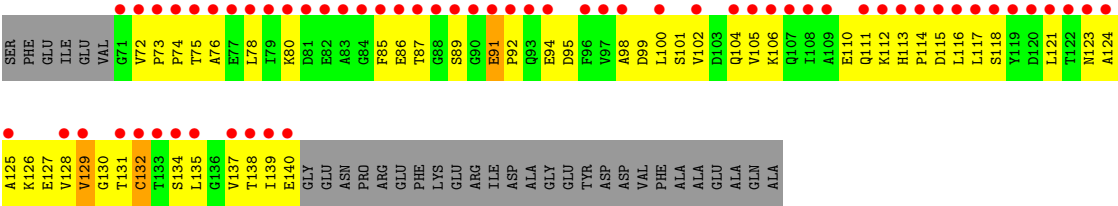


• Molecule 31: 50S ribosomal protein L44E



• 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, α , β , γ	212.04Å 299.41Å 575.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.21	Depositor EDS
% Data completeness (in resolution range)	97.9 (50.00-2.20) 88.8 (50.00-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.69 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.215 , 0.246 0.211 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	99040	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.38	0/65959	0.62	33/102870 (0.0%)
2	9	0.37	0/2905	0.60	1/4528 (0.0%)
3	4	0.35	0/40	0.68	0/60
4	A	0.40	0/1786	0.95	5/2408 (0.2%)
5	B	0.44	0/2690	1.01	19/3652 (0.5%)
6	C	0.44	0/1884	0.98	6/2551 (0.2%)
7	D	0.34	0/1111	0.85	6/1498 (0.4%)
8	E	0.38	0/1382	0.86	2/1880 (0.1%)
9	F	0.38	0/901	0.83	0/1224
10	G	0.31	0/241	0.76	0/324
11	H	0.37	0/1287	0.95	5/1725 (0.3%)
12	J	0.41	0/1136	0.94	3/1530 (0.2%)
13	K	0.42	0/1001	1.00	2/1347 (0.1%)
14	L	0.38	0/1130	0.99	6/1509 (0.4%)
15	M	0.41	0/1584	0.88	3/2119 (0.1%)
16	N	0.34	0/1474	1.02	9/1999 (0.5%)
17	O	0.41	0/874	0.91	4/1181 (0.3%)
18	P	0.39	0/1147	0.87	1/1528 (0.1%)
19	Q	0.41	0/749	1.03	3/1005 (0.3%)
20	R	0.44	0/1172	0.95	5/1578 (0.3%)
21	S	0.35	0/648	0.86	2/875 (0.2%)
22	T	0.36	0/958	0.95	3/1289 (0.2%)
23	U	0.40	0/417	0.87	1/562 (0.2%)
24	V	0.32	0/502	0.89	3/675 (0.4%)
25	W	0.49	1/1219 (0.1%)	0.95	3/1655 (0.2%)
26	X	0.43	0/664	0.94	3/895 (0.3%)
27	Y	0.44	0/1146	0.98	6/1536 (0.4%)
28	Z	0.34	0/589	0.88	0/787
29	1	0.48	0/438	0.94	1/578 (0.2%)
30	2	0.41	0/401	0.83	0/529
31	3	0.39	0/771	0.86	0/1024
32	I	0.34	0/526	0.89	2/716 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.39	1/98732 (0.0%)	0.72	137/147637 (0.1%)

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	40
2	9	0	1
All	All	1	41

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	W	35	VAL	CA-CB	5.70	1.58	1.54

All (137) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1563	G	C2'-C3'-O3'	14.37	131.06	109.50
19	Q	17	LYS	N-CA-C	-10.11	96.99	109.83
16	N	163	PHE	N-CA-C	-9.00	102.43	113.41
1	0	1942	A	C5'-C4'-C3'	8.75	129.12	116.00
1	0	1563	G	C4'-C3'-O3'	8.47	122.11	109.40
14	L	47	GLY	N-CA-C	8.15	120.31	112.08
5	B	222	LYS	N-CA-C	-7.77	99.02	110.52
1	0	871	G	C5'-C4'-O4'	-7.54	98.48	109.80
1	0	920	C	C2'-C3'-O3'	-7.33	102.71	113.70
5	B	323	LEU	N-CA-C	7.25	120.47	110.24
1	0	1819	G	C5'-C4'-C3'	7.21	126.81	116.00
1	0	1979	G	C2'-C3'-O3'	7.14	124.41	113.70
21	S	27	ALA	N-CA-C	-7.13	97.62	109.46
26	X	22	ASN	N-CA-C	7.10	119.88	111.71
16	N	135	VAL	N-CA-C	-7.05	106.26	113.10
1	0	1352	A	C2'-C3'-O3'	6.91	119.86	109.50
20	R	141	VAL	N-CA-C	6.88	117.75	108.11
1	0	1592	G	N9-C1'-C2'	6.71	122.06	112.00
12	J	36	VAL	N-CA-C	6.60	117.35	108.11
25	W	143	THR	N-CA-C	-6.56	104.17	111.71
1	0	1684	A	C2'-C3'-O3'	6.53	119.30	109.50
13	K	8	VAL	N-CA-C	6.50	117.27	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	L	57	VAL	N-CA-C	-6.47	106.48	112.43
5	B	266	ASN	N-CA-C	6.45	120.27	111.17
7	D	170	TYR	N-CA-C	6.43	119.96	111.28
12	J	112	ASP	N-CA-C	-6.41	101.03	110.52
6	C	78	ARG	N-CA-C	6.41	117.03	108.38
1	0	883	U	N1-C1'-C2'	6.39	121.59	112.00
20	R	137	ASN	N-CA-C	6.31	120.20	110.42
6	C	205	ARG	N-CA-C	6.31	119.82	111.75
2	9	3039	U	N1-C1'-C2'	6.26	121.39	112.00
26	X	12	ILE	N-CA-C	6.23	114.06	107.76
5	B	157	LYS	N-CA-C	-6.23	106.27	114.31
14	L	20	ASN	N-CA-C	6.23	117.95	111.03
4	A	222	GLY	N-CA-C	-6.22	106.51	113.79
11	H	160	SER	N-CA-C	-6.22	101.28	110.48
8	E	11	VAL	N-CA-C	6.12	118.68	109.20
20	R	122	GLN	N-CA-C	-6.10	99.92	109.25
15	M	8	ILE	N-CA-C	-6.10	104.56	110.72
16	N	51	GLY	CA-C-N	6.09	125.57	119.24
16	N	51	GLY	C-N-CA	6.09	125.57	119.24
23	U	50	GLU	N-CA-C	6.08	118.69	111.33
1	0	1504	A	N9-C1'-C2'	6.08	121.12	112.00
22	T	52	ARG	N-CA-C	6.00	123.57	110.80
15	M	89	THR	N-CA-C	5.98	117.67	111.03
22	T	16	LEU	N-CA-C	5.96	118.26	111.11
16	N	3	GLY	CA-C-N	5.95	126.11	119.32
16	N	3	GLY	C-N-CA	5.95	126.11	119.32
1	0	206	G	C5'-C4'-C3'	-5.94	107.09	116.00
4	A	70	ALA	N-CA-C	5.93	117.28	109.93
11	H	159	PRO	N-CA-C	5.92	119.51	111.22
6	C	84	VAL	N-CA-C	-5.89	101.98	109.58
1	0	1120	U	C5'-C4'-C3'	-5.87	107.19	116.00
27	Y	183	GLU	N-CA-C	-5.86	100.14	109.76
16	N	169	PRO	N-CA-C	-5.86	106.04	114.18
20	R	3	SER	N-CA-C	-5.86	100.25	109.50
5	B	117	GLU	N-CA-C	-5.83	106.70	113.88
21	S	57	THR	N-CA-C	5.79	118.37	110.55
14	L	145	LEU	N-CA-C	-5.75	105.01	111.28
24	V	42	ASN	CA-C-N	5.74	127.02	119.84
24	V	42	ASN	C-N-CA	5.74	127.02	119.84
1	0	2291	A	N9-C1'-C2'	5.72	120.58	112.00
1	0	1615	A	C5'-C4'-C3'	5.67	124.50	116.00
27	Y	143	TRP	N-CA-C	5.64	118.50	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W	35	VAL	N-CA-C	5.63	114.32	107.61
1	0	874	A	C4'-C3'-O3'	-5.62	104.57	113.00
22	T	78	THR	N-CA-C	5.62	116.78	108.86
1	0	921	G	N9-C1'-C2'	5.59	120.39	112.00
1	0	1819	G	C4'-C3'-C2'	-5.58	97.02	102.60
20	R	18	LEU	N-CA-C	-5.57	101.09	109.95
1	0	834	G	C2'-C3'-O3'	-5.56	105.37	113.70
1	0	2012	U	N1-C1'-C2'	5.56	120.33	112.00
16	N	42	HIS	N-CA-C	5.56	118.31	109.81
5	B	151	VAL	CA-C-N	5.55	125.22	119.05
5	B	151	VAL	C-N-CA	5.55	125.22	119.05
27	Y	230	ASN	CA-C-N	5.55	125.75	120.31
27	Y	230	ASN	C-N-CA	5.55	125.75	120.31
27	Y	178	HIS	N-CA-C	-5.55	102.13	109.84
6	C	186	TYR	N-CA-C	5.54	118.73	110.14
1	0	2301	A	N9-C1'-C2'	5.53	120.30	112.00
15	M	4	ALA	N-CA-C	-5.50	105.37	111.36
8	E	37	ASP	N-CA-C	5.47	119.24	112.24
12	J	105	LEU	N-CA-C	-5.46	101.08	109.76
27	Y	101	GLY	N-CA-C	5.46	122.11	112.83
6	C	175	LYS	N-CA-C	5.44	117.74	110.35
25	W	49	ASN	N-CA-C	5.42	118.69	111.75
18	P	56	GLY	N-CA-C	-5.41	101.99	111.46
5	B	123	ALA	N-CA-C	-5.40	105.40	111.28
5	B	23	THR	CA-C-N	5.38	125.32	119.78
5	B	23	THR	C-N-CA	5.38	125.32	119.78
5	B	120	ASP	CA-C-N	5.36	125.02	119.56
5	B	120	ASP	C-N-CA	5.36	125.02	119.56
6	C	192	ILE	N-CA-C	5.35	116.49	109.21
29	1	11	LYS	N-CA-C	5.35	118.03	107.98
17	O	43	VAL	N-CA-C	5.34	115.65	108.17
17	O	82	SER	N-CA-C	-5.34	103.83	110.41
1	0	2313	C	C5'-C4'-C3'	5.33	124.00	116.00
11	H	118	GLY	N-CA-C	5.29	119.32	112.54
4	A	198	ASP	N-CA-C	5.29	119.89	113.38
1	0	2768	A	N9-C1'-C2'	5.29	119.93	112.00
17	O	24	ALA	N-CA-C	-5.28	107.50	114.31
26	X	79	GLU	N-CA-C	5.27	117.77	111.71
32	I	91	GLU	CA-C-N	5.25	125.17	119.76
32	I	91	GLU	C-N-CA	5.25	125.17	119.76
17	O	66	GLY	N-CA-C	5.25	125.62	113.18
11	H	88	ARG	N-CA-C	5.23	119.51	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2467	A	O4'-C4'-C3'	-5.22	100.88	106.10
16	N	152	GLU	N-CA-C	-5.21	105.68	111.36
1	0	1819	G	C1'-O4'-C4'	-5.20	104.70	109.90
1	0	1942	A	C4'-C3'-C2'	-5.20	97.40	102.60
4	A	103	VAL	N-CA-C	5.19	113.65	107.73
5	B	154	VAL	CA-C-N	5.19	124.81	119.05
5	B	154	VAL	C-N-CA	5.19	124.81	119.05
5	B	111	ARG	N-CA-C	-5.18	106.95	113.28
14	L	44	GLU	N-CA-C	-5.17	102.65	109.84
7	D	15	GLU	CA-C-N	5.17	126.30	119.84
7	D	15	GLU	C-N-CA	5.17	126.30	119.84
24	V	64	GLY	N-CA-C	-5.14	108.14	115.64
1	0	1006	A	N9-C1'-C2'	5.14	119.71	112.00
7	D	169	THR	N-CA-C	5.12	116.25	107.28
1	0	1752	G	C5'-C4'-C3'	5.12	122.88	115.20
1	0	1261	A	N9-C1'-C2'	5.11	119.66	112.00
14	L	98	GLU	N-CA-C	-5.09	104.15	110.41
19	Q	49	ASN	N-CA-C	5.08	117.96	110.59
4	A	135	VAL	N-CA-C	5.06	115.20	108.27
11	H	116	ALA	N-CA-C	5.06	119.45	113.28
19	Q	68	GLY	N-CA-C	-5.06	102.77	111.47
7	D	136	ARG	CA-C-N	5.04	126.14	119.84
7	D	136	ARG	C-N-CA	5.04	126.14	119.84
1	0	820	G	N9-C1'-C2'	5.04	119.56	112.00
5	B	114	ASP	N-CA-C	-5.04	97.80	107.57
5	B	147	VAL	CA-C-N	5.03	126.12	119.84
5	B	147	VAL	C-N-CA	5.03	126.12	119.84
13	K	14	LYS	N-CA-C	-5.01	102.63	110.10
1	0	134	U	C5'-C4'-C3'	-5.01	108.48	116.00
1	0	1452	G	C5'-C4'-C3'	-5.00	108.49	116.00
5	B	224	LYS	N-CA-C	5.00	117.90	109.95

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	1563	G	C3'

All (41) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1078	A	Sidechain
1	0	1327	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	1340	G	Sidechain
1	0	1376	G	Sidechain
1	0	1430	G	Sidechain
1	0	1458	A	Sidechain
1	0	1592	G	Sidechain
1	0	1647	G	Sidechain
1	0	1726	G	Sidechain
1	0	1744	G	Sidechain
1	0	1819	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	191	A	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	2599	A	Sidechain
1	0	2607	U	Sidechain
1	0	2630	G	Sidechain
1	0	2679	G	Sidechain
1	0	2681	A	Sidechain
1	0	2842	G	Sidechain
1	0	333	G	Sidechain
1	0	396	U	Sidechain
1	0	458	G	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	795	G	Sidechain
1	0	817	G	Sidechain
1	0	952	G	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	29812	719	0
2	9	2600	0	1326	55	0
3	4	74	0	51	2	0
4	A	1753	0	1766	120	0
5	B	2625	0	2532	132	0
6	C	1859	0	1816	114	0
7	D	1094	0	1085	105	0
8	E	1357	0	1266	59	0
9	F	890	0	843	53	0
10	G	240	0	231	15	0
11	H	1266	0	1268	72	0
12	J	1120	0	1098	70	0
13	K	992	0	1031	50	0
14	L	1118	0	1076	63	0
15	M	1560	0	1568	68	0
16	N	1445	0	1401	93	0
17	O	865	0	873	39	0
18	P	1136	0	1123	40	0
19	Q	735	0	728	20	0
20	R	1149	0	1122	45	0
21	S	641	0	605	17	0
22	T	950	0	924	54	0
23	U	410	0	364	26	0
24	V	499	0	511	35	0
25	W	1196	0	1137	77	0
26	X	654	0	653	42	0
27	Y	1130	0	1133	56	0
28	Z	578	0	539	33	0
29	1	431	0	426	23	0
30	2	396	0	413	23	0
31	3	755	0	728	22	0
32	I	519	0	500	57	0
33	0	88	0	0	0	0
33	9	1	0	0	0	0
33	A	1	0	0	0	0
33	B	1	0	0	0	0
33	K	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	T	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	2	0	0	0	0
35	0	64	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	3	0	0	0	0
35	S	1	0	0	0	0
36	0	9	0	0	0	0
36	3	1	0	0	0	0
36	A	1	0	0	0	0
36	B	1	0	0	0	0
36	J	3	0	0	2	0
36	K	1	0	0	0	0
36	L	1	0	0	0	0
36	M	1	0	0	0	0
36	N	1	0	0	1	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	1	1	0	0	0	0
38	3	1	0	0	0	0
38	O	1	0	0	0	0
38	U	1	0	0	0	0
38	Z	1	0	0	0	0
39	0	5780	0	0	111	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	1	52	0	0	3	0
39	2	40	0	0	2	0
39	3	66	0	0	4	0
39	4	4	0	0	0	0
39	9	136	0	0	10	0
39	A	124	0	0	12	0
39	B	141	0	0	19	0
39	C	177	0	0	17	0
39	D	46	0	0	10	0
39	E	43	0	0	1	0
39	F	25	0	0	4	0
39	G	16	0	0	3	0
39	H	71	0	0	8	0
39	I	8	0	0	0	0
39	J	58	0	0	3	0
39	K	60	0	0	7	0
39	L	82	0	0	12	0
39	M	125	0	0	6	0
39	N	62	0	0	7	0
39	O	40	0	0	5	0
39	P	60	0	0	4	0
39	Q	49	0	0	3	0
39	R	83	0	0	4	0
39	S	30	0	0	0	0
39	T	36	0	0	4	0
39	U	28	0	0	4	0
39	V	12	0	0	1	0
39	W	68	0	0	4	0
39	X	26	0	0	6	0
39	Y	93	0	0	11	0
39	Z	29	0	0	2	0
All	All	99040	0	59949	2156	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 (2156) 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)
20:R:99:ALA:HB1	20:R:109:MET:HE1	1.29	1.14
1:O:1160:G:H5'	1:O:1161:A:H5'	1.32	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:236:THR:HG22	6:C:239:ALA:H	1.10	1.10
26:X:74:ALA:HB2	26:X:85:VAL:HG13	1.34	1.10
13:K:29:LEU:HB3	13:K:55:VAL:HG11	1.32	1.08
2:9:3006:C:H5''	16:N:37:ARG:NH1	1.68	1.07
25:W:21:LEU:HD21	25:W:48:VAL:HG11	1.27	1.07
9:F:91:VAL:HG12	9:F:92:GLY:H	1.24	1.02
1:0:871:G:C8	1:0:871:G:H5'	1.95	1.01
5:B:264:GLU:HG2	5:B:267:LYS:HE2	1.40	1.00
7:D:25:MET:HE2	7:D:41:LEU:HG	1.43	1.00
13:K:81:ARG:HB2	13:K:87:ARG:HH11	1.24	0.99
12:J:93:ARG:HB3	12:J:93:ARG:HH11	1.23	0.99
1:0:156:C:H5''	15:M:171:ARG:HD3	1.40	0.99
4:A:191:GLY:HA2	4:A:194:MET:HE2	1.44	0.98
24:V:8:ILE:HA	24:V:11:MET:HE3	1.40	0.98
12:J:19:MET:HE3	12:J:132:LEU:HD11	1.44	0.97
5:B:86:ALA:HA	39:B:9580:HOH:O	1.64	0.96
25:W:149:LEU:HG	25:W:153:MET:HE2	1.48	0.96
25:W:6:GLN:HB2	25:W:26:ILE:HD12	1.44	0.96
21:S:51:GLN:HE21	21:S:53:ASN:HD21	1.13	0.95
24:V:12:THR:HG22	24:V:15:GLU:HG3	1.48	0.95
2:9:3076:G:H3'	2:9:3077:A:H5''	1.49	0.95
1:0:2506:A:HO2'	1:0:2507:G:H8	0.97	0.94
25:W:137:GLN:HE21	25:W:141:HIS:HE1	1.11	0.94
1:0:871:G:H5'	1:0:871:G:H8	1.32	0.93
6:C:78:ARG:HH11	6:C:78:ARG:HG3	1.32	0.93
13:K:81:ARG:HB2	13:K:87:ARG:NH1	1.82	0.93
22:T:71:VAL:HG11	22:T:90:PRO:HB3	1.50	0.93
8:E:20:ILE:HD11	8:E:40:VAL:HG11	1.50	0.93
30:2:41:HIS:H	30:2:45:ASN:HD22	1.18	0.93
2:9:3006:C:H5''	16:N:37:ARG:HH12	1.29	0.92
26:X:37:LEU:HD13	26:X:85:VAL:HG21	1.48	0.92
1:0:1372:A:H3'	39:0:7690:HOH:O	1.70	0.92
4:A:211:LYS:HG2	4:A:212:PRO:HD2	1.52	0.92
29:1:25:LYS:HD2	30:2:49:GLU:H	1.31	0.92
7:D:28:GLY:HA2	7:D:69:ILE:HG23	1.52	0.92
13:K:10:GLN:NE2	13:K:10:GLN:H	1.66	0.91
16:N:144:GLY:O	16:N:147:ILE:HG22	1.71	0.91
13:K:74:VAL:HG11	13:K:113:ILE:HG12	1.50	0.91
26:X:30:MET:HE1	26:X:58:ALA:HB3	1.52	0.91
13:K:39:GLY:HA2	39:K:4183:HOH:O	1.70	0.90
5:B:190:MET:HE2	5:B:194:PHE:HD1	1.33	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1242:A:H5'	12:J:82:THR:HG23	1.52	0.90
18:P:115:SER:H	18:P:118:GLN:HE21	1.19	0.90
5:B:140:LEU:HA	39:B:9580:HOH:O	1.71	0.90
6:C:104:ASP:HA	6:C:107:ARG:HH12	1.33	0.90
28:Z:46:ARG:HD2	28:Z:59:TYR:HB2	1.49	0.90
1:0:289:G:H22	1:0:363:A:H2	1.19	0.89
2:9:3056:A:H2'	2:9:3057:A:H5''	1.52	0.89
5:B:162:MET:SD	5:B:310:ARG:HD3	2.11	0.89
5:B:212:GLN:HB2	5:B:257:THR:HG21	1.52	0.89
7:D:136:ARG:HH12	7:D:157:LEU:HA	1.36	0.89
13:K:10:GLN:H	13:K:10:GLN:HE21	0.89	0.89
26:X:25:ARG:HG2	39:X:5356:HOH:O	1.73	0.89
25:W:125:HIS:HD2	25:W:127:GLY:H	1.19	0.89
27:Y:235:GLU:CD	27:Y:235:GLU:H	1.79	0.89
1:0:2524:G:H21	1:0:2526:C:H41	1.21	0.88
15:M:99:ARG:HH21	15:M:170:ASN:HD22	1.14	0.88
7:D:58:VAL:HB	7:D:62:ASP:HB3	1.54	0.88
13:K:10:GLN:HE21	13:K:10:GLN:N	1.71	0.88
11:H:29:ALA:HB3	11:H:66:ARG:HH12	1.39	0.88
5:B:5:ARG:HH11	5:B:8:LYS:HE2	1.39	0.87
5:B:238:ASN:HD22	5:B:240:GLY:H	1.22	0.87
7:D:57:THR:HG23	7:D:63:ILE:HA	1.56	0.87
1:0:288:A:H61	1:0:364:C:H42	1.20	0.87
6:C:1:MET:HG2	6:C:2:GLN:H	1.36	0.87
13:K:74:VAL:HG13	13:K:113:ILE:HG23	1.55	0.87
11:H:46:GLN:HB3	11:H:167:PRO:HD2	1.54	0.87
13:K:14:LYS:HB2	13:K:45:PRO:HG2	1.57	0.87
1:0:542:A:H5'	1:0:542:A:H8	1.38	0.86
6:C:236:THR:HG22	6:C:239:ALA:N	1.89	0.86
13:K:32:ILE:HD11	13:K:56:SER:HB3	1.57	0.86
1:0:1603:A:H5'	1:0:1605:G:O4'	1.76	0.86
1:0:870:G:H2'	1:0:871:G:H5''	1.57	0.86
23:U:20:MET:HE2	23:U:30:HIS:NE2	1.90	0.86
9:F:58:GLU:HG3	9:F:61:MET:HE2	1.58	0.86
8:E:36:PRO:HD3	12:J:127:ILE:HD12	1.56	0.85
1:0:2812:A:H2	1:0:2814:A:H62	1.21	0.85
4:A:179:MET:HA	4:A:179:MET:HE3	1.56	0.85
1:0:1116:U:HO2'	1:0:1118:A:H2	0.86	0.84
18:P:115:SER:OG	18:P:118:GLN:HG3	1.77	0.84
1:0:2717:C:C2'	1:0:2718:C:H5''	2.07	0.84
4:A:192:VAL:HG12	4:A:207:GLN:HB3	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:51:VAL:HG23	5:B:329:TYR:O	1.78	0.84
8:E:69:ILE:HA	8:E:72:MET:HE3	1.60	0.84
16:N:83:LEU:HD13	16:N:175:LEU:HD23	1.60	0.84
13:K:109:LEU:HD13	13:K:113:ILE:HD11	1.60	0.83
16:N:113:SER:HB2	39:N:9356:HOH:O	1.77	0.83
6:C:127:ARG:NH2	6:C:225:PRO:HG2	1.92	0.83
1:O:1593:C:OP1	18:P:117:SER:HB3	1.77	0.83
1:O:1474:C:H6	1:O:1474:C:H5'	1.44	0.83
5:B:307:ARG:HH11	5:B:307:ARG:HG3	1.44	0.83
1:O:1041:U:H5'	39:L:9490:HOH:O	1.78	0.83
1:O:506:G:H22	1:O:509:A:H5''	1.42	0.83
25:W:88:THR:HB	39:W:6679:HOH:O	1.78	0.83
27:Y:187:VAL:HG23	27:Y:192:ASP:HB2	1.60	0.83
25:W:88:THR:HG23	25:W:110:GLN:NE2	1.94	0.82
4:A:192:VAL:HB	39:A:9582:HOH:O	1.78	0.82
15:M:102:GLU:OE1	15:M:164:THR:HG21	1.79	0.82
4:A:192:VAL:HG22	39:A:9621:HOH:O	1.78	0.82
1:O:560:C:H42	1:O:597:A:H61	1.23	0.82
1:O:1701:A:H4'	1:O:1702:U:H5''	1.61	0.82
5:B:18:ARG:HG3	5:B:256:GLN:HG3	1.61	0.82
1:O:1835:U:H5	1:O:1840:A:N7	1.77	0.82
1:O:2717:C:H2'	1:O:2718:C:H5''	1.62	0.82
39:O:5410:HOH:O	12:J:47:THR:HB	1.80	0.82
12:J:93:ARG:HB3	12:J:93:ARG:NH1	1.94	0.81
21:S:57:THR:HG22	21:S:59:ASP:H	1.45	0.81
4:A:153:ARG:HB2	4:A:153:ARG:HH11	1.46	0.81
24:V:1:THR:HG23	24:V:2:VAL:H	1.44	0.81
1:O:544:G:H2'	1:O:545:G:H5''	1.62	0.80
27:Y:154:ARG:HH12	27:Y:155:ARG:HG2	1.46	0.80
5:B:179:LEU:O	5:B:183:GLU:HG2	1.82	0.80
11:H:27:LYS:H	11:H:59:HIS:HD2	1.29	0.80
1:O:1205:U:H2'	1:O:1206:U:H5''	1.62	0.80
6:C:5:ILE:HD11	6:C:16:VAL:HG23	1.62	0.80
6:C:115:LEU:HD13	6:C:223:LEU:HD21	1.62	0.80
28:Z:37:HIS:HB2	28:Z:47:VAL:HB	1.63	0.80
4:A:199:HIS:HD2	4:A:201:PHE:H	1.27	0.79
25:W:137:GLN:HE21	25:W:141:HIS:CE1	2.00	0.79
1:O:559:U:H6	1:O:559:U:H5'	1.47	0.79
16:N:164:ASP:CG	16:N:167:ASP:HA	2.07	0.79
2:9:3039:U:H1'	2:9:3044:A:H61	1.48	0.79
4:A:191:GLY:HA2	4:A:194:MET:CE	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:107:ARG:NH1	6:C:107:ARG:HB3	1.98	0.79
39:O:6083:HOH:O	5:B:298:LYS:HG2	1.82	0.78
1:O:962:C:H1'	16:N:5:ARG:NH1	1.99	0.78
5:B:141:ARG:HD2	5:B:163:GLU:OE2	1.84	0.78
5:B:190:MET:HE2	5:B:194:PHE:CD1	2.18	0.78
25:W:21:LEU:HD22	25:W:26:ILE:CD1	2.14	0.78
25:W:21:LEU:CD2	25:W:48:VAL:HG11	2.13	0.78
1:O:645:U:OP2	14:L:4:LYS:HE2	1.84	0.78
7:D:23:VAL:HG21	7:D:45:THR:HG21	1.65	0.78
26:X:72:VAL:HG22	26:X:85:VAL:HG12	1.64	0.77
1:O:506:G:H22	1:O:509:A:C5'	1.97	0.77
6:C:246:ARG:HB3	6:C:246:ARG:NH1	1.99	0.77
1:O:871:G:H8	1:O:871:G:C5'	1.97	0.77
1:O:1667:A:H8	1:O:1667:A:H5'	1.50	0.77
9:F:53:ASP:OD1	9:F:80:GLN:HB2	1.84	0.77
20:R:25:PHE:CE2	20:R:29:LYS:HE2	2.19	0.77
1:O:2054:A:N3	20:R:128:ARG:NH2	2.33	0.77
1:O:2635:A:O2'	1:O:2636:C:H5'	1.85	0.77
22:T:71:VAL:HG11	22:T:90:PRO:CB	2.14	0.77
1:O:1160:G:C5'	1:O:1161:A:H5'	2.13	0.77
5:B:56:ASP:HB3	5:B:322:ARG:HE	1.50	0.76
1:O:2748:G:H2'	39:O:8086:HOH:O	1.86	0.76
4:A:35:GLY:O	4:A:36:ASP:HB3	1.86	0.76
1:O:656:G:H5'	17:O:3:THR:HG22	1.67	0.76
5:B:41:PHE:CD1	5:B:79:MET:HE2	2.21	0.76
8:E:84:MET:HE1	8:E:148:ILE:HD12	1.65	0.76
1:O:553:G:P	27:Y:204:ARG:HH22	2.09	0.75
22:T:49:GLU:HB3	22:T:59:GLU:HG2	1.67	0.75
5:B:5:ARG:NH1	5:B:8:LYS:HE2	2.02	0.75
9:F:50:VAL:HG13	9:F:60:VAL:HG11	1.68	0.75
4:A:192:VAL:CG1	4:A:207:GLN:HB3	2.16	0.75
12:J:45:VAL:HG11	12:J:121:LEU:HD22	1.68	0.75
16:N:7:LYS:HE3	19:Q:21:ARG:O	1.86	0.75
22:T:9:LYS:HE2	22:T:13:ARG:NH1	2.02	0.75
28:Z:11:SER:HB3	28:Z:23:ARG:HB2	1.69	0.75
6:C:5:ILE:HD11	6:C:16:VAL:CG2	2.17	0.75
1:O:2840:A:OP1	5:B:211:THR:HG23	1.85	0.75
7:D:135:VAL:HG21	7:D:139:TYR:CD1	2.22	0.75
16:N:80:SER:HB2	39:N:9335:HOH:O	1.87	0.75
1:O:871:G:C8	1:O:871:G:C5'	2.70	0.75
1:O:2506:A:O2'	1:O:2507:G:H8	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:21:LEU:HD22	25:W:26:ILE:HD11	1.69	0.75
1:0:236:A:H4'	1:0:237:G:H5'	1.69	0.74
1:0:1160:G:H5'	1:0:1161:A:C5'	2.16	0.74
2:9:3014:G:H5'	2:9:3014:G:H8	1.52	0.74
1:0:1973:A:H5'	1:0:1973:A:H8	1.52	0.74
7:D:58:VAL:HG12	7:D:60:GLU:HG2	1.68	0.74
26:X:76:ARG:HH11	26:X:76:ARG:HG3	1.52	0.74
1:0:1116:U:O2'	1:0:1118:A:H2	1.68	0.74
1:0:545:G:H5'	1:0:545:G:H8	1.51	0.74
25:W:13:MET:HE2	25:W:18:GLN:HA	1.70	0.74
39:0:7941:HOH:O	5:B:211:THR:HG21	1.85	0.74
6:C:236:THR:CG2	6:C:239:ALA:H	1.96	0.74
12:J:93:ARG:HH11	12:J:93:ARG:CB	2.01	0.73
1:0:2716:G:H5''	5:B:206:THR:HG21	1.70	0.73
6:C:115:LEU:HD21	6:C:243:VAL:HG13	1.68	0.73
1:0:2491:G:H1'	39:0:7383:HOH:O	1.88	0.73
6:C:132:ASP:HB3	39:C:9166:HOH:O	1.87	0.73
27:Y:200:THR:HG22	27:Y:201:GLU:HG3	1.70	0.73
1:0:1377:C:H5'	1:0:1377:C:H6	1.52	0.73
8:E:15:GLN:HG2	8:E:19:ASP:O	1.89	0.73
5:B:195:ARG:HG2	5:B:323:LEU:HD22	1.68	0.73
17:O:32:ARG:HE	17:O:35:LYS:HD2	1.54	0.73
1:0:2005:G:H3'	1:0:2005:G:OP2	1.89	0.73
9:F:58:GLU:HA	9:F:61:MET:HE2	1.69	0.73
39:0:4356:HOH:O	22:T:9:LYS:HD2	1.89	0.72
4:A:100:PRO:HG2	4:A:103:VAL:HG21	1.69	0.72
5:B:16:ARG:NH1	39:B:9614:HOH:O	2.20	0.72
5:B:201:ASP:HB2	5:B:312:ARG:HD2	1.71	0.72
25:W:13:MET:HE2	25:W:18:GLN:CA	2.19	0.72
26:X:71:ARG:HD3	39:X:2171:HOH:O	1.88	0.72
1:0:481:U:H5''	39:0:6210:HOH:O	1.90	0.72
6:C:246:ARG:HB3	6:C:246:ARG:HH11	1.52	0.72
11:H:99:LYS:HD3	11:H:119:LYS:HD3	1.72	0.72
1:0:1244:U:OP1	12:J:18:ILE:HD13	1.90	0.72
16:N:12:ARG:HD3	16:N:18:THR:OG1	1.90	0.72
1:0:1183:C:N4	1:0:1184:C:H41	1.88	0.72
1:0:1206:U:H5'	1:0:1206:U:H6	1.54	0.72
1:0:281:U:H2'	1:0:282:C:O4'	1.89	0.71
1:0:870:G:C2'	1:0:871:G:H5''	2.20	0.71
1:0:1118:A:H62	1:0:1244:U:H3	1.38	0.71
5:B:221:GLN:HE22	13:K:42:ASN:HD22	1.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:6:GLN:HB2	25:W:26:ILE:CD1	2.18	0.71
1:O:2270:G:H4'	4:A:223:ARG:HH12	1.56	0.71
25:W:88:THR:HG22	25:W:89:ASP:N	2.05	0.71
11:H:170:ASN:HD22	11:H:170:ASN:N	1.86	0.71
1:O:2765:C:H4'	39:O:6083:HOH:O	1.91	0.71
14:L:73:VAL:HG23	14:L:74:THR:H	1.55	0.71
1:O:1299:G:O6	14:L:6:ARG:HD3	1.90	0.71
1:O:1166:A:H1'	1:O:1192:A:C2	2.26	0.70
21:S:10:VAL:HG11	24:V:36:ALA:HA	1.73	0.70
12:J:74:ARG:O	12:J:78:ILE:HG12	1.92	0.70
13:K:29:LEU:HB3	13:K:55:VAL:CG1	2.18	0.70
2:9:3029:C:H2'	2:9:3030:C:H5'	1.73	0.70
31:3:70:ARG:HG3	31:3:77:ALA:HB2	1.74	0.70
1:O:56:G:H5''	24:V:50:ARG:NH1	2.06	0.70
6:C:78:ARG:HG3	6:C:78:ARG:NH1	2.03	0.70
18:P:115:SER:H	18:P:118:GLN:NE2	1.88	0.70
13:K:74:VAL:CG1	13:K:113:ILE:HG12	2.22	0.70
1:O:1166:A:H61	1:O:1180:U:H3	1.37	0.70
1:O:542:A:H5'	1:O:542:A:C8	2.25	0.70
1:O:1165:G:H4'	1:O:1174:A:O2'	1.91	0.70
1:O:1751:G:H2'	1:O:1752:G:H5''	1.74	0.70
15:M:99:ARG:NH2	15:M:170:ASN:HD22	1.89	0.70
15:M:187:LEU:CD2	15:M:194:ALA:HB3	2.21	0.70
24:V:12:THR:HG22	24:V:15:GLU:CG	2.20	0.70
25:W:125:HIS:CD2	25:W:127:GLY:H	2.07	0.70
31:3:70:ARG:HG2	39:3:9501:HOH:O	1.91	0.70
1:O:2524:G:N2	1:O:2526:C:H41	1.90	0.70
24:V:39:ALA:N	24:V:40:PRO:HD2	2.07	0.70
1:O:1205:U:H2'	1:O:1206:U:C5'	2.21	0.69
1:O:2586:U:H3	1:O:2592:G:H22	1.37	0.69
1:O:1159:G:H21	1:O:1189:A:H8	1.40	0.69
8:E:20:ILE:CD1	8:E:40:VAL:HG11	2.22	0.69
6:C:162:VAL:HG22	6:C:232:LEU:HD21	1.74	0.69
9:F:13:GLU:OE2	9:F:78:GLU:HG2	1.92	0.69
1:O:280:C:H2'	1:O:281:U:O4'	1.92	0.69
1:O:902:G:N7	14:L:18:HIS:HD2	1.90	0.69
1:O:2749:U:H5'	39:O:8486:HOH:O	1.92	0.69
1:O:2851:G:C2'	1:O:2852:A:H5'	2.23	0.69
4:A:105:VAL:HG11	4:A:154:ALA:HB1	1.75	0.69
6:C:104:ASP:HA	6:C:107:ARG:NH1	2.06	0.69
12:J:74:ARG:HB3	12:J:74:ARG:HH11	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:18:LEU:HB2	20:R:143:VAL:CG1	2.22	0.69
1:0:1118:A:H8	1:0:1118:A:H3'	1.58	0.69
1:0:1641:A:H2'	1:0:1642:A:H5'	1.73	0.69
9:F:96:ALA:HA	39:F:3111:HOH:O	1.92	0.69
12:J:75:PRO:HG2	12:J:105:LEU:HD21	1.73	0.69
15:M:164:THR:HG22	15:M:166:ALA:H	1.58	0.69
26:X:71:ARG:HB3	26:X:88:GLU:OE1	1.93	0.69
1:0:2524:G:H21	1:0:2526:C:N4	1.90	0.69
9:F:63:ILE:HB	9:F:64:PRO:HD3	1.75	0.69
8:E:15:GLN:HG3	8:E:20:ILE:HG12	1.74	0.69
11:H:56:GLN:HE21	11:H:126:ARG:HE	1.38	0.69
14:L:67:ARG:O	14:L:71:GLU:HG3	1.93	0.69
25:W:88:THR:HG22	25:W:89:ASP:H	1.56	0.69
2:9:3006:C:C5'	16:N:37:ARG:NH1	2.54	0.68
9:F:91:VAL:HG12	9:F:92:GLY:N	2.03	0.68
11:H:56:GLN:NE2	11:H:126:ARG:HE	1.91	0.68
26:X:37:LEU:CD1	26:X:85:VAL:HG21	2.22	0.68
27:Y:115:ARG:HB3	27:Y:115:ARG:HH11	1.59	0.68
1:0:2676:C:H4'	12:J:70:PHE:CD1	2.27	0.68
17:O:96:VAL:HG13	17:O:100:GLN:HB2	1.75	0.68
1:0:282:C:O2'	1:0:283:U:H5'	1.92	0.68
1:0:1118:A:H3'	1:0:1118:A:C8	2.28	0.68
1:0:2533:C:H5'	1:0:2533:C:H6	1.58	0.68
4:A:199:HIS:CD2	4:A:201:PHE:H	2.10	0.68
1:0:2534:C:H1'	39:O:4100:HOH:O	1.93	0.68
2:9:3014:G:H5'	2:9:3014:G:C8	2.28	0.68
20:R:8:ALA:HB1	20:R:13:THR:HG21	1.75	0.68
6:C:140:VAL:HB	39:C:9254:HOH:O	1.93	0.68
8:E:23:GLU:HG2	8:E:28:SER:HB3	1.76	0.68
9:F:2:VAL:HG22	9:F:57:GLU:OE1	1.93	0.68
1:0:1119:G:N2	1:0:1246:A:C2	2.56	0.68
1:0:2820:A:OP1	5:B:98:THR:HG22	1.93	0.68
22:T:26:THR:HA	22:T:39:ASN:HB3	1.76	0.68
1:0:544:G:C2'	1:0:545:G:H5''	2.22	0.68
4:A:105:VAL:CG1	4:A:154:ALA:HB1	2.24	0.68
16:N:169:PRO:O	16:N:172:PHE:HB3	1.94	0.68
23:U:17:THR:HG22	23:U:18:GLY:N	2.07	0.68
18:P:91:LYS:O	18:P:95:GLU:HG3	1.93	0.68
15:M:164:THR:HG22	15:M:166:ALA:N	2.09	0.68
1:0:1201:C:H2'	1:0:1202:A:H5'	1.74	0.67
5:B:102:THR:HG21	5:B:182:VAL:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:27:ARG:HG3	6:C:29:ASP:OD1	1.94	0.67
14:L:143:THR:HG22	14:L:144:ASP:H	1.57	0.67
27:Y:144:ARG:HH11	27:Y:144:ARG:CG	2.07	0.67
1:O:1116:U:O2'	1:O:1118:A:C2	2.46	0.67
1:O:1838:U:O2'	1:O:2644:C:H5'	1.94	0.67
1:O:1206:U:H2'	1:O:1207:A:O4'	1.94	0.67
9:F:37:THR:O	9:F:41:GLU:HG3	1.94	0.67
27:Y:144:ARG:HH11	27:Y:144:ARG:HG3	1.57	0.67
1:O:1189:A:H3'	39:O:8245:HOH:O	1.94	0.67
1:O:1979:G:H2'	39:O:3902:HOH:O	1.93	0.67
25:W:13:MET:HE3	25:W:17:ILE:HG22	1.74	0.67
1:O:1119:G:H2'	12:J:52:GLN:NE2	2.09	0.67
16:N:23:ARG:NH1	16:N:27:LEU:HD11	2.09	0.67
1:O:1878:G:H1'	39:O:6661:HOH:O	1.94	0.67
4:A:51:ARG:HB2	39:A:9594:HOH:O	1.94	0.67
29:1:25:LYS:HD2	30:2:49:GLU:N	2.07	0.67
5:B:53:LEU:HD11	5:B:327:VAL:HG22	1.76	0.67
17:O:32:ARG:O	17:O:32:ARG:HD3	1.94	0.67
1:O:797:A:H5'	28:Z:10:ARG:N	2.09	0.67
6:C:47:GLY:HA2	6:C:92:PRO:HB2	1.75	0.67
14:L:143:THR:HG22	14:L:144:ASP:N	2.10	0.67
11:H:58:ARG:HH11	11:H:58:ARG:HG3	1.60	0.67
1:O:1205:U:C2'	1:O:1206:U:H5''	2.25	0.67
15:M:80:GLY:O	15:M:81:ARG:HD2	1.93	0.67
22:T:71:VAL:HG12	22:T:72:ILE:N	2.10	0.67
32:I:74:PRO:C	32:I:112:LYS:HZ1	2.03	0.67
1:O:1666:C:H2'	1:O:1667:A:H5'	1.77	0.66
2:9:3039:U:H1'	2:9:3044:A:N6	2.09	0.66
2:9:3056:A:C2'	2:9:3057:A:H5''	2.23	0.66
20:R:18:LEU:HD12	20:R:143:VAL:HG11	1.77	0.66
6:C:118:THR:HG22	6:C:137:PRO:HB3	1.77	0.66
1:O:2081:A:H4'	12:J:69:TYR:CE1	2.30	0.66
6:C:129:HIS:CE1	6:C:231:ARG:HA	2.31	0.66
10:G:12:ILE:N	10:G:13:PRO:HD3	2.11	0.66
1:O:2270:G:H4'	4:A:223:ARG:NH1	2.10	0.66
2:9:3051:A:H5'	16:N:160:SER:HB3	1.77	0.66
4:A:48:ASP:HB3	39:A:9594:HOH:O	1.95	0.66
1:O:1474:C:H5'	1:O:1474:C:C6	2.31	0.66
1:O:396:U:O2'	1:O:418:C:H4'	1.96	0.66
1:O:797:A:C4'	28:Z:10:ARG:N	2.59	0.66
1:O:2420:G:O2'	1:O:2421:G:H5'	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3013:A:O2'	2:9:3014:G:H5''	1.95	0.66
15:M:107:ARG:HH11	15:M:107:ARG:HG3	1.60	0.66
25:W:48:VAL:O	25:W:48:VAL:HG12	1.95	0.66
25:W:21:LEU:HD21	25:W:48:VAL:CG1	2.16	0.66
27:Y:151:SER:O	27:Y:155:ARG:HG3	1.96	0.66
29:1:25:LYS:HE2	39:2:7213:HOH:O	1.95	0.66
14:L:80:ASP:HB2	14:L:90:ARG:O	1.95	0.66
17:O:45:LEU:CD1	17:O:88:LYS:HD2	2.26	0.66
25:W:81:ASP:OD1	25:W:92:ASP:HB2	1.95	0.66
32:I:106:LYS:O	32:I:110:GLU:HG3	1.96	0.66
11:H:166:SER:HB3	11:H:167:PRO:HD3	1.76	0.65
26:X:9:VAL:HG22	26:X:88:GLU:OE2	1.97	0.65
1:0:1701:A:H4'	1:0:1702:U:C5'	2.26	0.65
1:0:2291:A:C8	1:0:2309:C:H5'	2.31	0.65
2:9:3014:G:O2'	16:N:1:ALA:HB2	1.97	0.65
5:B:102:THR:HG23	5:B:182:VAL:HG12	1.77	0.65
14:L:133:VAL:HA	39:L:9471:HOH:O	1.97	0.65
25:W:13:MET:CE	25:W:17:ILE:HG22	2.26	0.65
5:B:102:THR:CG2	5:B:182:VAL:HG12	2.27	0.65
6:C:1:MET:HG2	6:C:2:GLN:N	2.11	0.65
20:R:99:ALA:CB	20:R:109:MET:HE1	2.18	0.65
1:0:558:C:C2'	1:0:559:U:H5''	2.27	0.65
16:N:11:ARG:HG3	16:N:14:ARG:NH1	2.12	0.65
17:O:42:GLU:HB2	39:O:2176:HOH:O	1.96	0.65
21:S:57:THR:HG22	21:S:59:ASP:N	2.12	0.65
11:H:166:SER:CB	11:H:167:PRO:CD	2.75	0.65
32:I:99:ASP:OD1	32:I:138:THR:HB	1.96	0.65
5:B:125:GLU:O	5:B:129:ARG:HG3	1.97	0.65
5:B:238:ASN:HD22	5:B:240:GLY:N	1.95	0.65
11:H:30:GLN:H	11:H:66:ARG:NH1	1.95	0.65
13:K:55:VAL:HG12	13:K:56:SER:N	2.11	0.65
1:0:2578:G:H5'	1:0:2578:G:H8	1.61	0.65
8:E:7:ILE:HD11	8:E:12:ASP:HA	1.79	0.65
25:W:4:LEU:HD22	25:W:52:VAL:HG21	1.78	0.64
1:0:2364:A:H5''	19:Q:15:LYS:HD3	1.79	0.64
4:A:153:ARG:HH11	4:A:153:ARG:CB	2.11	0.64
5:B:307:ARG:HG3	5:B:307:ARG:NH1	2.06	0.64
8:E:84:MET:HE1	8:E:148:ILE:CD1	2.27	0.64
1:0:2505:G:O2'	1:0:2506:A:H5'	1.98	0.64
7:D:54:ALA:HB2	7:D:69:ILE:HD12	1.79	0.64
24:V:56:ILE:O	24:V:60:GLN:HG3	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:102:VAL:O	32:I:106:LYS:HG3	1.97	0.64
1:0:470:U:O2'	29:1:16:HIS:HD2	1.81	0.64
27:Y:154:ARG:HB3	27:Y:154:ARG:HH11	1.61	0.64
1:0:541:C:H2'	1:0:542:A:C5'	2.27	0.64
14:L:36:ASP:HB2	39:L:9431:HOH:O	1.98	0.64
1:0:282:C:H1'	1:0:368:C:N4	2.12	0.64
2:9:3051:A:H5'	16:N:160:SER:CB	2.27	0.64
6:C:163:HIS:HD2	39:C:9241:HOH:O	1.80	0.64
27:Y:165:GLU:HB3	39:Y:9391:HOH:O	1.96	0.64
32:I:110:GLU:HA	32:I:113:HIS:CE1	2.33	0.64
2:9:3006:C:OP1	16:N:37:ARG:NH1	2.31	0.64
5:B:62:ARG:HA	5:B:65:MET:CE	2.28	0.64
5:B:254:GLN:HG2	5:B:255:GLY:N	2.10	0.64
20:R:106:GLY:HA2	20:R:109:MET:HE3	1.80	0.64
29:1:8:GLN:HE22	29:1:11:LYS:NZ	1.96	0.64
15:M:69:LYS:O	15:M:73:ARG:NH2	2.31	0.64
21:S:51:GLN:HE21	21:S:53:ASN:ND2	1.93	0.64
6:C:45:ASP:OD2	6:C:98:ARG:HD2	1.98	0.63
25:W:41:TYR:HA	25:W:44:MET:HE3	1.81	0.63
27:Y:144:ARG:CZ	39:Y:9409:HOH:O	2.45	0.63
4:A:36:ASP:HA	4:A:83:GLY:HA3	1.79	0.63
6:C:236:THR:HG21	39:C:9178:HOH:O	1.98	0.63
15:M:60:VAL:C	15:M:61:ILE:HD12	2.22	0.63
27:Y:187:VAL:HG23	27:Y:192:ASP:CB	2.28	0.63
1:0:949:U:H4'	19:Q:95:GLU:HA	1.78	0.63
4:A:179:MET:HG2	4:A:186:TRP:CB	2.28	0.63
1:0:962:C:H1'	16:N:5:ARG:HH12	1.63	0.63
22:T:41:ARG:HG2	22:T:41:ARG:HH11	1.61	0.63
1:0:541:C:C2'	1:0:542:A:H5''	2.28	0.63
1:0:2346:C:O2'	7:D:52:THR:HG21	1.98	0.63
1:0:2481:G:H5''	39:0:5130:HOH:O	1.97	0.63
16:N:154:LEU:O	16:N:155:GLU:HB3	1.98	0.63
1:0:111:C:O2'	29:1:20:ARG:HG2	1.99	0.63
1:0:681:G:N3	1:0:681:G:H5'	2.14	0.63
5:B:51:VAL:CG2	5:B:327:VAL:HG13	2.29	0.63
7:D:65:GLU:HA	39:D:6752:HOH:O	1.97	0.63
26:X:25:ARG:HD3	26:X:64:ALA:O	1.98	0.63
29:1:25:LYS:CD	30:2:49:GLU:H	2.06	0.63
1:0:1766:U:O2	1:0:1778:A:H5'	1.99	0.63
1:0:877:G:H5'	1:0:878:G:OP1	1.98	0.63
8:E:68:HIS:O	8:E:72:MET:HG3	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:115:GLU:HG3	22:T:116:ASP:N	2.13	0.63
1:O:289:G:N2	1:O:363:A:H2	1.94	0.62
1:O:1119:G:H22	1:O:1246:A:H2	1.39	0.62
39:O:7132:HOH:O	27:Y:155:ARG:HD2	1.98	0.62
6:C:139:VAL:HG13	39:C:9251:HOH:O	1.99	0.62
9:F:48:VAL:HG23	9:F:74:PHE:HB3	1.81	0.62
25:W:68:THR:HG23	25:W:69:ARG:HG2	1.79	0.62
28:Z:11:SER:CB	28:Z:23:ARG:HB2	2.28	0.62
5:B:215:VAL:HB	5:B:234:ARG:HH12	1.64	0.62
1:O:2769:C:C2'	1:O:2770:G:H5'	2.29	0.62
4:A:179:MET:HA	4:A:179:MET:CE	2.30	0.62
5:B:98:THR:HG21	5:B:127:GLN:OE1	1.99	0.62
1:O:1119:G:H8	12:J:52:GLN:HE22	1.46	0.62
1:O:2426:G:H1'	39:O:6634:HOH:O	1.98	0.62
7:D:54:ALA:CB	7:D:69:ILE:HD12	2.30	0.62
20:R:99:ALA:HB1	20:R:109:MET:CE	2.19	0.62
1:O:2896:A:N3	1:O:2896:A:H2'	2.15	0.62
20:R:18:LEU:HB2	20:R:143:VAL:HG12	1.80	0.62
7:D:170:TYR:O	7:D:171:ASP:HB3	1.99	0.62
1:O:1700:C:H5''	1:O:1701:A:OP2	1.99	0.62
1:O:2827:A:H2'	1:O:2828:G:O4'	1.99	0.62
14:L:91:VAL:HG13	14:L:120:LEU:HD23	1.81	0.62
18:P:59:ARG:NH2	18:P:66:GLN:HE22	1.98	0.62
26:X:30:MET:HE1	26:X:58:ALA:CB	2.29	0.62
27:Y:189:ASN:HA	27:Y:217:ILE:HD11	1.81	0.62
18:P:10:ALA:HA	18:P:13:VAL:HG12	1.80	0.62
22:T:38:ARG:NH1	39:T:6217:HOH:O	2.33	0.62
1:O:1183:C:H2'	39:O:6785:HOH:O	2.00	0.62
1:O:2769:C:O2'	1:O:2770:G:H5'	2.00	0.62
7:D:146:LYS:NZ	16:N:107:ASN:HD21	1.98	0.62
9:F:21:GLU:O	9:F:24:ARG:HG3	2.00	0.62
25:W:4:LEU:HD23	25:W:54:PHE:HB3	1.79	0.62
25:W:88:THR:HG23	25:W:110:GLN:HE21	1.63	0.62
1:O:1426:C:H2'	39:O:3214:HOH:O	1.98	0.62
7:D:136:ARG:NH1	7:D:157:LEU:HA	2.13	0.61
9:F:60:VAL:O	9:F:60:VAL:HG12	1.99	0.61
29:1:10:LYS:HG3	39:1:9488:HOH:O	1.99	0.61
1:O:1181:A:H5'	32:I:94:GLU:OE2	1.99	0.61
1:O:2064:U:H5'	1:O:2652:U:H4'	1.81	0.61
15:M:59:GLY:HA3	15:M:141:ILE:HD12	1.82	0.61
16:N:139:TRP:HA	16:N:139:TRP:CE3	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:757:C:OP1	14:L:27:ARG:HD2	2.00	0.61
17:O:87:THR:O	17:O:91:GLN:HG3	2.00	0.61
25:W:21:LEU:HB3	25:W:26:ILE:HG12	1.81	0.61
1:0:1377:C:H5'	1:0:1377:C:C6	2.36	0.61
39:9:4350:HOH:O	19:Q:25:PRO:HB2	1.99	0.61
1:0:1528:A:H2'	1:0:1529:G:O4'	2.01	0.61
5:B:275:GLY:O	5:B:291:ASP:HA	2.01	0.61
1:0:381:G:H5''	39:0:4905:HOH:O	1.99	0.61
1:0:1209:C:H2'	1:0:1210:G:H8	1.65	0.61
1:0:1666:C:O2'	1:0:1667:A:H5''	1.99	0.61
1:0:2468:A:H61	31:3:48:ASN:HD21	1.46	0.61
8:E:100:ASP:HB2	39:E:2789:HOH:O	2.01	0.61
15:M:79:ALA:HB3	15:M:81:ARG:NH1	2.15	0.61
1:0:1268:C:O2'	27:Y:169:ARG:HB2	2.00	0.61
6:C:194:PHE:CD2	6:C:234:VAL:HG11	2.34	0.61
12:J:75:PRO:HG2	12:J:105:LEU:CD2	2.30	0.61
13:K:81:ARG:HD3	13:K:87:ARG:NH1	2.16	0.61
15:M:27:ARG:HH12	15:M:44:THR:CG2	2.14	0.61
18:P:64:GLU:HG2	39:P:163:HOH:O	2.00	0.61
1:0:343:C:O2'	1:0:344:C:H5'	1.99	0.61
6:C:79:ARG:O	6:C:87:ARG:HG2	2.00	0.61
1:0:380:A:OP2	15:M:9:ARG:HD2	2.01	0.61
1:0:2003:U:H4'	1:0:2004:U:H5	1.65	0.61
1:0:2769:C:H2'	1:0:2770:G:O4'	2.00	0.61
7:D:58:VAL:CG1	7:D:60:GLU:HG2	2.30	0.61
7:D:84:LEU:HA	7:D:87:ALA:HB3	1.83	0.61
7:D:159:PRO:O	7:D:163:VAL:HG23	1.99	0.61
1:0:2507:G:H2'	1:0:2510:C:H42	1.66	0.60
6:C:246:ARG:HH11	6:C:246:ARG:CB	2.13	0.60
7:D:25:MET:HE2	7:D:41:LEU:CG	2.26	0.60
9:F:48:VAL:HG23	9:F:74:PHE:CB	2.31	0.60
17:O:59:VAL:HG23	17:O:111:VAL:HG22	1.83	0.60
18:P:89:ASN:OD1	18:P:92:GLU:HB2	2.00	0.60
18:P:115:SER:N	18:P:118:GLN:HE21	1.93	0.60
39:0:5188:HOH:O	4:A:206:ARG:HD3	1.99	0.60
39:0:7025:HOH:O	27:Y:141:THR:HG23	2.01	0.60
12:J:39:VAL:HG11	12:J:107:ASN:CG	2.27	0.60
1:0:221:G:H5''	39:0:6299:HOH:O	2.00	0.60
1:0:1184:C:H1'	39:0:7950:HOH:O	2.00	0.60
8:E:84:MET:HE2	8:E:133:VAL:CG2	2.31	0.60
17:O:53:GLN:HG2	17:O:56:GLU:OE1	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:56:G:H5''	24:V:50:ARG:HH12	1.64	0.60
1:0:541:C:H2'	1:0:542:A:H5''	1.83	0.60
1:0:1116:U:H3	1:0:1246:A:H62	1.49	0.60
39:0:9975:HOH:O	29:1:1:THR:HA	2.00	0.60
11:H:27:LYS:N	11:H:59:HIS:HD2	1.99	0.60
1:0:1175:G:H1'	1:0:1193:A:H2'	1.83	0.60
32:I:129:VAL:O	32:I:129:VAL:HG12	2.00	0.60
7:D:138:GLY:N	39:D:7597:HOH:O	2.35	0.60
26:X:31:ILE:O	26:X:35:GLU:HG3	2.02	0.60
1:0:308:U:H5'	22:T:97:ARG:NH2	2.16	0.60
6:C:107:ARG:HB3	6:C:107:ARG:HH11	1.64	0.60
9:F:58:GLU:HG3	9:F:61:MET:CE	2.32	0.60
21:S:51:GLN:NE2	21:S:53:ASN:HD21	1.92	0.60
1:0:138:U:H5''	1:0:139:C:OP2	2.02	0.60
15:M:27:ARG:NH1	15:M:44:THR:CG2	2.64	0.60
24:V:55:ARG:O	24:V:59:ILE:HG12	2.02	0.60
1:0:338:C:H4'	6:C:174:ILE:CD1	2.31	0.60
5:B:40:GLY:HA3	39:B:9642:HOH:O	2.01	0.60
16:N:164:ASP:OD1	16:N:167:ASP:HA	2.00	0.60
18:P:10:ALA:HA	18:P:13:VAL:CG1	2.31	0.60
23:U:45:GLU:HB2	23:U:48:ASN:ND2	2.16	0.60
1:0:1119:G:H2'	12:J:52:GLN:HE22	1.65	0.60
8:E:34:TRP:O	12:J:127:ILE:HD11	2.02	0.60
12:J:19:MET:CE	12:J:132:LEU:HD11	2.27	0.60
5:B:307:ARG:HB3	39:B:9647:HOH:O	2.01	0.59
6:C:77:ALA:O	6:C:78:ARG:HG3	2.01	0.59
11:H:21:THR:O	11:H:120:ILE:HD12	2.02	0.59
16:N:49:THR:HG22	16:N:56:ASP:HB2	1.84	0.59
18:P:80:ARG:HG2	18:P:87:ARG:CZ	2.32	0.59
28:Z:22:SER:O	28:Z:26:VAL:HG23	2.02	0.59
32:I:116:LEU:HD22	32:I:127:GLU:OE1	2.02	0.59
1:0:272:A:H5'	1:0:273:G:OP2	2.02	0.59
1:0:1681:G:H5''	1:0:1682:A:H5'	1.82	0.59
4:A:129:LEU:CD1	4:A:145:MET:HE1	2.33	0.59
1:0:883:U:H2'	1:0:883:U:O2	2.02	0.59
1:0:1118:A:H8	1:0:1119:G:H5''	1.67	0.59
9:F:46:GLU:OE1	9:F:100:ASP:HA	2.02	0.59
25:W:139:GLY:O	25:W:141:HIS:HD2	1.85	0.59
1:0:2073:G:OP2	1:0:2490:A:H5'	2.02	0.59
1:0:2718:C:H6	1:0:2718:C:H5'	1.68	0.59
6:C:2:GLN:HB3	39:C:9189:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:141:HIS:HB2	25:W:146:ILE:HG12	1.84	0.59
1:0:474:C:O3'	6:C:73:LEU:HD21	2.03	0.59
4:A:95:PRO:HG2	4:A:98:GLU:HG2	1.84	0.59
4:A:211:LYS:CG	4:A:212:PRO:HD2	2.29	0.59
13:K:30:LYS:O	13:K:55:VAL:HG13	2.02	0.59
22:T:49:GLU:OE2	22:T:97:ARG:HD2	2.03	0.59
17:O:45:LEU:HD11	17:O:88:LYS:HD2	1.84	0.59
32:I:132:CYS:HB3	32:I:137:VAL:HB	1.84	0.59
1:0:447:A:P	22:T:1:SER:HB2	2.43	0.59
4:A:209:PRO:O	4:A:211:LYS:N	2.34	0.59
8:E:81:GLU:HG2	8:E:134:SER:CB	2.33	0.59
23:U:39:ASN:ND2	23:U:44:ARG:HH11	2.00	0.59
31:3:6:ARG:NH1	31:3:21:GLU:HG3	2.17	0.59
1:0:524:A:H5''	20:R:29:LYS:HD3	1.84	0.59
4:A:94:LEU:HD12	4:A:98:GLU:HB2	1.85	0.59
8:E:107:PHE:O	8:E:110:GLU:HG3	2.03	0.59
18:P:9:LEU:O	18:P:13:VAL:HG12	2.03	0.59
22:T:49:GLU:CB	22:T:59:GLU:HG2	2.33	0.59
1:0:558:C:H2'	1:0:559:U:C5'	2.32	0.59
6:C:236:THR:H	6:C:239:ALA:HB3	1.68	0.59
15:M:27:ARG:NH1	15:M:44:THR:HG21	2.17	0.59
17:O:32:ARG:NE	17:O:35:LYS:HD2	2.18	0.59
1:0:95:A:H5''	1:0:97:G:O4'	2.03	0.58
9:F:48:VAL:HG12	9:F:97:ALA:HB2	1.85	0.58
31:3:38:ARG:HB3	31:3:42:ARG:HH12	1.68	0.58
1:0:475:G:C5'	6:C:73:LEU:HD23	2.33	0.58
1:0:538:C:OP2	27:Y:134:HIS:HE1	1.86	0.58
7:D:134:LEU:HD11	7:D:166:ILE:HD11	1.85	0.58
1:0:2563:U:H2'	1:0:2565:C:O5'	2.02	0.58
5:B:212:GLN:HB2	5:B:257:THR:CG2	2.28	0.58
17:O:97:SER:OG	17:O:100:GLN:HG3	2.03	0.58
1:0:796:A:HO2'	28:Z:10:ARG:N	2.00	0.58
1:0:1352:A:O2'	1:0:1353:C:OP1	2.20	0.58
1:0:2521:A:OP2	11:H:3:ALA:HB3	2.03	0.58
1:0:2721:U:H4'	13:K:87:ARG:HG3	1.85	0.58
4:A:66:ARG:HH11	4:A:66:ARG:HB2	1.68	0.58
12:J:74:ARG:NH1	12:J:76:ASP:HB2	2.19	0.58
1:0:69:A:H5'	1:0:69:A:C8	2.39	0.58
1:0:1182:C:H1'	1:0:1192:A:H8	1.67	0.58
39:O:7389:HOH:O	15:M:178:LYS:HB2	2.03	0.58
5:B:217:ARG:HG3	5:B:257:THR:HG22	1.85	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	2.03	0.58
32:I:125:ALA:O	32:I:129:VAL:HG23	2.03	0.58
5:B:145:HIS:HD2	5:B:146:THR:O	1.86	0.58
7:D:75:LEU:HD22	7:D:79:MET:HB3	1.85	0.58
14:L:104:ASP:HB2	39:L:9461:HOH:O	2.04	0.58
20:R:111:ILE:HG23	20:R:145:LEU:HD11	1.86	0.58
24:V:8:ILE:HG21	24:V:59:ILE:HG13	1.85	0.58
25:W:64:THR:O	25:W:68:THR:HG22	2.04	0.58
32:I:92:PRO:C	32:I:94:GLU:H	2.11	0.58
5:B:62:ARG:HA	5:B:65:MET:HE2	1.85	0.58
14:L:80:ASP:CB	14:L:90:ARG:HB3	2.32	0.58
16:N:176:ARG:HG3	16:N:180:LEU:HD13	1.86	0.58
1:O:1218:U:H2'	1:O:1219:U:C6	2.39	0.58
2:9:3054:A:H2	39:9:3535:HOH:O	1.85	0.58
20:R:39:THR:HB	20:R:42:GLU:HG3	1.84	0.58
25:W:110:GLN:NE2	25:W:110:GLN:HA	2.19	0.58
26:X:37:LEU:HD13	26:X:85:VAL:CG2	2.30	0.58
1:O:558:C:O2'	1:O:559:U:H5''	2.04	0.58
4:A:33:GLU:H	4:A:33:GLU:CD	2.10	0.58
8:E:88:TYR:HB3	8:E:93:MET:HE3	1.86	0.58
1:O:248:A:H5'	1:O:249:G:OP2	2.04	0.58
1:O:2878:U:H2'	1:O:2879:A:O4'	2.04	0.58
10:G:20:VAL:O	10:G:24:VAL:HG23	2.03	0.58
12:J:19:MET:HE2	12:J:79:PHE:HA	1.85	0.58
39:O:8128:HOH:O	31:3:60:LYS:HG3	2.03	0.57
4:A:206:ARG:HD3	4:A:206:ARG:H	1.67	0.57
7:D:57:THR:HG23	7:D:63:ILE:CA	2.33	0.57
8:E:88:TYR:CE1	8:E:92:PRO:HA	2.39	0.57
12:J:130:VAL:HG12	12:J:131:THR:N	2.19	0.57
15:M:164:THR:HG22	15:M:167:GLY:H	1.69	0.57
1:O:1979:G:O2'	1:O:1980:U:OP1	2.20	0.57
1:O:2676:C:H4'	12:J:70:PHE:CE1	2.39	0.57
4:A:153:ARG:HB2	4:A:153:ARG:NH1	2.18	0.57
10:G:12:ILE:HD12	39:G:692:HOH:O	2.04	0.57
11:H:154:TYR:HB2	39:H:9557:HOH:O	2.04	0.57
31:3:62:THR:HB	39:3:9481:HOH:O	2.03	0.57
7:D:13:MET:HA	7:D:137:PRO:HG2	1.86	0.57
7:D:24:HIS:HB2	7:D:72:LYS:CB	2.33	0.57
11:H:166:SER:CB	11:H:167:PRO:HD3	2.35	0.57
16:N:152:GLU:C	16:N:154:LEU:H	2.12	0.57
24:V:64:GLY:O	24:V:65:ASP:HB2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1625:U:H4'	39:0:5245:HOH:O	2.05	0.57
5:B:185:GLY:HA2	39:B:9631:HOH:O	2.03	0.57
15:M:182:LYS:O	15:M:194:ALA:HB2	2.05	0.57
1:0:960:G:H4'	39:0:7917:HOH:O	2.03	0.57
9:F:91:VAL:CG1	9:F:92:GLY:H	2.07	0.57
25:W:13:MET:HE2	25:W:18:GLN:N	2.18	0.57
4:A:125:ASN:HB3	4:A:158:VAL:HG12	1.87	0.57
5:B:72:THR:HB	39:B:9603:HOH:O	2.04	0.57
13:K:58:THR:HG22	13:K:59:LYS:HG3	1.85	0.57
14:L:80:ASP:HB3	14:L:90:ARG:HB3	1.87	0.57
21:S:77:VAL:O	21:S:80:ARG:HG2	2.05	0.57
22:T:71:VAL:CG1	22:T:90:PRO:HB3	2.31	0.57
1:0:2866:U:H4'	1:0:2867:G:H5'	1.85	0.57
12:J:74:ARG:HH12	12:J:76:ASP:HB2	1.69	0.57
16:N:48:VAL:CG1	16:N:55:ASP:HB3	2.34	0.57
1:0:1878:G:O2'	1:0:1879:U:OP2	2.22	0.57
1:0:2726:U:O2'	26:X:22:ASN:ND2	2.38	0.57
2:9:3069:U:OP1	16:N:4:PRO:HG3	2.05	0.57
7:D:23:VAL:HG21	7:D:45:THR:CG2	2.35	0.57
32:I:134:SER:O	32:I:135:LEU:HD23	2.05	0.57
1:0:475:G:H5'	6:C:73:LEU:HD23	1.86	0.57
1:0:1185:U:H4'	32:I:123:ASN:HB3	1.87	0.57
16:N:61:ALA:HB3	16:N:88:ALA:HB2	1.87	0.57
32:I:110:GLU:HA	32:I:113:HIS:NE2	2.19	0.57
1:0:241:A:C2	1:0:378:A:H4'	2.40	0.57
1:0:1819:G:H2'	1:0:1820:G:H4'	1.86	0.57
7:D:25:MET:SD	7:D:40:ILE:HD11	2.44	0.57
23:U:52:THR:HG22	23:U:54:THR:N	2.20	0.57
27:Y:115:ARG:NE	39:Y:9353:HOH:O	2.38	0.57
30:2:22:PRO:HG2	30:2:25:VAL:CG2	2.34	0.57
1:0:121:U:OP2	30:2:10:ARG:NH2	2.32	0.56
1:0:1594:C:OP2	18:P:120:ARG:HD2	2.05	0.56
39:0:3159:HOH:O	18:P:81:LYS:HG2	2.04	0.56
5:B:310:ARG:HD2	39:B:9590:HOH:O	2.04	0.56
11:H:20:ILE:HG23	11:H:120:ILE:HD11	1.86	0.56
11:H:158:THR:HB	11:H:159:PRO:HD3	1.87	0.56
28:Z:17:ARG:HD3	39:Z:9218:HOH:O	2.05	0.56
1:0:545:G:H5'	1:0:545:G:C8	2.36	0.56
1:0:1853:C:OP1	4:A:231:LYS:HG3	2.05	0.56
1:0:2644:C:O2'	1:0:2645:U:H5'	2.05	0.56
1:0:2717:C:O2'	1:0:2718:C:H5''	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:74:ILE:HD13	5:B:309:VAL:HG21	1.86	0.56
7:D:135:VAL:HG22	7:D:136:ARG:H	1.70	0.56
7:D:136:ARG:HB3	7:D:137:PRO:HD2	1.88	0.56
12:J:19:MET:HE1	12:J:78:ILE:HG22	1.87	0.56
15:M:57:LYS:HE2	15:M:140:ALA:O	2.05	0.56
32:I:113:HIS:N	32:I:114:PRO:HD2	2.21	0.56
1:O:164:G:H4'	14:L:30:ARG:HD3	1.87	0.56
1:O:2781:U:H1'	8:E:139:GLU:OE2	2.04	0.56
1:O:2851:G:O2'	1:O:2852:A:H5'	2.06	0.56
4:A:26:ASP:O	4:A:28:GLU:N	2.38	0.56
9:F:50:VAL:HG21	9:F:63:ILE:HG21	1.86	0.56
18:P:40:VAL:O	18:P:44:VAL:HG23	2.05	0.56
24:V:39:ALA:N	24:V:40:PRO:CD	2.68	0.56
25:W:88:THR:HG22	25:W:90:TYR:HD1	1.69	0.56
32:I:89:SER:HB2	32:I:95:ASP:HB2	1.88	0.56
1:O:1328:A:OP1	27:Y:169:ARG:HD2	2.06	0.56
15:M:99:ARG:HH21	15:M:170:ASN:ND2	1.96	0.56
15:M:107:ARG:HG3	15:M:107:ARG:NH1	2.21	0.56
5:B:80:ARG:HB2	5:B:145:HIS:CE1	2.41	0.56
8:E:101:GLU:HB2	8:E:116:THR:O	2.04	0.56
11:H:166:SER:HB2	11:H:167:PRO:CD	2.36	0.56
11:H:170:ASN:N	11:H:170:ASN:ND2	2.54	0.56
27:Y:154:ARG:HH12	27:Y:155:ARG:CG	2.16	0.56
1:O:926:A:O2'	14:L:41:HIS:HD2	1.89	0.56
5:B:85:ARG:NH1	39:B:9632:HOH:O	2.38	0.56
8:E:11:VAL:HG12	8:E:12:ASP:N	2.20	0.56
14:L:136:ALA:HB3	39:L:9471:HOH:O	2.05	0.56
16:N:154:LEU:HG	16:N:155:GLU:H	1.70	0.56
5:B:234:ARG:HB3	5:B:234:ARG:HH11	1.69	0.56
6:C:16:VAL:HG12	6:C:17:ASP:H	1.70	0.56
8:E:154:ILE:HD11	8:E:157:LYS:HB2	1.88	0.56
27:Y:235:GLU:CD	27:Y:235:GLU:N	2.53	0.56
2:9:3007:G:H5'	39:9:5071:HOH:O	2.06	0.56
5:B:91:PRO:O	12:J:144:THR:HG21	2.06	0.56
5:B:96:PRO:HG3	39:B:9632:HOH:O	2.05	0.56
9:F:46:GLU:O	9:F:73:PRO:HD2	2.05	0.56
16:N:22:GLN:HG2	16:N:26:LEU:HD22	1.88	0.56
23:U:17:THR:CG2	23:U:18:GLY:N	2.69	0.56
1:O:625:U:H5''	1:O:1044:C:N4	2.21	0.56
1:O:2812:A:C2	1:O:2814:A:N6	2.65	0.56
2:9:3002:U:OP2	2:9:3003:A:H5'	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:105:VAL:HG11	4:A:154:ALA:CB	2.35	0.56
13:K:4:LEU:HD22	13:K:116:GLU:HB3	1.88	0.56
16:N:176:ARG:O	16:N:180:LEU:HD13	2.05	0.56
22:T:9:LYS:CE	22:T:13:ARG:NH1	2.69	0.56
6:C:236:THR:HA	39:C:9254:HOH:O	2.05	0.56
9:F:1:PRO:H3	9:F:4:VAL:HG23	1.71	0.56
16:N:82:TYR:OH	16:N:176:ARG:NH1	2.39	0.56
27:Y:126:PRO:HG2	27:Y:128:PHE:CE1	2.41	0.56
39:O:5303:HOH:O	16:N:21:HIS:HD2	1.90	0.55
1:O:93:C:H5''	24:V:1:THR:HB	1.88	0.55
1:O:797:A:H4'	28:Z:10:ARG:N	2.21	0.55
1:O:2748:G:H1'	39:O:8464:HOH:O	2.04	0.55
1:O:2780:C:H1'	8:E:143:GLN:HE21	1.72	0.55
14:L:148:GLU:HB2	39:L:9487:HOH:O	2.05	0.55
18:P:143:ALA:HA	39:P:162:HOH:O	2.07	0.55
1:O:1165:G:H1'	1:O:1174:A:H1'	1.87	0.55
1:O:2502:C:C2'	1:O:2503:A:H5'	2.36	0.55
1:O:2265:U:H2'	1:O:2266:A:C8	2.42	0.55
4:A:194:MET:HE3	4:A:199:HIS:CB	2.36	0.55
19:Q:11:ARG:HD3	39:Q:5620:HOH:O	2.06	0.55
1:O:1787:C:OP1	18:P:68:LYS:HE2	2.06	0.55
1:O:2670:G:O2'	1:O:2671:U:H5'	2.06	0.55
16:N:139:TRP:HA	16:N:139:TRP:HE3	1.70	0.55
1:O:1244:U:H2'	12:J:47:THR:HG21	1.88	0.55
5:B:41:PHE:HB3	5:B:190:MET:HE1	1.88	0.55
5:B:41:PHE:CG	5:B:79:MET:HE2	2.42	0.55
15:M:59:GLY:HA3	15:M:141:ILE:CD1	2.37	0.55
28:Z:30:GLU:HA	28:Z:33:MET:HE3	1.89	0.55
1:O:447:A:OP2	22:T:1:SER:HB2	2.07	0.55
5:B:138:GLY:O	5:B:139:ASP:O	2.24	0.55
5:B:297:VAL:HB	39:B:9603:HOH:O	2.06	0.55
1:O:949:U:O2'	19:Q:40:HIS:HE1	1.89	0.55
1:O:960:G:H3'	1:O:960:G:N3	2.22	0.55
1:O:1946:C:H2'	1:O:1971:G:C8	2.42	0.55
7:D:59:GLY:O	7:D:61:PHE:N	2.40	0.55
11:H:167:PRO:O	11:H:168:ALA:HB2	2.07	0.55
16:N:143:ARG:NH2	16:N:169:PRO:HB2	2.21	0.55
32:I:138:THR:HG22	32:I:139:ILE:N	2.22	0.55
1:O:516:A:H5'	39:O:6210:HOH:O	2.06	0.55
2:9:3020:G:O2'	2:9:3021:G:H5'	2.06	0.55
4:A:88:ILE:HD13	4:A:100:PRO:HD3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:5:ARG:HH11	5:B:8:LYS:CE	2.17	0.55
6:C:170:ASP:O	6:C:171:GLU:HG3	2.07	0.55
13:K:125:ALA:C	13:K:127:ALA:H	2.15	0.55
14:L:90:ARG:NH2	14:L:121:ILE:HD11	2.22	0.55
22:T:89:ARG:HG3	22:T:89:ARG:O	2.07	0.55
1:O:1299:G:H5'	39:O:4667:HOH:O	2.06	0.55
1:O:1462:C:H2'	1:O:1463:A:C8	2.42	0.55
1:O:2406:U:H1'	39:O:7222:HOH:O	2.06	0.55
22:T:40:VAL:HG22	22:T:41:ARG:N	2.22	0.55
1:O:119:A:H2'	1:O:120:A:H5''	1.89	0.54
1:O:1552:G:N2	1:O:1634:G:H1'	2.23	0.54
1:O:2252:A:H2'	1:O:2253:G:O4'	2.06	0.54
5:B:58:PRO:HA	5:B:63:GLU:OE1	2.06	0.54
8:E:84:MET:HE2	8:E:133:VAL:HG23	1.88	0.54
13:K:109:LEU:HD13	13:K:113:ILE:CD1	2.36	0.54
25:W:88:THR:CG2	25:W:89:ASP:H	2.20	0.54
27:Y:133:HIS:HD2	39:Y:9380:HOH:O	1.90	0.54
1:O:2073:G:H3'	39:O:4424:HOH:O	2.07	0.54
1:O:2419:U:H5''	1:O:2420:G:H5'	1.88	0.54
15:M:187:LEU:HD23	15:M:194:ALA:HB3	1.89	0.54
16:N:154:LEU:O	16:N:155:GLU:CB	2.55	0.54
19:Q:32:GLU:HA	19:Q:71:TYR:OH	2.08	0.54
1:O:475:G:OP1	6:C:73:LEU:HD22	2.07	0.54
1:O:1384:C:H5'	26:X:30:MET:HG2	1.88	0.54
39:O:5272:HOH:O	28:Z:13:ARG:HD3	2.07	0.54
2:9:3048:C:H4'	16:N:141:ARG:HH21	1.73	0.54
4:A:194:MET:HE3	4:A:199:HIS:HB2	1.89	0.54
1:O:69:A:H5'	1:O:69:A:H8	1.73	0.54
1:O:151:A:H2'	1:O:152:A:O4'	2.07	0.54
6:C:129:HIS:HD2	6:C:165:ASP:OD2	1.90	0.54
17:O:25:VAL:HG23	17:O:26:TRP:H	1.72	0.54
1:O:156:C:H5''	15:M:171:ARG:CD	2.28	0.54
6:C:107:ARG:HH11	6:C:107:ARG:CB	2.20	0.54
8:E:93:MET:HE1	8:E:165:GLY:H	1.73	0.54
1:O:1187:U:O2'	1:O:1189:A:H2	1.91	0.54
1:O:2533:C:H5'	1:O:2533:C:C6	2.42	0.54
5:B:258:GLY:H	5:B:260:HIS:CE1	2.25	0.54
11:H:136:ALA:HB3	11:H:146:VAL:HG21	1.88	0.54
13:K:87:ARG:CZ	39:K:4854:HOH:O	2.54	0.54
14:L:65:ASP:CG	14:L:111:ALA:HB3	2.32	0.54
1:O:969:G:H1	1:O:999:C:H42	1.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1278:A:H4'	1:0:1279:U:C4	2.42	0.54
1:0:2362:A:H2'	1:0:2363:G:C8	2.43	0.54
5:B:75:GLU:C	5:B:77:PRO:HD3	2.33	0.54
5:B:140:LEU:HD23	39:B:9580:HOH:O	2.08	0.54
5:B:195:ARG:HD2	5:B:324:ASP:OD1	2.07	0.54
9:F:12:LEU:HD21	9:F:111:ILE:HG23	1.89	0.54
13:K:34:VAL:HG22	13:K:47:ALA:HB2	1.90	0.54
26:X:12:ILE:HD12	26:X:36:HIS:ND1	2.22	0.54
28:Z:72:GLU:OE1	28:Z:77:LYS:HE2	2.07	0.54
2:9:3029:C:C2'	2:9:3030:C:H5'	2.37	0.54
6:C:118:THR:CG2	6:C:137:PRO:HB3	2.38	0.54
7:D:64:ARG:NE	7:D:67:ASP:HB3	2.22	0.54
10:G:67:LEU:O	10:G:71:LEU:HG	2.07	0.54
29:1:25:LYS:HD2	30:2:48:ASP:HA	1.90	0.54
1:0:185:G:H4'	1:0:186:A:H4'	1.90	0.54
1:0:1595:G:O2'	1:0:1596:U:H5'	2.08	0.54
1:0:2851:G:H2'	1:0:2852:A:H5'	1.90	0.54
4:A:94:LEU:HD23	4:A:94:LEU:N	2.22	0.54
5:B:18:ARG:HE	5:B:256:GLN:NE2	2.06	0.54
7:D:146:LYS:HZ3	16:N:107:ASN:HD21	1.56	0.54
9:F:57:GLU:O	9:F:61:MET:HG3	2.07	0.54
22:T:75:GLU:O	22:T:76:ASP:HB2	2.08	0.54
25:W:13:MET:HE3	25:W:17:ILE:CG2	2.38	0.54
1:0:1778:A:H2'	1:0:1779:A:H5'	1.89	0.54
11:H:78:GLY:C	11:H:80:GLU:H	2.16	0.54
12:J:45:VAL:HG11	12:J:121:LEU:CD2	2.38	0.54
16:N:110:THR:HB	16:N:113:SER:OG	2.08	0.54
20:R:18:LEU:HD12	20:R:143:VAL:CG1	2.37	0.54
25:W:106:THR:OG1	25:W:109:GLU:HG3	2.08	0.54
1:0:1789:G:O6	18:P:73:HIS:HE1	1.91	0.53
1:0:2908:A:H2'	1:0:2909:G:O4'	2.06	0.53
5:B:268:ARG:NH2	5:B:325:PRO:HG3	2.23	0.53
7:D:23:VAL:HG22	7:D:73:VAL:HB	1.89	0.53
15:M:27:ARG:NH2	15:M:44:THR:HG23	2.22	0.53
15:M:164:THR:CG2	15:M:166:ALA:H	2.21	0.53
16:N:114:LYS:O	16:N:118:ILE:HG13	2.07	0.53
1:0:1189:A:H1'	1:0:1209:C:O4'	2.08	0.53
1:0:2346:C:H4'	7:D:52:THR:CG2	2.38	0.53
1:0:2890:A:H1'	23:U:56:ARG:NH2	2.22	0.53
4:A:107:ASN:OD1	4:A:120:ARG:HD2	2.07	0.53
6:C:214:THR:HG23	39:C:9240:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:27:LYS:H	11:H:59:HIS:CD2	2.18	0.53
18:P:103:THR:O	18:P:107:GLU:HG3	2.08	0.53
27:Y:99:ALA:HB2	27:Y:233:TYR:CE2	2.43	0.53
31:3:55:VAL:HG22	39:3:9444:HOH:O	2.07	0.53
1:0:1201:C:H5''	39:0:6774:HOH:O	2.08	0.53
6:C:98:ARG:NH1	39:C:9160:HOH:O	2.41	0.53
6:C:127:ARG:HD3	6:C:129:HIS:HE1	1.74	0.53
8:E:81:GLU:HG2	8:E:134:SER:HB3	1.90	0.53
19:Q:75:ILE:HD13	19:Q:84:ILE:HD11	1.90	0.53
1:0:2817:G:P	39:0:8491:HOH:O	2.67	0.53
15:M:64:ARG:HD2	39:M:9386:HOH:O	2.08	0.53
15:M:134:ILE:HG23	15:M:141:ILE:HD13	1.91	0.53
17:O:14:LEU:CD2	17:O:102:ILE:HD11	2.37	0.53
30:2:48:ASP:O	30:2:49:GLU:HB2	2.06	0.53
31:3:18:GLN:OE1	31:3:73:GLU:HB3	2.09	0.53
1:0:500:G:H21	20:R:98:ASN:HD21	1.55	0.53
1:0:2645:U:C6	1:0:2645:U:OP2	2.62	0.53
7:D:23:VAL:CG2	7:D:73:VAL:HB	2.38	0.53
13:K:99:ASP:OD1	13:K:101:ASN:N	2.41	0.53
27:Y:96:GLU:O	27:Y:235:GLU:HA	2.09	0.53
30:2:5:LYS:O	30:2:9:LYS:HG3	2.08	0.53
1:0:558:C:H2'	1:0:559:U:H5''	1.89	0.53
1:0:1053:G:OP1	11:H:12:PRO:HG3	2.08	0.53
1:0:2783:A:H5''	39:0:5797:HOH:O	2.07	0.53
13:K:34:VAL:CG2	13:K:47:ALA:HB2	2.39	0.53
25:W:4:LEU:O	25:W:32:CYS:HA	2.09	0.53
29:1:8:GLN:HE22	29:1:11:LYS:HZ1	1.54	0.53
32:I:100:LEU:O	32:I:139:ILE:HG23	2.09	0.53
4:A:132:ASP:OD1	4:A:133:ARG:N	2.41	0.53
5:B:264:GLU:HG2	5:B:267:LYS:CE	2.26	0.53
7:D:35:ALA:O	7:D:38:GLU:HG3	2.08	0.53
11:H:30:GLN:H	11:H:66:ARG:HH11	1.57	0.53
15:M:134:ILE:CG2	15:M:141:ILE:HD13	2.38	0.53
32:I:118:SER:HB2	32:I:123:ASN:HB2	1.91	0.53
1:0:656:G:H5'	17:O:3:THR:CG2	2.37	0.53
1:0:1119:G:N2	1:0:1246:A:N1	2.57	0.53
2:9:3029:C:O3'	7:D:138:GLY:HA2	2.09	0.53
11:H:40:ALA:HB1	11:H:137:TYR:CE2	2.44	0.53
15:M:183:THR:HG22	15:M:194:ALA:HB1	1.91	0.53
32:I:128:VAL:C	32:I:130:GLY:H	2.16	0.53
1:0:299:U:H5'	39:0:7830:HOH:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1400:C:H4'	26:X:56:GLU:HG2	1.90	0.53
1:0:1943:C:H4'	4:A:211:LYS:O	2.09	0.53
1:0:2807:U:P	5:B:27:ASN:HD21	2.32	0.53
5:B:214:PRO:HD2	39:B:9524:HOH:O	2.09	0.53
11:H:116:ALA:O	11:H:117:PHE:C	2.52	0.53
1:0:775:G:OP1	29:1:16:HIS:HE1	1.92	0.53
11:H:29:ALA:C	11:H:30:GLN:HG3	2.33	0.53
16:N:164:ASP:OD2	16:N:167:ASP:HA	2.08	0.53
26:X:43:VAL:HG12	26:X:44:ASP:N	2.23	0.53
31:3:48:ASN:ND2	31:3:50:GLY:H	2.07	0.53
1:0:541:C:H2'	1:0:542:A:H5'	1.90	0.52
1:0:1641:A:C2'	1:0:1642:A:H5'	2.38	0.52
1:0:2472:C:O2'	1:0:2634:G:H4'	2.08	0.52
1:0:2661:U:H3	1:0:2812:A:H62	1.57	0.52
4:A:76:VAL:HG23	28:Z:63:LYS:HB3	1.91	0.52
12:J:8:ALA:HA	12:J:35:THR:HG22	1.90	0.52
15:M:79:ALA:HB3	15:M:81:ARG:HH12	1.74	0.52
22:T:32:ARG:NH1	22:T:38:ARG:HH12	2.06	0.52
1:0:2100:A:H4'	6:C:64:GLY:O	2.08	0.52
17:O:22:GLY:HA2	39:O:2823:HOH:O	2.08	0.52
1:0:441:A:H1'	1:0:442:A:N7	2.23	0.52
14:L:97:VAL:HG12	14:L:98:GLU:O	2.09	0.52
1:0:447:A:OP1	22:T:2:LYS:HG2	2.09	0.52
8:E:133:VAL:HG12	8:E:141:VAL:HG13	1.92	0.52
11:H:28:ILE:HG23	39:H:9546:HOH:O	2.09	0.52
22:T:40:VAL:HG22	22:T:41:ARG:H	1.74	0.52
25:W:130:HIS:O	25:W:136:GLY:HA3	2.09	0.52
26:X:22:ASN:O	26:X:25:ARG:HG3	2.09	0.52
1:0:291:C:H2'	1:0:292:G:O4'	2.10	0.52
1:0:1328:A:C8	27:Y:169:ARG:HD3	2.45	0.52
5:B:329:TYR:CE2	23:U:15:PRO:HG2	2.44	0.52
20:R:113:HIS:HE1	20:R:144:GLU:CD	2.17	0.52
30:2:36:ASN:HB3	30:2:39:ARG:HG3	1.91	0.52
2:9:3050:G:H5''	16:N:159:TYR:HE1	1.74	0.52
15:M:30:GLU:O	15:M:34:GLU:HG3	2.09	0.52
24:V:5:VAL:HG23	39:V:2271:HOH:O	2.09	0.52
1:0:1167:G:H4'	32:I:135:LEU:CD2	2.40	0.52
4:A:26:ASP:O	4:A:26:ASP:CG	2.53	0.52
6:C:107:ARG:NE	39:C:9263:HOH:O	2.36	0.52
13:K:87:ARG:NH1	39:K:4066:HOH:O	2.43	0.52
23:U:9:CYS:O	23:U:52:THR:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:29:VAL:O	25:W:30:ASN:HB2	2.10	0.52
1:0:446:G:OP2	22:T:6:LYS:NZ	2.39	0.52
39:0:4582:HOH:O	22:T:82:THR:HA	2.09	0.52
2:9:3076:G:C3'	2:9:3077:A:H5''	2.32	0.52
5:B:8:LYS:HG3	5:B:220:VAL:HG12	1.92	0.52
24:V:1:THR:HG22	24:V:48:GLU:OE1	2.10	0.52
30:2:20:ARG:HD2	30:2:39:ARG:NH2	2.24	0.52
1:0:1189:A:O2'	1:0:1208:C:H2'	2.10	0.52
16:N:37:ARG:NE	39:N:9333:HOH:O	2.42	0.52
17:O:38:ARG:NH1	39:O:7674:HOH:O	2.43	0.52
1:0:407:A:H5'	39:0:6572:HOH:O	2.10	0.52
1:0:407:A:H2'	1:0:408:A:C8	2.45	0.52
1:0:848:C:H5'	39:0:7771:HOH:O	2.10	0.52
1:0:1080:C:H4'	1:0:1081:A:OP1	2.09	0.52
1:0:1555:G:H4'	1:0:1630:A:H2	1.75	0.52
1:0:2064:U:H5'	1:0:2652:U:O3'	2.10	0.52
5:B:62:ARG:HG2	5:B:65:MET:HE3	1.91	0.52
8:E:35:TYR:HA	12:J:127:ILE:HD12	1.92	0.52
13:K:55:VAL:CG1	13:K:56:SER:N	2.72	0.52
18:P:14:LEU:O	18:P:16:VAL:HG23	2.10	0.52
18:P:16:VAL:HG13	18:P:20:ARG:NH1	2.24	0.52
24:V:1:THR:HG23	24:V:2:VAL:N	2.19	0.52
1:0:2636:C:H3'	1:0:2637:A:C5'	2.40	0.51
7:D:25:MET:CE	7:D:37:ALA:HB1	2.40	0.51
17:O:25:VAL:HG11	17:O:111:VAL:HG11	1.93	0.51
19:Q:75:ILE:CD1	19:Q:84:ILE:HD11	2.40	0.51
1:0:1363:G:OP1	6:C:76:ARG:NH2	2.43	0.51
1:0:1451:C:H5'	1:0:1505:U:C5	2.45	0.51
1:0:1626:A:H2'	1:0:1627:G:O4'	2.10	0.51
1:0:2133:U:H4'	1:0:2134:G:H5'	1.91	0.51
1:0:2748:G:H8	39:0:8086:HOH:O	1.92	0.51
8:E:5:LEU:HD21	8:E:66:GLN:HG3	1.92	0.51
10:G:64:ASN:HD22	10:G:64:ASN:N	2.07	0.51
11:H:2:PRO:HD2	11:H:5:MET:SD	2.49	0.51
20:R:104:PHE:HB3	20:R:109:MET:HE2	1.92	0.51
22:T:38:ARG:HG3	22:T:38:ARG:HH11	1.76	0.51
24:V:39:ALA:C	24:V:41:GLU:H	2.19	0.51
28:Z:37:HIS:O	28:Z:45:ASP:HA	2.10	0.51
1:0:622:G:P	27:Y:148:GLY:HA3	2.49	0.51
1:0:1189:A:H1'	1:0:1209:C:C1'	2.40	0.51
1:0:1771:U:H5'	28:Z:20:ARG:HH21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2250:G:OP1	4:A:31:LYS:HD3	2.10	0.51
1:O:2694:A:H4'	8:E:91:PHE:CE1	2.46	0.51
4:A:149:ASP:OD1	4:A:151:GLN:HB2	2.09	0.51
1:O:316:A:H5'	22:T:54:ASP:OD2	2.09	0.51
1:O:1218:U:H2'	1:O:1219:U:H6	1.74	0.51
1:O:2717:C:H2'	1:O:2718:C:C5'	2.37	0.51
1:O:2795:C:O2'	1:O:2796:U:H5'	2.10	0.51
5:B:267:LYS:HE3	5:B:300:SER:O	2.10	0.51
6:C:142:ASP:OD1	6:C:237:GLU:HB3	2.11	0.51
8:E:116:THR:HG22	8:E:151:LEU:HD22	1.91	0.51
10:G:12:ILE:N	10:G:13:PRO:CD	2.74	0.51
12:J:131:THR:HG22	12:J:133:GLY:N	2.26	0.51
22:T:61:GLU:HG3	39:T:3851:HOH:O	2.09	0.51
22:T:71:VAL:HG13	22:T:91:LEU:O	2.11	0.51
25:W:5:VAL:O	25:W:52:VAL:HG22	2.10	0.51
31:3:25:VAL:HG22	31:3:68:LYS:HG3	1.91	0.51
32:I:131:THR:O	32:I:135:LEU:HG	2.10	0.51
1:O:1882:C:OP1	4:A:192:VAL:HG23	2.09	0.51
1:O:2502:C:H2'	1:O:2503:A:H5'	1.91	0.51
4:A:65:ARG:C	4:A:66:ARG:HG3	2.36	0.51
4:A:100:PRO:HG2	4:A:103:VAL:CG2	2.40	0.51
5:B:53:LEU:CD1	5:B:327:VAL:HG22	2.41	0.51
7:D:81:GLU:O	7:D:85:GLN:HG3	2.10	0.51
14:L:101:ASP:C	14:L:103:ALA:H	2.19	0.51
1:O:602:A:O2'	1:O:605:C:H4'	2.10	0.51
1:O:1118:A:C8	1:O:1119:G:H5''	2.45	0.51
5:B:190:MET:HA	5:B:190:MET:HE3	1.92	0.51
11:H:45:VAL:HA	11:H:167:PRO:O	2.10	0.51
16:N:143:ARG:NH1	16:N:173:ASP:OD2	2.43	0.51
20:R:106:GLY:HA2	20:R:109:MET:CE	2.41	0.51
1:O:65:C:O2'	1:O:66:G:H5'	2.10	0.51
1:O:485:A:N3	1:O:487:G:H5''	2.25	0.51
1:O:2632:G:H5''	4:A:210:GLY:HA3	1.92	0.51
1:O:2769:C:H2'	1:O:2770:G:C5'	2.40	0.51
39:O:5855:HOH:O	25:W:122:ARG:NH2	2.36	0.51
4:A:190:ARG:NH2	4:A:207:GLN:OE1	2.39	0.51
6:C:242:GLU:HG3	39:C:9186:HOH:O	2.10	0.51
9:F:48:VAL:CG2	9:F:74:PHE:HB3	2.40	0.51
14:L:145:LEU:HD23	14:L:145:LEU:C	2.35	0.51
18:P:16:VAL:HG12	18:P:17:GLY:N	2.25	0.51
25:W:80:ASP:O	25:W:84:VAL:HG23	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:621:C:H5'	27:Y:132:ASP:OD2	2.11	0.51
1:0:797:A:C5'	28:Z:10:ARG:N	2.72	0.51
1:0:2747:C:H4'	39:0:8486:HOH:O	2.10	0.51
4:A:125:ASN:CB	4:A:158:VAL:HG12	2.40	0.51
6:C:16:VAL:HG12	6:C:17:ASP:N	2.26	0.51
6:C:46:TYR:CE2	6:C:98:ARG:NH1	2.79	0.51
12:J:131:THR:HG22	12:J:134:GLU:H	1.74	0.51
13:K:115:ARG:HG3	13:K:116:GLU:N	2.26	0.51
16:N:179:LEU:HD23	16:N:184:ILE:HD12	1.92	0.51
18:P:98:ILE:HD12	18:P:102:ARG:NE	2.25	0.51
25:W:38:THR:HG22	25:W:39:ASP:N	2.25	0.51
32:I:78:LEU:HD12	32:I:112:LYS:NZ	2.26	0.51
1:0:120:A:H5'	29:1:20:ARG:HH21	1.76	0.51
1:0:709:G:O2'	17:O:25:VAL:HG12	2.09	0.51
1:0:1972:U:H2'	1:0:1973:A:C5'	2.41	0.51
39:0:4127:HOH:O	18:P:91:LYS:HD3	2.11	0.51
13:K:49:LEU:HD22	13:K:117:VAL:CG2	2.41	0.51
27:Y:216:ARG:HD2	39:Y:9367:HOH:O	2.10	0.51
1:0:644:G:O2'	14:L:4:LYS:HE3	2.11	0.51
1:0:1380:U:O4	1:0:2748:G:O2'	2.29	0.51
1:0:2416:G:O2'	16:N:25:ARG:HG2	2.10	0.51
6:C:129:HIS:HE1	6:C:231:ARG:HA	1.75	0.51
11:H:58:ARG:HG3	11:H:58:ARG:NH1	2.26	0.51
14:L:57:VAL:O	14:L:57:VAL:HG12	2.10	0.51
14:L:125:PHE:CZ	14:L:140:VAL:HG13	2.46	0.51
25:W:5:VAL:O	25:W:52:VAL:CG2	2.59	0.51
30:2:41:HIS:HD2	30:2:44:ARG:H	1.58	0.51
1:0:371:U:H2'	1:0:372:A:C8	2.46	0.50
1:0:564:G:H1'	39:0:6848:HOH:O	2.09	0.50
7:D:36:ASN:HA	39:D:7500:HOH:O	2.11	0.50
8:E:49:ILE:HD11	8:E:69:ILE:HD12	1.92	0.50
13:K:13:GLU:OE1	13:K:44:LEU:HD12	2.10	0.50
16:N:162:ASP:HA	39:N:9330:HOH:O	2.11	0.50
23:U:9:CYS:HA	23:U:52:THR:HG23	1.92	0.50
31:3:60:LYS:HG3	31:3:61:PRO:HD2	1.92	0.50
1:0:1506:U:H6	1:0:1506:U:H5'	1.76	0.50
2:9:3050:G:H5''	16:N:159:TYR:CE1	2.47	0.50
6:C:118:THR:O	6:C:136:VAL:HG13	2.10	0.50
7:D:51:ARG:HD3	39:D:7636:HOH:O	2.11	0.50
28:Z:42:CYS:SG	28:Z:43:GLY:N	2.85	0.50
29:1:21:ARG:HD2	29:1:37:CYS:SG	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:78:LEU:HD12	32:I:112:LYS:HZ3	1.76	0.50
1:O:20:G:H21	20:R:117:HIS:HD2	1.58	0.50
1:O:1687:C:O2	29:1:9:GLY:HA2	2.11	0.50
1:O:2480:G:H3'	39:O:4777:HOH:O	2.11	0.50
4:A:101:GLU:OE2	4:A:131:HIS:HB2	2.12	0.50
15:M:47:ASP:CG	15:M:48:LYS:N	2.70	0.50
20:R:111:ILE:HG23	20:R:145:LEU:CD1	2.41	0.50
32:I:102:VAL:HG12	32:I:106:LYS:HE3	1.93	0.50
1:O:1184:C:H4'	32:I:126:LYS:HB3	1.92	0.50
1:O:2704:C:O2	8:E:110:GLU:HB3	2.11	0.50
1:O:2825:C:H4'	1:O:2826:G:O5'	2.12	0.50
2:9:3049:G:O2'	2:9:3050:G:H5'	2.11	0.50
7:D:96:SER:C	7:D:98:PHE:H	2.18	0.50
7:D:167:GLU:C	7:D:169:THR:H	2.20	0.50
8:E:20:ILE:CD1	8:E:33:LEU:HD12	2.42	0.50
9:F:70:LYS:C	9:F:72:VAL:H	2.20	0.50
12:J:54:VAL:O	12:J:58:GLU:HG3	2.11	0.50
14:L:53:ARG:NH2	14:L:57:VAL:HG12	2.25	0.50
27:Y:209:VAL:HG12	27:Y:214:ARG:HG3	1.93	0.50
29:1:28:HIS:CE1	29:1:31:LYS:HE2	2.45	0.50
1:O:944:G:C8	25:W:23:MET:HE1	2.47	0.50
1:O:2912:C:H2'	1:O:2913:A:O4'	2.12	0.50
5:B:312:ARG:HD3	5:B:315:VAL:HG13	1.94	0.50
6:C:142:ASP:OD1	6:C:236:THR:HG23	2.11	0.50
25:W:65:VAL:HA	25:W:68:THR:HG22	1.92	0.50
1:O:2726:U:O2	1:O:2749:U:O5'	2.30	0.50
4:A:36:ASP:O	4:A:38:ILE:N	2.42	0.50
5:B:264:GLU:CG	5:B:267:LYS:HE2	2.28	0.50
7:D:50:VAL:O	7:D:71:ALA:HA	2.11	0.50
11:H:148:GLU:OE1	11:H:148:GLU:HA	2.12	0.50
15:M:68:ARG:O	15:M:68:ARG:HD3	2.11	0.50
32:I:91:GLU:HB2	32:I:95:ASP:OD2	2.12	0.50
1:O:558:C:H2'	1:O:559:U:H5'	1.94	0.50
1:O:625:U:H5'	39:O:3793:HOH:O	2.12	0.50
1:O:894:A:N1	6:C:87:ARG:NH2	2.59	0.50
1:O:1406:A:H4'	1:O:1407:A:H5''	1.94	0.50
1:O:2816:A:H2'	39:O:8491:HOH:O	2.12	0.50
5:B:146:THR:C	5:B:148:PRO:HD3	2.37	0.50
8:E:7:ILE:HD11	8:E:11:VAL:O	2.11	0.50
12:J:71:TYR:CD1	12:J:72:PRO:HD2	2.47	0.50
15:M:107:ARG:NH1	39:M:9378:HOH:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2032:U:H2'	1:0:2033:G:H5'	1.92	0.50
5:B:41:PHE:HA	5:B:79:MET:HE1	1.94	0.50
7:D:37:ALA:O	7:D:40:ILE:HG12	2.11	0.50
13:K:98:VAL:CG2	13:K:102:GLU:C	2.85	0.50
31:3:35:TRP:HD1	39:3:9487:HOH:O	1.94	0.50
1:0:1701:A:H5'	39:0:6821:HOH:O	2.11	0.49
1:0:1926:G:H2'	1:0:1927:A:C8	2.47	0.49
1:0:2032:U:H2'	1:0:2033:G:C5'	2.42	0.49
4:A:72:GLU:HG3	28:Z:66:GLY:HA2	1.92	0.49
11:H:157:ILE:HD11	11:H:161:CYS:SG	2.52	0.49
12:J:70:PHE:CG	12:J:70:PHE:O	2.65	0.49
16:N:64:SER:C	16:N:66:LEU:H	2.20	0.49
17:O:25:VAL:HG11	17:O:111:VAL:CG1	2.42	0.49
27:Y:144:ARG:CG	27:Y:144:ARG:NH1	2.69	0.49
28:Z:53:GLY:HA2	28:Z:67:GLY:O	2.12	0.49
1:0:136:C:H2'	1:0:137:U:O4'	2.12	0.49
1:0:329:A:OP2	6:C:206:ASN:HB2	2.13	0.49
1:0:870:G:OP2	4:A:3:ARG:HD3	2.12	0.49
1:0:1435:U:H5'	39:0:3214:HOH:O	2.12	0.49
5:B:81:ALA:O	5:B:186:GLY:HA3	2.11	0.49
13:K:14:LYS:HG3	13:K:32:ILE:O	2.12	0.49
15:M:98:GLN:O	15:M:102:GLU:HG3	2.11	0.49
16:N:86:LEU:HD21	16:N:180:LEU:CD1	2.43	0.49
18:P:125:LYS:HB3	18:P:130:GLU:HG3	1.93	0.49
19:Q:30:VAL:HG12	19:Q:30:VAL:O	2.12	0.49
26:X:9:VAL:HG13	26:X:88:GLU:OE2	2.11	0.49
1:0:1118:A:C8	1:0:1118:A:C3'	2.91	0.49
1:0:1667:A:H5'	1:0:1667:A:C8	2.38	0.49
1:0:1736:A:H1'	39:0:8155:HOH:O	2.12	0.49
1:0:1773:G:C8	28:Z:16:ALA:HA	2.47	0.49
7:D:170:TYR:O	7:D:171:ASP:CB	2.60	0.49
9:F:16:ALA:HA	9:F:111:ILE:HD13	1.94	0.49
9:F:50:VAL:CG1	9:F:60:VAL:HG11	2.41	0.49
1:0:666:A:H2'	1:0:667:C:O4'	2.13	0.49
1:0:1666:C:H2'	1:0:1667:A:C5'	2.42	0.49
4:A:105:VAL:HG12	4:A:106:CYS:N	2.27	0.49
6:C:19:PRO:HG2	6:C:22:PHE:CE1	2.48	0.49
6:C:246:ARG:NH1	39:C:9174:HOH:O	2.44	0.49
7:D:135:VAL:HG22	7:D:136:ARG:N	2.27	0.49
12:J:39:VAL:HG13	12:J:106:GLY:O	2.12	0.49
22:T:88:PRO:HB3	39:T:6320:HOH:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:66:THR:HG23	26:X:67:PRO:HD2	1.94	0.49
31:3:3:MET:O	31:3:90:PHE:HA	2.12	0.49
32:I:105:VAL:HG11	32:I:129:VAL:CG2	2.42	0.49
1:0:2748:G:OP1	1:0:2749:U:H5''	2.12	0.49
12:J:15:ARG:NH1	12:J:43:ARG:NH1	2.61	0.49
13:K:49:LEU:HD12	13:K:80:ILE:HD13	1.94	0.49
30:2:22:PRO:HG2	30:2:25:VAL:HG23	1.94	0.49
32:I:129:VAL:HG13	32:I:139:ILE:HD11	1.95	0.49
1:0:653:C:H2'	1:0:654:A:C8	2.48	0.49
1:0:936:C:OP1	17:O:35:LYS:NZ	2.46	0.49
1:0:2895:C:H4'	39:X:4132:HOH:O	2.12	0.49
6:C:25:PRO:HG2	39:C:9123:HOH:O	2.12	0.49
25:W:137:GLN:NE2	25:W:141:HIS:HE1	1.95	0.49
27:Y:117:LEU:HA	27:Y:174:VAL:HG11	1.94	0.49
1:0:399:C:H5'	15:M:179:GLY:O	2.12	0.49
1:0:2365:G:H5''	39:Q:6597:HOH:O	2.10	0.49
1:0:2443:C:O3'	14:L:56:LYS:HE3	2.11	0.49
2:9:3057:A:C8	7:D:141:VAL:HG21	2.47	0.49
7:D:23:VAL:HG23	7:D:23:VAL:O	2.13	0.49
9:F:48:VAL:HG12	9:F:97:ALA:CB	2.41	0.49
1:0:328:U:O4'	6:C:202:THR:HG22	2.13	0.49
1:0:1573:A:H2'	1:0:1574:C:O4'	2.12	0.49
6:C:153:VAL:O	6:C:157:LEU:HG	2.13	0.49
6:C:194:PHE:CE2	6:C:234:VAL:HG11	2.48	0.49
13:K:23:ASN:HD21	13:K:107:THR:HB	1.77	0.49
15:M:49:ALA:C	15:M:54:TYR:HB3	2.38	0.49
15:M:69:LYS:HG3	15:M:126:GLN:CA	2.42	0.49
20:R:39:THR:HG23	20:R:107:GLU:O	2.13	0.49
27:Y:145:LYS:HE2	39:Y:9403:HOH:O	2.13	0.49
5:B:243:ASN:HA	5:B:244:PRO:C	2.37	0.49
10:G:14:GLU:HB3	39:G:4173:HOH:O	2.13	0.49
12:J:142:ASN:O	12:J:144:THR:N	2.46	0.49
14:L:89:PHE:CD1	14:L:89:PHE:N	2.81	0.49
1:0:1853:C:O2'	4:A:217:ARG:NH2	2.46	0.49
1:0:2456:A:H2'	1:0:2457:U:C6	2.48	0.49
1:0:2626:C:H2'	1:0:2627:G:C8	2.48	0.49
39:O:3561:HOH:O	26:X:23:HIS:HD2	1.95	0.49
7:D:104:PHE:CE2	7:D:166:ILE:HD13	2.48	0.49
9:F:29:VAL:HG12	9:F:98:VAL:HA	1.94	0.49
21:S:57:THR:CG2	21:S:58:MET:N	2.75	0.49
22:T:69:LYS:O	22:T:71:VAL:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:64:GLY:O	24:V:65:ASP:CB	2.60	0.49
25:W:84:VAL:HG12	39:W:6679:HOH:O	2.11	0.49
1:O:449:A:C8	6:C:43:LYS:HG2	2.48	0.48
1:O:1165:G:O3'	1:O:1174:A:H4'	2.13	0.48
1:O:2694:A:H4'	8:E:91:PHE:HE1	1.77	0.48
1:O:2908:A:C2'	1:O:2909:G:H5'	2.42	0.48
4:A:81:GLN:HB2	4:A:92:ASN:ND2	2.28	0.48
5:B:17:LYS:O	5:B:260:HIS:HD2	1.95	0.48
12:J:50:GLU:O	12:J:54:VAL:HG23	2.13	0.48
15:M:169:ARG:NH2	39:M:9352:HOH:O	2.46	0.48
18:P:121:ASP:O	18:P:125:LYS:HG3	2.13	0.48
22:T:41:ARG:HG2	22:T:41:ARG:NH1	2.27	0.48
27:Y:99:ALA:HB2	27:Y:233:TYR:CZ	2.48	0.48
1:O:737:A:H2'	1:O:738:G:O4'	2.13	0.48
1:O:1209:C:H2'	1:O:1210:G:C8	2.48	0.48
4:A:36:ASP:O	4:A:36:ASP:CG	2.55	0.48
4:A:39:ALA:HB3	4:A:61:GLU:OE2	2.14	0.48
7:D:24:HIS:HB2	7:D:72:LYS:HB3	1.94	0.48
13:K:87:ARG:NE	39:K:4854:HOH:O	2.46	0.48
25:W:21:LEU:HD22	25:W:26:ILE:HD13	1.93	0.48
1:O:371:U:H2'	1:O:372:A:H8	1.77	0.48
1:O:558:C:C2'	1:O:559:U:C5'	2.91	0.48
1:O:656:G:C5'	17:O:3:THR:HG22	2.40	0.48
1:O:1198:U:H2'	1:O:1200:A:OP2	2.13	0.48
1:O:1675:C:H5''	30:2:5:LYS:HD2	1.95	0.48
39:O:4965:HOH:O	15:M:83:SER:HB3	2.13	0.48
4:A:36:ASP:C	4:A:38:ILE:H	2.21	0.48
5:B:7:ARG:HG2	5:B:7:ARG:HH11	1.78	0.48
6:C:140:VAL:HG12	6:C:141:SER:N	2.28	0.48
8:E:3:VAL:HG22	8:E:49:ILE:HB	1.94	0.48
10:G:12:ILE:HG13	39:G:6833:HOH:O	2.12	0.48
14:L:91:VAL:CG1	14:L:120:LEU:HD23	2.43	0.48
15:M:61:ILE:HD12	15:M:61:ILE:N	2.27	0.48
20:R:96:VAL:HG13	20:R:106:GLY:HA3	1.95	0.48
24:V:43:PRO:O	24:V:46:ILE:HG22	2.12	0.48
1:O:951:A:C2'	1:O:952:G:H5'	2.43	0.48
1:O:1603:A:H5''	1:O:1605:G:H5'	1.95	0.48
1:O:1972:U:H2'	1:O:1973:A:H5'	1.96	0.48
4:A:135:VAL:HG21	4:A:147:ARG:NH1	2.28	0.48
14:L:72:ASN:HB2	39:L:9480:HOH:O	2.13	0.48
14:L:97:VAL:O	14:L:100:ALA:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:145:LEU:O	14:L:148:GLU:HG3	2.13	0.48
23:U:20:MET:CG	23:U:28:THR:HG23	2.44	0.48
24:V:5:VAL:CG1	24:V:9:ARG:NH1	2.77	0.48
26:X:72:VAL:CG2	26:X:85:VAL:HG12	2.37	0.48
1:0:204:A:C2'	1:0:205:U:H5'	2.44	0.48
5:B:294:TYR:HE2	39:B:9644:HOH:O	1.95	0.48
11:H:75:LYS:O	11:H:75:LYS:HG2	2.13	0.48
26:X:43:VAL:CG1	26:X:44:ASP:N	2.76	0.48
32:I:139:ILE:HG22	32:I:140:GLU:N	2.29	0.48
1:0:776:A:OP1	29:1:28:HIS:HE1	1.96	0.48
1:0:820:G:O2'	1:0:856:G:H4'	2.14	0.48
1:0:1242:A:C5'	12:J:82:THR:HG23	2.36	0.48
1:0:2837:U:H2'	39:0:7353:HOH:O	2.13	0.48
6:C:107:ARG:NH1	39:C:9235:HOH:O	2.47	0.48
7:D:25:MET:HE1	7:D:37:ALA:O	2.14	0.48
7:D:128:LEU:C	7:D:128:LEU:HD23	2.39	0.48
18:P:16:VAL:HG13	18:P:20:ARG:CZ	2.43	0.48
1:0:1056:U:H2'	1:0:1057:A:O4'	2.13	0.48
1:0:1462:C:H2'	1:0:1463:A:H8	1.78	0.48
1:0:1717:A:H5''	18:P:54:LYS:HB2	1.95	0.48
2:9:3092:G:H2'	2:9:3093:A:C8	2.49	0.48
39:9:5071:HOH:O	16:N:18:THR:HG21	2.12	0.48
6:C:133:ARG:NE	6:C:138:VAL:HG22	2.29	0.48
7:D:82:GLU:HA	7:D:85:GLN:HE21	1.78	0.48
12:J:52:GLN:HG3	12:J:53:ILE:N	2.28	0.48
31:3:11:CYS:HB2	31:3:20:HIS:CE1	2.49	0.48
1:0:249:G:O2'	1:0:250:C:H5'	2.14	0.48
1:0:482:G:H4'	1:0:508:A:N1	2.29	0.48
1:0:634:G:O2'	1:0:1358:A:OP1	2.31	0.48
1:0:1159:G:H1	1:0:1208:C:H42	1.62	0.48
1:0:2820:A:H2'	1:0:2821:C:C6	2.47	0.48
4:A:88:ILE:O	4:A:88:ILE:HG22	2.13	0.48
11:H:1:LYS:HE2	11:H:1:LYS:HA	1.95	0.48
15:M:187:LEU:HD22	15:M:194:ALA:HB3	1.95	0.48
17:O:78:ALA:C	17:O:98:LEU:HD13	2.38	0.48
19:Q:3:SER:HB3	39:Q:5998:HOH:O	2.13	0.48
31:3:65:THR:CG2	31:3:67:LEU:HG	2.42	0.48
1:0:90:A:H2'	1:0:91:G:O4'	2.14	0.48
1:0:2072:G:H3'	1:0:2073:G:C5'	2.44	0.48
1:0:2348:C:H1'	7:D:131:THR:HG21	1.96	0.48
1:0:2421:G:H2'	39:0:4671:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3024:U:H3'	2:9:3025:G:H5'	1.95	0.48
5:B:84:LEU:HB2	5:B:182:VAL:HG21	1.96	0.48
8:E:93:MET:HE1	8:E:165:GLY:N	2.29	0.48
11:H:169:GLY:C	11:H:170:ASN:HD22	2.21	0.48
13:K:28:GLU:OE2	13:K:58:THR:HG21	2.14	0.48
20:R:132:ARG:NH2	39:R:9492:HOH:O	2.47	0.48
23:U:47:ARG:HG2	39:U:4381:HOH:O	2.14	0.48
25:W:142:ASP:HB3	25:W:145:GLY:H	1.79	0.48
1:0:834:G:H4'	1:0:835:U:OP2	2.14	0.48
1:0:1634:G:H3'	39:0:4492:HOH:O	2.13	0.48
1:0:1942:A:H3'	39:0:7839:HOH:O	2.14	0.48
1:0:2414:A:H2'	1:0:2415:A:C8	2.49	0.48
1:0:2453:G:H4'	14:L:50:GLY:C	2.38	0.48
4:A:223:ARG:NE	39:A:9560:HOH:O	2.46	0.48
7:D:173:GLU:O	7:D:174:VAL:C	2.57	0.48
12:J:103:VAL:HG12	39:J:5907:HOH:O	2.14	0.48
14:L:10:SER:O	14:L:11:ARG:HB3	2.13	0.48
14:L:21:ARG:N	39:L:9424:HOH:O	2.46	0.48
16:N:78:MET:HB2	16:N:79:PRO:HD3	1.96	0.48
17:O:57:THR:HB	17:O:111:VAL:HG23	1.96	0.48
20:R:18:LEU:HB2	20:R:143:VAL:HG13	1.95	0.48
25:W:88:THR:HG22	25:W:90:TYR:CD1	2.49	0.48
31:3:17:HIS:O	31:3:18:GLN:HG3	2.14	0.48
1:0:2363:G:O2'	19:Q:11:ARG:HG3	2.14	0.47
4:A:51:ARG:NH1	4:A:120:ARG:O	2.47	0.47
9:F:26:THR:HG21	9:F:102:GLY:C	2.39	0.47
13:K:81:ARG:HD3	13:K:87:ARG:CZ	2.44	0.47
32:I:72:VAL:HG11	32:I:111:GLN:O	2.13	0.47
1:0:1236:A:H2'	1:0:1237:U:O4'	2.14	0.47
1:0:1290:G:H3'	39:0:5735:HOH:O	2.13	0.47
1:0:1333:U:H2'	1:0:1334:C:C6	2.49	0.47
1:0:1477:C:H5'	1:0:1868:G:C5'	2.44	0.47
1:0:1750:C:H4'	39:0:7969:HOH:O	2.15	0.47
1:0:2587:OMU:O5'	1:0:2587:OMU:H6	2.13	0.47
17:O:80:ASP:OD1	17:O:81:PHE:N	2.47	0.47
22:T:38:ARG:NH1	22:T:38:ARG:HG3	2.29	0.47
27:Y:122:ARG:NH2	39:Y:9333:HOH:O	2.47	0.47
1:0:1044:C:H5''	39:0:9647:HOH:O	2.13	0.47
1:0:2911:C:O2'	1:0:2912:C:H5'	2.14	0.47
5:B:254:GLN:HG2	5:B:255:GLY:H	1.79	0.47
7:D:99:ASP:O	7:D:159:PRO:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:88:PRO:O	12:J:94:GLY:HA3	2.15	0.47
16:N:167:ASP:C	16:N:168:LEU:HG	2.39	0.47
17:O:98:LEU:O	17:O:102:ILE:HG13	2.15	0.47
25:W:110:GLN:HE21	25:W:110:GLN:HA	1.77	0.47
1:O:2505:G:C2'	1:O:2506:A:H5'	2.45	0.47
3:4:75:C:H2'	3:4:76:PPU:C8	2.44	0.47
4:A:36:ASP:HB2	4:A:85:SER:H	1.80	0.47
7:D:172:VAL:HG12	7:D:173:GLU:N	2.28	0.47
8:E:125:GLU:HB2	8:E:132:THR:HG23	1.97	0.47
22:T:71:VAL:CG1	22:T:72:ILE:N	2.77	0.47
32:I:113:HIS:N	32:I:114:PRO:CD	2.78	0.47
1:O:317:A:H5''	22:T:52:ARG:HD2	1.96	0.47
1:O:449:A:N7	6:C:43:LYS:HG2	2.29	0.47
1:O:926:A:O2'	14:L:41:HIS:CD2	2.67	0.47
1:O:1973:A:H5'	1:O:1973:A:C8	2.40	0.47
1:O:2711:U:H1'	39:O:4046:HOH:O	2.13	0.47
39:O:4783:HOH:O	27:Y:186:ARG:HD2	2.15	0.47
2:9:3008:G:O6	16:N:11:ARG:NH1	2.43	0.47
7:D:44:ILE:HG23	7:D:45:THR:HG23	1.97	0.47
10:G:24:VAL:O	10:G:28:GLU:HB2	2.14	0.47
18:P:141:ILE:C	18:P:143:ALA:H	2.22	0.47
28:Z:26:VAL:O	28:Z:30:GLU:HG3	2.14	0.47
1:O:1167:G:H4'	32:I:135:LEU:HD22	1.97	0.47
1:O:1181:A:N1	1:O:1192:A:O2'	2.47	0.47
6:C:236:THR:HG22	6:C:239:ALA:CB	2.45	0.47
7:D:76:ARG:O	7:D:77:ASP:HB2	2.14	0.47
9:F:101:ALA:HA	39:F:5413:HOH:O	2.15	0.47
13:K:98:VAL:HG22	13:K:102:GLU:C	2.39	0.47
16:N:170:GLU:HA	16:N:173:ASP:OD2	2.15	0.47
17:O:39:THR:O	17:O:115:ARG:NH2	2.47	0.47
21:S:57:THR:HG22	21:S:58:MET:N	2.29	0.47
1:O:396:U:H1'	39:O:8194:HOH:O	2.15	0.47
1:O:709:G:O2'	17:O:25:VAL:CG1	2.62	0.47
1:O:1066:U:H2'	1:O:1067:A:C8	2.49	0.47
1:O:1119:G:H8	12:J:52:GLN:NE2	2.09	0.47
1:O:1234:U:N3	5:B:244:PRO:HB3	2.30	0.47
1:O:1482:A:O2'	1:O:1483:C:H5'	2.15	0.47
1:O:2456:A:H2'	1:O:2457:U:H6	1.80	0.47
1:O:2541:U:H3	1:O:2618:G:H1	1.61	0.47
4:A:121:ALA:O	4:A:124:VAL:HG22	2.14	0.47
4:A:194:MET:CE	4:A:199:HIS:HB2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:280:VAL:HG13	5:B:333:GLU:O	2.14	0.47
6:C:236:THR:O	6:C:237:GLU:C	2.57	0.47
7:D:27:ILE:HD11	7:D:37:ALA:HB3	1.96	0.47
7:D:166:ILE:HB	39:D:6326:HOH:O	2.14	0.47
8:E:1:PRO:HG2	8:E:59:MET:SD	2.55	0.47
8:E:20:ILE:HD12	8:E:33:LEU:HD12	1.95	0.47
14:L:73:VAL:HG23	14:L:74:THR:N	2.24	0.47
14:L:145:LEU:HD23	14:L:145:LEU:O	2.15	0.47
17:O:25:VAL:HG23	17:O:26:TRP:N	2.29	0.47
22:T:96:VAL:HG13	22:T:97:ARG:N	2.29	0.47
26:X:34:ARG:NH1	26:X:48:VAL:O	2.45	0.47
28:Z:60:CYS:O	28:Z:61:ASP:HB2	2.15	0.47
32:I:72:VAL:CG1	32:I:73:PRO:HD2	2.44	0.47
1:O:1503:U:H2'	1:O:1504:A:O4'	2.15	0.47
4:A:131:HIS:O	4:A:132:ASP:HB2	2.14	0.47
5:B:171:VAL:HG23	5:B:172:SER:N	2.30	0.47
16:N:93:GLN:HE21	16:N:127:LEU:CD1	2.27	0.47
17:O:47:ARG:HH11	17:O:47:ARG:HG3	1.80	0.47
25:W:4:LEU:HD11	25:W:45:VAL:HG12	1.97	0.47
1:O:68:U:H4'	39:O:7269:HOH:O	2.14	0.47
1:O:920:C:H4'	1:O:921:G:C2	2.50	0.47
1:O:1342:C:C2'	1:O:1343:C:H5'	2.45	0.47
1:O:1684:A:H1'	30:2:43:ARG:HH22	1.79	0.47
1:O:2890:A:H1'	23:U:56:ARG:CZ	2.45	0.47
2:9:3041:C:O4'	7:D:50:VAL:HG22	2.14	0.47
4:A:109:GLU:HG2	4:A:116:GLY:N	2.30	0.47
6:C:154:VAL:O	6:C:158:GLU:HG3	2.15	0.47
6:C:168:ARG:NH2	6:C:190:ALA:O	2.48	0.47
7:D:41:LEU:HA	7:D:44:ILE:HG22	1.96	0.47
8:E:23:GLU:HG2	8:E:28:SER:CB	2.44	0.47
9:F:36:THR:HG23	9:F:97:ALA:HB2	1.97	0.47
11:H:76:GLU:C	11:H:77:LEU:HD23	2.40	0.47
11:H:169:GLY:HA3	39:H:9555:HOH:O	2.13	0.47
15:M:164:THR:CG2	15:M:165:GLY:N	2.78	0.47
26:X:7:GLU:HA	26:X:74:ALA:O	2.14	0.47
27:Y:106:THR:HG23	27:Y:107:PRO:HD2	1.96	0.47
1:O:1350:U:H2'	1:O:1351:G:O4'	2.15	0.47
1:O:2299:G:O6	19:Q:1:PRO:HA	2.15	0.47
1:O:2531:U:O2'	1:O:2532:A:H5'	2.14	0.47
39:9:5537:HOH:O	16:N:110:THR:HG22	2.16	0.47
4:A:39:ALA:O	4:A:61:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:128:LEU:HB2	39:D:6007:HOH:O	2.14	0.47
11:H:28:ILE:HG21	11:H:31:HIS:CE1	2.50	0.47
20:R:46:TYR:O	20:R:50:VAL:HG23	2.14	0.47
25:W:88:THR:CG2	25:W:89:ASP:N	2.72	0.47
1:O:88:G:H2'	1:O:89:G:C8	2.49	0.46
1:O:541:C:C2'	1:O:542:A:C5'	2.92	0.46
1:O:1098:A:H2'	1:O:1099:G:O4'	2.15	0.46
1:O:1714:C:O2'	1:O:1715:C:H5'	2.15	0.46
1:O:2353:A:H4'	1:O:2354:A:O5'	2.15	0.46
2:9:3039:U:C2'	2:9:3040:C:OP1	2.63	0.46
2:9:3107:C:H5	39:9:3167:HOH:O	1.97	0.46
6:C:136:VAL:HG22	6:C:137:PRO:HA	1.96	0.46
16:N:43:VAL:HG13	16:N:118:ILE:HD11	1.97	0.46
26:X:9:VAL:HG13	26:X:88:GLU:OE1	2.16	0.46
1:O:244:C:OP2	9:F:38:LYS:HE3	2.15	0.46
5:B:62:ARG:HA	5:B:65:MET:HE3	1.95	0.46
6:C:219:ASN:O	6:C:222:ASP:OD1	2.33	0.46
7:D:60:GLU:O	7:D:61:PHE:C	2.57	0.46
9:F:31:LYS:HE3	39:F:2623:HOH:O	2.15	0.46
10:G:19:GLU:HG2	10:G:66:LEU:HD13	1.98	0.46
11:H:59:HIS:HA	11:H:62:LEU:HD23	1.95	0.46
16:N:89:GLY:O	16:N:92:ALA:HB3	2.15	0.46
18:P:59:ARG:HH22	18:P:66:GLN:HE22	1.62	0.46
20:R:61:GLN:NE2	39:R:9449:HOH:O	2.48	0.46
20:R:114:VAL:HA	20:R:144:GLU:O	2.15	0.46
20:R:132:ARG:CZ	39:R:9492:HOH:O	2.63	0.46
23:U:17:THR:CG2	23:U:18:GLY:H	2.28	0.46
26:X:45:GLU:HG3	39:X:6178:HOH:O	2.14	0.46
27:Y:126:PRO:HG2	27:Y:128:PHE:CZ	2.50	0.46
30:2:10:ARG:HH11	30:2:49:GLU:CD	2.23	0.46
32:I:124:ALA:O	32:I:128:VAL:HG23	2.15	0.46
1:O:794:U:H3	1:O:819:A:H61	1.62	0.46
1:O:1067:A:H5'	39:O:4933:HOH:O	2.15	0.46
1:O:2769:C:H2'	1:O:2770:G:H5'	1.96	0.46
2:9:3051:A:H5'	16:N:160:SER:HB2	1.96	0.46
11:H:38:LYS:HE2	11:H:42:ASP:HB2	1.97	0.46
20:R:69:LYS:HB2	20:R:72:VAL:HG23	1.97	0.46
20:R:84:ALA:O	20:R:88:PHE:HD1	1.98	0.46
20:R:119:VAL:O	20:R:119:VAL:CG1	2.62	0.46
24:V:56:ILE:HG22	24:V:60:GLN:NE2	2.31	0.46
30:2:36:ASN:HB3	30:2:39:ARG:NE	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:259:G:H21	15:M:58:GLN:NE2	2.14	0.46
1:0:316:A:N3	1:0:336:G:O2'	2.43	0.46
1:0:497:A:H2'	1:0:498:A:C5'	2.45	0.46
1:0:1669:A:H2'	1:0:1670:G:C8	2.51	0.46
1:0:2338:G:H2'	7:D:129:ASP:OD1	2.16	0.46
1:0:2712:G:H5'	39:K:4183:HOH:O	2.16	0.46
1:0:2824:C:H5''	1:0:2825:C:H5'	1.97	0.46
4:A:34:ASP:OD1	4:A:35:GLY:N	2.49	0.46
4:A:203:GLY:HA2	39:A:9534:HOH:O	2.14	0.46
5:B:36:PRO:HA	5:B:167:GLY:O	2.16	0.46
6:C:5:ILE:HG13	6:C:15:GLU:HA	1.97	0.46
8:E:81:GLU:HG2	8:E:134:SER:HB2	1.97	0.46
22:T:20:HIS:HB3	22:T:41:ARG:HD2	1.96	0.46
24:V:42:ASN:O	24:V:44:GLY:N	2.48	0.46
1:0:368:C:H2'	1:0:369:G:H5'	1.97	0.46
1:0:952:G:N3	1:0:2302:A:H2'	2.31	0.46
1:0:1940:C:H4'	39:0:7839:HOH:O	2.15	0.46
1:0:2591:C:H2'	1:0:2592:G:O4'	2.15	0.46
1:0:2676:C:H6	1:0:2676:C:H5''	1.81	0.46
1:0:2779:G:H21	8:E:143:GLN:NE2	2.13	0.46
1:0:2831:C:O3'	20:R:71:LYS:HE2	2.16	0.46
1:0:2852:A:H5''	39:0:5799:HOH:O	2.15	0.46
1:0:2906:A:H5'	1:0:2907:C:O4'	2.15	0.46
2:9:3057:A:O2'	7:D:152:PRO:HD2	2.15	0.46
39:9:4707:HOH:O	16:N:147:ILE:HD12	2.15	0.46
7:D:21:VAL:HG23	7:D:80:ALA:HB1	1.97	0.46
9:F:65:GLU:O	9:F:69:GLU:HG2	2.16	0.46
11:H:47:ILE:HD12	11:H:146:VAL:CG1	2.45	0.46
16:N:43:VAL:CG1	16:N:118:ILE:HD11	2.46	0.46
16:N:87:LEU:HD21	16:N:91:ARG:NH2	2.30	0.46
20:R:122:GLN:HB3	20:R:138:SER:HB2	1.95	0.46
1:0:1666:C:C2'	1:0:1667:A:C5'	2.94	0.46
1:0:1748:U:H4'	39:0:8016:HOH:O	2.15	0.46
1:0:2346:C:H6	1:0:2346:C:O5'	1.98	0.46
1:0:2401:A:H2'	1:0:2402:A:C8	2.51	0.46
39:0:3175:HOH:O	25:W:119:HIS:HE1	1.98	0.46
2:9:3054:A:O2'	2:9:3055:U:H5'	2.15	0.46
5:B:175:LEU:O	5:B:175:LEU:HD23	2.16	0.46
7:D:27:ILE:HG22	7:D:28:GLY:N	2.29	0.46
12:J:92:GLN:HB3	39:J:1405:HOH:O	2.15	0.46
21:S:2:TRP:CH2	21:S:31:ARG:HB2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:U:17:THR:HG22	23:U:18:GLY:H	1.79	0.46
1:0:1007:A:H2'	11:H:19:TYR:CZ	2.51	0.46
39:0:7645:HOH:O	29:1:1:THR:HB	2.15	0.46
5:B:41:PHE:HA	5:B:79:MET:CE	2.45	0.46
5:B:307:ARG:HH11	5:B:307:ARG:CG	2.21	0.46
9:F:12:LEU:CD2	9:F:111:ILE:HG23	2.46	0.46
12:J:76:ASP:HA	39:J:5907:HOH:O	2.14	0.46
23:U:49:LEU:HG	39:U:3805:HOH:O	2.15	0.46
27:Y:212:ARG:HD2	39:Y:9399:HOH:O	2.15	0.46
29:1:28:HIS:CD2	29:1:31:LYS:HG3	2.51	0.46
30:2:22:PRO:HG2	30:2:25:VAL:HG21	1.97	0.46
1:0:137:U:H2'	1:0:139:C:C5	2.51	0.46
1:0:1120:U:H5''	1:0:1120:U:C6	2.51	0.46
1:0:1185:U:OP1	32:I:126:LYS:HD3	2.15	0.46
1:0:2320:U:H4'	1:0:2321:A:O4'	2.15	0.46
39:0:7912:HOH:O	22:T:9:LYS:HG3	2.14	0.46
4:A:123:GLY:HA3	4:A:162:GLY:HA2	1.98	0.46
9:F:39:SER:HB3	9:F:45:ALA:HB2	1.97	0.46
13:K:7:ASP:OD2	13:K:81:ARG:NH2	2.48	0.46
14:L:134:GLU:HG3	39:L:9454:HOH:O	2.15	0.46
1:0:424:C:H2'	1:0:425:U:C6	2.50	0.46
1:0:1168:C:H5''	32:I:87:THR:HG23	1.98	0.46
1:0:1667:A:H2'	1:0:1668:U:C6	2.51	0.46
1:0:2453:G:H5''	39:L:9437:HOH:O	2.15	0.46
4:A:126:ALA:HB1	4:A:138:VAL:CG1	2.46	0.46
5:B:51:VAL:HG21	5:B:327:VAL:HG13	1.97	0.46
7:D:154:LYS:N	7:D:154:LYS:HD2	2.31	0.46
8:E:35:TYR:HA	12:J:127:ILE:CD1	2.46	0.46
11:H:43:TYR:HA	11:H:44:PRO:HD3	1.78	0.46
11:H:119:LYS:HB2	11:H:119:LYS:HE3	1.75	0.46
12:J:19:MET:CE	12:J:132:LEU:HD21	2.46	0.46
1:0:432:G:O2'	1:0:433:C:H5'	2.16	0.46
1:0:470:U:O2'	29:1:16:HIS:CD2	2.65	0.46
1:0:999:C:H2'	1:0:1000:C:O4'	2.16	0.46
1:0:2515:C:H2'	1:0:2516:G:O4'	2.15	0.46
4:A:105:VAL:HG13	4:A:155:THR:O	2.15	0.46
5:B:97:LEU:O	5:B:98:THR:HG23	2.16	0.46
6:C:78:ARG:NH1	6:C:78:ARG:CG	2.75	0.46
7:D:95:THR:OG1	7:D:174:VAL:HG22	2.16	0.46
16:N:74:PRO:HG2	16:N:159:TYR:CE1	2.51	0.46
16:N:132:ASN:O	16:N:135:VAL:HG12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:47:THR:HB	22:T:100:ASP:HB3	1.97	0.46
25:W:139:GLY:O	25:W:141:HIS:CD2	2.68	0.46
27:Y:108:ASP:OD1	27:Y:108:ASP:N	2.49	0.46
30:2:49:GLU:HB2	39:2:131:HOH:O	2.15	0.46
31:3:65:THR:HG23	31:3:67:LEU:HG	1.98	0.46
1:0:588:G:O6	25:W:154:ARG:NH1	2.50	0.45
1:0:2329:C:O2'	1:0:2330:U:H5'	2.16	0.45
1:0:2635:A:C2'	1:0:2636:C:H5'	2.46	0.45
1:0:2649:A:H5'	1:0:2649:A:H8	1.81	0.45
2:9:3049:G:H2'	2:9:3050:G:O4'	2.17	0.45
4:A:33:GLU:OE1	4:A:33:GLU:N	2.31	0.45
11:H:69:ALA:HB2	11:H:153:ALA:HB2	1.98	0.45
15:M:43:PRO:HG3	15:M:62:VAL:HG21	1.97	0.45
1:0:256:C:H2'	1:0:257:G:O4'	2.16	0.45
1:0:263:U:O4'	9:F:59:ILE:HD13	2.16	0.45
1:0:834:G:H3'	1:0:835:U:H4'	1.99	0.45
1:0:1306:U:OP1	6:C:184:ARG:HD2	2.17	0.45
1:0:1342:C:O2'	1:0:1343:C:H5'	2.16	0.45
1:0:2612:A:H4'	39:0:4284:HOH:O	2.15	0.45
5:B:36:PRO:HB3	5:B:174:ARG:CB	2.47	0.45
14:L:120:LEU:HD12	14:L:133:VAL:HG21	1.98	0.45
15:M:72:ALA:HB2	15:M:93:ARG:HG2	1.98	0.45
15:M:74:LYS:HG2	15:M:75:ARG:N	2.30	0.45
23:U:11:THR:HG22	23:U:53:ASP:OD2	2.16	0.45
25:W:48:VAL:O	25:W:48:VAL:CG1	2.64	0.45
25:W:85:ALA:HB2	25:W:91:ASP:O	2.16	0.45
25:W:88:THR:CG2	25:W:90:TYR:HD1	2.27	0.45
27:Y:154:ARG:NH1	27:Y:155:ARG:HG2	2.24	0.45
1:0:120:A:H2'	1:0:120:A:N3	2.32	0.45
1:0:286:U:H2'	1:0:287:C:C6	2.52	0.45
1:0:1151:G:OP1	10:G:63:ARG:NH1	2.49	0.45
6:C:19:PRO:HG2	6:C:22:PHE:CD1	2.51	0.45
12:J:47:THR:HG22	12:J:48:GLY:N	2.32	0.45
15:M:34:GLU:HB3	15:M:38:GLU:HG3	1.98	0.45
21:S:10:VAL:HG11	24:V:36:ALA:CA	2.45	0.45
1:0:426:G:H2'	1:0:427:C:O4'	2.16	0.45
1:0:702:G:O2'	1:0:703:G:H5'	2.17	0.45
1:0:1441:G:O2'	1:0:1442:A:H5'	2.17	0.45
1:0:1751:G:C2'	1:0:1752:G:H5''	2.43	0.45
4:A:207:GLN:O	4:A:208:HIS:HB3	2.16	0.45
14:L:77:ALA:C	14:L:79:ASP:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:184:ARG:HG3	15:M:185:PRO:HA	1.99	0.45
20:R:119:VAL:O	20:R:119:VAL:HG12	2.17	0.45
23:U:4:ARG:HG2	23:U:4:ARG:HH11	1.81	0.45
27:Y:112:GLU:OE2	27:Y:115:ARG:NH1	2.49	0.45
1:0:64:G:H2'	1:0:65:C:O4'	2.17	0.45
1:0:284:C:H4'	1:0:285:A:H8	1.82	0.45
1:0:288:A:H2'	1:0:289:G:C8	2.50	0.45
1:0:319:A:H4'	1:0:338:C:C5	2.51	0.45
1:0:1131:G:H5'	2:9:3091:C:O4'	2.16	0.45
39:O:4996:HOH:O	4:A:11:ARG:CZ	2.64	0.45
9:F:60:VAL:HG13	9:F:63:ILE:HG13	1.97	0.45
24:V:39:ALA:O	24:V:41:GLU:N	2.42	0.45
26:X:9:VAL:HG13	26:X:88:GLU:CD	2.41	0.45
1:0:338:C:H4'	6:C:174:ILE:HD12	1.98	0.45
1:0:363:A:H1'	39:O:5847:HOH:O	2.15	0.45
1:0:2415:A:H2'	1:0:2416:G:H5'	1.98	0.45
7:D:10:PHE:CG	7:D:11:HIS:N	2.84	0.45
9:F:99:THR:HG23	9:F:99:THR:O	2.17	0.45
11:H:40:ALA:HB1	11:H:137:TYR:CD2	2.52	0.45
15:M:114:VAL:O	15:M:158:ARG:HD3	2.17	0.45
26:X:76:ARG:HG3	26:X:76:ARG:NH1	2.23	0.45
1:0:1167:G:H2'	1:0:1168:C:O4'	2.16	0.45
1:0:1203:G:O2'	1:0:1204:C:H5'	2.17	0.45
1:0:1252:A:H2'	1:0:1253:C:O4'	2.16	0.45
1:0:2019:A:H5'	39:O:5123:HOH:O	2.16	0.45
1:0:2402:A:O2'	1:0:2403:C:H5'	2.17	0.45
7:D:170:TYR:CD1	7:D:170:TYR:N	2.85	0.45
11:H:154:TYR:CD1	11:H:154:TYR:C	2.95	0.45
12:J:75:PRO:HD3	12:J:136:SER:OG	2.16	0.45
24:V:12:THR:OG1	24:V:13:PRO:HD2	2.16	0.45
28:Z:42:CYS:SG	28:Z:59:TYR:HD2	2.40	0.45
29:1:25:LYS:HD2	30:2:48:ASP:CA	2.46	0.45
32:I:101:SER:OG	32:I:104:GLN:HG3	2.16	0.45
1:0:432:G:H2'	1:0:433:C:H6	1.82	0.45
1:0:506:G:N2	1:0:509:A:H5''	2.21	0.45
4:A:101:GLU:HB3	4:A:129:LEU:O	2.15	0.45
7:D:10:PHE:CD1	7:D:11:HIS:N	2.85	0.45
8:E:101:GLU:OE2	8:E:115:ARG:HD3	2.17	0.45
14:L:67:ARG:HG2	14:L:67:ARG:HH11	1.81	0.45
25:W:78:ASP:OD2	25:W:79:VAL:N	2.50	0.45
25:W:125:HIS:HE1	39:W:3071:HOH:O	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:144:ARG:NH1	39:Y:9374:HOH:O	2.50	0.45
1:0:1086:A:C6	25:W:11:VAL:HG11	2.52	0.45
1:0:1484:G:H2'	39:0:9723:HOH:O	2.16	0.45
1:0:1592:G:O2'	1:0:1593:C:O4'	2.32	0.45
1:0:1734:C:OP1	5:B:234:ARG:NH1	2.50	0.45
1:0:2072:G:C6	1:0:2533:C:H1'	2.52	0.45
6:C:150:THR:HA	6:C:203:ALA:O	2.17	0.45
7:D:82:GLU:HA	7:D:85:GLN:NE2	2.32	0.45
14:L:143:THR:CG2	14:L:144:ASP:N	2.80	0.45
16:N:83:LEU:HD13	16:N:175:LEU:CD2	2.41	0.45
1:0:542:A:H2'	1:0:543:G:O4'	2.17	0.45
1:0:1724:U:H5''	39:0:4333:HOH:O	2.16	0.45
1:0:1847:A:OP1	4:A:175:LYS:HG3	2.16	0.45
1:0:2102:G:H5''	1:0:2538:A:C2	2.51	0.45
1:0:2724:U:H2'	1:0:2725:G:O4'	2.17	0.45
1:0:2883:A:H2'	1:0:2884:G:O4'	2.17	0.45
39:0:4690:HOH:O	5:B:216:LYS:HE2	2.16	0.45
24:V:56:ILE:HG22	24:V:60:GLN:HE21	1.80	0.45
25:W:11:VAL:O	25:W:12:ASN:HB2	2.17	0.45
25:W:65:VAL:HG12	25:W:116:LEU:HD13	1.98	0.45
1:0:362:G:H2'	1:0:363:A:C8	2.52	0.44
1:0:366:U:H2'	1:0:367:G:O4'	2.17	0.44
1:0:407:A:H8	39:0:5045:HOH:O	2.00	0.44
1:0:1175:G:H2'	1:0:1176:C:O4'	2.17	0.44
1:0:1527:A:H1'	1:0:1528:A:C8	2.52	0.44
1:0:2541:U:H1'	3:4:76:PPU:O2'	2.17	0.44
39:0:9836:HOH:O	4:A:11:ARG:HD3	2.17	0.44
2:9:3028:U:H2'	2:9:3029:C:C6	2.52	0.44
2:9:3044:A:O4'	7:D:76:ARG:NE	2.50	0.44
4:A:57:ALA:HB1	4:A:65:ARG:HE	1.82	0.44
5:B:294:TYR:CD1	5:B:294:TYR:C	2.95	0.44
6:C:72:LYS:HG2	6:C:77:ALA:HA	1.99	0.44
9:F:14:ASP:O	9:F:18:GLU:HG3	2.17	0.44
25:W:19:ASP:O	25:W:23:MET:HG3	2.17	0.44
32:I:92:PRO:C	32:I:94:GLU:N	2.76	0.44
1:0:220:C:H1'	39:0:6313:HOH:O	2.17	0.44
1:0:317:A:OP1	22:T:52:ARG:O	2.35	0.44
1:0:1189:A:H1'	1:0:1209:C:H1'	1.99	0.44
1:0:1380:U:O4	1:0:2043:U:H4'	2.17	0.44
39:9:3472:HOH:O	16:N:41:LYS:HD3	2.16	0.44
5:B:321:PRO:HA	39:B:9653:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:19:GLU:HG2	10:G:66:LEU:CD1	2.47	0.44
16:N:86:LEU:HD21	16:N:180:LEU:HD12	1.99	0.44
22:T:64:ASN:HB3	22:T:73:HIS:HB2	1.98	0.44
28:Z:32:GLU:HA	28:Z:35:GLU:HG3	1.99	0.44
30:2:48:ASP:O	30:2:49:GLU:CB	2.65	0.44
1:0:2243:C:H5''	39:0:4351:HOH:O	2.18	0.44
1:0:2894:C:O2'	1:0:2895:C:H5'	2.17	0.44
4:A:56:ALA:O	4:A:68:ILE:HG22	2.17	0.44
4:A:70:ALA:HA	4:A:71:PRO:HD3	1.81	0.44
5:B:321:PRO:HG3	39:B:9599:HOH:O	2.17	0.44
7:D:78:GLU:O	7:D:82:GLU:HG3	2.18	0.44
13:K:49:LEU:HD22	13:K:117:VAL:HG21	2.00	0.44
14:L:143:THR:O	14:L:147:GLU:HG3	2.18	0.44
26:X:37:LEU:HD11	26:X:85:VAL:HG11	1.99	0.44
26:X:74:ALA:CB	26:X:85:VAL:HG13	2.25	0.44
1:0:1202:A:H2'	1:0:1203:G:O4'	2.18	0.44
39:0:9728:HOH:O	5:B:229:ARG:HD2	2.16	0.44
12:J:74:ARG:HH12	12:J:76:ASP:CB	2.31	0.44
14:L:125:PHE:CE1	14:L:140:VAL:HG13	2.53	0.44
39:M:9334:HOH:O	31:3:46:ILE:HB	2.17	0.44
16:N:152:GLU:C	16:N:154:LEU:N	2.73	0.44
16:N:171:HIS:CE1	39:N:9363:HOH:O	2.70	0.44
20:R:113:HIS:HE1	20:R:144:GLU:OE1	1.99	0.44
24:V:8:ILE:CG2	24:V:59:ILE:HG13	2.46	0.44
1:0:806:A:H2'	1:0:807:A:O4'	2.17	0.44
1:0:870:G:C3'	1:0:871:G:H5''	2.48	0.44
7:D:51:ARG:HH11	7:D:68:PRO:HB3	1.83	0.44
10:G:27:ILE:HD13	10:G:71:LEU:HD23	1.98	0.44
18:P:97:ARG:HD2	39:P:159:HOH:O	2.17	0.44
23:U:52:THR:HG22	23:U:54:THR:H	1.80	0.44
26:X:20:GLU:HG3	26:X:21:PRO:CD	2.48	0.44
28:Z:10:ARG:HA	39:Z:9214:HOH:O	2.16	0.44
28:Z:11:SER:O	28:Z:14:PHE:HB2	2.17	0.44
1:0:664:U:O4	1:0:681:G:H5''	2.18	0.44
1:0:1180:U:O2'	32:I:92:PRO:HD2	2.18	0.44
1:0:1200:A:H3'	39:0:6312:HOH:O	2.18	0.44
1:0:1902:G:H2'	1:0:1903:U:O4'	2.17	0.44
1:0:2649:A:H5'	1:0:2649:A:C8	2.53	0.44
6:C:233:THR:HG22	6:C:234:VAL:N	2.32	0.44
8:E:15:GLN:NE2	8:E:40:VAL:O	2.51	0.44
9:F:60:VAL:HG13	9:F:63:ILE:CG1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:U:44:ARG:HB3	39:U:3805:HOH:O	2.17	0.44
32:I:85:PHE:CD1	32:I:98:ALA:HB2	2.53	0.44
32:I:105:VAL:HG11	32:I:129:VAL:HG22	1.99	0.44
1:O:56:G:C5'	24:V:50:ARG:HH12	2.30	0.44
1:O:308:U:C4	1:O:342:C:H1'	2.53	0.44
1:O:398:U:H2'	1:O:399:C:C6	2.53	0.44
1:O:1878:G:O2'	1:O:1879:U:P	2.75	0.44
1:O:2104:C:O2	1:O:2485:A:N1	2.50	0.44
1:O:2663:U:O2	39:O:8491:HOH:O	2.21	0.44
4:A:96:LEU:O	4:A:131:HIS:HE1	2.00	0.44
4:A:209:PRO:C	4:A:211:LYS:H	2.24	0.44
5:B:14:GLY:HA2	5:B:15:PRO:C	2.42	0.44
7:D:154:LYS:HD2	7:D:154:LYS:H	1.83	0.44
8:E:7:ILE:HA	8:E:8:PRO:HD3	1.92	0.44
12:J:42:GLU:O	12:J:131:THR:HG23	2.18	0.44
16:N:183:ASP:O	16:N:184:ILE:C	2.61	0.44
25:W:108:ARG:HG3	25:W:114:PRO:HG3	1.99	0.44
32:I:113:HIS:HE1	32:I:121:LEU:HD22	1.83	0.44
1:O:475:G:H5'	6:C:73:LEU:CD2	2.48	0.44
1:O:968:G:O2'	1:O:969:G:H5'	2.17	0.44
1:O:1295:G:H4'	39:L:9490:HOH:O	2.18	0.44
1:O:2549:C:H1'	5:B:248:ARG:NH2	2.33	0.44
2:9:3052:A:H2'	2:9:3053:G:O4'	2.18	0.44
18:P:13:VAL:HG21	18:P:41:ARG:HG2	2.00	0.44
23:U:14:GLU:OE1	23:U:15:PRO:HD2	2.17	0.44
1:O:125:U:H2'	39:O:4367:HOH:O	2.18	0.44
1:O:1201:C:C2'	1:O:1202:A:H5'	2.42	0.44
6:C:27:ARG:HG2	6:C:30:LEU:HG	1.98	0.44
7:D:167:GLU:OE2	7:D:173:GLU:HG2	2.18	0.44
8:E:84:MET:HE3	8:E:131:LEU:HD13	1.98	0.44
9:F:117:GLU:C	9:F:119:ARG:H	2.26	0.44
11:H:67:LEU:O	11:H:71:ARG:HB2	2.18	0.44
15:M:69:LYS:HG2	15:M:127:LYS:HG3	2.00	0.44
21:S:33:SER:OG	21:S:36:GLU:HG3	2.18	0.44
1:O:710:G:H5'	17:O:25:VAL:HG13	1.99	0.43
1:O:1163:G:H2'	1:O:1164:U:C5	2.53	0.43
1:O:1741:U:H3'	39:O:3379:HOH:O	2.18	0.43
1:O:2044:G:OP1	26:X:23:HIS:HE1	2.01	0.43
5:B:23:THR:HA	5:B:24:PRO:HD3	1.87	0.43
5:B:238:ASN:ND2	5:B:240:GLY:H	2.03	0.43
6:C:115:LEU:O	6:C:118:THR:HB	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:127:ARG:CZ	6:C:225:PRO:HG2	2.46	0.43
11:H:54:THR:O	11:H:55:VAL:HG13	2.17	0.43
14:L:80:ASP:HB2	14:L:90:ARG:HB3	2.00	0.43
16:N:154:LEU:HD11	16:N:157:PRO:HA	2.00	0.43
22:T:96:VAL:CG1	22:T:97:ARG:N	2.78	0.43
1:O:1299:G:N2	39:O:5261:HOH:O	2.51	0.43
1:O:1314:U:H2'	39:O:6429:HOH:O	2.17	0.43
1:O:1406:A:H4'	1:O:1407:A:C5'	2.48	0.43
5:B:85:ARG:HB2	5:B:99:GLU:HG2	1.99	0.43
7:D:94:ALA:HA	7:D:174:VAL:O	2.17	0.43
20:R:114:VAL:HG13	20:R:114:VAL:O	2.18	0.43
1:O:603:A:H5''	1:O:604:G:OP1	2.17	0.43
1:O:2435:U:H1'	39:O:5996:HOH:O	2.18	0.43
4:A:217:ARG:HH11	4:A:217:ARG:CG	2.32	0.43
5:B:16:ARG:NE	39:B:9556:HOH:O	2.39	0.43
5:B:115:VAL:HA	5:B:116:PRO:HD3	1.92	0.43
9:F:50:VAL:CG2	9:F:63:ILE:HG21	2.47	0.43
11:H:154:TYR:HA	11:H:157:ILE:HG12	2.00	0.43
1:O:1654:U:H2'	4:A:47:HIS:CD2	2.54	0.43
1:O:1817:U:O2	18:P:81:LYS:NZ	2.47	0.43
1:O:1878:G:H5''	39:O:3406:HOH:O	2.18	0.43
1:O:1966:U:H2'	1:O:1967:U:H2'	2.01	0.43
1:O:2090:G:H2'	1:O:2091:G:C8	2.53	0.43
2:9:3014:G:H2'	2:9:3015:C:H5'	2.00	0.43
2:9:3058:G:H1'	39:9:3839:HOH:O	2.17	0.43
4:A:179:MET:HG2	4:A:186:TRP:HB2	1.99	0.43
4:A:223:ARG:CZ	39:A:9560:HOH:O	2.66	0.43
7:D:88:LEU:N	7:D:89:PRO:CD	2.80	0.43
16:N:108:SER:C	16:N:110:THR:H	2.27	0.43
18:P:121:ASP:OD1	18:P:125:LYS:HE3	2.17	0.43
18:P:143:ALA:HB2	39:P:186:HOH:O	2.18	0.43
20:R:39:THR:HB	20:R:42:GLU:CG	2.47	0.43
1:O:1250:C:O2'	1:O:1251:C:H5'	2.19	0.43
1:O:1351:G:OP1	6:C:96:LYS:NZ	2.45	0.43
1:O:1473:U:O2'	1:O:1474:C:H5''	2.19	0.43
1:O:2506:A:O2'	1:O:2507:G:O5'	2.37	0.43
11:H:83:TYR:CD1	11:H:83:TYR:C	2.95	0.43
15:M:59:GLY:C	15:M:141:ILE:HD11	2.43	0.43
24:V:16:ARG:NH2	24:V:63:GLU:HG3	2.33	0.43
32:I:139:ILE:C	32:I:140:GLU:HG3	2.43	0.43
1:O:1291:A:H2	39:O:5858:HOH:O	2.01	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
1:0:2587:OMU:H2'	1:0:2589:U:H5''	1.99	0.43
2:9:3039:U:HO2'	2:9:3042:C:H5	1.61	0.43
4:A:53:ALA:HB3	39:A:9594:HOH:O	2.17	0.43
5:B:277:GLU:N	5:B:278:PRO:HD2	2.33	0.43
11:H:47:ILE:HD12	11:H:146:VAL:HG13	2.00	0.43
13:K:113:ILE:HD12	13:K:128:ALA:HB2	1.99	0.43
27:Y:189:ASN:C	27:Y:189:ASN:HD22	2.26	0.43
1:0:793:A:H5''	18:P:83:LYS:HG2	2.01	0.43
1:0:1119:G:C8	12:J:52:GLN:NE2	2.87	0.43
1:0:1470:A:OP1	15:M:93:ARG:HD2	2.17	0.43
1:0:2252:A:C5	1:0:2253:G:H1'	2.53	0.43
1:0:2300:A:H4'	1:0:2301:A:O5'	2.19	0.43
4:A:82:VAL:HG13	4:A:93:THR:HB	1.99	0.43
5:B:132:HIS:CE1	5:B:171:VAL:HG21	2.54	0.43
6:C:157:LEU:HD22	6:C:162:VAL:CG1	2.49	0.43
6:C:246:ARG:NE	39:C:9228:HOH:O	2.43	0.43
11:H:146:VAL:HG22	39:H:9543:HOH:O	2.18	0.43
39:K:7438:HOH:O	23:U:20:MET:HE1	2.19	0.43
14:L:144:ASP:HA	14:L:147:GLU:OE1	2.19	0.43
21:S:8:PRO:HD2	24:V:32:ALA:HA	2.00	0.43
25:W:54:PHE:CZ	25:W:140:LYS:HB2	2.53	0.43
1:0:1131:G:C6	1:0:1230:A:C4	3.06	0.43
5:B:71:VAL:HG11	5:B:296:LEU:HD22	2.00	0.43
7:D:25:MET:HE1	7:D:40:ILE:HD11	2.00	0.43
8:E:69:ILE:HA	8:E:72:MET:CE	2.40	0.43
12:J:90:LYS:HB2	36:J:9302:CL:CL	2.55	0.43
13:K:22:ASP:O	13:K:110:LYS:HE3	2.18	0.43
14:L:35:ARG:C	14:L:35:ARG:HD3	2.44	0.43
17:O:73:ASP:HA	17:O:92:VAL:O	2.19	0.43
28:Z:19:GLY:O	28:Z:23:ARG:HG2	2.18	0.43
28:Z:57:CYS:SG	28:Z:59:TYR:HB3	2.59	0.43
1:0:123:U:O2'	1:0:124:C:H5'	2.18	0.43
1:0:391:U:OP2	15:M:84:LYS:NZ	2.48	0.43
1:0:447:A:O2'	1:0:448:G:H5'	2.19	0.43
1:0:810:G:H1'	39:0:7750:HOH:O	2.19	0.43
1:0:920:C:H5''	1:0:921:G:O5'	2.19	0.43
1:0:1594:C:O2'	1:0:1607:A:H4'	2.18	0.43
1:0:2256:G:C2'	1:0:2257:G:H5'	2.49	0.43
1:0:2791:U:H1'	1:0:2792:A:H5''	2.01	0.43
2:9:3031:C:H2'	2:9:3032:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:57:THR:HA	39:D:5728:HOH:O	2.19	0.43
7:D:99:ASP:HB3	7:D:103:ASN:H	1.83	0.43
8:E:8:PRO:HB2	8:E:11:VAL:HG23	2.01	0.43
12:J:39:VAL:CG1	12:J:40:ASN:N	2.82	0.43
14:L:6:ARG:NH2	39:L:9444:HOH:O	2.51	0.43
15:M:58:GLN:HG3	39:M:9404:HOH:O	2.18	0.43
22:T:71:VAL:HG12	22:T:72:ILE:H	1.79	0.43
28:Z:56:GLN:HA	28:Z:62:TYR:O	2.19	0.43
1:O:949:U:C4'	19:Q:95:GLU:HA	2.46	0.43
1:O:2016:U:H2'	1:O:2017:U:O4'	2.19	0.43
1:O:2540:G:O2'	1:O:2541:U:H5''	2.19	0.43
4:A:33:GLU:O	4:A:34:ASP:HB2	2.18	0.43
5:B:84:LEU:HD13	5:B:84:LEU:C	2.44	0.43
6:C:46:TYR:CE1	6:C:92:PRO:HB3	2.54	0.43
6:C:200:PRO:HB3	6:C:212:VAL:HG23	2.01	0.43
7:D:18:ILE:HD13	7:D:84:LEU:CD1	2.49	0.43
7:D:60:GLU:O	7:D:60:GLU:HG3	2.19	0.43
11:H:3:ALA:HA	11:H:58:ARG:NH1	2.33	0.43
11:H:114:ARG:O	11:H:115:ALA:C	2.62	0.43
15:M:77:HIS:HD2	15:M:79:ALA:O	2.01	0.43
16:N:36:ALA:N	39:N:9333:HOH:O	2.52	0.43
17:O:26:TRP:HB2	39:O:3062:HOH:O	2.19	0.43
18:P:13:VAL:HG11	18:P:40:VAL:CG1	2.48	0.43
20:R:18:LEU:HG	20:R:91:LEU:HD13	2.01	0.43
30:2:20:ARG:HG3	30:2:21:VAL:N	2.34	0.43
32:I:101:SER:H	32:I:104:GLN:NE2	2.17	0.43
1:O:360:A:H2'	1:O:361:C:O4'	2.19	0.42
1:O:497:A:H2'	1:O:498:A:H5'	2.01	0.42
1:O:672:G:O6	6:C:213:ALA:HB1	2.19	0.42
1:O:1878:G:H4'	39:O:4709:HOH:O	2.19	0.42
1:O:2645:U:OP2	1:O:2645:U:H6	2.02	0.42
1:O:2831:C:H2'	1:O:2832:C:H5'	2.00	0.42
5:B:265:LEU:HD21	5:B:316:ARG:HD3	2.01	0.42
6:C:57:PRO:HG2	6:C:73:LEU:HD13	2.01	0.42
7:D:37:ALA:HA	39:D:5583:HOH:O	2.19	0.42
8:E:112:ALA:HA	8:E:113:PRO:HD3	1.89	0.42
9:F:80:GLN:HB3	39:F:2563:HOH:O	2.17	0.42
14:L:92:ASP:HA	14:L:121:ILE:HB	2.00	0.42
15:M:169:ARG:NH1	39:M:9372:HOH:O	2.52	0.42
16:N:119:GLN:O	16:N:123:ILE:HG13	2.18	0.42
29:1:10:LYS:N	39:1:9488:HOH:O	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:195:C:H2'	1:0:196:G:H5'	2.01	0.42
1:0:263:U:C2	9:F:59:ILE:CD1	3.02	0.42
1:0:935:G:H4'	17:O:38:ARG:HH12	1.84	0.42
1:0:2256:G:O2'	1:0:2257:G:H5'	2.20	0.42
1:0:2310:G:OP2	11:H:115:ALA:HA	2.18	0.42
1:0:2356:A:H2'	1:0:2357:G:O4'	2.18	0.42
4:A:179:MET:HG2	4:A:186:TRP:HB3	2.01	0.42
11:H:151:ARG:HA	11:H:154:TYR:CE2	2.54	0.42
12:J:74:ARG:NH1	12:J:105:LEU:HD11	2.33	0.42
16:N:36:ALA:HB1	16:N:118:ILE:HD12	2.01	0.42
16:N:37:ARG:CZ	39:N:9333:HOH:O	2.67	0.42
26:X:8:ARG:NH1	39:X:2479:HOH:O	2.51	0.42
27:Y:107:PRO:HB3	27:Y:182:PHE:CE2	2.54	0.42
27:Y:115:ARG:CZ	39:Y:9353:HOH:O	2.67	0.42
28:Z:36:ASP:HB3	28:Z:45:ASP:HB3	2.01	0.42
31:3:73:GLU:O	31:3:73:GLU:HG2	2.18	0.42
1:0:1701:A:P	39:0:4968:HOH:O	2.77	0.42
1:0:1826:C:O2'	1:0:1827:G:H5'	2.19	0.42
1:0:2270:G:C4'	4:A:223:ARG:HH12	2.28	0.42
1:0:2715:G:N2	5:B:264:GLU:OE1	2.53	0.42
2:9:3040:C:N4	7:D:53:LYS:HE3	2.34	0.42
8:E:18:LEU:HD13	8:E:34:TRP:CG	2.54	0.42
12:J:63:ILE:CG2	12:J:64:GLY:N	2.82	0.42
15:M:36:ALA:O	15:M:65:VAL:HA	2.19	0.42
16:N:137:ALA:HB1	16:N:141:ARG:HD3	2.01	0.42
22:T:3:GLN:HA	22:T:4:PRO:HD3	1.90	0.42
22:T:117:ASP:OD1	22:T:118:SER:N	2.51	0.42
1:0:612:U:H2'	1:0:613:C:C6	2.55	0.42
1:0:2067:A:H2'	1:0:2068:G:O4'	2.19	0.42
1:0:2241:C:O2'	1:0:2242:U:H5'	2.19	0.42
1:0:2636:C:C3'	1:0:2637:A:C5'	2.96	0.42
1:0:2718:C:H5'	1:0:2718:C:C6	2.51	0.42
4:A:94:LEU:HB2	4:A:95:PRO:HD2	2.00	0.42
4:A:164:ARG:CZ	39:A:9575:HOH:O	2.67	0.42
5:B:333:GLU:HB2	39:U:3564:HOH:O	2.18	0.42
9:F:5:ASP:O	9:F:119:ARG:NH1	2.52	0.42
16:N:108:SER:HA	16:N:109:PRO:HD3	1.82	0.42
32:I:72:VAL:HG13	32:I:73:PRO:HD2	2.01	0.42
1:0:522:U:O2'	1:0:1366:C:H5'	2.18	0.42
1:0:1369:A:H4'	20:R:64:SER:OG	2.19	0.42
1:0:2821:C:H4'	5:B:116:PRO:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:O:5543:HOH:O	11:H:58:ARG:HG3	2.18	0.42
2:9:3052:A:O2'	2:9:3053:G:H5'	2.20	0.42
4:A:201:PHE:HB3	39:A:9621:HOH:O	2.19	0.42
6:C:1:MET:HG2	6:C:2:GLN:HE21	1.84	0.42
12:J:47:THR:CG2	12:J:48:GLY:N	2.83	0.42
21:S:29:ASP:OD2	21:S:31:ARG:NH1	2.51	0.42
26:X:20:GLU:HG3	26:X:21:PRO:HD2	2.00	0.42
27:Y:178:HIS:CG	27:Y:179:PRO:HD2	2.55	0.42
32:I:112:LYS:C	32:I:114:PRO:HD2	2.43	0.42
1:0:130:C:H2'	39:O:3769:HOH:O	2.18	0.42
1:0:424:C:H2'	1:0:425:U:H6	1.84	0.42
1:0:1705:C:O2	1:0:2735:U:H5''	2.20	0.42
1:0:2324:G:N2	1:0:2377:U:H1'	2.34	0.42
1:0:2704:C:H2'	1:0:2705:U:O4'	2.20	0.42
1:0:2838:A:H2'	1:0:2839:C:C6	2.55	0.42
39:O:9737:HOH:O	15:M:82:ARG:HD2	2.19	0.42
2:9:3024:U:H3'	2:9:3025:G:C5'	2.50	0.42
5:B:69:VAL:HA	5:B:70:PRO:HD3	1.86	0.42
6:C:124:VAL:HA	6:C:230:GLY:O	2.18	0.42
26:X:73:ARG:HH12	26:X:88:GLU:HA	1.85	0.42
27:Y:115:ARG:HH11	27:Y:115:ARG:CB	2.29	0.42
32:I:76:ALA:O	32:I:80:LYS:HG3	2.20	0.42
1:0:185:G:C4'	1:0:186:A:H4'	2.49	0.42
1:0:1298:U:H2'	1:0:1299:G:C8	2.53	0.42
1:0:1603:A:H5''	1:0:1604:G:H3'	2.01	0.42
1:0:1759:A:N3	1:0:1818:C:H2'	2.35	0.42
1:0:1878:G:O2'	1:0:1879:U:C6	2.70	0.42
1:0:2880:A:H2'	1:0:2881:C:H5'	2.02	0.42
6:C:194:PHE:CD2	6:C:234:VAL:CG1	3.01	0.42
7:D:18:ILE:HG12	7:D:134:LEU:CD2	2.49	0.42
11:H:78:GLY:C	11:H:80:GLU:N	2.77	0.42
13:K:125:ALA:C	13:K:127:ALA:N	2.78	0.42
14:L:61:ALA:HB2	14:L:105:TYR:CZ	2.54	0.42
17:O:14:LEU:HG	17:O:102:ILE:HD11	2.01	0.42
25:W:110:GLN:NE2	25:W:110:GLN:CA	2.82	0.42
26:X:23:HIS:CD2	26:X:24:LYS:HG3	2.55	0.42
27:Y:151:SER:HB3	27:Y:154:ARG:HB3	2.02	0.42
27:Y:163:THR:HB	39:Y:9398:HOH:O	2.20	0.42
1:0:1419:U:H2'	1:0:1685:A:C2	2.54	0.42
1:0:1654:U:H2'	4:A:47:HIS:HD2	1.83	0.42
1:0:1992:U:OP2	13:K:66:ARG:HD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2676:C:H4'	12:J:70:PHE:HD1	1.78	0.42
5:B:24:PRO:HG3	5:B:204:GLY:HA2	2.00	0.42
5:B:87:TYR:OH	5:B:163:GLU:OE2	2.30	0.42
6:C:194:PHE:HA	6:C:234:VAL:HG13	2.02	0.42
7:D:18:ILE:HD13	7:D:84:LEU:HD12	2.01	0.42
14:L:94:ARG:NH1	14:L:143:THR:HG21	2.35	0.42
19:Q:33:PHE:HE2	19:Q:93:ARG:HG3	1.85	0.42
1:O:912:A:C4	1:O:1294:A:C2	3.06	0.42
1:O:1244:U:C6	12:J:47:THR:HG22	2.54	0.42
1:O:1287:A:O4'	25:W:117:ARG:HD3	2.20	0.42
1:O:1909:A:N1	1:O:2128:G:H1'	2.35	0.42
1:O:2568:A:H2'	1:O:2569:A:O4'	2.19	0.42
2:9:3005:G:OP1	16:N:17:ARG:NH2	2.52	0.42
4:A:36:ASP:OD2	4:A:85:SER:HB2	2.20	0.42
5:B:84:LEU:HD13	5:B:84:LEU:O	2.19	0.42
6:C:123:LEU:HD23	6:C:123:LEU:HA	1.92	0.42
9:F:20:LEU:O	9:F:23:ALA:HB3	2.20	0.42
11:H:66:ARG:HD3	39:H:9546:HOH:O	2.20	0.42
11:H:144:GLU:HG2	39:H:9535:HOH:O	2.19	0.42
32:I:80:LYS:HD3	32:I:86:GLU:O	2.19	0.42
1:O:308:U:H5'	22:T:97:ARG:HH21	1.85	0.42
1:O:1980:U:O2	1:O:2008:U:H4'	2.20	0.42
1:O:2508:C:H2'	39:O:7270:HOH:O	2.18	0.42
1:O:2697:A:H2'	1:O:2698:G:O4'	2.20	0.42
2:9:3003:A:OP2	2:9:3025:G:N2	2.52	0.42
5:B:301:VAL:HG11	5:B:309:VAL:HG11	2.02	0.42
9:F:28:ALA:CB	9:F:99:THR:HG23	2.49	0.42
10:G:23:ILE:O	10:G:27:ILE:HG13	2.20	0.42
11:H:28:ILE:HA	11:H:63:GLU:OE1	2.19	0.42
11:H:77:LEU:HD12	11:H:83:TYR:CD2	2.55	0.42
16:N:152:GLU:OE1	16:N:152:GLU:HA	2.20	0.42
1:O:87:C:C2	30:2:30:ASP:OD2	2.72	0.41
1:O:462:A:H2'	39:O:5457:HOH:O	2.20	0.41
1:O:1149:U:H5''	1:O:1151:G:O4'	2.20	0.41
1:O:1476:A:O2'	1:O:1477:C:H5'	2.20	0.41
1:O:1768:C:H2'	1:O:1769:C:O4'	2.19	0.41
1:O:2015:A:H2'	1:O:2016:U:O4'	2.20	0.41
1:O:2388:C:H5'	19:Q:83:THR:O	2.20	0.41
10:G:64:ASN:N	10:G:64:ASN:ND2	2.67	0.41
11:H:45:VAL:HG13	39:H:9525:HOH:O	2.19	0.41
12:J:71:TYR:CG	12:J:72:PRO:HD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:93:GLN:HE21	16:N:127:LEU:HD12	1.84	0.41
20:R:16:ALA:HB1	20:R:94:ASN:HD22	1.85	0.41
27:Y:155:ARG:HH21	27:Y:157:ILE:HD11	1.85	0.41
32:I:138:THR:HG22	32:I:139:ILE:H	1.84	0.41
1:O:920:C:OP1	14:L:37:LYS:NZ	2.51	0.41
1:O:2896:A:H5''	39:X:5399:HOH:O	2.21	0.41
4:A:94:LEU:HG	4:A:99:ILE:HD11	2.02	0.41
4:A:209:PRO:C	4:A:211:LYS:N	2.79	0.41
6:C:127:ARG:HD3	6:C:129:HIS:CE1	2.53	0.41
6:C:132:ASP:HB2	6:C:161:ASP:HB3	2.02	0.41
11:H:29:ALA:CB	11:H:66:ARG:HH12	2.20	0.41
24:V:29:ASN:O	24:V:33:VAL:HG23	2.20	0.41
26:X:80:GLU:O	26:X:80:GLU:HG2	2.20	0.41
1:O:349:U:O2'	1:O:350:C:H5'	2.21	0.41
1:O:1878:G:O2'	1:O:1879:U:C5	2.68	0.41
1:O:2256:G:H2'	1:O:2257:G:C5'	2.51	0.41
1:O:2337:G:O3'	7:D:97:GLN:HA	2.20	0.41
1:O:2866:U:C4	23:U:50:GLU:HB3	2.55	0.41
39:O:5855:HOH:O	25:W:119:HIS:CG	2.73	0.41
2:9:3064:C:C2'	2:9:3065:A:H5'	2.49	0.41
4:A:57:ALA:HA	4:A:67:LEU:HD23	2.02	0.41
5:B:190:MET:CE	5:B:194:PHE:CD1	2.96	0.41
6:C:166:ILE:HD11	6:C:207:LEU:HD13	2.02	0.41
8:E:102:VAL:HG13	8:E:116:THR:HG23	2.02	0.41
11:H:63:GLU:HA	39:H:9546:HOH:O	2.19	0.41
14:L:146:GLY:C	14:L:148:GLU:H	2.28	0.41
16:N:49:THR:HG22	16:N:56:ASP:CB	2.50	0.41
21:S:42:GLU:O	21:S:46:ASP:HA	2.21	0.41
22:T:112:LEU:CD2	22:T:119:ALA:HB3	2.50	0.41
1:O:314:G:N2	1:O:316:A:H3'	2.35	0.41
1:O:583:G:H2'	1:O:584:U:C6	2.56	0.41
1:O:883:U:O2	1:O:883:U:C2'	2.66	0.41
1:O:932:U:H2'	1:O:933:C:C6	2.56	0.41
1:O:2101:A:H2'	6:C:63:SER:OG	2.20	0.41
1:O:2506:A:O2'	1:O:2507:G:P	2.79	0.41
5:B:217:ARG:CG	5:B:257:THR:HG22	2.48	0.41
6:C:142:ASP:CG	6:C:237:GLU:HB3	2.45	0.41
9:F:79:GLN:HB2	9:F:82:ASP:OD2	2.20	0.41
13:K:109:LEU:CD1	13:K:113:ILE:HD11	2.42	0.41
14:L:92:ASP:HB3	14:L:95:ASP:OD2	2.21	0.41
16:N:182:GLY:O	16:N:183:ASP:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:45:LEU:HD12	17:O:88:LYS:HD2	2.02	0.41
20:R:39:THR:HG22	20:R:41:GLY:N	2.36	0.41
21:S:38:ALA:O	21:S:42:GLU:HG3	2.20	0.41
22:T:78:THR:HB	22:T:87:VAL:O	2.21	0.41
1:O:414:C:H5'	39:O:3274:HOH:O	2.20	0.41
1:O:500:G:O2'	20:R:94:ASN:ND2	2.53	0.41
1:O:506:G:H22	1:O:509:A:H5'	1.79	0.41
1:O:2265:U:H2'	1:O:2266:A:H8	1.82	0.41
1:O:2503:A:OP1	11:H:151:ARG:NH2	2.46	0.41
7:D:35:ALA:C	7:D:37:ALA:N	2.78	0.41
12:J:75:PRO:HB3	12:J:132:LEU:HB3	2.02	0.41
16:N:66:LEU:HG	16:N:175:LEU:HD21	2.02	0.41
26:X:43:VAL:CG1	26:X:47:ALA:HB3	2.51	0.41
27:Y:107:PRO:HD3	27:Y:182:PHE:CE1	2.56	0.41
32:I:135:LEU:HB2	32:I:137:VAL:HG23	2.02	0.41
1:O:177:A:H2'	1:O:178:U:O4'	2.20	0.41
1:O:611:U:H2'	1:O:612:U:C6	2.56	0.41
1:O:1279:U:O2	1:O:1279:U:H2'	2.20	0.41
1:O:1304:U:H2'	1:O:1305:C:C6	2.56	0.41
1:O:1363:G:P	6:C:76:ARG:HH22	2.43	0.41
1:O:1787:C:H4'	1:O:2883:A:O4'	2.20	0.41
1:O:1881:A:OP1	4:A:199:HIS:HE1	2.03	0.41
1:O:2338:G:OP1	7:D:97:GLN:HG2	2.21	0.41
5:B:16:ARG:NH2	39:B:9556:HOH:O	2.43	0.41
6:C:57:PRO:O	6:C:58:ALA:C	2.62	0.41
7:D:139:TYR:CE2	7:D:143:LYS:HE3	2.56	0.41
8:E:137:ASP:OD1	8:E:139:GLU:HB2	2.20	0.41
14:L:73:VAL:HG21	14:L:116:HIS:CD2	2.54	0.41
15:M:159:VAL:HG13	15:M:160:PHE:N	2.36	0.41
15:M:167:GLY:O	15:M:171:ARG:HG3	2.20	0.41
22:T:18:GLU:O	22:T:21:LYS:HG2	2.21	0.41
23:U:9:CYS:CA	23:U:52:THR:HG23	2.51	0.41
28:Z:10:ARG:HG3	28:Z:11:SER:N	2.36	0.41
1:O:1162:G:H1'	32:I:117:LEU:HD11	2.02	0.41
1:O:1181:A:H4'	32:I:92:PRO:HG2	2.02	0.41
1:O:2281:C:C2'	1:O:2282:U:H5'	2.50	0.41
1:O:2443:C:H5'	14:L:57:VAL:HG21	2.03	0.41
1:O:2456:A:H5'	39:O:6254:HOH:O	2.20	0.41
1:O:2564:G:OP2	1:O:2565:C:H5''	2.20	0.41
1:O:2784:A:H1'	8:E:60:SER:OG	2.21	0.41
7:D:22:VAL:HG22	7:D:74:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:20:ILE:HD12	8:E:33:LEU:CD1	2.50	0.41
9:F:111:ILE:O	9:F:115:VAL:HG23	2.19	0.41
12:J:63:ILE:HG22	12:J:64:GLY:N	2.35	0.41
22:T:43:ASN:C	22:T:45:GLY:H	2.29	0.41
29:1:42:SER:HB2	39:1:9465:HOH:O	2.20	0.41
1:0:559:U:H2'	1:0:560:C:O4'	2.21	0.41
1:0:960:G:N3	1:0:960:G:C2'	2.84	0.41
1:0:1132:A:N6	1:0:1229:C:H2'	2.36	0.41
1:0:1163:G:H5'	32:I:115:ASP:O	2.21	0.41
1:0:2283:G:C6	11:H:113:MET:HB3	2.56	0.41
2:9:3064:C:H2'	2:9:3065:A:H5'	2.02	0.41
4:A:52:SER:HB2	4:A:164:ARG:HH11	1.86	0.41
4:A:65:ARG:HG2	4:A:65:ARG:HH11	1.86	0.41
5:B:104:GLU:HB2	39:B:9631:HOH:O	2.20	0.41
7:D:135:VAL:HG21	7:D:139:TYR:CG	2.54	0.41
8:E:7:ILE:CD1	8:E:12:ASP:HA	2.48	0.41
14:L:144:ASP:O	14:L:147:GLU:HB2	2.21	0.41
15:M:27:ARG:HH22	15:M:44:THR:HG23	1.85	0.41
16:N:42:HIS:CG	16:N:62:HIS:HE1	2.39	0.41
16:N:77:ASN:OD1	16:N:79:PRO:HD2	2.21	0.41
25:W:119:HIS:HD2	25:W:120:PRO:O	2.04	0.41
25:W:125:HIS:HD2	25:W:127:GLY:N	2.02	0.41
1:0:185:G:O3'	1:0:186:A:H4'	2.21	0.41
1:0:517:U:H1'	39:0:8147:HOH:O	2.20	0.41
1:0:553:G:P	27:Y:204:ARG:NH2	2.86	0.41
1:0:855:U:H4'	1:0:856:G:O4'	2.20	0.41
1:0:1754:A:H2'	1:0:1755:A:O4'	2.20	0.41
1:0:1755:A:H2'	1:0:1756:G:O4'	2.21	0.41
1:0:2094:G:O6	1:0:2649:A:H2	2.03	0.41
1:0:2365:G:H4'	19:Q:45:PRO:O	2.21	0.41
1:0:2699:A:H2'	1:0:2700:G:O4'	2.20	0.41
4:A:36:ASP:CB	4:A:85:SER:H	2.33	0.41
4:A:68:ILE:HG12	4:A:69:LEU:N	2.35	0.41
4:A:94:LEU:HD12	4:A:98:GLU:CB	2.51	0.41
4:A:103:VAL:O	4:A:105:VAL:HG23	2.21	0.41
5:B:277:GLU:N	5:B:278:PRO:CD	2.84	0.41
7:D:25:MET:HE1	7:D:37:ALA:HB1	2.02	0.41
7:D:56:ARG:N	39:D:6752:HOH:O	2.52	0.41
9:F:60:VAL:O	9:F:60:VAL:CG1	2.68	0.41
12:J:39:VAL:HG11	12:J:107:ASN:CB	2.50	0.41
20:R:33:ARG:NH1	39:R:9452:HOH:O	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:27:LEU:HD23	22:T:98:VAL:HB	2.02	0.41
22:T:85:GLU:HG2	22:T:86:GLU:N	2.36	0.41
23:U:14:GLU:O	23:U:17:THR:HB	2.21	0.41
24:V:59:ILE:O	24:V:63:GLU:HG2	2.20	0.41
25:W:38:THR:HG22	25:W:40:ALA:H	1.85	0.41
26:X:23:HIS:NE2	26:X:24:LYS:HD2	2.36	0.41
31:3:24:LYS:HA	31:3:67:LEU:HD23	2.02	0.41
32:I:75:THR:O	32:I:76:ALA:C	2.64	0.41
1:0:17:G:H2'	1:0:18:C:C6	2.56	0.41
1:0:830:G:O2'	1:0:831:U:H5'	2.21	0.41
1:0:941:G:C5	1:0:942:U:C4	3.09	0.41
1:0:1352:A:HO2'	1:0:1353:C:P	2.44	0.41
1:0:2681:A:H4'	1:0:2682:C:H5'	2.03	0.41
1:0:2748:G:H4'	1:0:2749:U:C5'	2.51	0.41
4:A:171:LYS:NZ	39:A:9514:HOH:O	2.54	0.41
4:A:173:GLY:O	4:A:176:HIS:HB3	2.20	0.41
12:J:80:LYS:HE2	12:J:98:PHE:CE1	2.56	0.41
13:K:38:SER:O	39:K:4183:HOH:O	2.22	0.41
13:K:115:ARG:CG	13:K:116:GLU:N	2.84	0.41
14:L:93:VAL:HG12	14:L:97:VAL:HG23	2.02	0.41
15:M:68:ARG:NH2	15:M:73:ARG:HD3	2.36	0.41
16:N:42:HIS:ND1	16:N:63:SER:OG	2.53	0.41
16:N:176:ARG:HG3	16:N:180:LEU:CD1	2.51	0.41
18:P:131:PHE:CE1	18:P:137:LEU:HD13	2.56	0.41
22:T:14:ALA:HA	22:T:15:PRO:HD3	1.95	0.41
1:0:380:A:H2'	39:0:7729:HOH:O	2.21	0.40
1:0:2523:U:O2'	1:0:2524:G:H5'	2.22	0.40
1:0:2748:G:H4'	1:0:2749:U:H5'	2.02	0.40
1:0:2807:U:OP2	5:B:28:SER:HB2	2.21	0.40
6:C:133:ARG:NH1	39:C:9216:HOH:O	2.54	0.40
8:E:126:ILE:HB	8:E:131:LEU:CD2	2.51	0.40
12:J:54:VAL:HG11	12:J:138:THR:HG21	2.02	0.40
12:J:107:ASN:C	12:J:107:ASN:HD22	2.29	0.40
16:N:37:ARG:HD3	36:N:9307:CL:CL	2.58	0.40
17:O:112:ARG:HE	17:O:112:ARG:HB2	1.77	0.40
18:P:37:ARG:O	18:P:41:ARG:HG3	2.20	0.40
19:Q:64:GLU:HG3	19:Q:74:ASP:CG	2.46	0.40
27:Y:177:LYS:HD3	27:Y:181:GLY:O	2.21	0.40
1:0:294:C:H2'	1:0:295:C:O4'	2.21	0.40
1:0:951:A:O2'	1:0:952:G:H5'	2.21	0.40
1:0:1044:C:H3'	1:0:1045:G:H5''	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1131:G:H4'	2:9:3091:C:O4'	2.21	0.40
1:0:1745:G:H22	1:0:2033:G:H5'	1.86	0.40
1:0:2611:G:H5'	1:0:2613:G:C8	2.56	0.40
1:0:2754:G:H2'	1:0:2755:G:O4'	2.21	0.40
39:9:1361:HOH:O	16:N:41:LYS:HE3	2.21	0.40
4:A:186:TRP:CG	4:A:187:PRO:HA	2.57	0.40
6:C:133:ARG:HG3	6:C:133:ARG:HH11	1.85	0.40
6:C:162:VAL:CG2	6:C:232:LEU:HD21	2.48	0.40
11:H:39:ASP:HB3	11:H:41:ASP:OD2	2.21	0.40
13:K:78:LYS:HA	13:K:79:PRO:HD3	1.93	0.40
16:N:112:GLY:HA2	16:N:137:ALA:N	2.36	0.40
21:S:81:ILE:HG22	24:V:29:ASN:OD1	2.21	0.40
22:T:106:GLU:HG3	39:T:4913:HOH:O	2.21	0.40
31:3:55:VAL:HB	31:3:56:PRO:HD2	2.03	0.40
1:0:629:A:H2'	1:0:630:A:O4'	2.22	0.40
1:0:644:G:H5'	1:0:644:G:N3	2.37	0.40
1:0:921:G:H4'	1:0:924:G:N1	2.36	0.40
1:0:1099:G:OP1	25:W:129:LYS:HE3	2.22	0.40
1:0:1168:C:H5''	32:I:87:THR:CG2	2.51	0.40
1:0:1657:A:H2'	1:0:1658:A:C8	2.56	0.40
39:0:6895:HOH:O	4:A:205:GLY:HA3	2.22	0.40
5:B:255:GLY:O	5:B:257:THR:HG23	2.20	0.40
5:B:305:ASP:O	5:B:306:LYS:CB	2.67	0.40
17:O:23:GLY:C	39:O:3062:HOH:O	2.63	0.40
17:O:97:SER:H	17:O:100:GLN:NE2	2.20	0.40
19:Q:8:GLU:CD	19:Q:8:GLU:C	2.89	0.40
20:R:39:THR:CG2	20:R:107:GLU:O	2.70	0.40
24:V:60:GLN:O	24:V:65:ASP:N	2.54	0.40
32:I:99:ASP:HA	32:I:138:THR:O	2.21	0.40
1:0:1477:C:H5'	1:0:1868:G:H5'	2.04	0.40
1:0:1972:U:C2'	1:0:1973:A:H5''	2.51	0.40
1:0:2499:U:H2'	1:0:2500:C:H6	1.86	0.40
1:0:2565:C:H4'	39:0:5409:HOH:O	2.22	0.40
4:A:192:VAL:HG13	4:A:208:HIS:N	2.37	0.40
6:C:236:THR:C	39:C:9251:HOH:O	2.65	0.40
7:D:52:THR:HB	7:D:70:GLY:C	2.46	0.40
7:D:164:ALA:O	7:D:165:PHE:C	2.64	0.40
14:L:144:ASP:HA	14:L:147:GLU:CD	2.47	0.40
20:R:16:ALA:CB	20:R:94:ASN:HD22	2.34	0.40
23:U:35:LYS:HE2	23:U:51:TRP:CZ2	2.57	0.40
27:Y:95:THR:N	27:Y:236:VAL:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:204:A:H2'	1:0:205:U:H5'	2.02	0.40
1:0:226:A:H1'	1:0:393:G:C5	2.56	0.40
1:0:285:A:H2'	1:0:286:U:O4'	2.21	0.40
1:0:370:G:O2'	1:0:371:U:H5'	2.21	0.40
1:0:582:C:O2'	1:0:583:G:H5'	2.22	0.40
1:0:920:C:H5'	1:0:921:G:C4	2.56	0.40
1:0:1117:A:C2	1:0:1244:U:C2	3.10	0.40
1:0:1864:C:C5	15:M:75:ARG:HD2	2.57	0.40
1:0:2038:A:O2'	1:0:2039:A:H5'	2.21	0.40
1:0:2374:A:H2'	1:0:2375:G:C8	2.57	0.40
1:0:2857:C:H2'	1:0:2858:U:C6	2.57	0.40
4:A:166:ASP:HA	39:A:9607:HOH:O	2.20	0.40
6:C:140:VAL:CG1	6:C:141:SER:N	2.85	0.40
7:D:28:GLY:CA	7:D:69:ILE:HG23	2.37	0.40
7:D:40:ILE:HG13	7:D:41:LEU:N	2.37	0.40
7:D:49:PRO:HB3	39:D:5828:HOH:O	2.21	0.40
12:J:64:GLY:HA3	36:J:9321:CL:CL	2.58	0.40
14:L:40:PHE:CD1	14:L:40:PHE:C	3.00	0.40
15:M:66:SER:HB3	15:M:128:TRP:CD1	2.56	0.40
19:Q:62:THR:O	19:Q:64:GLU:HG2	2.22	0.40
25:W:91:ASP:HB2	39:W:5425:HOH:O	2.22	0.40
28:Z:39:CYS:SG	28:Z:41:ASN:HB3	2.60	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%)	208 (88%)	25 (11%)	2 (1%)	14	14
5	B	335/338 (99%)	315 (94%)	16 (5%)	4 (1%)	10	8
6	C	244/246 (99%)	225 (92%)	19 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	D	134/177 (76%)	107 (80%)	16 (12%)	11 (8%)	0	0
8	E	170/178 (96%)	164 (96%)	6 (4%)	0	100	100
9	F	117/120 (98%)	105 (90%)	8 (7%)	4 (3%)	3	1
10	G	25/348 (7%)	25 (100%)	0	0	100	100
11	H	156/171 (91%)	137 (88%)	15 (10%)	4 (3%)	4	2
12	J	140/145 (97%)	132 (94%)	5 (4%)	3 (2%)	5	3
13	K	130/132 (98%)	125 (96%)	5 (4%)	0	100	100
14	L	141/165 (86%)	119 (84%)	20 (14%)	2 (1%)	9	7
15	M	192/195 (98%)	183 (95%)	8 (4%)	1 (0%)	24	27
16	N	184/187 (98%)	165 (90%)	12 (6%)	7 (4%)	2	1
17	O	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
18	P	141/149 (95%)	136 (96%)	5 (4%)	0	100	100
19	Q	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
20	R	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
21	S	79/85 (93%)	75 (95%)	4 (5%)	0	100	100
22	T	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	14	14
23	U	51/66 (77%)	48 (94%)	3 (6%)	0	100	100
24	V	63/71 (89%)	58 (92%)	4 (6%)	1 (2%)	7	6
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%)	137 (98%)	3 (2%)	0	100	100
28	Z	71/83 (86%)	62 (87%)	6 (8%)	3 (4%)	2	1
29	1	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
30	2	42/50 (84%)	40 (95%)	2 (5%)	0	100	100
31	3	90/92 (98%)	86 (96%)	4 (4%)	0	100	100
32	I	68/162 (42%)	56 (82%)	10 (15%)	2 (3%)	3	2
All	All	3705/4431 (84%)	3432 (93%)	228 (6%)	45 (1%)	10	8

All (45) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	27	LEU
5	B	139	ASP

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Mol	Chain	Res	Type
11	H	166	SER
11	H	168	ALA
12	J	143	LYS
14	L	80	ASP
16	N	154	LEU
16	N	184	ILE
28	Z	81	ARG
4	A	37	VAL
7	D	27	ILE
7	D	60	GLU
7	D	61	PHE
7	D	97	GLN
7	D	171	ASP
9	F	101	ALA
22	T	53	GLY
24	V	43	PRO
28	Z	20	ARG
28	Z	21	VAL
7	D	28	GLY
7	D	56	ARG
11	H	16	ARG
11	H	81	GLY
12	J	5	GLU
12	J	65	ASN
14	L	102	ASP
16	N	65	ASP
16	N	155	GLU
16	N	164	ASP
16	N	167	ASP
5	B	34	GLY
5	B	185	GLY
7	D	16	PRO
7	D	137	PRO
7	D	173	GLU
9	F	71	GLY
32	I	132	CYS
7	D	164	ALA
15	M	83	SER
16	N	160	SER
32	I	129	VAL
9	F	100	ASP
9	F	27	GLY

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Mol	Chain	Res	Type
5	B	2	GLN

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%)	13	15
5	B	282/283 (100%)	262 (93%)	20 (7%)	13	16
6	C	193/193 (100%)	175 (91%)	18 (9%)	8	9
7	D	117/148 (79%)	112 (96%)	5 (4%)	26	35
8	E	152/156 (97%)	145 (95%)	7 (5%)	24	32
9	F	93/94 (99%)	91 (98%)	2 (2%)	45	61
10	G	27/283 (10%)	27 (100%)	0	100	100
11	H	132/138 (96%)	126 (96%)	6 (4%)	24	33
12	J	118/121 (98%)	112 (95%)	6 (5%)	21	27
13	K	106/106 (100%)	102 (96%)	4 (4%)	29	40
14	L	113/127 (89%)	109 (96%)	4 (4%)	32	43
15	M	158/159 (99%)	154 (98%)	4 (2%)	42	56
16	N	149/150 (99%)	143 (96%)	6 (4%)	28	38
17	O	93/94 (99%)	91 (98%)	2 (2%)	45	61
18	P	113/117 (97%)	111 (98%)	2 (2%)	51	68
19	Q	79/80 (99%)	76 (96%)	3 (4%)	29	40
20	R	117/122 (96%)	113 (97%)	4 (3%)	32	44
21	S	71/74 (96%)	71 (100%)	0	100	100
22	T	105/106 (99%)	101 (96%)	4 (4%)	29	40
23	U	44/52 (85%)	44 (100%)	0	100	100
24	V	51/57 (90%)	50 (98%)	1 (2%)	48	64
25	W	130/130 (100%)	125 (96%)	5 (4%)	29	40
26	X	66/74 (89%)	62 (94%)	4 (6%)	17	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Y	120/196 (61%)	109 (91%)	11 (9%)	8	9
28	Z	60/68 (88%)	60 (100%)	0	100	100
29	1	46/47 (98%)	45 (98%)	1 (2%)	45	61
30	2	42/46 (91%)	42 (100%)	0	100	100
31	3	79/79 (100%)	78 (99%)	1 (1%)	61	76
32	I	58/130 (45%)	58 (100%)	0	100	100
All	All	3093/3612 (86%)	2960 (96%)	133 (4%)	26	35

All (133) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	3	ARG
4	A	36	ASP
4	A	55	VAL
4	A	69	LEU
4	A	94	LEU
4	A	131	HIS
4	A	151	GLN
4	A	153	ARG
4	A	165	THR
4	A	175	LYS
4	A	179	MET
4	A	206	ARG
4	A	217	ARG
5	B	7	ARG
5	B	11	LEU
5	B	27	ASN
5	B	56	ASP
5	B	71	VAL
5	B	82	VAL
5	B	84	LEU
5	B	149	ASP
5	B	175	LEU
5	B	180	ASP
5	B	190	MET
5	B	195	ARG
5	B	234	ARG
5	B	251	VAL
5	B	254	GLN
5	B	264	GLU

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Mol	Chain	Res	Type
5	B	265	LEU
5	B	277	GLU
5	B	307	ARG
5	B	312	ARG
6	C	2	GLN
6	C	67	GLN
6	C	76	ARG
6	C	78	ARG
6	C	91	PRO
6	C	94	THR
6	C	101	ASP
6	C	136	VAL
6	C	162	VAL
6	C	187	ARG
6	C	214	THR
6	C	222	ASP
6	C	223	LEU
6	C	234	VAL
6	C	236	THR
6	C	240	LEU
6	C	243	VAL
6	C	246	ARG
7	D	24	HIS
7	D	50	VAL
7	D	61	PHE
7	D	137	PRO
7	D	170	TYR
8	E	3	VAL
8	E	7	ILE
8	E	86	VAL
8	E	102	VAL
8	E	108	LEU
8	E	154	ILE
8	E	155	ASN
9	F	12	LEU
9	F	46	GLU
11	H	18	GLU
11	H	51	VAL
11	H	84	LYS
11	H	154	TYR
11	H	159	PRO
11	H	170	ASN

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Mol	Chain	Res	Type
12	J	45	VAL
12	J	52	GLN
12	J	74	ARG
12	J	93	ARG
12	J	127	ILE
12	J	131	THR
13	K	4	LEU
13	K	10	GLN
13	K	49	LEU
13	K	84	ASP
14	L	35	ARG
14	L	43	HIS
14	L	89	PHE
14	L	140	VAL
15	M	46	LEU
15	M	93	ARG
15	M	99	ARG
15	M	164	THR
16	N	12	ARG
16	N	26	LEU
16	N	49	THR
16	N	65	ASP
16	N	127	LEU
16	N	139	TRP
17	O	3	THR
17	O	111	VAL
18	P	21	VAL
18	P	98	ILE
19	Q	16	ASN
19	Q	57	ASP
19	Q	95	GLU
20	R	39	THR
20	R	82	GLU
20	R	132	ARG
20	R	143	VAL
22	T	39	ASN
22	T	48	VAL
22	T	89	ARG
22	T	96	VAL
24	V	65	ASP
25	W	26	ILE
25	W	35	VAL

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Mol	Chain	Res	Type
25	W	52	VAL
25	W	142	ASP
25	W	146	ILE
26	X	8	ARG
26	X	79	GLU
26	X	82	GLU
26	X	85	VAL
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	163	THR
27	Y	189	ASN
27	Y	200	THR
27	Y	203	VAL
27	Y	235	GLU
29	1	29	THR
31	3	22	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (97) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	199	HIS
5	B	27	ASN
5	B	145	HIS
5	B	177	HIS
5	B	221	GLN
5	B	238	ASN
5	B	256	GLN
5	B	260	HIS
5	B	332	ASN
6	C	2	GLN
6	C	39	GLN
6	C	129	HIS
6	C	178	GLN
7	D	47	GLN
7	D	85	GLN
7	D	103	ASN
7	D	133	ASN
8	E	106	ASN

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Mol	Chain	Res	Type
8	E	143	GLN
9	F	80	GLN
10	G	64	ASN
11	H	31	HIS
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	52	GLN
12	J	107	ASN
13	K	10	GLN
14	L	18	HIS
14	L	41	HIS
14	L	42	ASN
15	M	24	GLN
15	M	26	GLN
15	M	58	GLN
15	M	77	HIS
15	M	143	ASN
15	M	170	ASN
16	N	22	GLN
16	N	93	GLN
16	N	107	ASN
16	N	153	GLN
17	O	100	GLN
18	P	50	GLN
18	P	66	GLN
18	P	73	HIS
18	P	118	GLN
19	Q	16	ASN
19	Q	40	HIS
19	Q	67	GLN
20	R	22	GLN
20	R	61	GLN
20	R	94	ASN
20	R	98	ASN
20	R	102	GLN
20	R	113	HIS
20	R	117	HIS
20	R	122	GLN

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Mol	Chain	Res	Type
20	R	140	GLN
21	S	25	GLN
21	S	51	GLN
21	S	53	ASN
21	S	55	GLN
21	S	75	GLN
22	T	37	GLN
22	T	39	ASN
22	T	43	ASN
22	T	73	HIS
23	U	39	ASN
23	U	48	ASN
24	V	60	GLN
25	W	27	HIS
25	W	28	HIS
25	W	110	GLN
25	W	119	HIS
25	W	125	HIS
25	W	141	HIS
26	X	22	ASN
27	Y	133	HIS
27	Y	134	HIS
27	Y	149	GLN
27	Y	153	GLN
27	Y	189	ASN
29	1	8	GLN
29	1	16	HIS
29	1	28	HIS
30	2	16	ASN
30	2	18	ASN
30	2	41	HIS
30	2	45	ASN
31	3	20	HIS
31	3	30	GLN
31	3	48	ASN
32	I	104	GLN
32	I	113	HIS

5.3.3 RNA ⓘ

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2922 (93%)	242 (8%)	35 (1%)
2	9	121/122 (99%)	16 (13%)	2 (1%)
3	4	1/3 (33%)	0	0
All	All	2867/3047 (94%)	258 (8%)	37 (1%)

All (258) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G
1	0	86	A
1	0	87	C
1	0	88	G
1	0	114	A
1	0	115	U
1	0	120	A
1	0	130	C
1	0	141	C
1	0	151	A
1	0	166	A
1	0	169	A
1	0	170	U
1	0	186	A
1	0	191	A
1	0	192	A
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	284	C
1	0	308	U
1	0	309	C
1	0	318	C
1	0	336	G
1	0	337	A
1	0	358	G

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Mol	Chain	Res	Type
1	0	381	G
1	0	397	A
1	0	417	G
1	0	461	C
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	588	G
1	0	604	G
1	0	620	A
1	0	632	A
1	0	644	G
1	0	645	U
1	0	660	A
1	0	688	A
1	0	698	A
1	0	701	U
1	0	702	G
1	0	759	C
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	840	U
1	0	846	A
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	875	A
1	0	877	G
1	0	878	G
1	0	885	G
1	0	898	G

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Mol	Chain	Res	Type
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	1164	U
1	0	1165	G
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U
1	0	1192	A
1	0	1193	A
1	0	1206	U
1	0	1208	C
1	0	1216	G
1	0	1232	A
1	0	1233	A
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1246	A
1	0	1247	A
1	0	1279	U
1	0	1289	C

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Mol	Chain	Res	Type
1	0	1331	A
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	1634	G
1	0	1656	A
1	0	1667	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1686	C
1	0	1692	C
1	0	1693	A
1	0	1701	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1730	G
1	0	1731	C
1	0	1752	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1879	U

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Mol	Chain	Res	Type
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	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2110	G
1	0	2243	C
1	0	2258	A
1	0	2271	G
1	0	2272	G
1	0	2291	A
1	0	2317	C
1	0	2321	A
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2379	G
1	0	2422	U
1	0	2462	G
1	0	2465	A
1	0	2469	A
1	0	2476	C
1	0	2480	G
1	0	2483	A
1	0	2507	G

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Mol	Chain	Res	Type
1	0	2509	A
1	0	2511	A
1	0	2533	C
1	0	2537	G
1	0	2541	U
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G
1	0	2645	U
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	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2761	A
1	0	2762	C
1	0	2768	A
1	0	2786	G
1	0	2792	A
1	0	2800	A
1	0	2811	A
1	0	2812	A
1	0	2825	C
1	0	2852	A
1	0	2853	U
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2903	C
1	0	2914	A
2	9	3002	U

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Mol	Chain	Res	Type
2	9	3014	G
2	9	3022	G
2	9	3023	U
2	9	3024	U
2	9	3025	G
2	9	3040	C
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

All (37) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	69	A
1	0	129	A
1	0	169	A
1	0	338	C
1	0	603	A
1	0	644	G
1	0	699	C
1	0	834	G
1	0	857	A
1	0	871	G
1	0	877	G
1	0	1080	C
1	0	1232	A
1	0	1237	U
1	0	1246	A
1	0	1352	A
1	0	1506	U
1	0	1563	G
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1752	G
1	0	1856	C

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Mol	Chain	Res	Type
1	0	1942	A
1	0	1979	G
1	0	2011	A
1	0	2313	C
1	0	2320	U
1	0	2467	A
1	0	2536	C
1	0	2649	A
1	0	2718	C
1	0	2761	A
1	0	2791	U
1	0	2852	A
2	9	3043	G
2	9	3065	A

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

6 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	19,22,23	0.24	0	25,31,34	0.46	0
1	PSU	0	2621	1	18,21,22	1.67	2 (11%)	21,30,33	1.38	3 (14%)
1	1MA	0	628	1	21,25,26	0.69	1 (4%)	30,37,40	0.78	1 (3%)
1	OMG	0	2588	3,1	23,26,27	0.28	0	32,38,41	0.41	0
3	PPU	4	76	3,1	37,40,41	1.03	1 (2%)	47,57,60	0.79	2 (4%)
1	UR3	0	2619	1	19,22,23	0.50	0	26,32,35	0.73	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	0	2587	1	-	0/9/27/28	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	1MA	0	628	1	-	2/7/25/26	0/3/3/3
1	OMG	0	2588	3,1	-	0/9/27/28	0/3/3/3
3	PPU	4	76	3,1	-	0/25/43/44	0/4/4/4
1	UR3	0	2619	1	-	0/7/25/26	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4	76	PPU	OC-CM	-5.82	1.26	1.42
1	0	2621	PSU	C2-N1	5.56	1.43	1.36
1	0	2621	PSU	C6-C5	3.48	1.39	1.35
1	0	628	1MA	C6-N6	2.39	1.33	1.28

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	C6-C5-C4	3.55	120.57	118.17
1	0	2621	PSU	C6-N1-C2	-3.35	119.58	122.69
1	0	2619	UR3	C4-N3-C2	2.94	126.94	124.58
3	4	76	PPU	C2-N1-C6	2.94	119.00	111.83
1	0	628	1MA	N1-C2-N3	2.78	129.30	126.00
1	0	2621	PSU	O2-C2-N1	2.71	125.58	122.79
3	4	76	PPU	CM-OC-CZ	2.24	122.31	117.50

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	0	628	1MA	C2'-C1'-N9-C8
1	0	628	1MA	C2'-C1'-N9-C4

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
3	4	76	PPU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 312 ligands modelled in this entry, 312 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2749/2922 (94%)	-0.19	81 (2%) 53 50	26, 46, 90, 148	0
2	9	122/122 (100%)	0.41	8 (6%) 24 21	39, 62, 87, 147	0
3	4	2/3 (66%)	0.14	0 100 100	52, 52, 52, 62	0
4	A	237/240 (98%)	0.69	22 (9%) 14 12	30, 52, 82, 104	0
5	B	337/338 (99%)	0.54	10 (2%) 52 49	31, 50, 72, 85	0
6	C	246/246 (100%)	0.50	9 (3%) 45 42	28, 47, 68, 81	0
7	D	140/177 (79%)	2.19	66 (47%) 0 0	56, 90, 119, 127	0
8	E	172/178 (96%)	1.01	20 (11%) 9 7	42, 60, 78, 83	0
9	F	119/120 (99%)	1.45	34 (28%) 1 1	47, 71, 99, 108	0
10	G	29/348 (8%)	1.91	11 (37%) 1 0	68, 89, 97, 98	0
11	H	160/171 (93%)	1.02	18 (11%) 10 8	44, 60, 92, 99	0
12	J	142/145 (97%)	0.49	5 (3%) 47 44	36, 47, 66, 86	0
13	K	132/132 (100%)	0.26	2 (1%) 72 69	34, 45, 66, 69	0
14	L	145/165 (87%)	1.12	28 (19%) 3 2	30, 64, 110, 119	0
15	M	194/195 (99%)	0.64	24 (12%) 8 6	35, 46, 67, 79	0
16	N	186/187 (99%)	1.29	37 (19%) 3 2	44, 62, 104, 112	0
17	O	115/116 (99%)	0.74	5 (4%) 40 36	41, 53, 66, 74	0
18	P	143/149 (95%)	0.66	5 (3%) 47 44	40, 51, 65, 78	0
19	Q	95/96 (98%)	0.48	3 (3%) 50 47	41, 47, 63, 74	0
20	R	150/155 (96%)	0.16	2 (1%) 75 73	31, 44, 62, 70	0
21	S	81/85 (95%)	0.89	8 (9%) 13 10	43, 62, 82, 95	0
22	T	119/120 (99%)	0.94	10 (8%) 17 14	43, 56, 79, 107	0
23	U	53/66 (80%)	0.69	2 (3%) 44 41	42, 51, 67, 75	0
24	V	65/71 (91%)	1.74	19 (29%) 1 1	54, 78, 111, 116	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	0.49	3 (1%) 66 63	36, 48, 69, 78	0
26	X	82/92 (89%)	0.94	13 (15%) 5 3	41, 53, 79, 97	0
27	Y	142/241 (58%)	0.33	5 (3%) 47 44	31, 43, 62, 82	0
28	Z	73/83 (87%)	1.70	27 (36%) 1 0	49, 73, 86, 92	0
29	1	56/57 (98%)	-0.11	0 100 100	30, 35, 42, 50	0
30	2	46/50 (92%)	1.02	8 (17%) 4 3	38, 58, 73, 83	0
31	3	92/92 (100%)	0.72	3 (3%) 49 46	37, 55, 68, 79	0
32	I	70/162 (43%)	3.46	61 (87%) 0 0	107, 120, 137, 139	0
All	All	6648/7478 (88%)	0.41	549 (8%) 17 15	26, 51, 94, 148	0

All (549) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
24	V	1	THR	9.7
7	D	10	PHE	9.1
32	I	133	THR	8.3
15	M	70	GLY	8.0
16	N	166	ALA	7.6
7	D	107	GLY	7.4
7	D	63	ILE	6.7
2	9	3001	U	6.7
32	I	88	GLY	6.4
16	N	168	LEU	6.4
32	I	90	GLY	6.4
24	V	2	VAL	6.3
32	I	117	LEU	6.3
12	J	70	PHE	6.2
32	I	121	LEU	6.1
7	D	174	VAL	6.1
32	I	118	SER	6.0
32	I	85	PHE	5.9
17	O	22	GLY	5.8
2	9	3002	U	5.8
28	Z	10	ARG	5.7
14	L	82	ALA	5.6
1	0	2748	G	5.5
16	N	154	LEU	5.5
32	I	76	ALA	5.4
15	M	74	LYS	5.3

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Mol	Chain	Res	Type	RSRZ
30	2	49	GLU	5.3
1	0	1173	A	5.3
24	V	43	PRO	5.2
16	N	165	ALA	5.2
4	A	37	VAL	5.2
28	Z	82	SER	5.2
24	V	40	PRO	5.1
8	E	10	ASP	5.1
28	Z	22	SER	5.1
11	H	168	ALA	5.0
14	L	78	ALA	5.0
15	M	75	ARG	5.0
7	D	135	VAL	4.9
1	0	2637	A	4.9
11	H	111	ASP	4.8
22	T	119	ALA	4.8
24	V	39	ALA	4.8
7	D	154	LYS	4.8
32	I	102	VAL	4.8
32	I	89	SER	4.7
8	E	45	ASP	4.7
9	F	102	GLY	4.7
26	X	88	GLU	4.6
22	T	117	ASP	4.6
32	I	79	ILE	4.6
32	I	106	LYS	4.6
32	I	132	CYS	4.6
14	L	77	ALA	4.6
26	X	87	ALA	4.5
32	I	135	LEU	4.5
7	D	61	PHE	4.5
1	0	10	U	4.5
32	I	96	PHE	4.5
1	0	1161	A	4.4
10	G	12	ILE	4.4
16	N	163	PHE	4.4
32	I	87	THR	4.4
32	I	75	THR	4.4
18	P	143	ALA	4.3
14	L	148	GLU	4.3
15	M	79	ALA	4.3
28	Z	11	SER	4.3

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Mol	Chain	Res	Type	RSRZ
7	D	69	ILE	4.2
14	L	149	ARG	4.2
32	I	137	VAL	4.2
32	I	134	SER	4.2
32	I	128	VAL	4.2
14	L	81	VAL	4.2
8	E	154	ILE	4.1
7	D	57	THR	4.1
32	I	139	ILE	4.1
32	I	129	VAL	4.1
32	I	116	LEU	4.1
1	0	2747	C	4.1
1	0	2102	G	4.0
21	S	81	ILE	4.0
5	B	57	GLU	4.0
4	A	36	ASP	4.0
8	E	12	ASP	4.0
28	Z	29	ILE	4.0
4	A	237	GLY	4.0
17	O	23	GLY	4.0
7	D	44	ILE	4.0
5	B	1	PRO	3.9
32	I	109	ALA	3.9
26	X	66	THR	3.9
7	D	105	SER	3.9
11	H	167	PRO	3.9
16	N	158	LEU	3.9
11	H	40	ALA	3.9
7	D	172	VAL	3.9
7	D	59	GLY	3.9
28	Z	16	ALA	3.9
32	I	114	PRO	3.8
7	D	18	ILE	3.8
16	N	167	ASP	3.8
15	M	78	LYS	3.8
26	X	85	VAL	3.8
1	0	1175	G	3.7
9	F	101	ALA	3.7
14	L	145	LEU	3.7
32	I	78	LEU	3.7
22	T	116	ASP	3.7
7	D	128	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
12	J	4	ALA	3.7
14	L	91	VAL	3.6
1	0	514	G	3.6
7	D	26	GLY	3.6
27	Y	236	VAL	3.6
32	I	93	GLN	3.6
9	F	22	VAL	3.6
15	M	88	VAL	3.6
1	0	138	U	3.6
7	D	153	THR	3.6
16	N	134	ASP	3.5
16	N	95	ALA	3.5
2	9	3024	U	3.5
15	M	89	THR	3.5
1	0	2345	A	3.5
1	0	2645	U	3.5
7	D	101	THR	3.5
1	0	497	A	3.5
1	0	1169	U	3.5
7	D	55	LYS	3.4
32	I	124	ALA	3.4
17	O	1	SER	3.4
14	L	146	GLY	3.4
32	I	119	TYR	3.4
14	L	150	GLN	3.4
8	E	126	ILE	3.4
32	I	122	THR	3.4
11	H	169	GLY	3.4
7	D	171	ASP	3.4
26	X	65	ASN	3.4
7	D	50	VAL	3.4
15	M	71	SER	3.4
21	S	1	SER	3.4
14	L	75	LEU	3.3
16	N	169	PRO	3.3
32	I	92	PRO	3.3
4	A	32	VAL	3.3
15	M	72	ALA	3.3
26	X	83	ALA	3.3
4	A	31	LYS	3.3
32	I	108	ILE	3.3
32	I	97	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	0	288	A	3.3
1	0	1964	U	3.3
16	N	186	LEU	3.3
19	Q	17	LYS	3.3
32	I	125	ALA	3.3
15	M	80	GLY	3.3
21	S	19	ASP	3.3
32	I	120	ASP	3.3
1	0	1524	U	3.3
1	0	2004	U	3.3
8	E	172	PRO	3.3
14	L	83	GLU	3.3
16	N	159	TYR	3.3
6	C	16	VAL	3.3
10	G	26	MET	3.2
15	M	77	HIS	3.2
2	9	3122	C	3.2
32	I	138	THR	3.2
7	D	170	TYR	3.2
9	F	8	VAL	3.2
32	I	105	VAL	3.2
4	A	35	GLY	3.2
16	N	164	ASP	3.2
7	D	11	HIS	3.2
24	V	46	ILE	3.2
28	Z	14	PHE	3.2
24	V	36	ALA	3.2
7	D	12	GLU	3.2
1	0	1165	G	3.2
1	0	2769	C	3.2
8	E	87	PHE	3.2
32	I	80	LYS	3.2
7	D	60	GLU	3.2
16	N	137	ALA	3.2
30	2	35	ARG	3.1
8	E	123	ASP	3.1
16	N	162	ASP	3.1
21	S	2	TRP	3.1
1	0	1929	G	3.1
10	G	27	ILE	3.1
26	X	84	ILE	3.1
1	0	1164	U	3.1

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Mol	Chain	Res	Type	RSRZ
10	G	71	LEU	3.1
1	0	1951	G	3.1
11	H	112	GLY	3.1
16	N	161	GLY	3.1
24	V	44	GLY	3.1
7	D	134	LEU	3.1
14	L	130	ARG	3.1
32	I	100	LEU	3.1
4	A	38	ILE	3.1
7	D	36	ASN	3.1
9	F	105	ASP	3.1
7	D	17	ARG	3.1
10	G	23	ILE	3.0
32	I	131	THR	3.0
10	G	63	ARG	3.0
32	I	98	ALA	3.0
14	L	99	GLU	3.0
12	J	46	ILE	3.0
9	F	24	ARG	3.0
28	Z	23	ARG	3.0
28	Z	12	GLY	3.0
25	W	86	GLU	3.0
1	0	737	A	3.0
1	0	1192	A	3.0
1	0	1202	A	3.0
32	I	107	GLN	3.0
25	W	108	ARG	3.0
22	T	118	SER	3.0
4	A	205	GLY	3.0
16	N	1	ALA	3.0
7	D	157	LEU	3.0
1	0	960	G	3.0
7	D	35	ALA	2.9
24	V	20	LEU	2.9
7	D	155	HIS	2.9
9	F	91	VAL	2.9
28	Z	21	VAL	2.9
32	I	72	VAL	2.9
14	L	55	GLN	2.9
7	D	52	THR	2.9
9	F	90	GLU	2.9
32	I	74	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
11	H	170	ASN	2.9
7	D	137	PRO	2.9
20	R	150	PRO	2.9
1	0	1176	C	2.9
16	N	184	ILE	2.9
1	0	1279	U	2.9
1	0	1171	A	2.9
1	0	1199	A	2.9
7	D	104	PHE	2.9
10	G	24	VAL	2.9
32	I	140	GLU	2.9
26	X	46	ASP	2.9
4	A	211	LYS	2.8
9	F	119	ARG	2.8
15	M	76	ARG	2.8
27	Y	216	ARG	2.8
22	T	44	ALA	2.8
1	0	1172	G	2.8
1	0	2237	G	2.8
5	B	119	HIS	2.8
7	D	54	ALA	2.8
11	H	171	ALA	2.8
32	I	113	HIS	2.8
11	H	137	TYR	2.8
5	B	183	GLU	2.8
9	F	78	GLU	2.8
7	D	22	VAL	2.8
7	D	58	VAL	2.8
8	E	124	VAL	2.8
9	F	111	ILE	2.8
31	3	62	THR	2.8
22	T	53	GLY	2.8
24	V	38	GLY	2.8
9	F	104	ALA	2.8
28	Z	25	ARG	2.8
1	0	1162	G	2.7
1	0	1523	G	2.7
18	P	121	ASP	2.7
32	I	111	GLN	2.7
32	I	84	GLY	2.7
9	F	9	PRO	2.7
1	0	128	A	2.7

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Mol	Chain	Res	Type	RSRZ
22	T	115	GLU	2.7
7	D	56	ARG	2.7
30	2	44	ARG	2.7
11	H	140	VAL	2.7
5	B	2	GLN	2.7
7	D	86	THR	2.7
28	Z	34	ASN	2.7
28	Z	78	THR	2.7
1	0	1167	G	2.7
32	I	94	GLU	2.7
9	F	31	LYS	2.7
28	Z	46	ARG	2.7
25	W	76	ASP	2.7
7	D	27	ILE	2.7
16	N	68	GLU	2.7
22	T	114	SER	2.7
1	0	1188	A	2.7
1	0	1170	U	2.7
9	F	16	ALA	2.7
32	I	83	ALA	2.7
27	Y	108	ASP	2.7
32	I	123	ASN	2.7
8	E	53	GLU	2.7
16	N	170	GLU	2.7
31	3	41	GLU	2.7
16	N	157	PRO	2.7
1	0	1166	A	2.7
28	Z	59	TYR	2.6
27	Y	106	THR	2.6
26	X	61	ARG	2.6
18	P	116	SER	2.6
11	H	32	LYS	2.6
16	N	73	ALA	2.6
28	Z	24	ARG	2.6
8	E	11	VAL	2.6
1	0	1168	C	2.6
16	N	175	LEU	2.6
24	V	3	LEU	2.6
7	D	99	ASP	2.6
31	3	18	GLN	2.6
32	I	112	LYS	2.6
1	0	2103	A	2.6

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Mol	Chain	Res	Type	RSRZ
32	I	82	GLU	2.6
28	Z	80	ARG	2.6
6	C	132	ASP	2.6
7	D	62	ASP	2.6
9	F	108	VAL	2.6
14	L	97	VAL	2.6
1	0	282	C	2.6
32	I	91	GLU	2.5
1	0	2538	A	2.5
15	M	1	ALA	2.5
4	A	63	GLY	2.5
7	D	89	PRO	2.5
5	B	51	VAL	2.5
1	0	999	C	2.5
1	0	1204	C	2.5
19	Q	95	GLU	2.5
15	M	73	ARG	2.5
15	M	81	ARG	2.5
30	2	39	ARG	2.5
7	D	90	LEU	2.5
1	0	441	A	2.5
4	A	97	ALA	2.5
5	B	139	ASP	2.5
14	L	80	ASP	2.5
16	N	76	GLY	2.5
32	I	73	PRO	2.5
7	D	131	THR	2.5
10	G	29	SER	2.5
26	X	79	GLU	2.5
15	M	82	ARG	2.5
28	Z	18	TYR	2.5
28	Z	20	ARG	2.5
1	0	1160	G	2.5
5	B	56	ASP	2.5
28	Z	45	ASP	2.5
28	Z	19	GLY	2.5
7	D	21	VAL	2.5
9	F	103	GLU	2.5
32	I	77	GLU	2.5
1	0	1174	A	2.5
7	D	53	LYS	2.5
7	D	138	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
6	C	76	ARG	2.4
8	E	81	GLU	2.4
5	B	21	SER	2.4
9	F	115	VAL	2.4
14	L	57	VAL	2.4
2	9	3023	U	2.4
9	F	89	LEU	2.4
16	N	180	LEU	2.4
14	L	100	ALA	2.4
19	Q	18	PRO	2.4
24	V	41	GLU	2.4
28	Z	44	GLU	2.4
1	0	1203	G	2.4
14	L	143	THR	2.4
24	V	33	VAL	2.4
28	Z	33	MET	2.4
4	A	34	ASP	2.4
9	F	7	ASP	2.4
14	L	102	ASP	2.4
24	V	42	ASN	2.4
30	2	48	ASP	2.4
10	G	22	ALA	2.4
16	N	67	ALA	2.4
15	M	69	LYS	2.4
4	A	82	VAL	2.4
1	0	287	C	2.4
7	D	29	HIS	2.4
11	H	154	TYR	2.4
7	D	37	ALA	2.4
7	D	102	GLY	2.4
16	N	2	THR	2.4
15	M	83	SER	2.4
1	0	1190	G	2.4
7	D	106	PHE	2.4
1	0	284	C	2.4
1	0	2508	C	2.4
6	C	245	GLU	2.4
16	N	139	TRP	2.4
1	0	2511	A	2.3
24	V	47	LYS	2.3
1	0	970	U	2.3
1	0	289	G	2.3

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Mol	Chain	Res	Type	RSRZ
1	0	1197	G	2.3
9	F	60	VAL	2.3
15	M	107	ARG	2.3
8	E	6	GLU	2.3
32	I	86	GLU	2.3
18	P	18	LYS	2.3
8	E	13	ALA	2.3
1	0	1967	U	2.3
11	H	166	SER	2.3
4	A	84	VAL	2.3
16	N	43	VAL	2.3
1	0	1193	A	2.3
30	2	26	MET	2.3
4	A	33	GLU	2.3
18	P	111	GLU	2.3
26	X	7	GLU	2.3
32	I	104	GLN	2.3
9	F	49	PHE	2.3
7	D	75	LEU	2.3
15	M	84	LYS	2.3
1	0	735	C	2.3
1	0	1189	A	2.3
32	I	71	GLY	2.3
4	A	86	ALA	2.3
9	F	19	ALA	2.3
14	L	111	ALA	2.3
15	M	194	ALA	2.3
28	Z	79	VAL	2.3
1	0	1163	G	2.2
1	0	1195	G	2.2
7	D	100	ASP	2.2
14	L	36	ASP	2.2
26	X	22	ASN	2.2
1	0	1201	C	2.2
4	A	206	ARG	2.2
7	D	51	ARG	2.2
11	H	162	ARG	2.2
15	M	68	ARG	2.2
26	X	80	GLU	2.2
9	F	93	SER	2.2
11	H	38	LYS	2.2
8	E	7	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
9	F	17	LEU	2.2
7	D	165	PHE	2.2
14	L	93	VAL	2.2
11	H	39	ASP	2.2
32	I	81	ASP	2.2
1	0	2344	G	2.2
23	U	47	ARG	2.2
23	U	56	ARG	2.2
24	V	13	PRO	2.2
1	0	806	A	2.2
1	0	2768	A	2.2
9	F	117	GLU	2.2
1	0	2541	U	2.2
13	K	118	ALA	2.2
22	T	107	LYS	2.2
7	D	74	THR	2.2
14	L	121	ILE	2.2
15	M	91	ILE	2.2
7	D	88	LEU	2.2
6	C	1	MET	2.2
1	0	2526	C	2.2
14	L	147	GLU	2.2
21	S	12	GLU	2.2
30	2	37	HIS	2.2
1	0	1981	A	2.2
21	S	74	ALA	2.2
16	N	179	LEU	2.2
28	Z	81	ARG	2.2
4	A	64	ASP	2.2
5	B	171	VAL	2.2
21	S	20	PHE	2.2
6	C	64	GLY	2.2
16	N	70	GLY	2.2
1	0	883	U	2.2
1	0	2419	U	2.2
2	9	3065	A	2.2
8	E	88	TYR	2.1
17	O	102	ILE	2.1
24	V	5	VAL	2.1
7	D	98	PHE	2.1
11	H	36	LYS	2.1
16	N	149	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
16	N	152	GLU	2.1
22	T	106	GLU	2.1
1	0	1177	A	2.1
12	J	47	THR	2.1
20	R	13	THR	2.1
16	N	69	TYR	2.1
6	C	8	LEU	2.1
7	D	40	ILE	2.1
8	E	20	ILE	2.1
7	D	43	GLU	2.1
14	L	98	GLU	2.1
24	V	65	ASP	2.1
7	D	68	PRO	2.1
8	E	102	VAL	2.1
10	G	20	VAL	2.1
9	F	79	GLN	2.1
4	A	204	GLY	2.1
7	D	66	GLY	2.1
1	0	969	G	2.1
2	9	3025	G	2.1
4	A	153	ARG	2.1
9	F	99	THR	2.1
9	F	116	GLU	2.1
27	Y	191	ASP	2.1
4	A	208	HIS	2.1
6	C	2	GLN	2.1
28	Z	15	GLY	2.1
13	K	27	ARG	2.1
1	0	1184	C	2.1
1	0	1965	C	2.1
17	O	21	SER	2.1
9	F	10	ALA	2.1
16	N	148	ALA	2.1
8	E	125	GLU	2.1
7	D	166	ILE	2.1
21	S	21	GLN	2.1
30	2	46	ASP	2.1
4	A	209	PRO	2.1
9	F	1	PRO	2.1
28	Z	26	VAL	2.1
8	E	46	THR	2.0
1	0	1191	A	2.0

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Mol	Chain	Res	Type	RSRZ
7	D	13	MET	2.0
9	F	69	GLU	2.0
1	0	1525	G	2.0
2	9	3022	G	2.0
11	H	37	GLN	2.0
10	G	73	ASP	2.0
16	N	138	ASP	2.0
32	I	115	ASP	2.0
6	C	5	ILE	2.0
16	N	74	PRO	2.0
7	D	23	VAL	2.0
24	V	45	ARG	2.0
1	0	1205	U	2.0
12	J	5	GLU	2.0
1	0	2850	C	2.0
14	L	62	ALA	2.0
9	F	25	ASP	2.0
9	F	118	LEU	2.0
15	M	15	PRO	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PPU	4	76	37/38	0.93	0.12	48,54,66,71	0
1	PSU	0	2621	20/21	0.96	0.07	37,40,50,51	0
1	UR3	0	2619	21/22	0.96	0.08	45,45,49,50	0
1	OMG	0	2588	24/25	0.97	0.07	30,35,40,41	0
1	1MA	0	628	23/24	0.98	0.06	29,33,36,37	0
1	OMU	0	2587	21/22	0.98	0.06	33,36,38,39	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
37	SR	0	9601	1/1	0.57	0.28	200,200,200,200	0
37	SR	0	9547	1/1	0.60	0.34	200,200,200,200	0
33	MG	0	8050	1/1	0.64	0.22	93,93,93,93	0
35	NA	0	9122	1/1	0.66	0.46	96,96,96,96	0
35	NA	0	9171	1/1	0.66	0.27	61,61,61,61	0
35	NA	0	9184	1/1	0.68	0.37	102,102,102,102	0
33	MG	0	8014	1/1	0.69	0.30	73,73,73,73	0
33	MG	0	8045	1/1	0.71	0.32	84,84,84,84	0
33	MG	0	8082	1/1	0.72	0.50	107,107,107,107	0
33	MG	0	8065	1/1	0.73	0.29	93,93,93,93	0
33	MG	B	8055	1/1	0.74	0.15	108,108,108,108	0
34	K	0	9001	1/1	0.75	0.43	116,116,116,116	0
35	NA	0	9129	1/1	0.76	0.38	85,85,85,85	0
33	MG	0	8092	1/1	0.77	0.35	81,81,81,81	0
35	NA	0	9164	1/1	0.77	0.29	59,59,59,59	0
35	NA	0	9173	1/1	0.78	0.20	70,70,70,70	0
33	MG	0	8040	1/1	0.78	0.43	100,100,100,100	0
37	SR	0	9501	1/1	0.79	0.20	200,200,200,200	0
33	MG	0	8047	1/1	0.79	0.38	91,91,91,91	0
35	NA	0	9152	1/1	0.79	0.50	78,78,78,78	0
33	MG	0	8090	1/1	0.80	0.26	80,80,80,80	0
35	NA	0	9170	1/1	0.82	0.42	94,94,94,94	0
33	MG	0	8024	1/1	0.83	0.49	77,77,77,77	0
33	MG	0	8052	1/1	0.83	0.30	68,68,68,68	0
35	NA	0	9168	1/1	0.83	0.24	57,57,57,57	0
35	NA	0	9179	1/1	0.83	0.34	100,100,100,100	0
37	SR	0	9590	1/1	0.84	0.18	178,178,178,178	0
33	MG	0	8059	1/1	0.85	0.14	78,78,78,78	0
33	MG	0	8061	1/1	0.85	0.16	95,95,95,95	0
37	SR	0	9484	1/1	0.86	0.16	147,147,147,147	0
37	SR	0	9500	1/1	0.86	0.46	200,200,200,200	0
35	NA	0	9172	1/1	0.86	0.26	70,70,70,70	0
33	MG	0	8085	1/1	0.86	0.23	91,91,91,91	0
35	NA	0	9185	1/1	0.86	0.24	46,46,46,46	0
35	NA	D	9151	1/1	0.86	0.18	63,63,63,63	0
37	SR	0	9537	1/1	0.87	0.18	154,154,154,154	0
33	MG	0	8072	1/1	0.88	0.20	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
37	SR	0	9529	1/1	0.88	0.16	138,138,138,138	0
35	NA	0	9120	1/1	0.88	0.18	64,64,64,64	0
37	SR	0	9452	1/1	0.88	0.14	114,114,114,114	0
35	NA	0	9182	1/1	0.88	0.11	78,78,78,78	0
35	NA	0	9140	1/1	0.88	0.16	60,60,60,60	0
34	K	0	9002	1/1	0.89	0.21	89,89,89,89	0
33	MG	0	8101	1/1	0.89	0.13	59,59,59,59	0
33	MG	0	8084	1/1	0.89	0.49	74,74,74,74	0
35	NA	0	9166	1/1	0.89	0.19	67,67,67,67	0
35	NA	0	9126	1/1	0.89	0.16	59,59,59,59	0
35	NA	0	9127	1/1	0.89	0.14	57,57,57,57	0
33	MG	0	8094	1/1	0.89	0.17	67,67,67,67	0
35	NA	S	9112	1/1	0.89	0.11	59,59,59,59	0
36	CL	0	9316	1/1	0.89	0.23	69,69,69,69	0
37	SR	B	9521	1/1	0.89	0.44	199,199,199,199	0
33	MG	0	8076	1/1	0.90	0.09	61,61,61,61	0
33	MG	0	8022	1/1	0.90	0.35	74,74,74,74	0
33	MG	0	8107	1/1	0.90	0.24	67,67,67,67	0
33	MG	9	8095	1/1	0.90	0.19	46,46,46,46	0
35	NA	0	9157	1/1	0.90	0.18	47,47,47,47	0
35	NA	0	9163	1/1	0.90	0.14	66,66,66,66	0
35	NA	0	9174	1/1	0.90	0.20	65,65,65,65	0
33	MG	0	8057	1/1	0.90	0.18	85,85,85,85	0
33	MG	0	8060	1/1	0.91	0.20	71,71,71,71	0
35	NA	0	9165	1/1	0.91	0.25	47,47,47,47	0
35	NA	0	9113	1/1	0.91	0.10	65,65,65,65	0
35	NA	0	9181	1/1	0.91	0.10	50,50,50,50	0
35	NA	0	9167	1/1	0.91	0.15	56,56,56,56	0
33	MG	0	8097	1/1	0.91	0.12	62,62,62,62	0
35	NA	0	9169	1/1	0.91	0.31	104,104,104,104	0
33	MG	0	8063	1/1	0.91	0.10	70,70,70,70	0
35	NA	0	9124	1/1	0.91	0.14	47,47,47,47	0
37	SR	0	9626	1/1	0.91	0.43	128,128,128,128	0
33	MG	0	8104	1/1	0.91	0.16	76,76,76,76	0
33	MG	0	8103	1/1	0.92	0.18	62,62,62,62	0
35	NA	9	9183	1/1	0.92	0.18	66,66,66,66	0
35	NA	0	9175	1/1	0.92	0.19	52,52,52,52	0
35	NA	0	9154	1/1	0.92	0.19	59,59,59,59	0
37	SR	0	9539	1/1	0.92	0.46	162,162,162,162	0
33	MG	T	8073	1/1	0.92	0.15	46,46,46,46	0
35	NA	0	9162	1/1	0.92	0.14	58,58,58,58	0
37	SR	0	9459	1/1	0.92	0.11	101,101,101,101	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
37	SR	0	9468	1/1	0.92	0.12	113,113,113,113	0
33	MG	0	8093	1/1	0.92	0.15	42,42,42,42	0
33	MG	0	8116	1/1	0.93	0.09	62,62,62,62	0
35	NA	0	9125	1/1	0.93	0.27	115,115,115,115	0
33	MG	0	8118	1/1	0.93	0.21	76,76,76,76	0
37	SR	0	9474	1/1	0.93	0.07	112,112,112,112	0
33	MG	0	8039	1/1	0.93	0.09	65,65,65,65	0
37	SR	0	9490	1/1	0.93	0.21	109,109,109,109	0
35	NA	0	9116	1/1	0.93	0.17	58,58,58,58	0
33	MG	0	8001	1/1	0.93	0.16	20,20,20,20	0
37	SR	0	9504	1/1	0.93	0.10	105,105,105,105	0
35	NA	B	9161	1/1	0.93	0.35	62,62,62,62	0
35	NA	C	9104	1/1	0.93	0.10	34,34,34,34	0
35	NA	0	9141	1/1	0.93	0.11	62,62,62,62	0
35	NA	J	9146	1/1	0.93	0.07	55,55,55,55	0
35	NA	R	9186	1/1	0.93	0.15	69,69,69,69	0
33	MG	0	8108	1/1	0.93	0.15	74,74,74,74	0
35	NA	0	9177	1/1	0.93	0.17	63,63,63,63	0
36	CL	A	9309	1/1	0.93	0.30	68,68,68,68	0
33	MG	0	8046	1/1	0.94	0.07	40,40,40,40	0
37	SR	0	9475	1/1	0.94	0.09	77,77,77,77	0
35	NA	0	9132	1/1	0.94	0.16	51,51,51,51	0
35	NA	0	9118	1/1	0.94	0.24	60,60,60,60	0
33	MG	0	8042	1/1	0.94	0.08	60,60,60,60	0
35	NA	0	9149	1/1	0.94	0.15	42,42,42,42	0
36	CL	0	9315	1/1	0.94	0.11	58,58,58,58	0
33	MG	0	8099	1/1	0.94	0.13	59,59,59,59	0
35	NA	0	9102	1/1	0.94	0.36	57,57,57,57	0
36	CL	B	9319	1/1	0.94	0.24	52,52,52,52	0
36	CL	L	9310	1/1	0.94	0.12	54,54,54,54	0
37	SR	0	9405	1/1	0.94	0.11	60,60,60,60	0
35	NA	0	9107	1/1	0.94	0.12	61,61,61,61	0
35	NA	0	9111	1/1	0.94	0.11	57,57,57,57	0
33	MG	0	8041	1/1	0.94	0.12	50,50,50,50	0
37	SR	0	9482	1/1	0.95	0.40	102,102,102,102	0
35	NA	0	9158	1/1	0.95	0.12	63,63,63,63	0
33	MG	A	8066	1/1	0.95	0.17	53,53,53,53	0
33	MG	0	8089	1/1	0.95	0.09	54,54,54,54	0
33	MG	0	8080	1/1	0.95	0.12	47,47,47,47	0
35	NA	0	9134	1/1	0.95	0.16	51,51,51,51	0
37	SR	0	9505	1/1	0.95	0.30	85,85,85,85	0
35	NA	0	9139	1/1	0.95	0.12	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8114	1/1	0.95	0.13	63,63,63,63	0
33	MG	0	8067	1/1	0.95	0.10	42,42,42,42	0
35	NA	0	9143	1/1	0.95	0.06	43,43,43,43	0
37	SR	0	9581	1/1	0.95	0.11	121,121,121,121	0
33	MG	0	8021	1/1	0.95	0.09	55,55,55,55	0
33	MG	0	8013	1/1	0.95	0.22	22,22,22,22	0
35	NA	0	9108	1/1	0.95	0.07	35,35,35,35	0
37	SR	9	9588	1/1	0.95	0.07	114,114,114,114	0
35	NA	0	9110	1/1	0.95	0.12	46,46,46,46	0
37	SR	H	9486	1/1	0.95	0.35	109,109,109,109	0
33	MG	0	8058	1/1	0.96	0.11	45,45,45,45	0
35	NA	0	9123	1/1	0.96	0.10	41,41,41,41	0
33	MG	0	8088	1/1	0.96	0.05	45,45,45,45	0
35	NA	0	9150	1/1	0.96	0.11	38,38,38,38	0
33	MG	0	8043	1/1	0.96	0.07	49,49,49,49	0
35	NA	M	9147	1/1	0.96	0.07	43,43,43,43	0
33	MG	0	8098	1/1	0.96	0.09	39,39,39,39	0
33	MG	0	8113	1/1	0.96	0.10	50,50,50,50	0
35	NA	0	9114	1/1	0.96	0.10	46,46,46,46	0
37	SR	0	9509	1/1	0.96	0.06	81,81,81,81	0
37	SR	0	9515	1/1	0.96	0.31	87,87,87,87	0
35	NA	0	9159	1/1	0.96	0.10	46,46,46,46	0
37	SR	0	9534	1/1	0.96	0.29	100,100,100,100	0
35	NA	0	9160	1/1	0.96	0.07	39,39,39,39	0
35	NA	0	9178	1/1	0.96	0.20	51,51,51,51	0
35	NA	0	9130	1/1	0.96	0.10	49,49,49,49	0
36	CL	N	9307	1/1	0.96	0.12	52,52,52,52	0
35	NA	0	9115	1/1	0.96	0.10	39,39,39,39	0
37	SR	0	9447	1/1	0.96	0.06	67,67,67,67	0
33	MG	0	8054	1/1	0.96	0.06	58,58,58,58	0
33	MG	0	8115	1/1	0.96	0.05	56,56,56,56	0
37	SR	0	9465	1/1	0.96	0.06	100,100,100,100	0
37	SR	F	9595	1/1	0.96	0.10	105,105,105,105	0
33	MG	0	8044	1/1	0.96	0.06	39,39,39,39	0
37	SR	0	9469	1/1	0.97	0.07	79,79,79,79	0
33	MG	0	8051	1/1	0.97	0.08	26,26,26,26	0
35	NA	Q	9148	1/1	0.97	0.04	44,44,44,44	0
37	SR	0	9477	1/1	0.97	0.06	84,84,84,84	0
35	NA	R	9138	1/1	0.97	0.06	56,56,56,56	0
37	SR	0	9483	1/1	0.97	0.05	68,68,68,68	0
33	MG	0	8102	1/1	0.97	0.06	56,56,56,56	0
33	MG	0	8096	1/1	0.97	0.06	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
37	SR	0	9495	1/1	0.97	0.06	88,88,88,88	0
36	CL	0	9303	1/1	0.97	0.07	46,46,46,46	0
36	CL	0	9313	1/1	0.97	0.06	51,51,51,51	0
33	MG	0	8091	1/1	0.97	0.13	45,45,45,45	0
35	NA	0	9135	1/1	0.97	0.08	50,50,50,50	0
36	CL	0	9322	1/1	0.97	0.34	53,53,53,53	0
35	NA	0	9105	1/1	0.97	0.06	43,43,43,43	0
37	SR	0	9517	1/1	0.97	0.07	91,91,91,91	0
37	SR	0	9522	1/1	0.97	0.06	104,104,104,104	0
35	NA	0	9106	1/1	0.97	0.15	37,37,37,37	0
37	SR	0	9530	1/1	0.97	0.06	84,84,84,84	0
36	CL	J	9301	1/1	0.97	0.18	53,53,53,53	0
36	CL	J	9321	1/1	0.97	0.09	53,53,53,53	0
33	MG	0	8117	1/1	0.97	0.05	43,43,43,43	0
33	MG	0	8106	1/1	0.97	0.05	43,43,43,43	0
37	SR	0	9560	1/1	0.97	0.08	97,97,97,97	0
37	SR	0	9570	1/1	0.97	0.15	98,98,98,98	0
33	MG	0	8083	1/1	0.97	0.05	54,54,54,54	0
37	SR	0	9433	1/1	0.97	0.07	76,76,76,76	0
33	MG	0	8025	1/1	0.97	0.20	25,25,25,25	0
33	MG	0	8112	1/1	0.97	0.06	43,43,43,43	0
37	SR	9	9503	1/1	0.97	0.06	114,114,114,114	0
35	NA	0	9128	1/1	0.97	0.10	45,45,45,45	0
37	SR	A	9437	1/1	0.97	0.05	67,67,67,67	0
35	NA	0	9155	1/1	0.97	0.19	55,55,55,55	0
37	SR	0	9467	1/1	0.97	0.06	67,67,67,67	0
35	NA	0	9156	1/1	0.97	0.11	53,53,53,53	0
35	NA	0	9131	1/1	0.98	0.06	48,48,48,48	0
37	SR	0	9480	1/1	0.98	0.05	87,87,87,87	0
33	MG	0	8027	1/1	0.98	0.10	39,39,39,39	0
36	CL	0	9317	1/1	0.98	0.08	50,50,50,50	0
33	MG	0	8028	1/1	0.98	0.04	37,37,37,37	0
37	SR	0	9488	1/1	0.98	0.05	76,76,76,76	0
37	SR	0	9489	1/1	0.98	0.09	85,85,85,85	0
33	MG	0	8070	1/1	0.98	0.06	26,26,26,26	0
33	MG	0	8056	1/1	0.98	0.05	46,46,46,46	0
33	MG	K	8069	1/1	0.98	0.09	29,29,29,29	0
36	CL	J	9302	1/1	0.98	0.05	48,48,48,48	0
33	MG	0	8075	1/1	0.98	0.04	36,36,36,36	0
33	MG	Y	8109	1/1	0.98	0.09	41,41,41,41	0
37	SR	0	9506	1/1	0.98	0.15	66,66,66,66	0
37	SR	0	9508	1/1	0.98	0.09	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
36	CL	M	9318	1/1	0.98	0.05	41,41,41,41	0
33	MG	0	8031	1/1	0.98	0.05	50,50,50,50	0
36	CL	R	9306	1/1	0.98	0.05	44,44,44,44	0
36	CL	Y	9320	1/1	0.98	0.10	43,43,43,43	0
36	CL	3	9304	1/1	0.98	0.05	55,55,55,55	0
33	MG	0	8110	1/1	0.98	0.14	36,36,36,36	0
37	SR	0	9532	1/1	0.98	0.10	103,103,103,103	0
37	SR	0	9427	1/1	0.98	0.04	52,52,52,52	0
37	SR	0	9429	1/1	0.98	0.04	60,60,60,60	0
37	SR	0	9431	1/1	0.98	0.04	55,55,55,55	0
37	SR	0	9545	1/1	0.98	0.09	79,79,79,79	0
35	NA	0	9101	1/1	0.98	0.07	47,47,47,47	0
37	SR	0	9446	1/1	0.98	0.04	83,83,83,83	0
37	SR	0	9566	1/1	0.98	0.11	77,77,77,77	0
37	SR	0	9568	1/1	0.98	0.04	75,75,75,75	0
33	MG	0	8079	1/1	0.98	0.03	34,34,34,34	0
35	NA	R	9137	1/1	0.98	0.04	36,36,36,36	0
37	SR	0	9454	1/1	0.98	0.08	74,74,74,74	0
37	SR	0	9455	1/1	0.98	0.05	67,67,67,67	0
33	MG	0	8036	1/1	0.98	0.04	60,60,60,60	0
37	SR	9	9481	1/1	0.98	0.08	80,80,80,80	0
33	MG	0	8037	1/1	0.98	0.09	39,39,39,39	0
33	MG	0	8015	1/1	0.98	0.03	34,34,34,34	0
33	MG	0	8019	1/1	0.98	0.05	58,58,58,58	0
37	SR	A	9497	1/1	0.98	0.04	91,91,91,91	0
36	CL	0	9305	1/1	0.98	0.07	54,54,54,54	0
36	CL	0	9311	1/1	0.98	0.07	57,57,57,57	0
33	MG	0	8012	1/1	0.98	0.13	41,41,41,41	0
37	SR	S	9470	1/1	0.98	0.04	100,100,100,100	0
38	CD	O	9205	1/1	0.98	0.06	75,75,75,75	0
37	SR	0	9466	1/1	0.99	0.10	84,84,84,84	0
33	MG	0	8020	1/1	0.99	0.03	37,37,37,37	0
36	CL	O	9308	1/1	0.99	0.10	60,60,60,60	0
33	MG	0	8029	1/1	0.99	0.08	33,33,33,33	0
37	SR	0	9473	1/1	0.99	0.07	69,69,69,69	0
33	MG	0	8030	1/1	0.99	0.03	39,39,39,39	0
36	CL	0	9314	1/1	0.99	0.14	45,45,45,45	0
33	MG	0	8002	1/1	0.99	0.03	28,28,28,28	0
37	SR	0	9478	1/1	0.99	0.03	70,70,70,70	0
37	SR	0	9406	1/1	0.99	0.06	38,38,38,38	0
37	SR	0	9407	1/1	0.99	0.02	43,43,43,43	0
37	SR	0	9410	1/1	0.99	0.02	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
37	SR	0	9411	1/1	0.99	0.02	40,40,40,40	0
37	SR	0	9412	1/1	0.99	0.02	42,42,42,42	0
37	SR	0	9413	1/1	0.99	0.03	44,44,44,44	0
37	SR	0	9414	1/1	0.99	0.03	52,52,52,52	0
37	SR	0	9416	1/1	0.99	0.03	43,43,43,43	0
37	SR	0	9498	1/1	0.99	0.07	59,59,59,59	0
37	SR	0	9417	1/1	0.99	0.03	59,59,59,59	0
37	SR	0	9420	1/1	0.99	0.03	56,56,56,56	0
37	SR	0	9421	1/1	0.99	0.03	64,64,64,64	0
37	SR	0	9422	1/1	0.99	0.04	54,54,54,54	0
37	SR	0	9423	1/1	0.99	0.04	54,54,54,54	0
37	SR	0	9425	1/1	0.99	0.04	55,55,55,55	0
37	SR	0	9426	1/1	0.99	0.04	67,67,67,67	0
33	MG	0	8032	1/1	0.99	0.07	43,43,43,43	0
35	NA	0	9117	1/1	0.99	0.12	39,39,39,39	0
33	MG	0	8003	1/1	0.99	0.03	32,32,32,32	0
37	SR	0	9432	1/1	0.99	0.06	62,62,62,62	0
33	MG	0	8004	1/1	0.99	0.03	30,30,30,30	0
37	SR	0	9434	1/1	0.99	0.03	55,55,55,55	0
37	SR	0	9435	1/1	0.99	0.04	65,65,65,65	0
37	SR	0	9438	1/1	0.99	0.05	63,63,63,63	0
37	SR	0	9440	1/1	0.99	0.06	61,61,61,61	0
37	SR	0	9441	1/1	0.99	0.06	60,60,60,60	0
37	SR	0	9442	1/1	0.99	0.05	59,59,59,59	0
37	SR	0	9443	1/1	0.99	0.04	57,57,57,57	0
37	SR	0	9444	1/1	0.99	0.07	50,50,50,50	0
37	SR	0	9445	1/1	0.99	0.05	56,56,56,56	0
35	NA	0	9136	1/1	0.99	0.05	34,34,34,34	0
33	MG	0	8038	1/1	0.99	0.10	20,20,20,20	0
37	SR	0	9585	1/1	0.99	0.06	83,83,83,83	0
37	SR	0	9449	1/1	0.99	0.04	59,59,59,59	0
37	SR	0	9451	1/1	0.99	0.04	62,62,62,62	0
33	MG	0	8068	1/1	0.99	0.10	46,46,46,46	0
37	SR	0	9629	1/1	0.99	0.05	65,65,65,65	0
37	SR	0	9453	1/1	0.99	0.06	69,69,69,69	0
33	MG	0	8008	1/1	0.99	0.10	17,17,17,17	0
36	CL	K	9312	1/1	0.99	0.09	46,46,46,46	0
37	SR	A	9436	1/1	0.99	0.10	61,61,61,61	0
37	SR	0	9456	1/1	0.99	0.07	69,69,69,69	0
37	SR	0	9457	1/1	0.99	0.04	47,47,47,47	0
37	SR	B	9458	1/1	0.99	0.06	68,68,68,68	0
33	MG	0	8026	1/1	0.99	0.05	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
37	SR	0	9461	1/1	0.99	0.09	76,76,76,76	0
37	SR	0	9462	1/1	0.99	0.04	64,64,64,64	0
37	SR	R	9418	1/1	0.99	0.03	54,54,54,54	0
37	SR	0	9464	1/1	0.99	0.08	74,74,74,74	0
37	SR	1	9460	1/1	0.99	0.05	52,52,52,52	0
37	SR	3	9439	1/1	0.99	0.06	63,63,63,63	0
33	MG	0	8009	1/1	0.99	0.02	28,28,28,28	0
38	CD	Z	9203	1/1	0.99	0.04	78,78,78,78	0
38	CD	1	9202	1/1	0.99	0.09	51,51,51,51	0
38	CD	3	9204	1/1	0.99	0.06	60,60,60,60	0
37	SR	0	9428	1/1	1.00	0.06	49,49,49,49	0
37	SR	0	9448	1/1	1.00	0.06	60,60,60,60	0
37	SR	L	9409	1/1	1.00	0.01	40,40,40,40	0
37	SR	0	9415	1/1	1.00	0.02	50,50,50,50	0
37	SR	0	9450	1/1	1.00	0.04	62,62,62,62	0
37	SR	1	9419	1/1	1.00	0.02	40,40,40,40	0
37	SR	0	9430	1/1	1.00	0.01	44,44,44,44	0
33	MG	0	8074	1/1	1.00	0.10	23,23,23,23	0
37	SR	0	9424	1/1	1.00	0.02	45,45,45,45	0
38	CD	U	9201	1/1	1.00	0.02	48,48,48,48	0
33	MG	0	8017	1/1	1.00	0.06	28,28,28,28	0
37	SR	0	9408	1/1	1.00	0.03	39,39,39,39	0
33	MG	0	8005	1/1	1.00	0.03	35,35,35,35	0

6.5 Other polymers

There are no such residues in this entry.