



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 04:31 AM UTC

PDB ID : 5ZET / pdb_00005zet
EMDB ID : EMD-6922
Title : M. smegmatis P/P state 50S ribosomal subunit
Authors : Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.
Deposited on : 2018-02-28
Resolution : 3.20 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

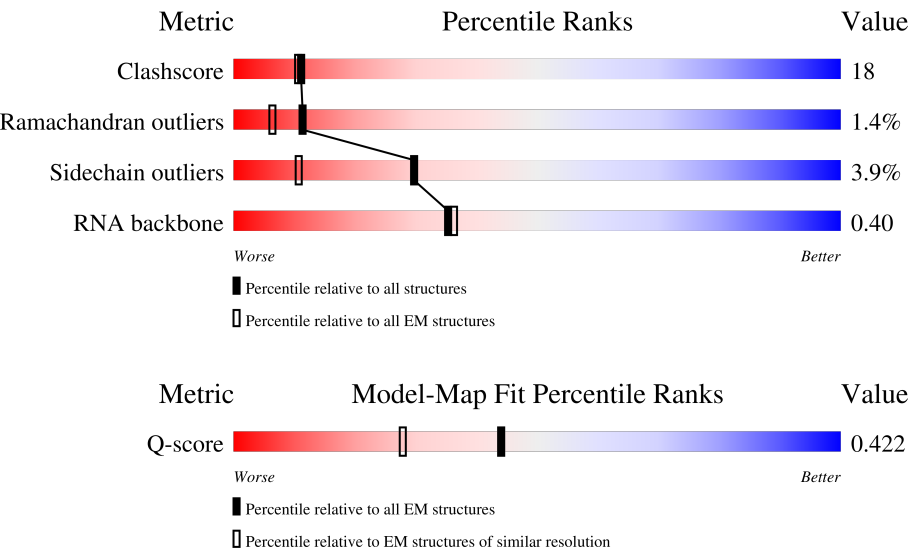
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



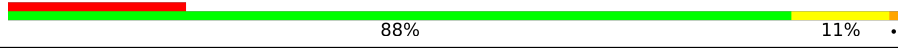
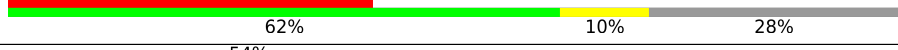
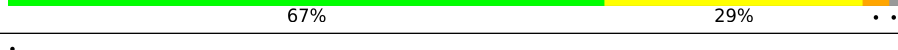
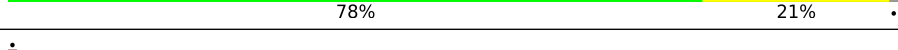
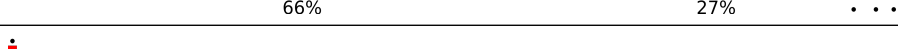
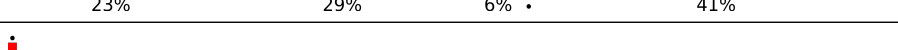
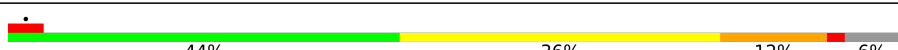
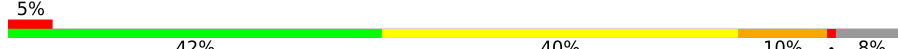
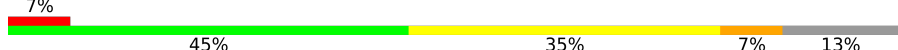
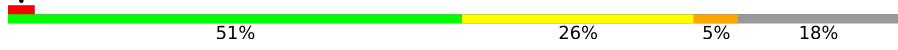
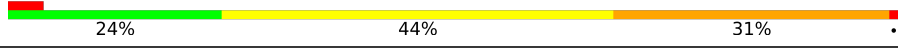
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	278	56%36% . .
2	D	217	81%16% . .
3	E	215	53%39% . . .

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Mol	Chain	Length	Quality of chain
4	F	187	
5	G	179	
6	H	151	
7	I	175	
8	J	142	
9	K	147	
10	L	122	
11	M	147	
12	N	138	
13	O	199	
14	P	127	
15	Q	113	
16	R	129	
17	S	103	
18	T	153	
19	U	100	
20	V	105	
21	W	215	
22	X	88	
23	Y	64	
24	Z	77	
25	B	118	
26	A	3120	
27	1	61	
28	2	75	

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Mol	Chain	Length	Quality of chain
29	3	57	82%12%5%
30	4	55	18%56%13%9%
31	5	47	49%40%6%
32	6	64	66%33%
33	7	37	49%49%
34	8	24	79%17%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 97374 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	273	Total	C	N	O	S	0	0
			2097	1290	435	368	4		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	207	Total	C	N	O	S	0	0
			1553	959	292	300	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	181	Total	C	N	O	S	0	0
			1437	903	269	259	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	147	Total	C	N	O	S	0	0
			1138	727	208	201	2		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	121	Total	C	N	O	S	0	0
			930	580	178	169	3		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	134	Total	C	N	O	S	0	0
			1074	680	211	181	2		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	P	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	R	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	S	102	Total	C	N	O	0	0
			768	487	140	141		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	U	94	Total	C	N	O	0	0
			739	469	135	135		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	97	Total	C	N	O	S	0	0
			731	456	137	136	2		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	W	188	Total	C	N	O	0	0
			1407	869	251	287		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	X	82	Total	C	N	O	0	0
			604	372	127	105		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 25 is a RNA chain called P-tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B	117	Total	C	N	O	P	0	0
			2501	1116	462	806	117		

- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	3102	Total	C	N	O	P	0	0
			66623	29694	12253	21574	3102		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	1	60	Total	C	N	O	0	0
			483	298	97	88		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	66	Total	C	N	O	S	0	0
			510	316	93	96	5		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	50	Total	C	N	O	S	0	0
			416	254	86	72	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	6	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

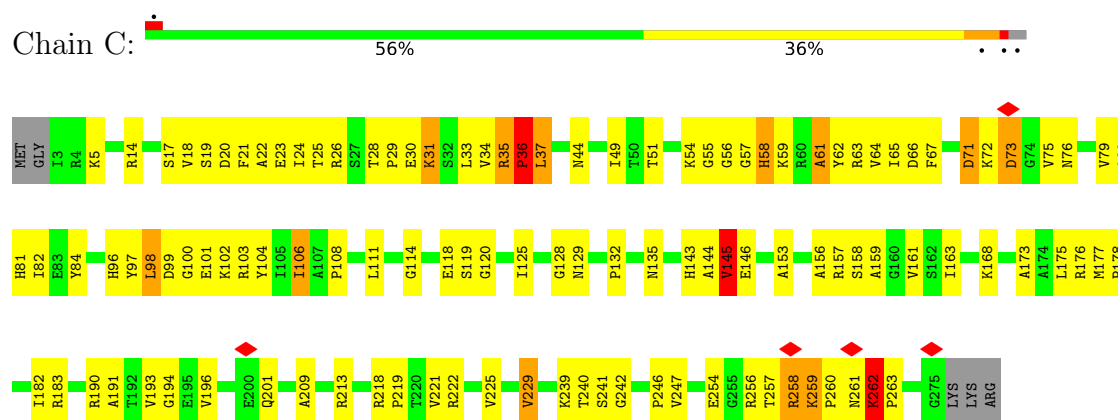
- Molecule 34 is a protein called Uncharacterized protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	8	23	Total	C	N	O	0	0
			189	111	50	28		

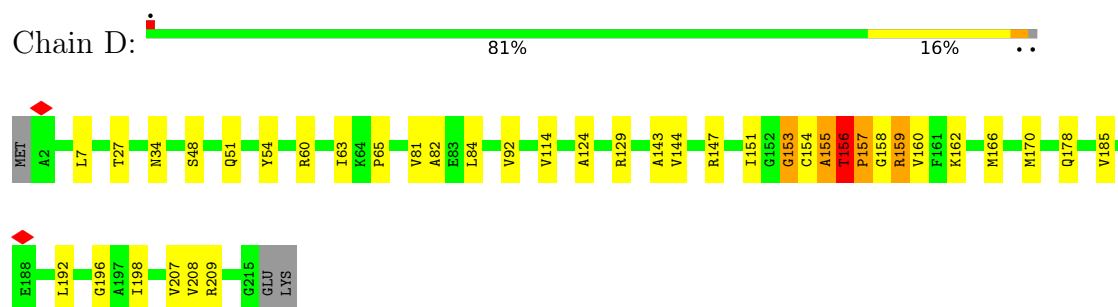
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

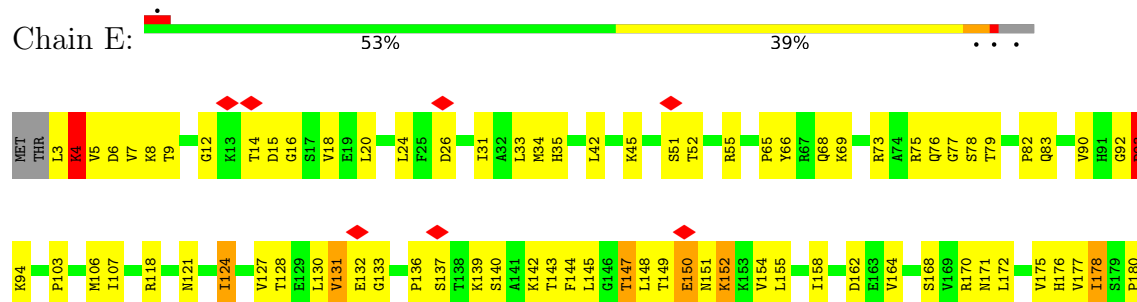
- Molecule 1: 50S ribosomal protein L2

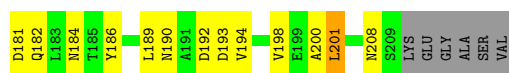


- Molecule 2: 50S ribosomal protein L3

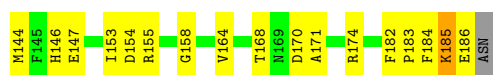
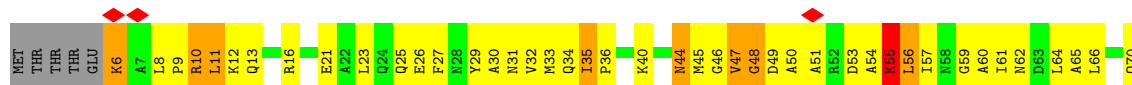


- Molecule 3: 50S ribosomal protein L4

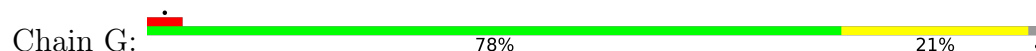




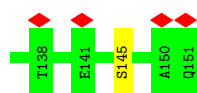
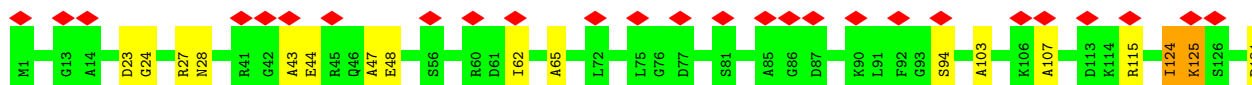
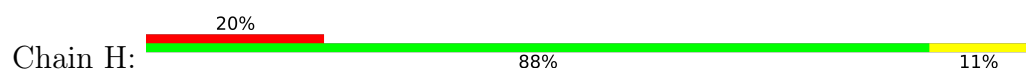
• Molecule 4: 50S ribosomal protein L5



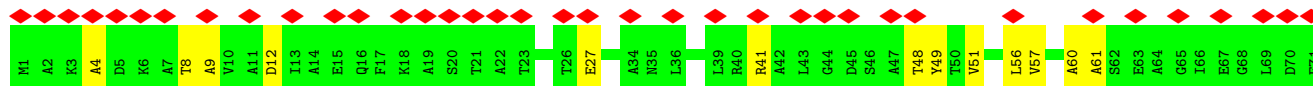
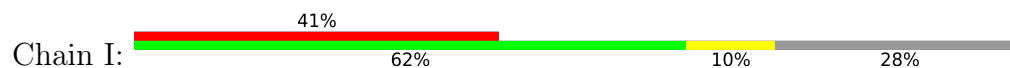
• Molecule 5: 50S ribosomal protein L6



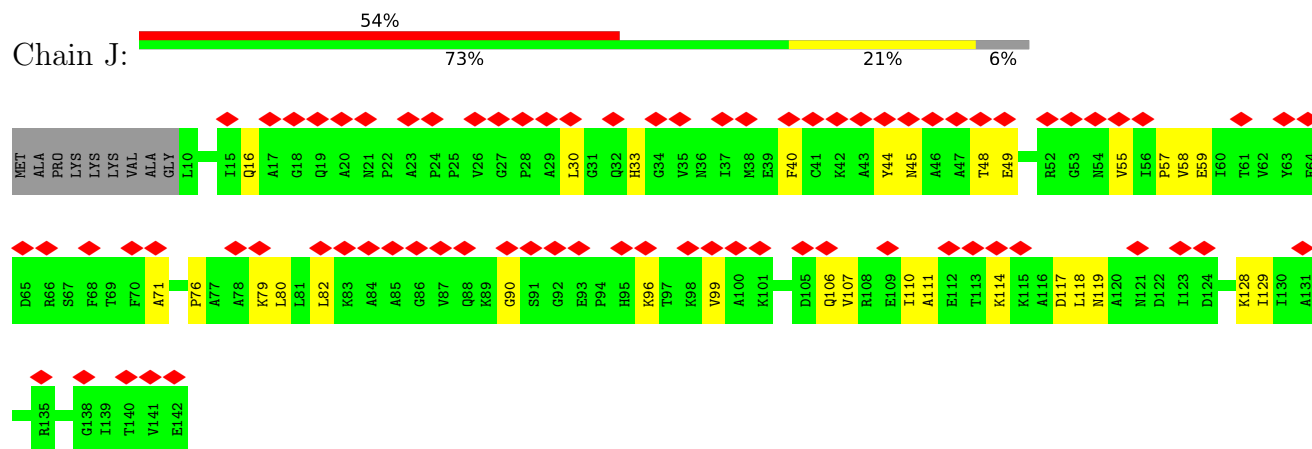
• Molecule 6: 50S ribosomal protein L9



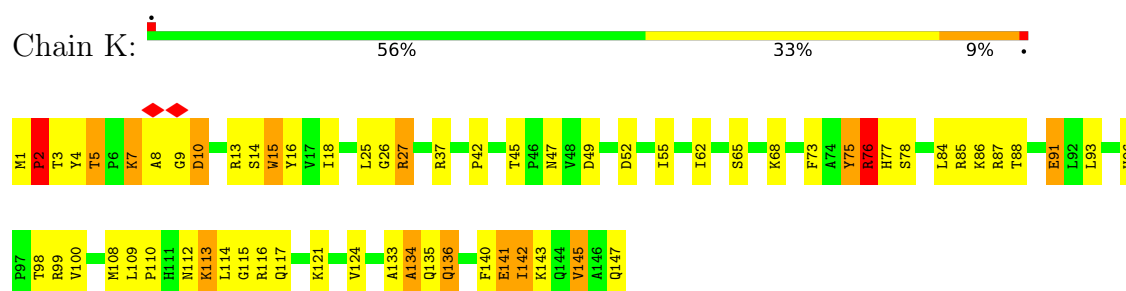
• Molecule 7: 50S ribosomal protein L10



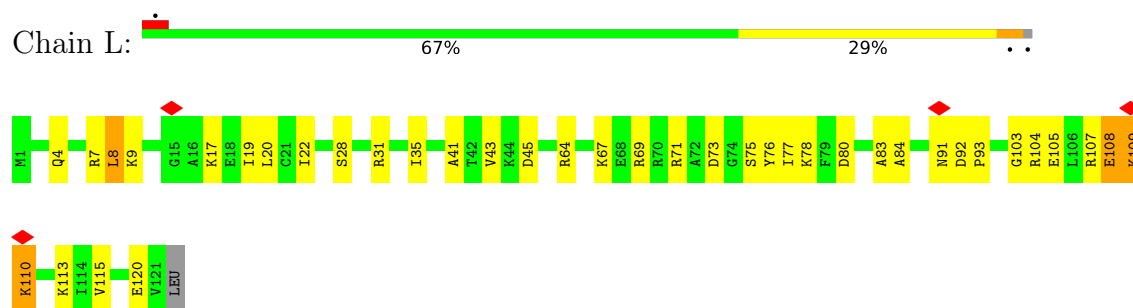
- Molecule 8: 50S ribosomal protein L11



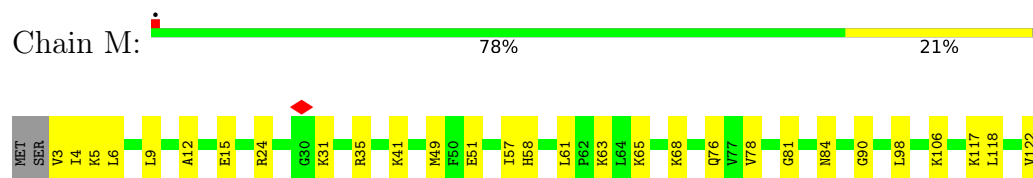
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14

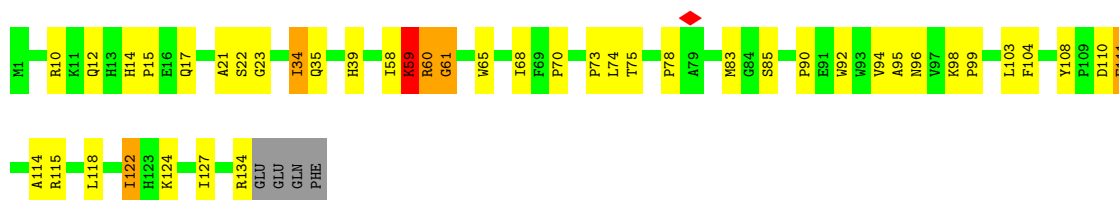


- Molecule 11: 50S ribosomal protein L15

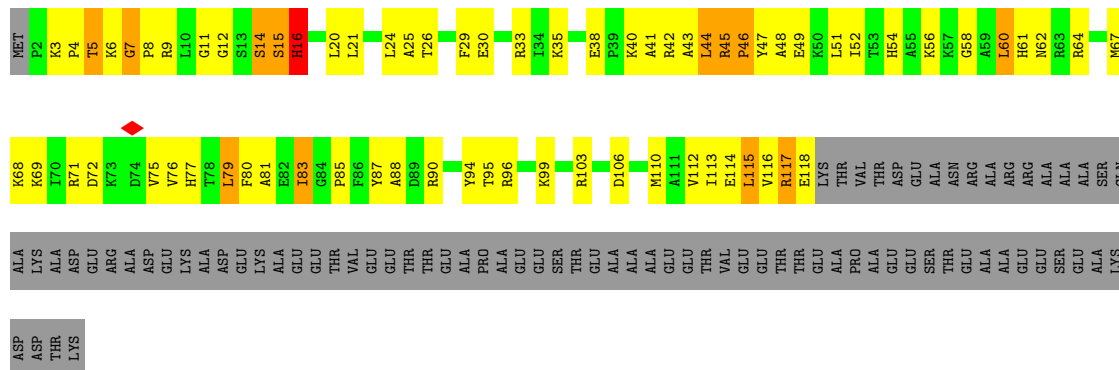
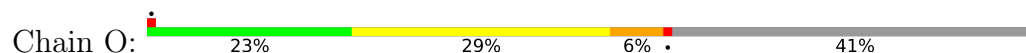


- Molecule 12: 50S ribosomal protein L16

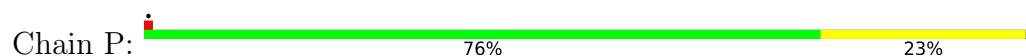




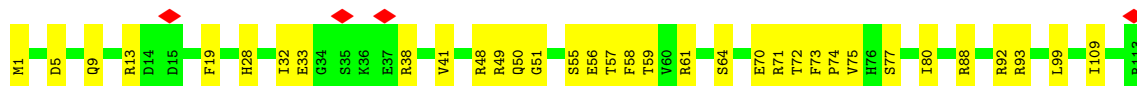
• Molecule 13: 50S ribosomal protein L17



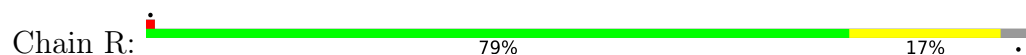
• Molecule 14: 50S ribosomal protein L18



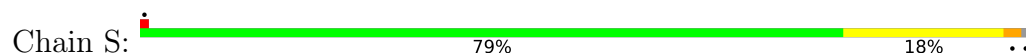
• Molecule 15: 50S ribosomal protein L19

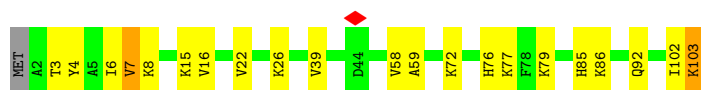


• Molecule 16: 50S ribosomal protein L20

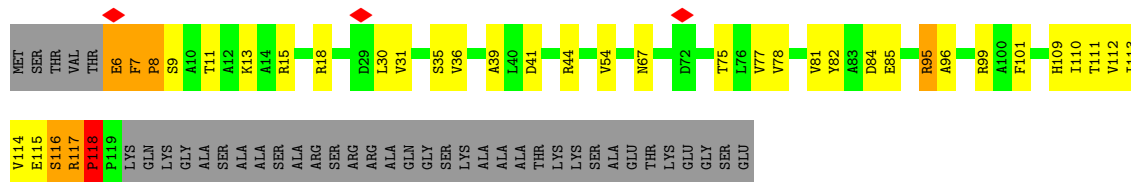


• Molecule 17: 50S ribosomal protein L21

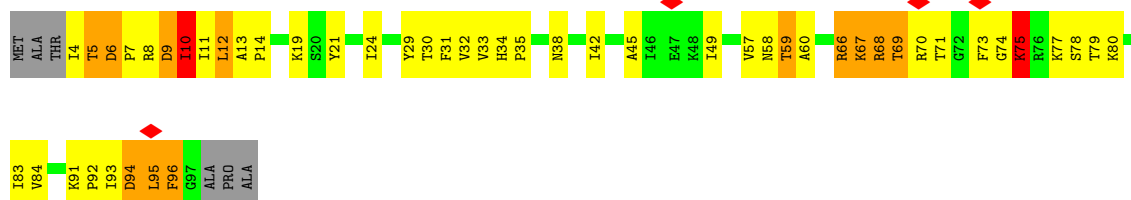




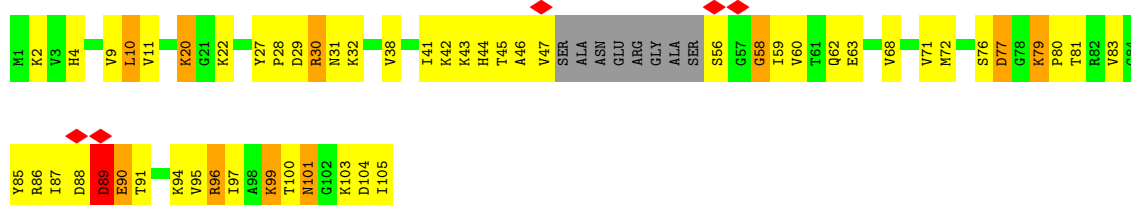
- Molecule 18: 50S ribosomal protein L22



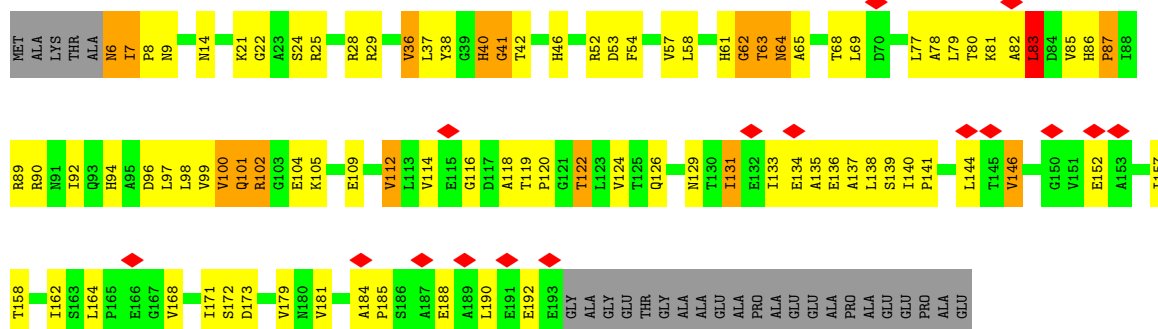
- Molecule 19: 50S ribosomal protein L23



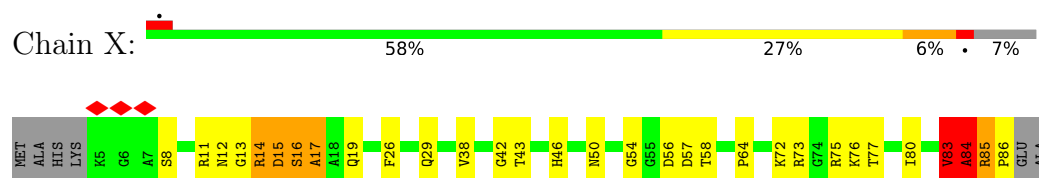
- Molecule 20: 50S ribosomal protein L24



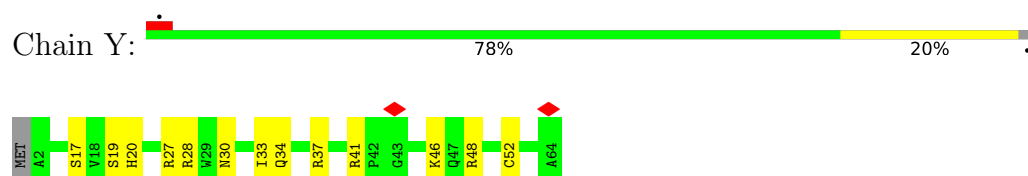
- Molecule 21: 50S ribosomal protein L25



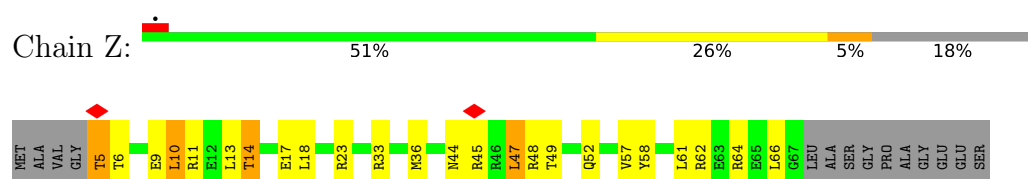
- Molecule 22: 50S ribosomal protein L27



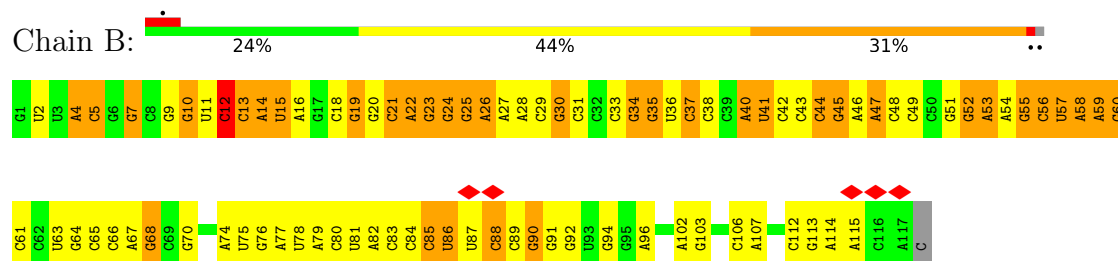
- Molecule 23: 50S ribosomal protein L28



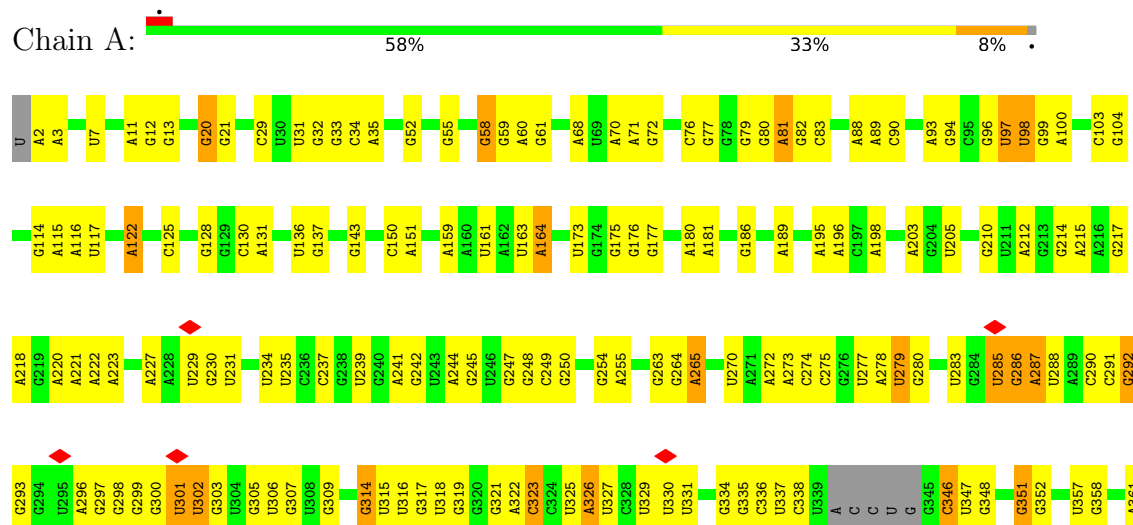
- Molecule 24: 50S ribosomal protein L29

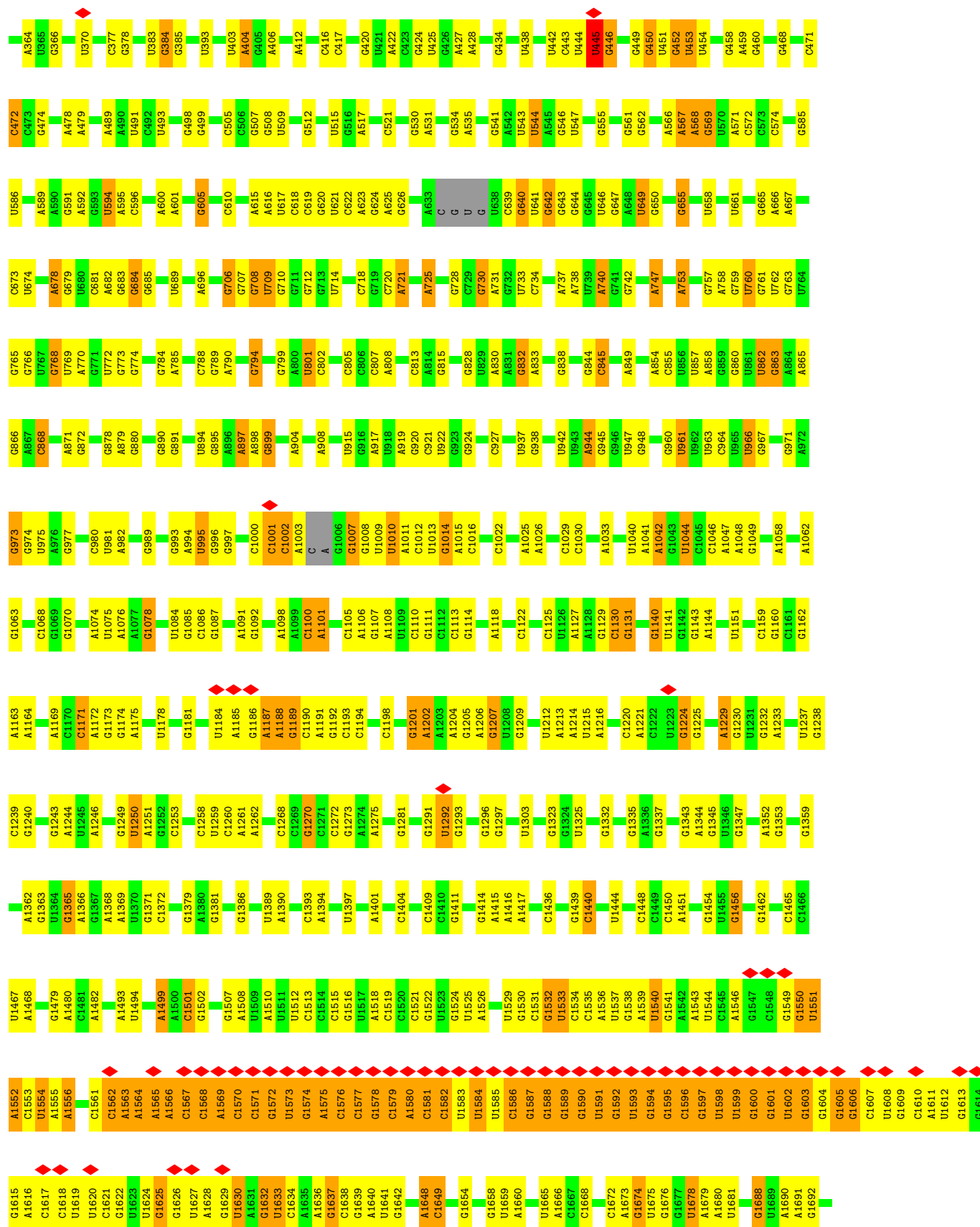


- Molecule 25: P-tRNA^{fMet}



- Molecule 26: 23S rRNA





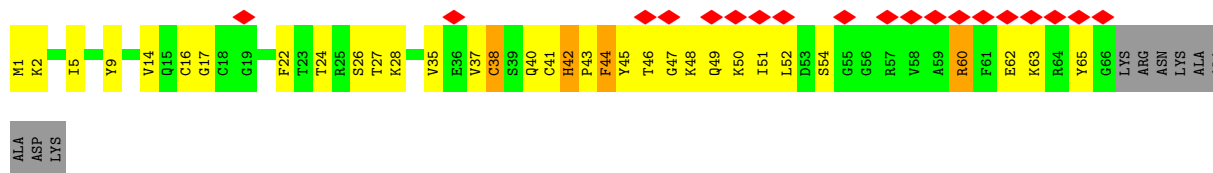
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G2798	C2799	G2800	A2801	C2802	C2803	U2810	A2814	C2815	A2826	G2827	U2828	U2833	U2837	A2838	U2839	C2843	G2851	U2852	C2853	U2860	U2861	C2862	C2865	A2866	C2870	U2873	C2876	U2877	A2878	C2879	U2880	A2881	C2885	A2886	G2887	G2888	C2891	G2892	C2893	C2894	A2895	C2896	G2897	C2900										
U2906	C2907	U2908	C2909	U2913	A2914	C2915	A2926	C2932	C2933	C2936	C2937	C2938	C2942	C2950	C2956	C2957	C2958	C2962	C2963	C2964	C2967	C2972	C2973	C2976	C2977	U2980	A2981	C2982	C2985	A2986	C2987	C2988	C2989	C2990	U2993	C2994	U2995	G3001	A3002	C3003	C3004	A3005	U3009	U3010										
C3011	C3012	C3013	C3014	C3015	C3016	C3017	A3021	G3022	G3023	A3024	G3025	U3029	A3030	C3037	C3038	C3039	G3040	C3041	A3042	G3043	A3044	C3045	C3046	A3047	A3052	G3055	A3056	U3057	G3070	A3071	U3082	C3088	A3093	A3094	C3095	U3096	C3101	U3102	C3105	C3106	G3107	A3112	A3113	A3114	A3115	A3119								

C

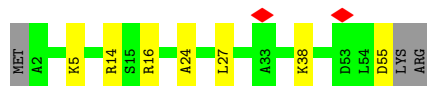
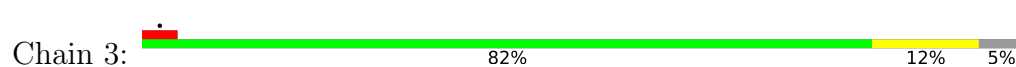
- Molecule 27: 50S ribosomal protein L30



- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



- Molecule 30: 50S ribosomal protein L33 1



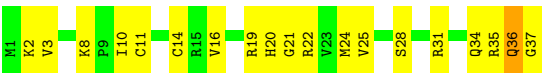
- Molecule 31: 50S ribosomal protein L34



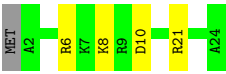
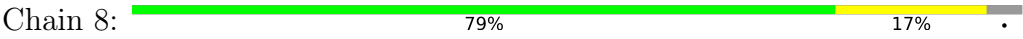
- Molecule 32: 50S ribosomal protein L35



- Molecule 33: 50S ribosomal protein L36



● Molecule 34: Uncharacterized protein bL37



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.781	Depositor
Minimum map value	-0.495	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	361.19998, 361.19998, 361.19998	wwPDB
Map dimensions	344, 344, 344	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	C	1.01	0/2140	1.16	14/2879 (0.5%)
2	D	0.53	0/1609	0.77	2/2165 (0.1%)
3	E	0.86	0/1576	1.06	3/2132 (0.1%)
4	F	0.63	0/1459	1.13	14/1962 (0.7%)
5	G	0.31	0/1369	0.60	0/1848
6	H	0.30	0/1027	0.69	2/1398 (0.1%)
7	I	0.22	0/925	0.56	0/1246
8	J	0.27	0/1006	0.71	0/1364
9	K	0.80	0/1165	1.21	16/1578 (1.0%)
10	L	0.89	0/938	1.12	6/1257 (0.5%)
11	M	0.49	0/1091	0.72	0/1457
12	N	0.92	0/1100	1.19	7/1482 (0.5%)
13	O	0.84	1/936 (0.1%)	1.33	16/1256 (1.3%)
14	P	0.38	0/966	0.62	0/1298
15	Q	0.46	0/921	0.70	0/1236
16	R	0.51	0/1000	0.64	0/1341
17	S	0.44	0/778	0.63	0/1048
18	T	0.95	1/887 (0.1%)	1.16	7/1204 (0.6%)
19	U	0.75	0/749	1.04	4/1006 (0.4%)
20	V	0.66	0/737	1.05	4/987 (0.4%)
21	W	0.65	1/1422 (0.1%)	1.18	9/1941 (0.5%)
22	X	0.92	0/613	1.04	1/821 (0.1%)
23	Y	0.52	0/478	0.77	0/641
24	Z	0.69	0/530	0.92	0/708
25	B	0.32	0/2797	0.55	1/4357 (0.0%)
26	A	0.48	0/74597	0.51	4/116386 (0.0%)
27	1	0.84	0/486	1.00	1/651 (0.2%)
28	2	0.40	0/520	0.84	1/698 (0.1%)
29	3	0.54	0/427	0.70	0/572
30	4	0.71	0/424	1.05	2/567 (0.4%)
31	5	0.95	0/375	1.34	4/493 (0.8%)
32	6	1.00	0/507	1.03	1/672 (0.1%)
33	7	0.85	0/302	1.02	0/401
34	8	0.46	0/191	0.75	0/247

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.54	3/106048 (0.0%)	0.65	119/159299 (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	C	0	4
2	D	0	2
3	E	0	5
4	F	0	1
9	K	0	1
12	N	0	1
13	O	0	1
18	T	0	1
22	X	0	2
All	All	0	18

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	W	7	ILE	C-N	6.25	1.39	1.33
18	T	117	ARG	C-N	5.74	1.40	1.33
13	O	45	ARG	C-N	5.50	1.40	1.34

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	W	62	GLY	N-CA-C	19.02	133.80	111.93
12	N	61	GLY	N-CA-C	14.65	128.50	111.36
21	W	61	HIS	CA-C-N	11.66	131.18	120.10
21	W	61	HIS	C-N-CA	11.66	131.18	120.10
4	F	117	ARG	N-CA-C	10.63	122.86	111.28
4	F	114	ALA	N-CA-C	10.38	122.59	111.28
18	T	118	PRO	N-CA-C	9.34	122.09	110.70
13	O	83	ILE	N-CA-C	8.89	118.89	110.53
9	K	10	ASP	N-CA-C	8.51	120.56	111.28
9	K	27	ARG	N-CA-C	-8.38	102.65	113.12
4	F	55	LYS	N-CA-C	8.27	120.29	111.28
18	T	118	PRO	CA-N-CD	-8.15	100.58	112.00
12	N	111	GLU	N-CA-C	7.92	119.91	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	5	8	PHE	N-CA-C	7.88	119.50	111.07
31	5	7	THR	N-CA-C	7.84	127.50	110.80
13	O	45	ARG	CA-C-N	-7.61	111.13	119.19
13	O	45	ARG	C-N-CA	-7.61	111.13	119.19
4	F	56	LEU	N-CA-C	7.48	120.38	111.33
6	H	124	ILE	CA-C-N	7.03	134.97	121.54
6	H	124	ILE	C-N-CA	7.03	134.97	121.54
28	2	54	SER	N-CA-C	6.99	119.99	110.55
18	T	118	PRO	CB-CA-C	6.92	119.36	110.92
20	V	58	GLY	N-CA-C	6.73	120.81	112.73
9	K	9	GLY	N-CA-C	6.72	120.79	112.73
30	4	22	ASN	N-CA-C	6.70	120.40	110.48
13	O	46	PRO	CA-N-CD	-6.66	102.68	112.00
10	L	108	GLU	N-CA-C	-6.65	96.64	110.80
9	K	76	ARG	N-CA-C	-6.61	98.12	108.90
4	F	54	ALA	N-CA-C	6.55	118.50	111.36
26	A	2085	C	C2'-C3'-O3'	6.40	119.10	109.50
10	L	110	LYS	N-CA-C	6.39	126.08	113.29
13	O	44	LEU	N-CA-C	-6.34	104.37	111.28
22	X	11	ARG	N-CA-C	-6.33	99.56	109.25
9	K	145	VAL	N-CA-C	6.30	116.95	107.75
9	K	7	LYS	N-CA-C	-6.21	102.34	110.53
30	4	23	TYR	N-CA-C	-6.18	98.91	109.24
18	T	31	VAL	N-CA-CB	-6.16	104.35	112.36
9	K	134	ALA	N-CA-C	-6.14	102.85	110.41
4	F	153	ILE	N-CA-CB	-6.08	106.57	112.65
13	O	16	HIS	N-CA-C	-6.08	104.65	111.28
13	O	88	ALA	CA-C-N	6.07	136.88	126.32
13	O	88	ALA	C-N-CA	6.07	136.88	126.32
27	1	52	HIS	N-CA-C	6.07	117.97	111.36
4	F	77	ALA	N-CA-C	6.05	119.39	109.76
25	B	12	C	O4'-C1'-C2'	-6.05	101.55	107.60
9	K	5	THR	CA-C-N	-6.04	113.54	119.76
9	K	5	THR	C-N-CA	-6.04	113.54	119.76
4	F	71	LYS	CA-C-N	-6.01	113.59	119.90
4	F	71	LYS	C-N-CA	-6.01	113.59	119.90
21	W	116	GLY	N-CA-C	5.98	120.48	110.56
4	F	35	ILE	CA-C-N	-5.95	114.48	120.31
4	F	35	ILE	C-N-CA	-5.95	114.48	120.31
1	C	262	LYS	CA-C-N	-5.95	114.63	120.52
1	C	262	LYS	C-N-CA	-5.95	114.63	120.52
19	U	8	ARG	N-CA-C	-5.95	106.67	114.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	6	15	ARG	CB-CG-CD	-5.88	97.77	111.30
10	L	110	LYS	CA-C-N	-5.87	113.34	123.25
10	L	110	LYS	C-N-CA	-5.87	113.34	123.25
1	C	259	LYS	CA-C-N	-5.86	114.22	120.03
1	C	259	LYS	C-N-CA	-5.86	114.22	120.03
9	K	5	THR	N-CA-C	-5.85	96.09	108.73
4	F	48	GLY	N-CA-C	-5.78	107.67	115.36
10	L	109	LYS	N-CA-C	5.78	117.83	108.41
1	C	145	VAL	CA-C-N	5.77	132.56	121.54
1	C	145	VAL	C-N-CA	5.77	132.56	121.54
9	K	136	GLN	CA-C-N	-5.74	113.84	119.76
9	K	136	GLN	C-N-CA	-5.74	113.84	119.76
12	N	59	LYS	N-CA-C	-5.74	102.80	110.55
13	O	7	GLY	CA-C-N	-5.73	114.36	120.03
13	O	7	GLY	C-N-CA	-5.73	114.36	120.03
20	V	89	ASP	N-CA-C	-5.73	105.04	111.28
21	W	173	ASP	CA-C-N	5.70	125.80	119.87
21	W	173	ASP	C-N-CA	5.70	125.80	119.87
13	O	30	GLU	N-CA-C	5.66	117.53	111.36
20	V	79	LYS	CA-C-N	-5.56	114.53	120.03
20	V	79	LYS	C-N-CA	-5.56	114.53	120.03
4	F	141	GLU	CA-C-N	5.55	132.13	121.54
4	F	141	GLU	C-N-CA	5.55	132.13	121.54
18	T	117	ARG	CA-C-N	-5.54	114.67	120.38
18	T	117	ARG	C-N-CA	-5.54	114.67	120.38
10	L	64	ARG	CB-CG-CD	-5.51	98.63	111.30
19	U	12	LEU	CA-CB-CG	5.50	135.56	116.30
12	N	61	GLY	CA-C-N	5.50	131.56	122.43
12	N	61	GLY	C-N-CA	5.50	131.56	122.43
13	O	3	LYS	CA-C-N	-5.48	114.14	119.78
13	O	3	LYS	C-N-CA	-5.48	114.14	119.78
3	E	147	THR	N-CA-C	-5.47	105.32	111.28
1	C	80	ALA	N-CA-C	-5.46	106.67	113.55
9	K	133	ALA	N-CA-C	-5.44	105.35	111.28
1	C	28	THR	CA-C-N	-5.42	114.66	120.03
1	C	28	THR	C-N-CA	-5.42	114.66	120.03
13	O	60	LEU	N-CA-C	-5.42	99.26	110.80
9	K	15	TRP	N-CA-C	5.41	117.68	110.53
21	W	89	ARG	N-CA-C	-5.37	102.25	110.14
31	5	9	GLN	CA-C-N	-5.35	114.21	119.93
31	5	9	GLN	C-N-CA	-5.35	114.21	119.93
1	C	157	ARG	CB-CG-CD	-5.32	99.07	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	2	PRO	CA-N-CD	-5.29	104.59	112.00
18	T	116	SER	N-CA-C	5.29	117.73	108.52
9	K	108	MET	CA-CB-CG	5.29	124.68	114.10
26	A	445	U	P-O3'-C3'	5.29	128.13	120.20
19	U	11	ILE	CA-C-N	-5.29	113.99	122.08
19	U	11	ILE	C-N-CA	-5.29	113.99	122.08
26	A	2085	C	P-O3'-C3'	5.26	128.09	120.20
2	D	156	THR	CA-C-N	-5.23	113.30	119.84
2	D	156	THR	C-N-CA	-5.23	113.30	119.84
3	E	93	PRO	CA-C-N	5.23	134.56	121.80
3	E	93	PRO	C-N-CA	5.23	134.56	121.80
26	A	2094	G	P-O3'-C3'	5.18	127.98	120.20
13	O	45	ARG	C-N-CD	5.14	146.07	125.00
1	C	98	LEU	N-CA-C	-5.11	105.79	111.36
21	W	152	GLU	N-CA-C	5.09	117.40	109.52
1	C	28	THR	N-CA-C	5.06	117.95	110.32
21	W	122	THR	N-CA-C	5.05	117.72	109.59
12	N	68	ILE	CA-C-N	-5.04	113.97	121.83
12	N	68	ILE	C-N-CA	-5.04	113.97	121.83
1	C	201	GLN	CA-C-N	5.03	131.15	121.54
1	C	201	GLN	C-N-CA	5.03	131.15	121.54
13	O	41	ALA	N-CA-C	5.02	116.76	111.28

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	144	ALA	Peptide
1	C	229	VAL	Peptide
1	C	246	PRO	Peptide
1	C	61	ALA	Peptide
2	D	153	GLY	Peptide
2	D	156	THR	Peptide
3	E	131	VAL	Peptide
3	E	137	SER	Peptide
3	E	158	ILE	Peptide
3	E	162	ASP	Peptide
3	E	93	PRO	Peptide
4	F	81	ILE	Peptide
9	K	91	GLU	Peptide
12	N	78	PRO	Peptide
13	O	61	HIS	Peptide

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Mol	Chain	Res	Type	Group
18	T	95	ARG	Peptide
22	X	83	VAL	Peptide
22	X	84	ALA	Peptide

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	C	2097	0	2147	212	0
2	D	1587	0	1629	70	0
3	E	1553	0	1587	149	0
4	F	1437	0	1463	212	0
5	G	1348	0	1399	26	0
6	H	1018	0	988	12	0
7	I	918	0	959	13	0
8	J	990	0	1021	28	0
9	K	1138	0	1174	119	0
10	L	930	0	989	58	0
11	M	1078	0	1151	46	0
12	N	1074	0	1116	67	0
13	O	919	0	959	158	0
14	P	956	0	989	41	0
15	Q	907	0	938	31	0
16	R	988	0	1038	20	0
17	S	768	0	820	48	0
18	T	873	0	909	54	0
19	U	739	0	777	123	0
20	V	731	0	782	114	0
21	W	1407	0	1423	159	0
22	X	604	0	622	56	0
23	Y	470	0	484	9	0
24	Z	527	0	537	56	0
25	B	2501	0	1269	294	0
26	A	66623	0	33514	1038	0
27	1	483	0	513	22	0
28	2	510	0	497	60	0
29	3	423	0	463	12	0
30	4	416	0	421	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	5	372	0	406	41	0
32	6	502	0	541	31	0
33	7	298	0	320	26	0
34	8	189	0	205	4	0
All	All	97374	0	64050	2879	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 18.

All (2879) 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)
17:S:3:THR:CG2	17:S:102:ILE:HD13	1.26	1.66
19:U:83:ILE:HD11	26:A:1456:G:C2	1.14	1.64
26:A:1561:C:C4	26:A:1562:C:C5	1.86	1.62
26:A:1565:A:N3	26:A:1606:G:C5	1.69	1.60
17:S:58:VAL:HG23	17:S:103:LYS:CG	1.24	1.60
26:A:1561:C:C4	26:A:1562:C:H5	1.16	1.59
13:O:29:PHE:CB	13:O:79:LEU:HD12	1.29	1.54
4:F:117:ARG:NH1	4:F:146:HIS:CD2	1.72	1.54
3:E:192:ASP:HB3	11:M:5:LYS:NZ	1.21	1.53
3:E:144:PHE:CG	3:E:148:LEU:HD11	1.42	1.53
20:V:4:HIS:CE1	20:V:96:ARG:NH1	1.75	1.53
26:A:1580:A:N6	26:A:1592:G:C5	1.78	1.51
19:U:83:ILE:CD1	26:A:1456:G:C2	1.85	1.51
33:7:22:ARG:NH2	33:7:37:GLY:HA2	1.25	1.51
17:S:3:THR:CG2	17:S:102:ILE:CD1	1.83	1.51
21:W:77:LEU:HB3	21:W:100:VAL:CG2	1.40	1.48
1:C:25:THR:HG21	1:C:81:HIS:CA	1.44	1.47
17:S:3:THR:HG22	17:S:102:ILE:CD1	1.38	1.47
20:V:4:HIS:CE1	20:V:96:ARG:HH12	1.32	1.45
3:E:144:PHE:CD1	3:E:148:LEU:HD21	1.51	1.44
17:S:58:VAL:CG2	17:S:103:LYS:HG2	1.48	1.43
4:F:132:THR:CG2	14:P:6:VAL:HG21	1.48	1.43
3:E:182:GLN:NE2	26:A:706:G:H8	1.06	1.43
2:D:154:CYS:CB	26:A:2798:G:O3'	1.68	1.42
25:B:20:G:N2	25:B:63:U:H3	1.11	1.42
26:A:1580:A:N6	26:A:1592:G:C4	1.85	1.42
9:K:142:ILE:CG2	26:A:1130:C:H41	1.33	1.41
26:A:1565:A:N3	26:A:1606:G:C6	1.86	1.41
19:U:4:ILE:HD13	24:Z:58:TYR:CE1	1.57	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:2:LYS:HD2	20:V:83:VAL:CG1	1.52	1.39
2:D:155:ALA:CB	26:A:2796:A:C8	2.02	1.39
19:U:19:LYS:HD2	26:A:1508:A:N6	1.30	1.39
25:B:18:C:C2'	25:B:19:G:H5''	1.51	1.37
4:F:51:ALA:O	4:F:85:LYS:NZ	1.58	1.36
25:B:24:G:C5	25:B:56:C:O2	1.75	1.36
1:C:26:ARG:HD2	1:C:81:HIS:CD2	1.61	1.35
19:U:83:ILE:HD11	26:A:1456:G:N2	1.42	1.34
13:O:29:PHE:HB3	13:O:79:LEU:CD1	1.54	1.34
25:B:29:C:N3	25:B:55:G:N2	1.76	1.34
26:A:1578:G:C4	26:A:1592:G:N1	1.97	1.33
13:O:90:ARG:NH2	13:O:118:GLU:HG3	1.41	1.32
13:O:90:ARG:HH22	13:O:118:GLU:CG	1.39	1.32
19:U:4:ILE:HD13	24:Z:58:TYR:CZ	1.63	1.32
4:F:183:PRO:O	4:F:184:PHE:CD2	1.79	1.32
26:A:1580:A:C6	26:A:1592:G:C4	2.17	1.31
25:B:4:A:C2	25:B:25:G:O6	1.84	1.31
3:E:144:PHE:CE1	3:E:148:LEU:HD21	1.66	1.30
13:O:29:PHE:CG	13:O:79:LEU:HD11	1.65	1.30
25:B:24:G:N7	25:B:56:C:O2	1.64	1.29
13:O:29:PHE:CB	13:O:79:LEU:CD1	2.07	1.29
13:O:81:ALA:O	13:O:85:PRO:CD	1.79	1.29
22:X:17:ALA:CB	26:A:2485:C:OP2	1.80	1.29
9:K:142:ILE:CG2	26:A:1130:C:N4	1.94	1.28
26:A:1561:C:C5	26:A:1562:C:H5	1.49	1.28
26:A:1570:C:N4	26:A:1602:U:O2	1.66	1.28
19:U:83:ILE:HD11	26:A:1456:G:N3	1.48	1.28
26:A:1595:G:H5''	26:A:1596:C:C6	1.68	1.27
25:B:18:C:H2'	25:B:19:G:C5'	1.63	1.27
30:4:15:CYS:O	30:4:20:HIS:CB	1.82	1.27
30:4:15:CYS:O	30:4:20:HIS:HB2	1.27	1.27
26:A:1565:A:C2	26:A:1606:G:N7	2.01	1.26
2:D:154:CYS:N	26:A:2798:G:O2'	1.67	1.26
19:U:19:LYS:NZ	26:A:1508:A:H61	1.31	1.26
4:F:73:GLU:HG2	25:B:42:C:C5	1.71	1.26
4:F:183:PRO:O	4:F:184:PHE:HD2	0.92	1.26
19:U:19:LYS:CD	26:A:1508:A:N6	1.98	1.26
25:B:19:G:N2	25:B:65:C:N3	1.83	1.26
13:O:33:ARG:HD3	13:O:114:GLU:OE2	1.19	1.26
13:O:75:VAL:O	13:O:79:LEU:HB3	1.09	1.25
1:C:25:THR:CG2	1:C:81:HIS:HB3	1.66	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:29:PHE:CG	13:O:79:LEU:CD1	2.16	1.25
3:E:151:ASN:O	3:E:152:LYS:CG	1.83	1.25
13:O:33:ARG:CD	13:O:114:GLU:OE2	1.84	1.25
26:A:1595:G:H8	26:A:1596:C:C6	1.54	1.24
4:F:51:ALA:C	4:F:85:LYS:NZ	1.87	1.24
13:O:81:ALA:O	13:O:85:PRO:HD2	1.11	1.24
26:A:1580:A:C6	26:A:1591:U:O2	1.91	1.24
4:F:46:GLY:O	4:F:47:VAL:CG2	1.86	1.23
25:B:40:A:N6	28:2:1:MET:H2	1.37	1.23
21:W:105:LYS:HZ1	21:W:136:GLU:CD	1.46	1.23
26:A:1570:C:N4	26:A:1602:U:C2	2.07	1.23
1:C:25:THR:HG21	1:C:81:HIS:CB	1.69	1.22
17:S:58:VAL:CG2	17:S:103:LYS:CG	2.07	1.22
26:A:1561:C:N3	26:A:1562:C:C5	2.06	1.21
9:K:142:ILE:HG21	26:A:1130:C:N4	1.50	1.21
1:C:96:HIS:CE1	1:C:102:LYS:HZ3	1.57	1.21
2:D:154:CYS:HB2	26:A:2799:C:P	1.80	1.20
14:P:41:ASN:ND2	25:B:7:G:O2'	1.73	1.20
21:W:6:ASN:HB2	21:W:138:LEU:O	1.36	1.20
26:A:1565:A:C2	26:A:1606:G:C5	2.28	1.20
9:K:141:GLU:CD	9:K:143:LYS:HG2	1.66	1.20
13:O:8:PRO:HG3	26:A:1870:U:C4	1.75	1.20
3:E:144:PHE:CE1	3:E:148:LEU:CD2	2.23	1.20
10:L:7:ARG:NH2	10:L:20:LEU:HD12	1.55	1.20
14:P:50:GLN:NE2	25:B:7:G:H21	1.38	1.20
26:A:1590:G:C5	26:A:1591:U:H5	1.58	1.20
1:C:72:LYS:HG3	1:C:75:VAL:HG21	1.21	1.19
2:D:154:CYS:SG	26:A:2796:A:H5''	1.80	1.19
3:E:7:VAL:HG23	3:E:16:GLY:C	1.65	1.19
21:W:100:VAL:CG1	21:W:137:ALA:HB1	1.71	1.19
25:B:24:G:HO2'	25:B:56:C:N4	1.37	1.19
25:B:25:G:N2	25:B:114:A:N3	1.88	1.19
25:B:24:G:O2'	25:B:56:C:N4	1.74	1.19
1:C:54:LYS:HZ2	26:A:2031:G:C4'	1.55	1.19
3:E:151:ASN:O	3:E:152:LYS:HG3	1.01	1.19
8:J:96:LYS:CE	21:W:120:PRO:HB2	1.73	1.19
2:D:154:CYS:HB3	26:A:2798:G:C3'	1.72	1.18
2:D:155:ALA:CB	26:A:2796:A:N7	2.04	1.18
3:E:182:GLN:NE2	26:A:706:G:C8	1.97	1.17
26:A:1595:G:H5''	26:A:1596:C:C5	1.80	1.17
33:7:22:ARG:NH2	33:7:37:GLY:CA	2.01	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:THR:CG2	1:C:81:HIS:CB	2.20	1.17
21:W:105:LYS:NZ	21:W:136:GLU:CD	2.03	1.16
12:N:85:SER:OG	22:X:8:SER:HB3	1.43	1.16
2:D:154:CYS:HB3	26:A:2798:G:O3'	1.24	1.16
26:A:1580:A:N6	26:A:1591:U:C2	2.13	1.16
1:C:73:ASP:HB3	1:C:120:GLY:CA	1.76	1.16
9:K:142:ILE:HG22	26:A:1130:C:H41	1.03	1.16
21:W:6:ASN:CB	21:W:138:LEU:O	1.93	1.16
4:F:46:GLY:O	4:F:47:VAL:HG22	1.00	1.15
22:X:17:ALA:HB2	26:A:2485:C:OP2	1.34	1.15
3:E:144:PHE:CD1	3:E:148:LEU:HD11	1.80	1.15
10:L:7:ARG:HH22	10:L:20:LEU:HD12	1.00	1.15
1:C:258:ARG:HA	26:A:2015:U:H5''	1.28	1.15
13:O:9:ARG:HG2	13:O:14:SER:HB3	1.25	1.15
19:U:91:LYS:HG2	19:U:92:PRO:CD	1.77	1.15
20:V:45:THR:O	26:A:571:A:O2'	1.65	1.15
26:A:1578:G:C4	26:A:1592:G:C2	2.26	1.15
33:7:22:ARG:HH22	33:7:37:GLY:CA	1.49	1.15
2:D:155:ALA:HB3	26:A:2796:A:H8	1.08	1.14
9:K:3:THR:CG2	26:A:1113:C:O2	1.96	1.14
21:W:105:LYS:CE	21:W:136:GLU:OE2	1.96	1.14
30:4:29:ARG:HH21	30:4:34:ASP:CB	1.58	1.14
19:U:4:ILE:CD1	24:Z:58:TYR:CE1	2.31	1.14
26:A:1601:G:C2'	26:A:1602:U:H5'	1.78	1.14
28:2:41:CYS:HB3	28:2:43:PRO:HD2	1.29	1.14
2:D:154:CYS:HA	26:A:2799:C:H5'	1.17	1.13
4:F:132:THR:HG21	14:P:6:VAL:CG2	1.75	1.13
26:A:1595:G:C8	26:A:1596:C:C6	2.36	1.13
4:F:45:MET:CE	4:F:64:LEU:HD21	1.78	1.13
26:A:1595:G:C8	26:A:1596:C:H6	1.66	1.13
30:4:19:LYS:CD	30:4:44:ASN:HB2	1.77	1.13
19:U:19:LYS:CE	26:A:1508:A:H61	1.60	1.13
26:A:1590:G:C5	26:A:1591:U:C5	2.36	1.12
26:A:1595:G:C5'	26:A:1596:C:C6	2.31	1.13
17:S:3:THR:HG21	17:S:102:ILE:CD1	1.62	1.12
21:W:77:LEU:CB	21:W:100:VAL:HG23	1.79	1.12
25:B:19:G:H2'	25:B:20:G:H5'	1.32	1.12
20:V:4:HIS:CE1	20:V:96:ARG:CZ	2.33	1.12
1:C:96:HIS:CE1	1:C:102:LYS:NZ	2.16	1.11
4:F:46:GLY:C	4:F:47:VAL:HG22	1.74	1.11
9:K:25:LEU:O	26:A:1258:C:OP1	1.65	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:79:LEU:HG	13:O:83:ILE:HD12	1.27	1.11
26:A:1580:A:N1	26:A:1592:G:C1'	2.14	1.11
9:K:141:GLU:OE1	9:K:143:LYS:HG2	1.50	1.11
13:O:90:ARG:NH2	13:O:118:GLU:CG	2.04	1.11
14:P:42:ARG:NH1	25:B:48:C:OP1	1.83	1.11
2:D:154:CYS:CA	26:A:2799:C:H5'	1.80	1.11
25:B:4:A:H2	25:B:25:G:O6	1.24	1.11
25:B:10:G:N1	25:B:107:A:C2	2.17	1.11
25:B:58:A:C5	25:B:59:A:N7	2.19	1.11
3:E:144:PHE:CD1	3:E:148:LEU:CD2	2.31	1.11
21:W:100:VAL:CG1	21:W:137:ALA:CB	2.27	1.11
4:F:51:ALA:HB2	4:F:90:MET:HE1	1.22	1.10
21:W:101:GLN:HB3	21:W:104:GLU:HB2	1.30	1.10
13:O:90:ARG:NH2	13:O:118:GLU:CB	2.14	1.10
26:A:1601:G:H2'	26:A:1602:U:H5'	1.31	1.10
2:D:155:ALA:HB2	26:A:2796:A:C8	1.78	1.10
9:K:112:ASN:ND2	26:A:650:G:OP1	1.84	1.10
26:A:1581:C:H42	26:A:1591:U:H1'	1.14	1.10
17:S:103:LYS:HZ3	17:S:103:LYS:HA	1.06	1.10
3:E:192:ASP:CB	11:M:5:LYS:NZ	2.14	1.09
1:C:25:THR:HG23	1:C:81:HIS:HB3	1.17	1.09
21:W:9:ASN:ND2	21:W:57:VAL:HG13	1.66	1.09
24:Z:6:THR:HG22	24:Z:10:LEU:HD11	1.21	1.09
24:Z:13:LEU:HD11	24:Z:17:GLU:HB2	1.34	1.09
30:4:15:CYS:CB	30:4:20:HIS:HA	1.83	1.09
1:C:25:THR:CG2	1:C:81:HIS:CA	2.30	1.09
20:V:28:PRO:HG2	26:A:83:C:OP1	1.49	1.09
25:B:57:U:H2'	25:B:58:A:H5''	1.35	1.09
25:B:78:U:O2	26:A:977:G:O2'	1.71	1.09
26:A:1580:A:N6	26:A:1592:G:N7	1.99	1.09
1:C:26:ARG:CD	1:C:81:HIS:CD2	2.36	1.08
3:E:7:VAL:N	3:E:16:GLY:O	1.84	1.08
26:A:2510:A:P	30:4:31:ASN:OD1	2.10	1.08
30:4:19:LYS:HD2	30:4:44:ASN:HB2	1.10	1.08
25:B:40:A:N6	28:2:1:MET:N	2.01	1.08
26:A:1580:A:N6	26:A:1592:G:C8	2.07	1.08
30:4:15:CYS:HB2	30:4:20:HIS:HA	1.35	1.08
9:K:13:ARG:NH2	9:K:49:ASP:O	1.86	1.08
20:V:4:HIS:ND1	20:V:96:ARG:NH1	2.02	1.08
13:O:75:VAL:O	13:O:79:LEU:CB	2.01	1.08
17:S:59:ALA:O	17:S:103:LYS:NZ	1.87	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:100:VAL:HG12	21:W:137:ALA:CB	1.84	1.07
25:B:58:A:H5'	25:B:58:A:H8	1.17	1.07
1:C:30:GLU:OE1	1:C:33:LEU:HD12	1.54	1.07
4:F:73:GLU:OE1	25:B:41:U:H5	1.35	1.07
19:U:19:LYS:HZ2	26:A:1508:A:N6	1.52	1.07
26:A:1580:A:N6	26:A:1591:U:O2	1.87	1.07
2:D:155:ALA:HB3	26:A:2796:A:C8	1.81	1.07
21:W:100:VAL:HG12	21:W:137:ALA:HB2	1.37	1.07
10:L:80:ASP:OD2	15:Q:61:ARG:NH1	1.86	1.06
21:W:77:LEU:CB	21:W:100:VAL:CG2	2.33	1.06
20:V:62:GLN:HG2	20:V:63:GLU:N	1.53	1.06
26:A:1565:A:C2	26:A:1606:G:C8	2.44	1.06
4:F:132:THR:HG21	14:P:6:VAL:HG21	1.10	1.06
11:M:51:GLU:CG	32:6:57:ARG:NH1	2.19	1.06
14:P:42:ARG:HH12	25:B:48:C:P	1.77	1.06
17:S:6:ILE:O	17:S:7:VAL:HG23	1.54	1.06
3:E:144:PHE:CG	3:E:148:LEU:CD1	2.38	1.06
4:F:99:ARG:HD2	25:B:45:G:C8	1.89	1.06
21:W:37:LEU:CD1	21:W:69:LEU:CD1	2.33	1.06
1:C:55:GLY:HA3	1:C:218:ARG:CD	1.86	1.05
4:F:132:THR:HG22	14:P:6:VAL:HG21	1.37	1.05
26:A:1581:C:H42	26:A:1591:U:C1'	1.69	1.05
26:A:1608:U:H2'	26:A:1609:G:H8	1.16	1.05
26:A:1608:U:H2'	26:A:1609:G:C8	1.90	1.05
21:W:77:LEU:HB3	21:W:100:VAL:HG21	1.30	1.05
4:F:45:MET:HE3	4:F:64:LEU:CD2	1.86	1.05
4:F:183:PRO:C	4:F:184:PHE:HD2	1.63	1.05
20:V:28:PRO:CG	26:A:83:C:OP1	2.03	1.05
30:4:11:ILE:HD13	30:4:27:LYS:HG2	1.37	1.05
4:F:45:MET:HE3	4:F:64:LEU:HD21	1.34	1.05
20:V:2:LYS:CD	20:V:83:VAL:HG11	1.85	1.05
26:A:1570:C:N4	26:A:1602:U:H3	1.53	1.05
26:A:1570:C:N4	26:A:1602:U:N3	2.03	1.05
4:F:73:GLU:HG2	25:B:42:C:C6	1.91	1.04
21:W:101:GLN:O	21:W:101:GLN:NE2	1.87	1.04
21:W:102:ARG:NH2	21:W:138:LEU:HD11	1.72	1.04
26:A:1580:A:N6	26:A:1592:G:N9	2.03	1.04
26:A:1595:G:C3'	26:A:1596:C:H5'	1.87	1.04
4:F:138:GLY:HA3	26:A:2529:A:H5''	1.38	1.04
19:U:91:LYS:CG	19:U:92:PRO:HD2	1.87	1.04
26:A:1595:G:H3'	26:A:1596:C:H5'	1.07	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:150:GLU:O	3:E:193:ASP:OD2	1.75	1.04
4:F:118:ILE:H	4:F:118:ILE:HD12	1.17	1.04
19:U:19:LYS:CE	26:A:1508:A:N6	2.20	1.04
2:D:154:CYS:HB3	26:A:2798:G:C2'	1.88	1.04
4:F:49:ASP:HB2	4:F:56:LEU:HD11	1.09	1.04
26:A:1572:G:O6	26:A:1600:G:N1	1.91	1.04
1:C:54:LYS:HZ2	26:A:2031:G:H4'	1.10	1.03
9:K:141:GLU:OE2	9:K:143:LYS:CG	2.06	1.03
17:S:58:VAL:HG23	17:S:103:LYS:HG3	1.07	1.03
18:T:18:ARG:NH1	26:A:1436:C:O2'	1.92	1.03
26:A:1580:A:N6	26:A:1591:U:N3	2.06	1.03
25:B:19:G:H5'	25:B:19:G:H8	1.23	1.03
12:N:60:ARG:HH12	26:A:1193:C:H5''	1.18	1.02
25:B:10:G:N1	25:B:107:A:H2	1.52	1.02
10:L:7:ARG:HH22	10:L:20:LEU:CD1	1.72	1.02
13:O:90:ARG:HH22	13:O:118:GLU:HG3	0.87	1.02
21:W:188:GLU:O	21:W:192:GLU:OE1	1.76	1.02
25:B:60:G:O2'	25:B:61:C:H5'	1.55	1.02
26:A:1590:G:C4	26:A:1591:U:C5	2.47	1.02
21:W:100:VAL:HG11	21:W:137:ALA:HB1	1.38	1.02
9:K:141:GLU:OE2	9:K:143:LYS:HG2	1.58	1.02
19:U:5:THR:HG22	19:U:6:ASP:H	1.24	1.02
26:A:1561:C:C2	26:A:1562:C:C6	2.48	1.02
26:A:1565:A:N3	26:A:1606:G:N7	2.04	1.02
2:D:155:ALA:HB1	26:A:2796:A:N7	1.71	1.01
13:O:16:HIS:HD2	26:A:1390:A:C8	1.77	1.01
26:A:2509:C:C5	30:4:8:ARG:NH1	2.28	1.01
3:E:192:ASP:CB	11:M:5:LYS:HZ1	1.72	1.00
4:F:9:PRO:HD2	4:F:12:LYS:NZ	1.75	1.00
26:A:1563:A:N6	26:A:1607:C:H41	1.59	1.00
21:W:77:LEU:HB3	21:W:100:VAL:HG23	1.01	1.00
26:A:1564:A:H2'	26:A:1565:A:H5''	1.44	1.00
28:2:41:CYS:HB2	28:2:44:PHE:CZ	1.97	1.00
1:C:26:ARG:HD2	1:C:81:HIS:NE2	1.76	1.00
1:C:54:LYS:NZ	26:A:2031:G:O3'	1.94	1.00
25:B:58:A:C4	25:B:59:A:C8	2.49	0.99
26:A:2980:U:OP2	33:7:19:ARG:NH1	1.95	0.99
20:V:62:GLN:CG	20:V:63:GLU:H	1.75	0.99
1:C:25:THR:CG2	1:C:81:HIS:HA	1.90	0.99
10:L:8:LEU:CD1	10:L:19:ILE:HG13	1.92	0.99
20:V:2:LYS:CD	20:V:83:VAL:CG1	2.37	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:5:5:LYS:HB3	31:5:9:GLN:NE2	1.76	0.99
13:O:33:ARG:HD3	13:O:114:GLU:CD	1.86	0.99
1:C:55:GLY:HA3	1:C:218:ARG:HD2	1.43	0.99
4:F:10:ARG:HG2	4:F:10:ARG:HH11	1.27	0.99
4:F:49:ASP:HB2	4:F:56:LEU:CD1	1.93	0.99
14:P:108:THR:OG1	25:B:47:A:O2'	1.79	0.99
25:B:40:A:H61	28:2:1:MET:N	1.58	0.99
28:2:44:PHE:O	28:2:48:LYS:HG3	1.61	0.99
9:K:141:GLU:CD	9:K:143:LYS:CG	2.35	0.99
25:B:57:U:C2'	25:B:58:A:H5''	1.93	0.99
19:U:19:LYS:NZ	26:A:1508:A:N6	2.09	0.98
20:V:62:GLN:HG2	20:V:63:GLU:H	0.84	0.98
3:E:66:TYR:CD1	3:E:73:ARG:NH1	2.31	0.98
26:A:1580:A:C6	26:A:1592:G:N9	2.31	0.98
21:W:105:LYS:NZ	21:W:136:GLU:OE2	1.92	0.98
21:W:105:LYS:HE2	21:W:136:GLU:OE2	1.61	0.98
25:B:60:G:H5'	25:B:60:G:H8	1.25	0.98
26:A:1565:A:C4	26:A:1606:G:C6	2.50	0.98
30:4:15:CYS:CA	30:4:20:HIS:HA	1.93	0.98
18:T:9:SER:HB3	18:T:115:GLU:CB	1.92	0.98
31:5:8:PHE:CE2	31:5:10:PRO:HG3	1.99	0.98
30:4:19:LYS:HD2	30:4:44:ASN:CB	1.93	0.98
4:F:117:ARG:NH1	4:F:146:HIS:HD2	1.24	0.97
12:N:85:SER:OG	22:X:8:SER:CB	2.11	0.97
13:O:90:ARG:CZ	13:O:118:GLU:HG3	1.94	0.97
2:D:154:CYS:SG	26:A:2796:A:H2'	2.04	0.97
17:S:58:VAL:HG22	17:S:103:LYS:HG2	1.45	0.97
26:A:1563:A:H61	26:A:1607:C:H41	1.05	0.97
3:E:7:VAL:CG2	3:E:16:GLY:HA3	1.95	0.97
13:O:8:PRO:CG	26:A:1870:U:C5	2.48	0.97
20:V:46:ALA:HB2	26:A:571:A:O3'	1.65	0.97
1:C:54:LYS:NZ	26:A:2031:G:C4'	2.28	0.97
12:N:111:GLU:OE2	12:N:115:ARG:NE	1.97	0.97
14:P:50:GLN:NE2	25:B:7:G:N2	2.13	0.96
17:S:3:THR:CG2	17:S:102:ILE:HD11	1.93	0.96
13:O:79:LEU:HG	13:O:83:ILE:CD1	1.96	0.96
1:C:54:LYS:HZ2	26:A:2031:G:C5'	1.76	0.96
12:N:61:GLY:O	12:N:108:TYR:CE1	2.17	0.96
8:J:96:LYS:HE3	21:W:120:PRO:HB2	1.48	0.96
21:W:87:PRO:O	21:W:90:ARG:NH2	1.97	0.96
26:A:1595:G:H3'	26:A:1596:C:C5'	1.95	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:11:ILE:CD1	30:4:27:LYS:HG2	1.95	0.96
18:T:75:THR:HB	18:T:118:PRO:HD3	1.46	0.96
20:V:2:LYS:HG2	20:V:83:VAL:HB	1.47	0.96
21:W:21:LYS:NZ	25:B:80:C:H42	1.64	0.96
4:F:66:LEU:HD23	28:2:27:THR:CG2	1.95	0.95
13:O:90:ARG:HH22	13:O:118:GLU:CB	1.75	0.95
26:A:1580:A:N1	26:A:1592:G:H1'	1.78	0.95
1:C:25:THR:HG21	1:C:81:HIS:HA	0.99	0.95
1:C:256:ARG:HA	1:C:256:ARG:HE	1.28	0.95
10:L:8:LEU:HD11	10:L:19:ILE:HG13	1.47	0.95
25:B:54:A:O2'	25:B:55:G:H5'	1.64	0.95
19:U:91:LYS:HG2	19:U:92:PRO:HD2	0.96	0.95
25:B:25:G:H21	25:B:114:A:C2'	1.79	0.95
4:F:109:ARG:HG3	4:F:113:ILE:HD12	1.48	0.95
25:B:96:A:H2	26:A:977:G:N3	1.62	0.95
18:T:44:ARG:HH12	29:3:55:ASP:H	1.09	0.95
9:K:112:ASN:CG	26:A:650:G:OP1	2.08	0.95
4:F:116:PRO:HB2	28:2:37:VAL:HG11	1.48	0.95
25:B:24:G:C8	25:B:56:C:C2	2.55	0.95
10:L:8:LEU:H	10:L:8:LEU:HD12	1.32	0.94
25:B:24:G:O2'	25:B:56:C:C4	2.17	0.94
13:O:8:PRO:HG3	26:A:1870:U:C5	2.02	0.94
26:A:1551:U:H3	26:A:1619:U:H3	1.12	0.94
26:A:1570:C:C4	26:A:1602:U:O2	2.20	0.94
17:S:6:ILE:O	17:S:7:VAL:CG2	2.15	0.94
24:Z:13:LEU:HD11	24:Z:17:GLU:CB	1.95	0.94
25:B:58:A:C5	25:B:59:A:C8	2.55	0.94
26:A:1554:U:H3	26:A:1617:C:N4	1.64	0.94
11:M:51:GLU:HG2	32:6:57:ARG:NH1	1.79	0.94
3:E:9:THR:OG1	3:E:12:GLY:O	1.85	0.94
17:S:3:THR:HG21	17:S:102:ILE:HD12	1.46	0.94
18:T:18:ARG:CZ	26:A:1436:C:O2'	2.16	0.94
12:N:60:ARG:HG2	12:N:60:ARG:HH21	1.27	0.94
19:U:4:ILE:HD13	24:Z:58:TYR:OH	1.68	0.94
25:B:82:A:H2	25:B:91:G:H1	1.05	0.94
26:A:1581:C:H2'	26:A:1582:C:C6	2.03	0.94
20:V:96:ARG:HD2	20:V:105:ILE:HG23	1.50	0.93
4:F:66:LEU:HD23	28:2:27:THR:HG21	1.48	0.93
30:4:36:LEU:HD21	30:4:38:ILE:HD12	1.48	0.93
18:T:9:SER:HB3	18:T:115:GLU:HB2	1.50	0.93
2:D:154:CYS:CB	26:A:2799:C:H5'	1.97	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:49:ASP:CB	4:F:56:LEU:HD11	1.96	0.93
4:F:110:LEU:HD23	4:F:111:ILE:N	1.83	0.93
20:V:2:LYS:CG	20:V:83:VAL:HB	1.99	0.93
26:A:1595:G:OP2	26:A:1596:C:C4	2.22	0.93
4:F:44:ASN:OD1	26:A:2537:C:O4'	1.86	0.93
13:O:9:ARG:HG2	13:O:14:SER:CB	1.99	0.93
3:E:144:PHE:HD1	3:E:148:LEU:HD21	1.33	0.93
22:X:15:ASP:OD2	26:A:2487:C:N4	2.01	0.93
30:4:29:ARG:NH2	30:4:34:ASP:CB	2.31	0.92
26:A:1597:G:N3	26:A:1598:U:C6	2.37	0.92
4:F:109:ARG:HD2	4:F:147:GLU:OE2	1.69	0.92
30:4:12:THR:HG22	30:4:22:ASN:HB3	1.50	0.92
9:K:68:LYS:NZ	26:A:1140:G:O6	2.01	0.92
24:Z:9:GLU:O	24:Z:11:ARG:N	2.03	0.92
4:F:105:GLU:HG3	28:2:24:THR:HG22	1.52	0.92
17:S:58:VAL:HG23	17:S:103:LYS:HG2	0.98	0.92
22:X:64:PRO:HB3	26:A:759:G:H1	1.34	0.92
25:B:58:A:C4	25:B:59:A:H8	1.84	0.92
2:D:154:CYS:SG	26:A:2796:A:OP1	2.28	0.92
3:E:144:PHE:CD1	3:E:148:LEU:CD1	2.52	0.92
19:U:19:LYS:HD2	26:A:1508:A:H62	0.84	0.92
19:U:83:ILE:HD12	26:A:1456:G:C2	2.05	0.92
21:W:87:PRO:HA	21:W:90:ARG:HH22	1.35	0.92
4:F:73:GLU:OE1	25:B:41:U:C5	2.23	0.92
1:C:72:LYS:HG3	1:C:75:VAL:CG2	2.00	0.92
26:A:1580:A:N6	26:A:1591:U:H3	1.66	0.92
26:A:1580:A:N1	26:A:1591:U:O2	2.02	0.91
26:A:1583:U:O2	26:A:1589:G:N1	2.03	0.91
1:C:30:GLU:OE2	1:C:102:LYS:HD3	1.68	0.91
2:D:154:CYS:HB3	26:A:2798:G:O2'	1.71	0.91
2:D:156:THR:HG21	26:A:2256:G:H21	1.36	0.91
19:U:83:ILE:CD1	26:A:1456:G:N2	2.11	0.91
25:B:19:G:N2	25:B:64:G:N1	2.19	0.91
30:4:29:ARG:HH21	30:4:34:ASP:HB3	1.34	0.91
4:F:168:THR:OG1	14:P:4:LYS:O	1.89	0.91
18:T:115:GLU:OE2	18:T:117:ARG:NH1	2.04	0.91
3:E:7:VAL:HB	3:E:16:GLY:HA3	1.52	0.91
3:E:192:ASP:HB3	11:M:5:LYS:HZ3	1.33	0.91
26:A:1561:C:N3	26:A:1562:C:C6	2.39	0.91
19:U:4:ILE:CD1	24:Z:58:TYR:CZ	2.51	0.90
30:4:15:CYS:HB2	30:4:20:HIS:CA	2.01	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:83:LEU:CD1	21:W:92:ILE:HG23	2.01	0.90
1:C:54:LYS:NZ	26:A:2031:G:H4'	1.83	0.90
10:L:108:GLU:HG3	10:L:109:LYS:H	1.36	0.90
30:4:9:PRO:HD2	30:4:27:LYS:O	1.71	0.90
13:O:9:ARG:CG	13:O:14:SER:HB3	2.01	0.90
26:A:2086:U:H3	26:A:2096:G:H1	0.97	0.90
25:B:4:A:H2	25:B:25:G:C6	1.90	0.90
26:A:2508:C:OP1	30:4:7:VAL:HG11	1.71	0.90
13:O:29:PHE:CD1	13:O:79:LEU:HD11	2.06	0.90
30:4:29:ARG:NH2	30:4:34:ASP:HB2	1.87	0.90
25:B:96:A:C2	26:A:977:G:N3	2.39	0.90
26:A:1561:C:N4	26:A:1562:C:N4	2.19	0.90
25:B:58:A:H5'	25:B:58:A:C8	2.07	0.90
26:A:1565:A:H2'	26:A:1566:A:C8	2.05	0.90
26:A:2571:C:O2'	30:4:23:TYR:OH	1.77	0.90
26:A:1563:A:N7	26:A:1565:A:N7	2.20	0.89
1:C:256:ARG:O	26:A:2014:G:H4'	1.71	0.89
26:A:1564:A:C2'	26:A:1565:A:H5''	2.02	0.89
1:C:37:LEU:HD23	1:C:62:TYR:HB2	1.54	0.89
1:C:73:ASP:HB3	1:C:120:GLY:HA2	1.50	0.89
3:E:144:PHE:CD2	3:E:148:LEU:HD11	2.07	0.89
21:W:83:LEU:HD11	21:W:92:ILE:HD12	1.55	0.89
1:C:96:HIS:HE1	1:C:102:LYS:NZ	1.70	0.89
1:C:258:ARG:HA	26:A:2015:U:C5'	2.01	0.89
25:B:19:G:C2'	25:B:20:G:H5'	2.03	0.89
25:B:20:G:C2'	25:B:21:C:H5'	2.02	0.89
26:A:325:U:H3	26:A:450:G:H1	0.94	0.89
3:E:7:VAL:O	3:E:14:THR:HA	1.73	0.89
12:N:58:ILE:CG2	12:N:108:TYR:CE1	2.55	0.89
26:A:1597:G:N3	26:A:1598:U:C5	2.41	0.89
13:O:8:PRO:CG	26:A:1870:U:C4	2.55	0.89
20:V:42:LYS:HD2	26:A:586:U:H5''	1.53	0.88
25:B:20:G:N1	25:B:63:U:O4	2.05	0.88
25:B:24:G:C5	25:B:56:C:C2	2.61	0.88
26:A:1571:C:O2'	26:A:1572:G:H5''	1.73	0.88
25:B:19:G:H5'	25:B:19:G:C8	2.07	0.88
26:A:1561:C:C2	26:A:1562:C:H6	1.92	0.88
25:B:58:A:C6	25:B:59:A:N7	2.40	0.88
26:A:1575:A:O2'	26:A:1576:C:H5'	1.72	0.88
26:A:1597:G:C4	26:A:1598:U:H5	1.91	0.88
31:5:22:ARG:O	31:5:26:ARG:HD3	1.73	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:29:C:H42	25:B:55:G:H1	1.18	0.88
30:4:18:CYS:SG	30:4:19:LYS:N	2.47	0.88
20:V:2:LYS:HD2	20:V:83:VAL:HG11	0.88	0.88
2:D:154:CYS:CB	26:A:2799:C:P	2.52	0.88
19:U:83:ILE:CD1	26:A:1456:G:N3	2.20	0.88
22:X:83:VAL:HG13	22:X:85:ARG:HA	1.54	0.88
26:A:1578:G:H22	26:A:1592:G:C2'	1.87	0.88
26:A:1580:A:C6	26:A:1591:U:C2	2.56	0.88
30:4:19:LYS:HB2	30:4:21:ARG:NH2	1.89	0.88
14:P:41:ASN:ND2	25:B:7:G:HO2'	1.70	0.87
25:B:25:G:H21	25:B:114:A:C1'	1.86	0.87
1:C:256:ARG:HA	1:C:256:ARG:NE	1.88	0.87
13:O:117:ARG:HD3	13:O:118:GLU:H	1.39	0.87
1:C:73:ASP:HB3	1:C:120:GLY:HA3	1.56	0.87
13:O:8:PRO:HG2	26:A:1870:U:C5	2.10	0.87
20:V:83:VAL:HG11	20:V:96:ARG:HG3	1.57	0.87
26:A:1597:G:C4	26:A:1598:U:C5	2.62	0.87
26:A:2509:C:H5	30:4:8:ARG:NH1	1.69	0.87
11:M:58:HIS:CD2	32:6:7:HIS:HE1	1.93	0.87
17:S:3:THR:HG22	17:S:102:ILE:HD11	1.51	0.87
26:A:1598:U:O4	26:A:1601:G:C6	2.28	0.87
1:C:29:PRO:CG	1:C:34:VAL:HG21	2.05	0.87
8:J:45:ASN:O	8:J:49:GLU:HB2	1.74	0.87
21:W:29:ARG:NH1	25:B:90:G:H5'	1.89	0.87
4:F:99:ARG:CD	25:B:45:G:C8	2.57	0.87
22:X:15:ASP:CG	26:A:2487:C:H41	1.83	0.87
25:B:28:A:H61	25:B:56:C:H42	1.21	0.86
26:A:1561:C:N4	26:A:1562:C:C5	2.41	0.86
3:E:150:GLU:OE1	3:E:193:ASP:OD1	1.92	0.86
28:2:41:CYS:HB3	28:2:43:PRO:CD	2.03	0.86
26:A:1578:G:H22	26:A:1592:G:H2'	1.40	0.86
26:A:1550:G:H1	26:A:1620:U:H3	0.86	0.86
4:F:74:VAL:O	25:B:41:U:O4	1.93	0.86
4:F:99:ARG:CD	25:B:45:G:H8	1.88	0.86
21:W:37:LEU:HD11	21:W:69:LEU:CD1	2.06	0.86
25:B:24:G:N7	25:B:56:C:C2	2.44	0.86
26:A:1582:C:O2'	26:A:1583:U:H5'	1.75	0.86
30:4:11:ILE:HD13	30:4:27:LYS:CG	2.06	0.86
13:O:4:PRO:HG3	26:A:3094:A:C2	2.10	0.85
20:V:29:ASP:OD1	20:V:30:ARG:N	2.09	0.85
21:W:77:LEU:HD22	21:W:100:VAL:HG21	1.57	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1566:A:O2'	26:A:1567:C:H5'	1.75	0.85
12:N:60:ARG:O	21:W:190:LEU:HD11	1.76	0.85
20:V:4:HIS:HE1	20:V:96:ARG:NH2	1.74	0.85
3:E:7:VAL:CB	3:E:16:GLY:HA3	2.05	0.85
19:U:4:ILE:HD13	24:Z:58:TYR:HE1	1.40	0.85
26:A:1590:G:C6	26:A:1591:U:C5	2.64	0.85
18:T:6:GLU:C	18:T:8:PRO:HD3	2.01	0.85
25:B:4:A:C2	25:B:25:G:C6	2.63	0.85
3:E:68:GLN:OE1	26:A:790:A:O2'	1.94	0.85
25:B:20:G:O2'	25:B:21:C:H5'	1.77	0.85
26:A:2510:A:OP2	30:4:31:ASN:OD1	1.94	0.85
26:A:1601:G:O2'	26:A:1602:U:C5'	2.24	0.85
20:V:97:ILE:HD12	20:V:103:LYS:O	1.77	0.84
24:Z:18:LEU:HD13	24:Z:61:LEU:CD2	2.07	0.84
13:O:29:PHE:CE2	13:O:51:LEU:HD12	2.11	0.84
17:S:103:LYS:HZ3	17:S:103:LYS:CA	1.90	0.84
25:B:19:G:N2	25:B:65:C:C2	2.44	0.84
25:B:19:G:H2'	25:B:20:G:C5'	2.07	0.84
19:U:19:LYS:CD	26:A:1508:A:H61	1.78	0.84
3:E:144:PHE:CE1	3:E:148:LEU:HD22	2.09	0.84
9:K:3:THR:HG21	26:A:1113:C:O2	1.75	0.84
2:D:155:ALA:HB2	26:A:2796:A:N7	1.83	0.84
13:O:20:LEU:HD11	13:O:40:LYS:HZ2	1.41	0.84
21:W:37:LEU:HD12	21:W:69:LEU:HD11	1.59	0.84
19:U:29:TYR:CE1	19:U:93:ILE:CG2	2.60	0.84
24:Z:13:LEU:CD1	24:Z:17:GLU:HB2	2.07	0.84
1:C:55:GLY:CA	1:C:218:ARG:CD	2.54	0.84
26:A:1556:A:H61	26:A:1615:G:H1	1.26	0.84
12:N:58:ILE:HG21	12:N:108:TYR:CE1	2.13	0.84
26:A:2510:A:OP1	30:4:31:ASN:OD1	1.95	0.83
1:C:25:THR:HG22	1:C:82:ILE:N	1.92	0.83
1:C:76:ASN:O	1:C:98:LEU:CD2	2.25	0.83
8:J:96:LYS:HE2	21:W:120:PRO:HB2	1.59	0.83
13:O:96:ARG:NH2	13:O:116:VAL:HG12	1.93	0.83
21:W:37:LEU:HD12	21:W:69:LEU:CD1	2.08	0.83
3:E:90:VAL:HG11	26:A:678:A:O5'	1.77	0.83
4:F:99:ARG:HD2	25:B:45:G:H8	1.40	0.83
14:P:50:GLN:CD	25:B:7:G:H21	1.86	0.83
21:W:101:GLN:HB3	21:W:104:GLU:CB	2.08	0.83
25:B:59:A:H2'	25:B:60:G:H5'	1.59	0.83
25:B:82:A:C2	25:B:91:G:N1	2.45	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:17:ALA:CB	26:A:2485:C:P	2.66	0.83
30:4:37:GLU:O	30:4:38:ILE:HG13	1.78	0.83
4:F:105:GLU:CG	28:2:24:THR:HG22	2.07	0.83
19:U:19:LYS:HZ2	26:A:1508:A:H61	1.01	0.83
26:A:860:G:HO2'	26:A:863:G:HO2'	1.27	0.83
21:W:86:HIS:O	21:W:90:ARG:NH2	2.10	0.83
30:4:29:ARG:HH21	30:4:34:ASP:HB2	1.43	0.83
4:F:108:ASP:O	4:F:111:ILE:HG22	1.76	0.83
25:B:18:C:H2'	25:B:19:G:H5''	0.83	0.83
33:7:22:ARG:CZ	33:7:37:GLY:HA2	2.07	0.83
25:B:25:G:N2	25:B:114:A:H1'	1.94	0.83
4:F:132:THR:CG2	14:P:6:VAL:CG2	2.40	0.83
26:A:2508:C:OP1	30:4:7:VAL:CG1	2.27	0.83
2:D:154:CYS:HB2	26:A:2799:C:OP1	1.79	0.82
3:E:145:LEU:HA	3:E:148:LEU:HD12	1.58	0.82
21:W:83:LEU:CD1	21:W:92:ILE:HD12	2.09	0.82
2:D:154:CYS:H	26:A:2798:G:HO2'	1.27	0.82
22:X:83:VAL:HG12	22:X:85:ARG:HB2	1.62	0.82
3:E:14:THR:HG22	3:E:15:ASP:H	1.44	0.82
24:Z:13:LEU:O	24:Z:64:ARG:NH1	2.12	0.82
25:B:20:G:N2	25:B:63:U:N3	1.89	0.82
26:A:1580:A:N1	26:A:1592:G:N9	2.27	0.82
26:A:1595:G:H8	26:A:1596:C:C5	1.96	0.82
19:U:77:LYS:NZ	19:U:79:THR:HG22	1.93	0.82
21:W:8:PRO:HB2	21:W:68:THR:OG1	1.80	0.82
26:A:1580:A:C2	26:A:1592:G:H1'	2.14	0.82
2:D:154:CYS:SG	26:A:2796:A:C5'	2.66	0.82
4:F:118:ILE:HD11	4:F:144:MET:HE3	1.61	0.82
25:B:36:U:O2'	25:B:37:C:H5'	1.80	0.82
9:K:112:ASN:OD1	9:K:113:LYS:N	2.11	0.82
25:B:85:C:O2'	25:B:86:U:O4'	1.97	0.82
26:A:1561:C:N4	26:A:1562:C:H41	1.76	0.82
4:F:116:PRO:CB	28:2:37:VAL:HG11	2.09	0.82
24:Z:13:LEU:HD11	24:Z:17:GLU:OE1	1.79	0.82
10:L:109:LYS:HD2	10:L:110:LYS:HZ1	1.42	0.81
11:M:51:GLU:HG3	32:6:57:ARG:NH1	1.93	0.81
13:O:14:SER:O	13:O:15:SER:OG	1.96	0.81
25:B:19:G:N2	25:B:65:C:C4	2.47	0.81
12:N:60:ARG:NH1	26:A:1193:C:H5''	1.94	0.81
19:U:91:LYS:CG	19:U:92:PRO:CD	2.51	0.81
24:Z:6:THR:HG22	24:Z:10:LEU:CD1	2.09	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1567:C:O2'	26:A:1568:C:OP2	1.96	0.81
26:A:1602:U:H2'	26:A:1603:G:C8	2.16	0.81
1:C:29:PRO:HB2	1:C:34:VAL:CG2	2.09	0.81
3:E:45:LYS:HG3	26:A:709:U:O4	1.80	0.81
4:F:45:MET:HB2	4:F:94:ALA:O	1.81	0.81
13:O:79:LEU:CG	13:O:83:ILE:HD12	2.10	0.81
17:S:103:LYS:HA	17:S:103:LYS:NZ	1.95	0.81
13:O:81:ALA:O	13:O:85:PRO:CG	2.28	0.81
1:C:54:LYS:NZ	26:A:2031:G:H5''	1.94	0.81
26:A:1566:A:N3	26:A:1605:G:C6	2.48	0.81
26:A:1582:C:C2'	26:A:1583:U:H5'	2.10	0.81
28:2:41:CYS:CB	28:2:43:PRO:HD2	2.10	0.81
26:A:1561:C:C5	26:A:1562:C:C5	2.41	0.81
30:4:21:ARG:HG3	30:4:44:ASN:OD1	1.81	0.81
25:B:21:C:H2'	25:B:22:A:O4'	1.81	0.81
3:E:51:SER:OG	26:A:35:A:H5'	1.81	0.80
26:A:1580:A:H62	26:A:1591:U:H3	1.25	0.80
9:K:113:LYS:HD2	26:A:616:A:OP1	1.81	0.80
26:A:1561:C:C2	26:A:1562:C:C5	2.68	0.80
26:A:1570:C:H42	26:A:1602:U:H3	0.80	0.80
26:A:1570:C:O2'	26:A:1571:C:H5'	1.80	0.80
9:K:26:GLY:O	26:A:1262:A:N6	2.14	0.80
19:U:19:LYS:HE3	26:A:1454:G:H5'	1.62	0.80
22:X:15:ASP:HB2	26:A:2486:U:O4	1.81	0.80
31:5:5:LYS:HB3	31:5:9:GLN:HE21	1.47	0.80
3:E:24:LEU:HD21	3:E:208:ASN:OD1	1.82	0.80
9:K:3:THR:HG23	26:A:1113:C:N3	1.97	0.80
13:O:4:PRO:HG3	26:A:3094:A:N1	1.97	0.80
13:O:33:ARG:HG3	13:O:114:GLU:CG	2.11	0.80
26:A:1561:C:C4	26:A:1562:C:C4	2.69	0.80
30:4:9:PRO:CD	30:4:27:LYS:O	2.30	0.80
1:C:56:GLY:CA	26:A:807:C:OP1	2.29	0.80
25:B:60:G:H5'	25:B:60:G:C8	2.15	0.80
1:C:30:GLU:OE1	1:C:33:LEU:CD1	2.29	0.80
21:W:40:HIS:O	21:W:42:THR:N	2.14	0.80
26:A:1561:C:N4	26:A:1562:C:C4	2.50	0.80
2:D:154:CYS:HG	26:A:2796:A:P	2.05	0.79
25:B:18:C:C2'	25:B:19:G:C5'	2.40	0.79
26:A:351:G:H1	26:A:444:U:H3	1.27	0.79
26:A:1581:C:N4	26:A:1591:U:C1'	2.45	0.79
26:A:1596:C:O2'	26:A:1597:G:O4'	2.00	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:30:G:N1	25:B:54:A:C2	2.48	0.79
21:W:98:LEU:HD23	21:W:99:VAL:N	1.97	0.79
4:F:45:MET:CE	4:F:64:LEU:CD2	2.52	0.79
26:A:1578:G:N7	26:A:1592:G:O6	2.15	0.79
26:A:1600:G:C3'	26:A:1601:G:H5''	2.11	0.79
4:F:55:LYS:HB2	4:F:55:LYS:NZ	1.97	0.79
9:K:112:ASN:HD21	26:A:650:G:P	2.04	0.79
21:W:9:ASN:HD22	21:W:57:VAL:HG13	1.41	0.79
22:X:17:ALA:HB3	26:A:2485:C:OP2	1.82	0.79
18:T:75:THR:HB	18:T:118:PRO:CD	2.12	0.79
25:B:96:A:H2	26:A:977:G:C2	2.00	0.79
5:G:171:ARG:NH2	33:7:28:SER:O	2.16	0.79
4:F:120:ASP:OD2	4:F:122:ARG:NH1	2.16	0.79
4:F:182:PHE:CD2	4:F:184:PHE:HE2	2.01	0.79
25:B:19:G:N2	25:B:64:G:H1	1.80	0.79
1:C:54:LYS:NZ	26:A:2031:G:C5'	2.46	0.79
1:C:55:GLY:HA3	1:C:218:ARG:CG	2.13	0.79
3:E:7:VAL:CG2	3:E:16:GLY:CA	2.61	0.79
26:A:1561:C:C2'	26:A:1562:C:H5'	2.13	0.79
1:C:257:THR:HB	26:A:2014:G:O2'	1.82	0.79
2:D:154:CYS:HA	26:A:2799:C:C5'	2.07	0.79
3:E:118:ARG:HH11	11:M:3:VAL:HG13	1.48	0.79
13:O:81:ALA:C	13:O:85:PRO:HD2	2.08	0.79
26:A:1563:A:C5	26:A:1565:A:N7	2.50	0.78
3:E:8:LYS:O	3:E:127:VAL:HA	1.82	0.78
14:P:42:ARG:NH1	25:B:48:C:P	2.46	0.78
21:W:102:ARG:HH21	21:W:138:LEU:HD21	1.45	0.78
33:7:22:ARG:HD3	33:7:36:GLN:O	1.83	0.78
12:N:61:GLY:O	12:N:108:TYR:HE1	1.59	0.78
20:V:2:LYS:NZ	20:V:85:TYR:CE2	2.51	0.78
22:X:14:ARG:NH2	26:A:2503:G:N7	2.30	0.78
12:N:61:GLY:O	12:N:108:TYR:CD1	2.36	0.78
21:W:37:LEU:CD1	21:W:69:LEU:HD11	2.11	0.78
26:A:1541:G:O6	26:A:1630:U:C4	2.36	0.78
3:E:145:LEU:CA	3:E:148:LEU:HD12	1.98	0.78
12:N:134:ARG:HH21	21:W:129:ASN:HD21	1.30	0.78
13:O:42:ARG:O	13:O:45:ARG:HB3	1.83	0.78
20:V:47:VAL:C	20:V:56:SER:HA	2.09	0.78
21:W:87:PRO:CA	21:W:90:ARG:HH22	1.96	0.78
26:A:725:A:OP2	32:6:47:ARG:NH2	2.16	0.78
28:2:48:LYS:O	28:2:52:LEU:HG	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:13:ARG:NE	9:K:121:LYS:HZ3	1.82	0.78
19:U:29:TYR:CE1	19:U:93:ILE:HG22	2.19	0.78
26:A:1578:G:C5	26:A:1592:G:N1	2.18	0.78
2:D:154:CYS:HB2	26:A:2799:C:C5'	2.14	0.78
4:F:117:ARG:NH1	4:F:146:HIS:NE2	2.30	0.78
25:B:25:G:N2	25:B:114:A:C1'	2.47	0.78
10:L:107:ARG:NH1	15:Q:33:GLU:HG3	1.99	0.78
26:A:1541:G:O6	26:A:1630:U:C5	2.36	0.78
13:O:16:HIS:CD2	26:A:1390:A:C8	2.68	0.77
24:Z:5:THR:HG23	24:Z:6:THR:H	1.47	0.77
25:B:59:A:C2'	25:B:60:G:H5'	2.14	0.77
9:K:141:GLU:OE1	9:K:143:LYS:CG	2.27	0.77
21:W:40:HIS:O	21:W:40:HIS:ND1	2.16	0.77
30:4:36:LEU:HG	30:4:37:GLU:N	1.99	0.77
9:K:3:THR:CG2	26:A:1113:C:C2	2.66	0.77
12:N:60:ARG:NE	26:A:1194:C:OP2	2.17	0.77
19:U:77:LYS:HG3	26:A:55:G:H5''	1.66	0.77
26:A:1601:G:O2'	26:A:1602:U:H5'	1.82	0.77
28:2:44:PHE:O	28:2:48:LYS:HE3	1.84	0.77
3:E:51:SER:HB3	26:A:34:C:O2'	1.84	0.77
13:O:33:ARG:HG3	13:O:114:GLU:HG3	1.66	0.77
13:O:33:ARG:HD2	13:O:114:GLU:OE2	1.85	0.77
26:A:1595:G:H5'	26:A:1596:C:C6	2.20	0.77
10:L:92:ASP:OD2	10:L:93:PRO:HD2	1.85	0.77
19:U:7:PRO:O	19:U:49:ILE:HD11	1.84	0.77
26:A:1554:U:H3	26:A:1617:C:H42	1.31	0.77
26:A:1566:A:H1'	26:A:1605:G:H1	1.47	0.77
2:D:154:CYS:CB	26:A:2798:G:O2'	2.33	0.77
17:S:103:LYS:C	17:S:103:LYS:HD3	2.10	0.77
19:U:69:THR:OG1	19:U:73:PHE:O	2.03	0.77
3:E:107:ILE:CD1	26:A:710:G:OP1	2.33	0.77
11:M:61:LEU:CD2	32:6:24:ARG:HH11	1.96	0.77
20:V:44:HIS:HA	20:V:58:GLY:O	1.84	0.77
26:A:1563:A:N6	26:A:1607:C:N4	2.33	0.77
2:D:154:CYS:HB2	26:A:2799:C:H5'	1.67	0.77
13:O:33:ARG:NH2	13:O:114:GLU:OE2	2.16	0.77
1:C:35:ARG:HG3	1:C:36:PRO:CD	2.14	0.76
4:F:53:ASP:O	4:F:56:LEU:CD2	2.33	0.76
17:S:6:ILE:C	17:S:7:VAL:HG23	2.10	0.76
25:B:54:A:C2'	25:B:55:G:H5'	2.15	0.76
25:B:84:C:H2'	25:B:85:C:H5'	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:78:ARG:NH2	26:A:2522:A:OP1	2.19	0.76
21:W:37:LEU:CD1	21:W:69:LEU:HD13	2.15	0.76
1:C:35:ARG:HD2	1:C:36:PRO:HD3	1.66	0.76
26:A:1600:G:C2'	26:A:1601:G:H5''	2.15	0.76
30:4:15:CYS:O	30:4:20:HIS:HB3	1.80	0.76
17:S:3:THR:HG22	17:S:102:ILE:HD13	0.76	0.76
1:C:57:GLY:O	1:C:58:HIS:O	2.02	0.76
3:E:121:ASN:HD22	11:M:3:VAL:HG22	1.50	0.76
13:O:20:LEU:HD11	13:O:40:LYS:NZ	2.00	0.76
28:2:47:GLY:O	28:2:51:ILE:HG13	1.85	0.76
3:E:7:VAL:HG23	3:E:16:GLY:CA	2.15	0.76
13:O:43:ALA:C	13:O:46:PRO:HD2	2.11	0.76
20:V:4:HIS:CE1	20:V:96:ARG:NH2	2.50	0.76
26:A:802:C:H1'	31:5:7:THR:HG22	1.67	0.76
26:A:1597:G:C2	26:A:1598:U:C5	2.73	0.76
30:4:12:THR:CG2	30:4:22:ASN:HB3	2.16	0.76
11:M:63:LYS:HE3	32:6:12:LYS:HG2	1.68	0.76
11:M:51:GLU:HG2	32:6:57:ARG:CZ	2.16	0.76
16:R:50:ARG:HG2	16:R:53:ARG:HH21	1.51	0.76
4:F:182:PHE:HD2	4:F:184:PHE:HE2	1.32	0.75
8:J:44:TYR:O	8:J:48:THR:HB	1.87	0.75
13:O:95:THR:HG22	13:O:115:LEU:HD23	1.68	0.75
13:O:29:PHE:HE2	13:O:51:LEU:CD1	1.99	0.75
17:S:6:ILE:HG22	17:S:7:VAL:N	1.99	0.75
21:W:29:ARG:HH12	25:B:90:G:C5'	2.00	0.75
31:5:8:PHE:CD2	31:5:10:PRO:HG3	2.21	0.75
9:K:13:ARG:HH21	9:K:49:ASP:C	1.94	0.75
22:X:15:ASP:CB	26:A:2487:C:H41	1.98	0.75
24:Z:13:LEU:HD21	24:Z:17:GLU:C	2.11	0.75
26:A:1586:C:H3'	26:A:1587:G:H5''	1.68	0.75
30:4:15:CYS:C	30:4:20:HIS:CB	2.59	0.75
1:C:57:GLY:O	1:C:58:HIS:C	2.29	0.75
18:T:95:ARG:NH2	26:A:863:G:OP1	2.18	0.75
33:7:35:ARG:HG2	33:7:36:GLN:H	1.50	0.75
1:C:76:ASN:HB2	1:C:98:LEU:HD21	1.68	0.75
6:H:103:ALA:O	6:H:107:ALA:HB3	1.86	0.75
25:B:82:A:H2	25:B:91:G:N1	1.82	0.75
1:C:239:LYS:HE2	26:A:2196:G:OP2	1.85	0.75
9:K:96:HIS:HB3	9:K:99:ARG:HG2	1.66	0.75
18:T:41:ASP:OD2	29:3:27:LEU:HD13	1.86	0.75
24:Z:13:LEU:HD21	24:Z:17:GLU:CB	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:16:HIS:CD2	26:A:1390:A:C4	2.75	0.75
13:O:29:PHE:CE2	13:O:51:LEU:CD1	2.69	0.75
26:A:1601:G:O2'	26:A:1602:U:H5''	1.86	0.75
4:F:32:VAL:O	4:F:33:MET:HB2	1.86	0.74
4:F:168:THR:HG21	14:P:3:HIS:CE1	2.21	0.74
18:T:44:ARG:NH1	29:3:55:ASP:H	1.85	0.74
19:U:5:THR:HG22	19:U:6:ASP:N	2.01	0.74
20:V:86:ARG:HD3	20:V:97:ILE:HG13	1.68	0.74
20:V:96:ARG:NH2	20:V:96:ARG:HB2	2.01	0.74
26:A:1590:G:C4	26:A:1591:U:C6	2.74	0.74
24:Z:13:LEU:HD21	24:Z:17:GLU:HB3	1.68	0.74
26:A:1565:A:H2	26:A:1606:G:C8	1.98	0.74
18:T:116:SER:OG	18:T:118:PRO:HG2	1.86	0.74
27:1:51:HIS:H	27:1:51:HIS:CD2	2.03	0.74
30:4:18:CYS:HB2	30:4:45:CYS:SG	2.27	0.74
3:E:7:VAL:CG2	3:E:16:GLY:C	2.54	0.74
4:F:45:MET:CB	4:F:94:ALA:O	2.34	0.74
9:K:3:THR:HG23	26:A:1113:C:C2	2.22	0.74
21:W:83:LEU:HD11	21:W:92:ILE:HG23	1.68	0.74
21:W:87:PRO:C	21:W:90:ARG:HH22	1.95	0.74
1:C:35:ARG:HG3	1:C:36:PRO:HD2	1.68	0.74
1:C:256:ARG:CZ	1:C:258:ARG:HE	1.99	0.74
18:T:96:ALA:O	26:A:866:G:OP2	2.04	0.74
20:V:97:ILE:CD1	20:V:103:LYS:O	2.36	0.74
30:4:36:LEU:HD21	30:4:38:ILE:CD1	2.17	0.74
4:F:9:PRO:HD2	4:F:12:LYS:HZ1	1.50	0.74
22:X:15:ASP:CB	26:A:2486:U:O4	2.35	0.74
1:C:256:ARG:HD3	1:C:258:ARG:CD	2.17	0.74
26:A:2644:C:OP1	32:6:34:GLU:OE2	2.05	0.74
28:2:41:CYS:HB2	28:2:44:PHE:CE2	2.22	0.74
24:Z:18:LEU:HD13	24:Z:61:LEU:HD23	1.68	0.74
25:B:25:G:H21	25:B:114:A:H1'	1.50	0.74
25:B:84:C:C4	25:B:85:C:N3	2.55	0.74
25:B:10:G:H1	25:B:107:A:H2	0.80	0.74
25:B:28:A:H61	25:B:56:C:N4	1.85	0.74
1:C:23:GLU:O	1:C:82:ILE:HB	1.86	0.73
33:7:22:ARG:HH22	33:7:37:GLY:HA2	0.93	0.73
33:7:35:ARG:HG2	33:7:36:GLN:N	2.03	0.73
4:F:64:LEU:HB2	4:F:72:PRO:HG3	1.70	0.73
26:A:1563:A:O2'	26:A:1564:A:H5'	1.87	0.73
4:F:11:LEU:HD13	4:F:108:ASP:HB2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:60:ARG:HG2	12:N:60:ARG:NH2	2.03	0.73
13:O:20:LEU:HD23	13:O:20:LEU:C	2.13	0.73
13:O:90:ARG:NH2	13:O:118:GLU:HB2	2.03	0.73
22:X:13:GLY:C	22:X:14:ARG:HG3	2.13	0.73
26:A:1563:A:H61	26:A:1607:C:N4	1.82	0.73
4:F:185:LYS:O	4:F:185:LYS:HE2	1.88	0.73
21:W:29:ARG:NH1	25:B:90:G:C5'	2.51	0.73
26:A:1561:C:H41	26:A:1562:C:H41	1.34	0.73
26:A:1703:G:H1	26:A:1726:C:H42	1.33	0.73
1:C:55:GLY:HA3	1:C:218:ARG:HG3	1.71	0.73
4:F:6:LYS:HE2	4:F:6:LYS:HA	1.70	0.73
26:A:801:U:O2'	31:5:7:THR:O	2.05	0.73
1:C:20:ASP:OD2	1:C:22:ALA:HB2	1.89	0.73
10:L:109:LYS:HD2	10:L:110:LYS:NZ	2.02	0.73
20:V:42:LYS:CD	26:A:586:U:H5''	2.18	0.73
26:A:1601:G:C2'	26:A:1602:U:C5'	2.62	0.73
15:Q:51:GLY:HA2	15:Q:56:GLU:HG3	1.71	0.73
19:U:77:LYS:HD3	19:U:79:THR:HG23	1.70	0.73
1:C:262:LYS:CE	26:A:2309:U:OP1	2.37	0.73
12:N:59:LYS:HZ3	12:N:59:LYS:HB2	1.53	0.73
3:E:151:ASN:C	3:E:152:LYS:HG3	2.06	0.72
1:C:56:GLY:HA3	26:A:807:C:OP1	1.90	0.72
20:V:86:ARG:HB3	20:V:97:ILE:CG1	2.19	0.72
13:O:79:LEU:C	13:O:79:LEU:HD23	2.15	0.72
17:S:59:ALA:H	17:S:103:LYS:HE2	1.53	0.72
25:B:24:G:N7	25:B:56:C:O2'	2.21	0.72
9:K:96:HIS:CB	9:K:99:ARG:CG	2.68	0.72
25:B:18:C:O2'	25:B:19:G:H5''	1.89	0.72
4:F:183:PRO:C	4:F:184:PHE:CD2	2.50	0.72
12:N:59:LYS:HB2	12:N:59:LYS:NZ	2.05	0.72
12:N:65:TRP:HZ3	26:A:989:G:HO2'	1.36	0.72
13:O:33:ARG:CG	13:O:114:GLU:HG2	2.19	0.72
30:4:15:CYS:HB2	30:4:20:HIS:N	2.05	0.72
1:C:55:GLY:CA	1:C:218:ARG:HD2	2.17	0.72
26:A:1561:C:H2'	26:A:1562:C:H5'	1.71	0.72
26:A:1604:G:H2'	26:A:1605:G:H5''	1.72	0.72
1:C:25:THR:HG22	1:C:82:ILE:H	1.53	0.72
3:E:14:THR:HG22	3:E:15:ASP:N	2.04	0.72
4:F:105:GLU:HG3	28:2:24:THR:CG2	2.20	0.72
10:L:8:LEU:HD12	10:L:8:LEU:N	2.03	0.72
13:O:90:ARG:NH1	13:O:118:GLU:HG3	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1566:A:C2'	26:A:1605:G:O6	2.38	0.72
1:C:257:THR:HG22	26:A:2020:A:O2'	1.90	0.72
3:E:149:THR:C	3:E:150:GLU:HG3	2.13	0.72
4:F:74:VAL:O	25:B:41:U:C4	2.42	0.72
26:A:2363:A:H61	26:A:2374:U:H3	1.36	0.72
22:X:15:ASP:HB2	26:A:2486:U:C4	2.25	0.71
25:B:81:U:H3	25:B:92:G:H22	1.38	0.71
26:A:1581:C:N4	26:A:1591:U:H1'	1.98	0.71
22:X:26:PHE:H	22:X:29:GLN:HE21	1.38	0.71
25:B:57:U:C3'	25:B:58:A:H5''	2.20	0.71
26:A:1572:G:OP2	26:A:1594:G:OP2	2.08	0.71
31:5:6:ARG:NH1	31:5:6:ARG:HB2	2.05	0.71
3:E:24:LEU:CD2	3:E:208:ASN:OD1	2.38	0.71
4:F:44:ASN:OD1	26:A:2536:U:H2'	1.90	0.71
19:U:66:ARG:HA	19:U:75:LYS:HA	1.72	0.71
26:A:964:C:O2'	27:1:21:GLU:HG2	1.90	0.71
26:A:1600:G:OP1	26:A:1600:G:H4'	1.88	0.71
4:F:45:MET:HE3	4:F:64:LEU:CG	2.21	0.71
19:U:73:PHE:HZ	31:5:43:ARG:HH22	1.37	0.71
26:A:1600:G:H3'	26:A:1601:G:H5''	1.70	0.71
19:U:83:ILE:HD13	26:A:1456:G:C2	2.19	0.71
21:W:87:PRO:O	21:W:90:ARG:CZ	2.39	0.71
2:D:154:CYS:SG	26:A:2798:G:O3'	2.48	0.71
14:P:50:GLN:HE22	25:B:7:G:N2	1.87	0.71
26:A:279:U:H3	26:A:307:G:H1	1.39	0.71
26:A:290:C:H42	26:A:298:G:H1	1.38	0.71
3:E:143:THR:O	3:E:147:THR:OG1	2.09	0.71
13:O:16:HIS:CD2	26:A:1390:A:C5	2.78	0.71
13:O:117:ARG:HD3	13:O:118:GLU:N	2.06	0.71
21:W:21:LYS:HZ1	25:B:80:C:H42	1.37	0.71
24:Z:18:LEU:CD1	24:Z:61:LEU:CD2	2.69	0.71
1:C:54:LYS:NZ	26:A:2031:G:C3'	2.54	0.71
2:D:154:CYS:SG	26:A:2796:A:C2'	2.79	0.71
9:K:142:ILE:HG22	9:K:143:LYS:N	2.06	0.71
13:O:4:PRO:CG	26:A:3094:A:C2	2.73	0.71
20:V:96:ARG:O	20:V:97:ILE:HD13	1.91	0.71
26:A:1704:U:H3	26:A:1725:G:H1	1.39	0.70
9:K:112:ASN:ND2	26:A:650:G:P	2.64	0.70
26:A:1566:A:O2'	26:A:1605:G:O6	2.09	0.70
26:A:2075:G:HO2'	26:A:2107:G:H1	0.77	0.70
4:F:9:PRO:HD2	4:F:12:LYS:CE	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:68:ARG:O	19:U:69:THR:HG23	1.92	0.70
25:B:20:G:N2	25:B:63:U:C2	2.52	0.70
26:A:1554:U:N3	26:A:1617:C:N4	2.33	0.70
1:C:33:LEU:O	1:C:64:VAL:HG22	1.91	0.70
2:D:156:THR:HG21	26:A:2256:G:N2	2.05	0.70
13:O:29:PHE:CD2	13:O:79:LEU:HD11	2.24	0.70
30:4:15:CYS:CB	30:4:20:HIS:CA	2.63	0.70
2:D:156:THR:O	26:A:2795:C:O2'	2.09	0.70
20:V:42:LYS:HD3	20:V:59:ILE:HD11	1.73	0.70
25:B:19:G:C5'	25:B:19:G:H8	2.03	0.70
26:A:1580:A:C6	26:A:1592:G:N3	2.58	0.70
4:F:66:LEU:HA	28:2:27:THR:HG21	1.74	0.70
13:O:5:THR:O	13:O:6:LYS:HB3	1.92	0.70
14:P:45:ARG:NH1	25:B:52:G:N7	2.17	0.70
26:A:1578:G:N3	26:A:1592:G:N2	2.17	0.70
13:O:33:ARG:HD3	13:O:114:GLU:CG	2.21	0.70
21:W:105:LYS:HZ3	21:W:136:GLU:CD	1.99	0.70
24:Z:13:LEU:CD1	24:Z:17:GLU:OE1	2.39	0.70
26:A:802:C:O4'	31:5:7:THR:HA	1.92	0.70
26:A:1566:A:N3	26:A:1605:G:N1	2.39	0.70
1:C:25:THR:CB	1:C:81:HIS:HD1	2.03	0.70
13:O:33:ARG:CG	13:O:114:GLU:CG	2.70	0.70
2:D:154:CYS:CA	26:A:2798:G:O2'	2.39	0.69
9:K:7:LYS:O	9:K:10:ASP:OD1	2.10	0.69
13:O:29:PHE:CZ	13:O:51:LEU:HD12	2.25	0.69
13:O:33:ARG:CD	13:O:114:GLU:CG	2.70	0.69
25:B:29:C:C2	25:B:55:G:N2	2.58	0.69
25:B:60:G:H8	25:B:60:G:C5'	2.02	0.69
26:A:997:G:H1	26:A:1010:U:H3	1.40	0.69
9:K:134:ALA:C	9:K:135:GLN:HG2	2.17	0.69
26:A:1556:A:N6	26:A:1615:G:H1	1.89	0.69
27:1:19:GLN:CG	27:1:50:VAL:HG12	2.21	0.69
9:K:47:ASN:HD21	26:A:623:A:H2	1.39	0.69
13:O:90:ARG:NH2	13:O:118:GLU:HB3	2.07	0.69
21:W:77:LEU:CB	21:W:100:VAL:HG21	2.11	0.69
22:X:83:VAL:HG13	22:X:86:PRO:HD3	1.72	0.69
20:V:62:GLN:CG	20:V:63:GLU:N	2.39	0.69
24:Z:18:LEU:CD1	24:Z:61:LEU:HD23	2.22	0.69
26:A:966:U:H5'	27:1:49:THR:OG1	1.92	0.69
1:C:262:LYS:HE2	26:A:2309:U:OP1	1.93	0.69
21:W:37:LEU:HD11	21:W:69:LEU:HD12	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:38:CYS:SG	28:2:40:GLN:NE2	2.64	0.69
4:F:182:PHE:HD2	4:F:184:PHE:CE2	2.09	0.69
17:S:58:VAL:CG2	17:S:103:LYS:HG3	1.94	0.69
25:B:24:G:C4	25:B:56:C:N3	2.61	0.69
9:K:13:ARG:CZ	9:K:121:LYS:HZ3	2.06	0.69
9:K:25:LEU:HD12	9:K:26:GLY:H	1.56	0.69
30:4:18:CYS:CB	30:4:45:CYS:SG	2.81	0.69
4:F:73:GLU:CG	25:B:42:C:C6	2.73	0.69
9:K:3:THR:HG22	26:A:1113:C:O2	1.92	0.69
25:B:24:G:C6	25:B:56:C:O2	2.42	0.69
26:A:802:C:C4'	31:5:7:THR:HA	2.21	0.69
26:A:1563:A:N1	26:A:1607:C:N4	2.41	0.69
9:K:96:HIS:CB	9:K:99:ARG:HG3	2.23	0.69
30:4:15:CYS:N	30:4:20:HIS:HA	2.07	0.69
1:C:26:ARG:CD	1:C:81:HIS:CG	2.76	0.69
10:L:92:ASP:OD2	10:L:93:PRO:CD	2.41	0.69
25:B:40:A:C8	28:2:2:LYS:HE3	2.27	0.69
25:B:58:A:H8	25:B:58:A:C5'	2.02	0.69
26:A:753:A:H61	26:A:762:U:H3	1.41	0.69
26:A:1566:A:O2'	26:A:1605:G:N1	2.26	0.69
21:W:24:SER:OG	25:B:76:G:H5''	1.92	0.68
22:X:83:VAL:CG1	22:X:86:PRO:HD3	2.23	0.68
26:A:1566:A:O2'	26:A:1605:G:C6	2.37	0.68
10:L:8:LEU:CD1	10:L:19:ILE:CG1	2.71	0.68
19:U:83:ILE:CD1	26:A:1456:G:N1	2.52	0.68
20:V:46:ALA:HB1	26:A:572:C:OP1	1.94	0.68
25:B:19:G:C2	25:B:65:C:N3	2.59	0.68
26:A:2702:A:OP1	33:7:31:ARG:NH1	2.26	0.68
13:O:20:LEU:HD21	13:O:24:LEU:HD11	1.73	0.68
18:T:81:VAL:HG12	18:T:112:VAL:HG12	1.75	0.68
2:D:155:ALA:CB	26:A:2796:A:H8	1.65	0.68
21:W:64:ASN:ND2	21:W:109:GLU:O	2.27	0.68
21:W:101:GLN:CB	21:W:104:GLU:HB2	2.16	0.68
26:A:1608:U:O2'	26:A:1609:G:H5'	1.93	0.68
1:C:58:HIS:HE1	26:A:1788:G:H21	1.41	0.68
19:U:4:ILE:CD1	24:Z:58:TYR:HE1	2.00	0.68
21:W:22:GLY:HA3	25:B:92:G:OP2	1.93	0.68
25:B:40:A:H61	28:2:1:MET:H3	1.37	0.68
25:B:44:C:OP2	28:2:1:MET:N	2.27	0.68
3:E:7:VAL:HG23	3:E:16:GLY:O	1.92	0.68
9:K:4:TYR:CD2	16:R:100:VAL:HG11	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1590:G:C4	26:A:1591:U:H5	1.97	0.68
1:C:73:ASP:OD1	1:C:73:ASP:N	2.26	0.68
13:O:9:ARG:N	13:O:9:ARG:HD2	2.09	0.68
21:W:58:LEU:O	21:W:62:GLY:HA3	1.93	0.68
26:A:1580:A:O2'	26:A:1581:C:H5''	1.94	0.68
28:2:41:CYS:C	28:2:43:PRO:HD2	2.19	0.68
4:F:47:VAL:HG21	4:F:93:GLY:N	2.09	0.68
25:B:24:G:C8	25:B:56:C:O2	2.37	0.68
1:C:76:ASN:O	1:C:98:LEU:HD22	1.92	0.68
9:K:96:HIS:HB3	9:K:99:ARG:CG	2.23	0.68
9:K:113:LYS:N	9:K:113:LYS:HD3	2.06	0.68
20:V:43:LYS:O	20:V:59:ILE:HA	1.93	0.68
22:X:19:GLN:N	22:X:19:GLN:OE1	2.26	0.68
22:X:83:VAL:HG12	22:X:85:ARG:CB	2.24	0.68
25:B:25:G:O2'	25:B:26:A:H5'	1.94	0.68
4:F:45:MET:HG2	4:F:60:ALA:HB1	1.76	0.67
4:F:120:ASP:CG	4:F:122:ARG:HH11	2.01	0.67
13:O:47:TYR:OH	13:O:69:LYS:HG2	1.92	0.67
26:A:1939:U:H3	26:A:1955:A:H62	1.40	0.67
2:D:114:VAL:HG12	2:D:208:VAL:HG12	1.74	0.67
9:K:142:ILE:O	9:K:143:LYS:HB2	1.95	0.67
25:B:83:C:H4'	27:1:52:HIS:ND1	2.08	0.67
26:A:1574:G:O6	26:A:1600:G:N7	2.27	0.67
26:A:1609:G:O2'	26:A:1610:C:H5'	1.94	0.67
30:4:11:ILE:HD13	30:4:27:LYS:CD	2.24	0.67
4:F:79:LYS:HE3	4:F:81:ILE:HG12	1.76	0.67
10:L:108:GLU:HG3	10:L:109:LYS:N	2.08	0.67
26:A:1541:G:O6	26:A:1630:U:O4	2.12	0.67
26:A:1572:G:O6	26:A:1600:G:C2	2.47	0.67
26:A:2349:A:H61	26:A:2386:U:H5'	1.58	0.67
30:4:34:ASP:OD2	30:4:35:ARG:HG2	1.95	0.67
1:C:26:ARG:HG3	1:C:81:HIS:CG	2.29	0.67
1:C:29:PRO:CB	1:C:34:VAL:HG21	2.25	0.67
9:K:25:LEU:HD12	9:K:26:GLY:N	2.10	0.67
12:N:58:ILE:HG23	12:N:108:TYR:CZ	2.30	0.67
18:T:9:SER:HB3	18:T:115:GLU:HB3	1.72	0.67
21:W:101:GLN:HE21	21:W:101:GLN:C	2.01	0.67
10:L:7:ARG:HG2	10:L:7:ARG:HH21	1.58	0.67
18:T:75:THR:O	18:T:118:PRO:HD3	1.95	0.67
26:A:1567:C:N3	26:A:1603:G:O6	2.27	0.67
26:A:1577:C:H5	26:A:1594:G:O6	1.78	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:35:ARG:NH2	1:C:35:ARG:HG2	2.09	0.67
22:X:75:ARG:HE	26:A:2558:C:N4	1.93	0.67
24:Z:18:LEU:HB3	24:Z:61:LEU:HD21	1.76	0.67
26:A:1568:C:C3'	26:A:1569:A:H8	2.06	0.67
30:4:28:ASN:OD1	30:4:31:ASN:N	2.27	0.67
1:C:25:THR:HG23	1:C:81:HIS:CB	1.98	0.67
25:B:10:G:C6	25:B:107:A:N1	2.62	0.67
26:A:747:A:N6	26:A:768:G:O2'	2.28	0.67
26:A:1540:U:H3	26:A:1632:G:H1	1.43	0.67
26:A:1592:G:O2'	26:A:1593:U:H6	1.77	0.67
1:C:22:ALA:O	1:C:23:GLU:HB2	1.94	0.67
9:K:113:LYS:HD3	9:K:113:LYS:H	1.60	0.67
9:K:142:ILE:HG22	26:A:1130:C:N4	1.78	0.67
25:B:35:G:C2	25:B:36:U:C5	2.83	0.67
3:E:144:PHE:CD1	3:E:148:LEU:CG	2.77	0.67
13:O:95:THR:HG22	13:O:115:LEU:CD2	2.25	0.67
20:V:30:ARG:O	20:V:31:ASN:HB2	1.95	0.67
25:B:20:G:H2'	25:B:21:C:H5'	1.77	0.67
3:E:107:ILE:HD11	26:A:710:G:OP1	1.95	0.67
18:T:67:ASN:ND2	26:A:574:C:O2'	2.29	0.67
19:U:9:ASP:N	19:U:9:ASP:OD1	2.25	0.67
30:4:36:LEU:HG	30:4:37:GLU:H	1.60	0.67
1:C:29:PRO:HG2	1:C:34:VAL:HG21	1.75	0.66
1:C:222:ARG:NH1	26:A:2006:A:OP2	2.28	0.66
4:F:111:ILE:HD11	4:F:182:PHE:HA	1.76	0.66
6:H:43:ALA:O	6:H:47:ALA:HB3	1.95	0.66
9:K:3:THR:HG23	26:A:1113:C:O2	1.95	0.66
22:X:76:LYS:NZ	26:A:973:G:OP1	2.27	0.66
25:B:2:U:H3	25:B:115:A:H61	1.43	0.66
26:A:1583:U:O2	26:A:1589:G:C2	2.49	0.66
10:L:109:LYS:C	10:L:110:LYS:HG3	2.17	0.66
19:U:69:THR:CG2	19:U:73:PHE:O	2.43	0.66
30:4:15:CYS:C	30:4:20:HIS:HA	2.20	0.66
1:C:56:GLY:HA2	26:A:807:C:OP1	1.95	0.66
19:U:10:ILE:HD13	19:U:10:ILE:N	2.10	0.66
4:F:32:VAL:O	4:F:33:MET:CB	2.43	0.66
26:A:1568:C:H2'	26:A:1569:A:C8	2.30	0.66
13:O:20:LEU:HD21	13:O:24:LEU:CD1	2.24	0.66
20:V:4:HIS:HE1	20:V:96:ARG:HH22	1.39	0.66
20:V:96:ARG:HG3	20:V:96:ARG:HH21	1.61	0.66
21:W:9:ASN:HD21	21:W:57:VAL:HG13	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:85:C:H2'	25:B:86:U:H5''	1.75	0.66
26:A:1568:C:H3'	26:A:1569:A:C8	2.30	0.66
26:A:1607:C:H6	26:A:1607:C:O5'	1.78	0.66
25:B:12:C:O2'	25:B:13:C:OP2	2.11	0.66
26:A:1578:G:N2	26:A:1592:G:H2'	2.09	0.66
3:E:201:LEU:O	3:E:201:LEU:HD23	1.94	0.66
20:V:43:LYS:NZ	20:V:43:LYS:HB3	2.09	0.66
21:W:8:PRO:CB	21:W:68:THR:OG1	2.44	0.66
4:F:87:ARG:HB3	4:F:90:MET:HG3	1.78	0.66
9:K:96:HIS:HB2	9:K:99:ARG:HG3	1.77	0.66
26:A:1577:C:O2'	26:A:1578:G:H5'	1.95	0.66
1:C:100:GLY:O	26:A:1720:G:O2'	2.14	0.66
9:K:27:ARG:HH11	9:K:27:ARG:HG3	1.59	0.66
28:2:14:VAL:HB	28:2:22:PHE:HB2	1.78	0.65
26:A:1568:C:H3'	26:A:1569:A:H8	1.61	0.65
32:6:26:LYS:NZ	32:6:45:ASP:O	2.28	0.65
1:C:29:PRO:HB2	1:C:34:VAL:HG21	1.77	0.65
11:M:61:LEU:HD21	32:6:24:ARG:HH11	1.60	0.65
12:N:124:LYS:NZ	26:A:2691:C:O2	2.29	0.65
18:T:41:ASP:CG	29:3:38:LYS:HB2	2.20	0.65
26:A:1830:C:H4'	31:5:10:PRO:HD3	1.79	0.65
31:5:5:LYS:O	31:5:6:ARG:HG2	1.96	0.65
3:E:45:LYS:HG3	26:A:709:U:C4	2.31	0.65
4:F:6:LYS:HE2	4:F:6:LYS:CA	2.26	0.65
20:V:72:MET:HG2	20:V:80:PRO:HB2	1.78	0.65
25:B:70:G:H22	25:B:103:G:H1	1.43	0.65
4:F:110:LEU:HD23	4:F:111:ILE:H	1.60	0.65
21:W:102:ARG:NH2	21:W:138:LEU:HD21	2.12	0.65
1:C:35:ARG:HG2	1:C:35:ARG:HH21	1.59	0.65
2:D:144:VAL:HG22	2:D:147:ARG:HE	1.62	0.65
9:K:25:LEU:HD22	9:K:62:ILE:CD1	2.27	0.65
26:A:1563:A:H8	26:A:1563:A:OP2	1.80	0.65
31:5:6:ARG:O	31:5:7:THR:OG1	2.09	0.65
1:C:25:THR:HG1	1:C:81:HIS:CE1	2.09	0.65
4:F:45:MET:HA	4:F:45:MET:HE2	1.78	0.65
9:K:85:ARG:NH2	26:A:2866:A:OP2	2.26	0.65
9:K:116:ARG:NH2	26:A:615:A:H5''	2.12	0.65
18:T:116:SER:C	18:T:118:PRO:HD2	2.21	0.65
26:A:1573:U:H1'	26:A:1574:G:P	2.37	0.65
3:E:8:LYS:HE3	3:E:148:LEU:HD22	1.79	0.65
3:E:7:VAL:HB	3:E:16:GLY:CA	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:57:ILE:HG12	4:F:91:PRO:HB2	1.77	0.65
9:K:96:HIS:CB	9:K:99:ARG:HG2	2.25	0.65
13:O:77:HIS:CG	26:A:1674:G:H2'	2.11	0.65
20:V:2:LYS:CE	20:V:83:VAL:HG12	2.27	0.65
22:X:16:SER:O	22:X:17:ALA:HB3	1.96	0.65
21:W:77:LEU:CD2	21:W:100:VAL:HG21	2.26	0.64
4:F:46:GLY:O	4:F:47:VAL:CB	2.46	0.64
20:V:45:THR:C	26:A:571:A:O2'	2.38	0.64
25:B:79:A:H2	25:B:94:G:H1	1.42	0.64
30:4:47:THR:OG1	30:4:49:GLN:NE2	2.30	0.64
21:W:9:ASN:ND2	21:W:57:VAL:CG1	2.53	0.64
26:A:1573:U:H1'	26:A:1574:G:OP1	1.97	0.64
30:4:18:CYS:SG	30:4:19:LYS:NZ	2.70	0.64
4:F:10:ARG:HG2	4:F:10:ARG:NH1	2.05	0.64
26:A:1563:A:C6	26:A:1607:C:N4	2.65	0.64
26:A:1592:G:HO2'	26:A:1593:U:H6	1.43	0.64
3:E:107:ILE:HD11	26:A:710:G:H5''	1.79	0.64
25:B:96:A:H2	26:A:977:G:N2	1.96	0.64
1:C:108:PRO:HD2	1:C:111:LEU:HD22	1.80	0.64
20:V:99:LYS:NZ	20:V:99:LYS:HB3	2.12	0.64
26:A:1610:C:O5'	26:A:1610:C:H6	1.80	0.64
3:E:192:ASP:HB3	11:M:5:LYS:HZ1	0.81	0.64
22:X:17:ALA:HB1	26:A:2485:C:P	2.37	0.64
26:A:1565:A:C2	26:A:1606:G:C4	2.86	0.64
31:5:6:ARG:HB2	31:5:6:ARG:HH11	1.62	0.64
4:F:55:LYS:HB2	4:F:55:LYS:HZ2	1.63	0.64
13:O:29:PHE:CD2	13:O:79:LEU:CD1	2.77	0.64
19:U:75:LYS:O	26:A:61:G:H5'	1.96	0.64
25:B:29:C:N4	25:B:55:G:H1	1.94	0.64
1:C:37:LEU:HD23	1:C:62:TYR:CB	2.27	0.64
13:O:56:LYS:NZ	13:O:94:TYR:OH	2.21	0.64
1:C:256:ARG:CD	1:C:258:ARG:HD2	2.28	0.64
3:E:150:GLU:HB2	3:E:193:ASP:OD2	1.98	0.64
4:F:53:ASP:O	4:F:56:LEU:HD21	1.97	0.64
10:L:80:ASP:OD2	15:Q:61:ARG:CZ	2.46	0.64
13:O:45:ARG:NH1	26:A:3102:U:O2	2.31	0.64
2:D:48:SER:HB2	2:D:92:VAL:HG21	1.80	0.63
4:F:132:THR:HG21	14:P:6:VAL:HG22	1.77	0.63
9:K:1:MET:N	9:K:2:PRO:HD3	2.13	0.63
10:L:91:ASN:OD1	10:L:92:ASP:N	2.30	0.63
12:N:60:ARG:CZ	26:A:1194:C:P	2.86	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:2:LYS:NZ	20:V:85:TYR:CD2	2.62	0.63
20:V:96:ARG:HH21	20:V:96:ARG:CG	2.11	0.63
13:O:33:ARG:CD	13:O:114:GLU:CD	2.58	0.63
18:T:44:ARG:HH12	29:3:55:ASP:N	1.90	0.63
18:T:75:THR:CB	18:T:118:PRO:HG3	2.28	0.63
21:W:104:GLU:HA	21:W:104:GLU:OE1	1.98	0.63
26:A:1582:C:H2'	26:A:1583:U:H5'	1.79	0.63
1:C:25:THR:CG2	1:C:82:ILE:N	2.62	0.63
4:F:11:LEU:HD13	4:F:108:ASP:CB	2.27	0.63
11:M:76:GLN:NE2	26:A:720:C:N3	2.46	0.63
19:U:4:ILE:N	19:U:4:ILE:HD12	2.13	0.63
4:F:66:LEU:CD2	28:2:27:THR:CG2	2.73	0.63
4:F:118:ILE:HD12	4:F:118:ILE:N	2.02	0.63
20:V:89:ASP:N	20:V:89:ASP:OD1	2.31	0.63
25:B:35:G:C2	25:B:36:U:C4	2.85	0.63
3:E:149:THR:HG23	3:E:150:GLU:HG3	1.79	0.63
4:F:49:ASP:CB	4:F:56:LEU:CD1	2.65	0.63
4:F:66:LEU:CD2	28:2:27:THR:HG22	2.28	0.63
5:G:55:ARG:HD2	5:G:62:SER:HB3	1.81	0.63
19:U:5:THR:CG2	19:U:6:ASP:H	2.07	0.63
19:U:69:THR:HG21	26:A:61:G:O2'	1.98	0.63
26:A:1598:U:O4	26:A:1601:G:N1	2.31	0.63
31:5:26:ARG:HD2	31:5:26:ARG:N	2.12	0.63
1:C:240:THR:HG22	1:C:242:GLY:H	1.64	0.63
3:E:3:LEU:HD11	3:E:26:ASP:OD1	1.99	0.63
20:V:28:PRO:HG3	26:A:83:C:OP1	1.98	0.63
20:V:86:ARG:HB3	20:V:97:ILE:HG12	1.80	0.63
24:Z:48:ARG:O	24:Z:52:GLN:NE2	2.31	0.63
25:B:57:U:H2'	25:B:58:A:C5'	2.21	0.63
26:A:1581:C:C2'	26:A:1582:C:C6	2.79	0.63
26:A:1604:G:C2'	26:A:1605:G:H5''	2.28	0.63
4:F:11:LEU:HD22	4:F:108:ASP:N	2.13	0.63
3:E:52:THR:OG1	3:E:92:GLY:HA3	1.99	0.63
3:E:118:ARG:NH1	11:M:4:ILE:O	2.31	0.63
9:K:96:HIS:HB2	9:K:99:ARG:CG	2.29	0.63
13:O:26:THR:HG23	13:O:75:VAL:HG21	1.81	0.63
25:B:19:G:C6	25:B:20:G:N7	2.67	0.63
25:B:25:G:N2	25:B:114:A:C4	2.62	0.63
10:L:92:ASP:OD2	10:L:93:PRO:N	2.32	0.63
26:A:1564:A:C3'	26:A:1565:A:H5''	2.28	0.63
30:4:22:ASN:OD1	30:4:22:ASN:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:THR:HG21	1:C:81:HIS:CG	2.34	0.62
1:C:37:LEU:CD2	1:C:62:TYR:HD1	2.12	0.62
4:F:70:GLN:NE2	25:B:43:C:H4'	2.14	0.62
9:K:25:LEU:HD22	9:K:62:ILE:HD12	1.81	0.62
19:U:6:ASP:OD2	24:Z:23:ARG:HG3	1.98	0.62
25:B:82:A:N1	25:B:91:G:O6	2.32	0.62
25:B:84:C:C2'	25:B:85:C:H5'	2.28	0.62
26:A:1586:C:C3'	26:A:1587:G:H5''	2.28	0.62
28:2:38:CYS:HB2	28:2:40:GLN:NE2	2.14	0.62
31:5:38:ARG:HA	31:5:45:LEU:HD21	1.80	0.62
1:C:35:ARG:HH21	1:C:35:ARG:CG	2.12	0.62
4:F:118:ILE:HG13	4:F:144:MET:HG2	1.79	0.62
10:L:7:ARG:HH21	10:L:7:ARG:CG	2.12	0.62
19:U:29:TYR:CZ	19:U:93:ILE:HB	2.34	0.62
20:V:43:LYS:HG2	26:A:568:A:H4'	1.81	0.62
25:B:21:C:C6	25:B:21:C:H3'	2.35	0.62
26:A:1563:A:C5	26:A:1565:A:C5	2.87	0.62
26:A:1571:C:N3	26:A:1601:G:N2	2.47	0.62
30:4:15:CYS:CB	30:4:20:HIS:H	2.12	0.62
3:E:69:LYS:HE2	26:A:2668:G:OP2	1.98	0.62
5:G:154:ARG:HD2	5:G:155:PRO:HD2	1.82	0.62
25:B:40:A:H8	28:2:2:LYS:HE3	1.63	0.62
26:A:1590:G:C6	26:A:1591:U:C4	2.86	0.62
1:C:96:HIS:HE1	1:C:102:LYS:HZ2	1.45	0.62
1:C:257:THR:CG2	26:A:2020:A:O2'	2.47	0.62
19:U:29:TYR:CD1	19:U:93:ILE:HG21	2.34	0.62
19:U:60:ALA:HB2	26:A:1456:G:H4'	1.81	0.62
20:V:83:VAL:CG1	20:V:96:ARG:HG3	2.27	0.62
1:C:37:LEU:CD2	1:C:62:TYR:CD1	2.81	0.62
13:O:33:ARG:HG3	13:O:114:GLU:HG2	1.78	0.62
17:S:6:ILE:CG2	17:S:7:VAL:N	2.63	0.62
25:B:24:G:C4	25:B:56:C:C2	2.88	0.62
25:B:88:C:H2'	25:B:89:C:C5	2.35	0.62
28:2:44:PHE:O	28:2:48:LYS:CG	2.42	0.62
4:F:9:PRO:HD2	4:F:12:LYS:HZ2	1.64	0.62
13:O:11:GLY:O	13:O:12:GLY:C	2.42	0.62
25:B:21:C:H3'	25:B:21:C:H6	1.65	0.62
25:B:60:G:C2'	25:B:61:C:H5'	2.29	0.62
3:E:118:ARG:HH11	11:M:3:VAL:CG1	2.13	0.62
17:S:6:ILE:HG22	17:S:7:VAL:H	1.64	0.62
19:U:69:THR:HG23	19:U:73:PHE:O	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1603:G:C2	26:A:1604:G:C5	2.88	0.62
26:A:1609:G:H2'	26:A:1610:C:C6	2.35	0.62
25:B:79:A:C2	25:B:94:G:N1	2.58	0.62
26:A:1122:C:H2'	26:A:1129:G:H2'	1.82	0.62
4:F:76:ARG:NH1	25:B:41:U:H3	1.98	0.62
13:O:67:MET:HG3	13:O:76:VAL:HG11	1.81	0.62
19:U:29:TYR:CE1	19:U:93:ILE:HG21	2.34	0.62
30:4:19:LYS:HD3	30:4:44:ASN:HB2	1.80	0.62
26:A:1563:A:C8	26:A:1565:A:N7	2.68	0.62
1:C:63:ARG:HH12	26:A:1788:G:P	2.22	0.61
2:D:60:ARG:NH2	26:A:3052:A:OP1	2.33	0.61
4:F:126:PRO:O	4:F:174:ARG:NH1	2.33	0.61
7:I:27:GLU:HB2	7:I:106:LYS:HE3	1.81	0.61
9:K:141:GLU:CD	9:K:143:LYS:HG3	2.25	0.61
25:B:59:A:H2'	25:B:59:A:N3	2.14	0.61
4:F:51:ALA:HB2	4:F:90:MET:CE	2.15	0.61
11:M:84:ASN:ND2	11:M:117:LYS:O	2.33	0.61
20:V:2:LYS:CD	20:V:83:VAL:HG12	2.30	0.61
30:4:11:ILE:HD13	30:4:27:LYS:HD3	1.81	0.61
30:4:19:LYS:HG3	30:4:21:ARG:HG2	1.82	0.61
1:C:256:ARG:NE	1:C:258:ARG:HE	1.97	0.61
13:O:7:GLY:O	13:O:9:ARG:NH1	2.33	0.61
25:B:19:G:C8	25:B:19:G:H3'	2.35	0.61
1:C:256:ARG:HD3	1:C:258:ARG:NE	2.14	0.61
3:E:192:ASP:CB	11:M:5:LYS:HZ3	1.96	0.61
1:C:73:ASP:CB	1:C:120:GLY:HA3	2.28	0.61
8:J:96:LYS:HE3	21:W:120:PRO:CB	2.27	0.61
10:L:107:ARG:NH1	15:Q:33:GLU:CG	2.63	0.61
11:M:51:GLU:CG	32:6:57:ARG:HH11	2.11	0.61
12:N:60:ARG:CZ	26:A:1194:C:OP2	2.48	0.61
13:O:43:ALA:CA	13:O:46:PRO:HD2	2.30	0.61
20:V:86:ARG:HD3	20:V:97:ILE:CG1	2.30	0.61
21:W:102:ARG:NH2	21:W:138:LEU:CD1	2.57	0.61
28:2:16:CYS:SG	28:2:17:GLY:N	2.74	0.61
20:V:86:ARG:CB	20:V:97:ILE:HG13	2.30	0.61
21:W:40:HIS:C	21:W:42:THR:H	2.09	0.61
4:F:45:MET:HB3	4:F:94:ALA:N	2.16	0.61
26:A:1610:C:H2'	26:A:1611:A:H8	1.65	0.61
26:A:1754:G:O6	26:A:1759:A:N1	2.33	0.61
30:4:13:LEU:O	30:4:23:TYR:N	2.34	0.61
30:4:18:CYS:HG	30:4:45:CYS:HG	1.42	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:110:PRO:O	9:K:115:GLY:HA3	2.01	0.61
13:O:8:PRO:HG3	26:A:1870:U:N3	2.14	0.61
4:F:77:ALA:HB2	4:F:92:ILE:HD11	1.82	0.60
19:U:57:VAL:HG22	19:U:84:VAL:HG12	1.82	0.60
19:U:68:ARG:HB2	26:A:1450:C:OP1	2.01	0.60
1:C:241:SER:OG	26:A:2127:G:OP1	2.18	0.60
26:A:2256:G:N2	26:A:2796:A:OP2	2.33	0.60
3:E:7:VAL:H	3:E:16:GLY:C	1.99	0.60
10:L:109:LYS:HG2	10:L:110:LYS:HG3	1.82	0.60
1:C:25:THR:CG2	1:C:81:HIS:CG	2.83	0.60
3:E:121:ASN:ND2	11:M:3:VAL:HG22	2.16	0.60
24:Z:18:LEU:HD13	24:Z:61:LEU:HD21	1.82	0.60
3:E:35:HIS:HE1	26:A:1359:G:O2'	1.85	0.60
3:E:121:ASN:ND2	11:M:3:VAL:CG2	2.64	0.60
3:E:155:LEU:HB3	3:E:194:VAL:HG12	1.83	0.60
8:J:129:ILE:HA	26:A:1198:C:H1'	1.84	0.60
9:K:77:HIS:CD2	9:K:78:SER:O	2.54	0.60
1:C:262:LYS:HD2	1:C:262:LYS:N	2.17	0.60
2:D:27:THR:HG21	2:D:198:ILE:HG12	1.84	0.60
8:J:57:PRO:HD3	8:J:76:PRO:HD3	1.84	0.60
11:M:61:LEU:HD22	32:6:24:ARG:HH11	1.64	0.60
13:O:43:ALA:O	13:O:46:PRO:HD2	2.02	0.60
20:V:59:ILE:O	20:V:59:ILE:HG12	2.02	0.60
26:A:808:A:O2'	26:A:1468:A:N3	2.35	0.60
19:U:4:ILE:O	19:U:4:ILE:HG22	2.01	0.60
25:B:25:G:N2	25:B:114:A:C2'	2.61	0.60
26:A:1562:C:O2'	26:A:1563:A:H5'	2.02	0.60
27:1:51:HIS:H	27:1:51:HIS:HD2	1.46	0.60
1:C:54:LYS:HZ3	26:A:2031:G:H5''	1.65	0.60
3:E:42:LEU:O	26:A:531:A:N6	2.34	0.60
3:E:186:TYR:CE1	11:M:6:LEU:HD11	2.37	0.60
8:J:111:ALA:HA	8:J:114:LYS:HB2	1.83	0.60
10:L:104:ARG:HH12	15:Q:33:GLU:HB2	1.67	0.60
20:V:99:LYS:HB3	20:V:99:LYS:HZ2	1.66	0.60
25:B:24:G:C8	25:B:56:C:H2'	2.37	0.60
26:A:2713:G:OP1	34:8:6:ARG:NH2	2.33	0.60
33:7:22:ARG:CD	33:7:36:GLN:O	2.49	0.60
5:G:63:ARG:HB3	26:A:2973:A:H4'	1.84	0.60
19:U:69:THR:C	19:U:71:THR:H	2.09	0.60
4:F:44:ASN:HD22	4:F:44:ASN:C	2.10	0.59
13:O:9:ARG:HG2	13:O:14:SER:CA	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:16:HIS:CD2	26:A:1390:A:N9	2.70	0.59
20:V:89:ASP:O	20:V:90:GLU:C	2.43	0.59
25:B:24:G:C2'	25:B:56:C:C4	2.85	0.59
25:B:36:U:O5'	25:B:36:U:H6	1.84	0.59
25:B:60:G:O2'	25:B:61:C:C5'	2.42	0.59
30:4:15:CYS:HB2	30:4:20:HIS:H	1.66	0.59
1:C:261:ASN:O	1:C:262:LYS:HB2	2.03	0.59
3:E:4:LYS:HD3	3:E:5:VAL:N	2.17	0.59
4:F:46:GLY:C	4:F:47:VAL:CG2	2.49	0.59
12:N:75:THR:HA	12:N:90:PRO:HA	1.84	0.59
21:W:6:ASN:O	21:W:6:ASN:ND2	2.35	0.59
21:W:36:VAL:HG21	25:B:74:A:H2	1.67	0.59
25:B:34:G:C6	25:B:44:C:C5	2.89	0.59
25:B:84:C:C4	25:B:85:C:C2	2.90	0.59
25:B:87:U:H3'	25:B:88:C:O4'	2.02	0.59
1:C:21:PHE:O	1:C:24:ILE:HG13	2.02	0.59
1:C:73:ASP:O	1:C:119:SER:O	2.19	0.59
1:C:257:THR:HG22	1:C:257:THR:O	2.01	0.59
1:C:262:LYS:HE3	26:A:2309:U:OP1	2.02	0.59
15:Q:5:ASP:O	15:Q:9:GLN:HB3	2.02	0.59
26:A:325:U:O2	26:A:450:G:N2	2.30	0.59
27:1:50:VAL:O	27:1:50:VAL:HG23	2.01	0.59
18:T:75:THR:HB	18:T:118:PRO:CG	2.32	0.59
3:E:45:LYS:CG	26:A:709:U:O4	2.49	0.59
25:B:19:G:C8	25:B:19:G:C3'	2.85	0.59
26:A:1608:U:C2	26:A:1609:G:N7	2.69	0.59
1:C:254:GLU:HG2	1:C:254:GLU:O	2.03	0.59
25:B:4:A:N3	25:B:25:G:O6	2.34	0.59
13:O:90:ARG:HH21	13:O:118:GLU:CB	2.10	0.59
18:T:82:TYR:HD2	18:T:111:THR:HB	1.68	0.59
19:U:4:ILE:CD1	24:Z:58:TYR:OH	2.46	0.59
19:U:73:PHE:HZ	31:5:43:ARG:NH2	2.01	0.59
21:W:29:ARG:HH11	25:B:90:G:H5'	1.65	0.59
26:A:285:U:H3'	26:A:286:G:H4'	1.85	0.59
1:C:37:LEU:HD21	1:C:62:TYR:HD1	1.67	0.59
3:E:107:ILE:HD12	26:A:710:G:OP1	2.02	0.59
3:E:127:VAL:O	3:E:198:VAL:HG23	2.02	0.59
12:N:60:ARG:O	21:W:190:LEU:CD1	2.51	0.59
18:T:75:THR:HB	18:T:118:PRO:HG3	1.83	0.59
20:V:2:LYS:HD2	20:V:83:VAL:CB	2.32	0.59
24:Z:18:LEU:CD1	24:Z:61:LEU:HD21	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:993:G:N2	26:A:1015:A:OP2	2.36	0.59
26:A:1552:A:N6	26:A:1616:A:OP2	2.35	0.59
11:M:68:LYS:NZ	26:A:244:A:OP1	2.36	0.59
18:T:84:ASP:OD1	26:A:20:G:N2	2.23	0.59
18:T:85:GLU:O	26:A:21:G:O2'	2.20	0.59
20:V:45:THR:C	26:A:571:A:HO2'	2.08	0.59
25:B:60:G:C2'	25:B:61:C:C5'	2.80	0.59
26:A:1604:G:H2'	26:A:1605:G:C5'	2.31	0.59
33:7:2:LYS:NZ	33:7:31:ARG:O	2.32	0.59
1:C:62:TYR:CE1	26:A:2033:U:H3'	2.38	0.59
1:C:96:HIS:CE1	1:C:102:LYS:HZ2	2.14	0.59
3:E:144:PHE:CD2	3:E:148:LEU:CD1	2.79	0.59
19:U:77:LYS:HE2	19:U:79:THR:HA	1.84	0.59
19:U:77:LYS:HZ3	19:U:79:THR:HG22	1.67	0.59
20:V:43:LYS:HB3	20:V:43:LYS:HZ3	1.68	0.59
20:V:86:ARG:CD	20:V:97:ILE:HG13	2.32	0.59
25:B:55:G:H8	25:B:55:G:O5'	1.86	0.59
26:A:1573:U:O2'	26:A:1574:G:OP1	2.17	0.59
30:4:28:ASN:CG	30:4:31:ASN:HB2	2.28	0.59
1:C:31:LYS:HE3	26:A:1648:A:O2'	2.03	0.58
4:F:70:GLN:OE1	4:F:96:VAL:HG23	2.03	0.58
15:Q:19:PHE:HA	15:Q:88:ARG:HH12	1.68	0.58
26:A:858:A:O2'	26:A:1877:U:OP1	2.20	0.58
26:A:1174:G:O2'	26:A:1221:A:N6	2.36	0.58
2:D:154:CYS:CB	26:A:2799:C:C5'	2.72	0.58
20:V:86:ARG:HB3	20:V:97:ILE:HG13	1.85	0.58
25:B:31:C:H42	25:B:51:G:H1	1.51	0.58
25:B:96:A:C2	26:A:977:G:N2	2.71	0.58
26:A:1568:C:C3'	26:A:1569:A:C8	2.86	0.58
3:E:170:ARG:NH2	26:A:422:A:O2'	2.36	0.58
13:O:52:ILE:HD12	13:O:94:TYR:HB2	1.85	0.58
17:S:72:LYS:NZ	26:A:1337:G:N7	2.51	0.58
26:A:1595:G:O5'	26:A:1596:C:OP2	2.21	0.58
12:N:58:ILE:CG2	12:N:108:TYR:CZ	2.87	0.58
20:V:96:ARG:CZ	20:V:96:ARG:HB2	2.33	0.58
21:W:6:ASN:HB3	21:W:138:LEU:O	1.96	0.58
24:Z:18:LEU:CB	24:Z:61:LEU:HD21	2.33	0.58
26:A:1187:A:H4'	26:A:1188:A:H5''	1.85	0.58
3:E:164:VAL:O	3:E:168:SER:OG	2.20	0.58
12:N:58:ILE:HG21	12:N:108:TYR:CD1	2.36	0.58
13:O:29:PHE:HB3	13:O:79:LEU:HD12	0.60	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:58:ASN:HD22	26:A:1456:G:H21	1.49	0.58
21:W:82:ALA:O	21:W:83:LEU:HB2	2.04	0.58
28:2:45:TYR:O	28:2:49:GLN:HG3	2.03	0.58
3:E:9:THR:HG22	3:E:128:THR:OG1	2.04	0.58
12:N:85:SER:HG	22:X:8:SER:HB3	1.64	0.58
26:A:1397:U:H3	26:A:1401:A:H62	1.50	0.58
26:A:1568:C:C2'	26:A:1569:A:C8	2.87	0.58
1:C:51:THR:HG21	1:C:54:LYS:HE3	1.86	0.58
1:C:176:ARG:HG3	1:C:182:ILE:HG12	1.86	0.58
14:P:39:VAL:HA	14:P:103:ASP:HB3	1.86	0.58
24:Z:62:ARG:O	24:Z:62:ARG:HD3	2.03	0.58
25:B:4:A:C2	25:B:26:A:N6	2.71	0.58
25:B:84:C:N4	25:B:85:C:N3	2.52	0.58
26:A:1201:G:N2	26:A:1204:A:OP2	2.34	0.58
26:A:1584:U:C5	26:A:1586:C:OP2	2.57	0.58
3:E:90:VAL:CG1	26:A:678:A:O5'	2.51	0.58
5:G:2:SER:N	26:A:2973:A:OP1	2.37	0.58
18:T:6:GLU:HG3	18:T:6:GLU:O	2.03	0.58
26:A:122:A:OP2	31:5:22:ARG:NH1	2.37	0.58
26:A:1000:C:OP2	26:A:1002:C:N4	2.36	0.58
4:F:11:LEU:HD22	4:F:108:ASP:HB3	1.85	0.58
4:F:53:ASP:O	4:F:56:LEU:HD22	2.02	0.58
13:O:16:HIS:HD2	26:A:1390:A:N9	2.02	0.58
19:U:19:LYS:CD	26:A:1508:A:H62	1.78	0.58
22:X:83:VAL:HG13	22:X:83:VAL:O	2.04	0.58
26:A:1574:G:H5''	26:A:1575:A:OP1	2.04	0.58
26:A:1584:U:C6	26:A:1586:C:OP2	2.57	0.58
10:L:76:TYR:O	15:Q:71:ARG:HD2	2.04	0.57
13:O:29:PHE:HE2	13:O:51:LEU:HD12	1.56	0.57
19:U:94:ASP:O	19:U:96:PHE:N	2.28	0.57
21:W:102:ARG:HH22	21:W:138:LEU:HD11	1.66	0.57
26:A:1703:G:H1	26:A:1726:C:N4	2.01	0.57
1:C:256:ARG:HG3	1:C:258:ARG:HD2	1.86	0.57
1:C:260:PRO:O	1:C:263:PRO:HD3	2.04	0.57
12:N:59:LYS:C	12:N:60:ARG:HG3	2.29	0.57
30:4:13:LEU:N	30:4:23:TYR:O	2.34	0.57
1:C:55:GLY:CA	1:C:218:ARG:HD3	2.33	0.57
26:A:1249:G:N2	26:A:1250:U:O4	2.35	0.57
26:A:1600:G:H3'	26:A:1601:G:C5'	2.34	0.57
9:K:15:TRP:CD1	9:K:15:TRP:H	2.23	0.57
15:Q:13:ARG:NH1	15:Q:80:ILE:O	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:9:SER:HB2	18:T:114:VAL:O	2.04	0.57
25:B:10:G:C2	25:B:107:A:H2	2.19	0.57
25:B:21:C:C6	25:B:21:C:C3'	2.88	0.57
3:E:144:PHE:HE1	3:E:148:LEU:CD2	2.05	0.57
12:N:134:ARG:HH21	21:W:129:ASN:ND2	2.00	0.57
14:P:50:GLN:NE2	25:B:7:G:C2	2.69	0.57
15:Q:19:PHE:O	15:Q:49:ARG:NH1	2.37	0.57
20:V:4:HIS:CG	20:V:96:ARG:NH1	2.71	0.57
25:B:14:A:OP2	25:B:70:G:O2'	2.22	0.57
4:F:23:LEU:CD2	4:F:29:TYR:OH	2.53	0.57
8:J:44:TYR:O	8:J:48:THR:CB	2.51	0.57
26:A:1518:A:HO2'	26:A:1692:G:HO2'	1.52	0.57
26:A:2508:C:OP2	30:4:8:ARG:HG3	2.04	0.57
1:C:256:ARG:HD3	1:C:258:ARG:HD2	1.85	0.57
3:E:51:SER:HB2	26:A:35:A:H4'	1.87	0.57
9:K:142:ILE:HG21	26:A:1130:C:H42	1.63	0.57
13:O:20:LEU:CD2	13:O:24:LEU:HD12	2.34	0.57
24:Z:13:LEU:CD2	24:Z:17:GLU:C	2.78	0.57
26:A:1573:U:O4	26:A:1596:C:N4	2.28	0.57
26:A:1608:U:O5'	26:A:1608:U:H6	1.87	0.57
13:O:79:LEU:HD23	13:O:80:PHE:N	2.18	0.57
26:A:1100:C:O2	34:8:21:ARG:NH2	2.37	0.57
26:A:1590:G:O2'	26:A:1591:U:O4'	2.20	0.57
26:A:1996:U:OP2	26:A:2001:A:N6	2.36	0.57
4:F:47:VAL:HG23	4:F:48:GLY:H	1.69	0.57
4:F:109:ARG:O	4:F:113:ILE:HB	2.04	0.57
5:G:95:TYR:HE2	5:G:161:LYS:HB3	1.69	0.57
13:O:20:LEU:CD1	13:O:40:LYS:NZ	2.68	0.57
13:O:24:LEU:HB3	13:O:44:LEU:HD22	1.86	0.57
25:B:24:G:N7	25:B:56:C:C2'	2.68	0.57
1:C:20:ASP:O	1:C:21:PHE:HB2	2.04	0.57
1:C:26:ARG:HG3	1:C:81:HIS:ND1	2.19	0.57
8:J:96:LYS:CE	21:W:120:PRO:CB	2.66	0.57
20:V:2:LYS:HD2	20:V:83:VAL:HG12	1.73	0.57
20:V:2:LYS:CE	20:V:85:TYR:CE2	2.88	0.57
21:W:98:LEU:HD23	21:W:98:LEU:C	2.29	0.57
26:A:1042:A:H1'	27:1:42:GLN:HE22	1.69	0.57
1:C:25:THR:OG1	1:C:81:HIS:ND1	1.92	0.56
9:K:13:ARG:CZ	9:K:121:LYS:NZ	2.68	0.56
10:L:78:LYS:HD3	15:Q:70:GLU:OE1	2.04	0.56
19:U:83:ILE:HD13	26:A:1456:G:N3	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:301:U:H5'	26:A:302:U:H4'	1.85	0.56
30:4:13:LEU:O	30:4:22:ASN:HA	2.05	0.56
3:E:75:ARG:NH1	26:A:2669:G:OP1	2.38	0.56
6:H:115:ARG:NH1	26:A:163:U:O2	2.37	0.56
8:J:30:LEU:HA	8:J:33:HIS:HD2	1.69	0.56
13:O:56:LYS:HD3	13:O:87:TYR:O	2.05	0.56
18:T:117:ARG:N	18:T:118:PRO:HD2	2.20	0.56
20:V:42:LYS:O	26:A:568:A:O2'	2.23	0.56
30:4:49:GLN:O	30:4:51:HIS:HD2	1.87	0.56
3:E:143:THR:O	3:E:147:THR:CB	2.53	0.56
4:F:64:LEU:HD11	4:F:94:ALA:O	2.05	0.56
4:F:99:ARG:HD3	25:B:45:G:H8	1.66	0.56
4:F:130:ASP:OD2	4:F:134:ASN:ND2	2.38	0.56
17:S:4:TYR:CD2	17:S:15:LYS:HE3	2.41	0.56
20:V:42:LYS:HG3	26:A:586:U:H4'	1.86	0.56
26:A:346:C:H41	26:A:445:U:H3	1.53	0.56
26:A:1530:G:H21	26:A:1805:G:H22	1.54	0.56
26:A:1580:A:N1	26:A:1592:G:O4'	2.38	0.56
26:A:3014:A:H62	26:A:3113:A:H2	1.53	0.56
27:1:19:GLN:HG3	27:1:50:VAL:HG12	1.87	0.56
30:4:15:CYS:CB	30:4:20:HIS:N	2.68	0.56
30:4:32:ASP:HB2	30:4:33:PRO:CD	2.35	0.56
1:C:73:ASP:CB	1:C:120:GLY:CA	2.68	0.56
24:Z:18:LEU:HD22	24:Z:57:VAL:HG13	1.86	0.56
26:A:1882:A:H61	26:A:2220:C:H42	1.52	0.56
1:C:258:ARG:HG2	1:C:259:LYS:N	2.19	0.56
13:O:44:LEU:HD23	13:O:113:ILE:HD12	1.87	0.56
19:U:60:ALA:HB2	26:A:1456:G:C4'	2.36	0.56
25:B:30:G:C6	25:B:54:A:N1	2.74	0.56
25:B:35:G:N3	25:B:35:G:H2'	2.21	0.56
26:A:995:U:O4	26:A:1014:G:N2	2.38	0.56
26:A:1563:A:N6	26:A:1565:A:C6	2.73	0.56
26:A:1601:G:H2'	26:A:1602:U:H6	1.70	0.56
26:A:1602:U:H2'	26:A:1603:G:N7	2.20	0.56
26:A:1607:C:C5	26:A:1608:U:C4	2.93	0.56
26:A:2329:G:O6	26:A:2406:U:O2	2.24	0.56
3:E:51:SER:CB	26:A:35:A:H5'	2.35	0.56
3:E:184:ASN:ND2	26:A:708:G:N2	2.54	0.56
26:A:1566:A:H2'	26:A:1605:G:O6	2.06	0.56
26:A:2747:G:HO2'	26:A:2988:A:HO2'	1.52	0.56
4:F:10:ARG:HH11	4:F:10:ARG:CG	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:30:G:O6	25:B:54:A:N1	2.39	0.56
11:M:58:HIS:CD2	32:6:7:HIS:CE1	2.84	0.56
13:O:103:ARG:HD3	13:O:110:MET:HE3	1.88	0.56
17:S:4:TYR:CE2	17:S:15:LYS:HE3	2.41	0.56
26:A:1577:C:O2'	26:A:1578:G:O4'	2.24	0.56
30:4:12:THR:HG23	30:4:24:ILE:HG22	1.87	0.56
1:C:132:PRO:HA	1:C:190:ARG:HA	1.87	0.56
17:S:6:ILE:CG2	17:S:7:VAL:H	2.19	0.56
20:V:2:LYS:CG	20:V:83:VAL:CB	2.79	0.56
21:W:62:GLY:O	21:W:63:THR:HG23	2.05	0.56
21:W:105:LYS:HZ2	21:W:135:ALA:HA	1.71	0.56
26:A:159:A:OP2	26:A:164:A:N6	2.30	0.56
26:A:1563:A:C5	26:A:1565:A:C8	2.93	0.56
26:A:1565:A:H2'	26:A:1566:A:N7	2.21	0.56
26:A:1603:G:H2'	26:A:1604:G:C8	2.39	0.56
26:A:2086:U:O4	26:A:2096:G:O6	2.23	0.56
27:1:21:GLU:OE2	27:1:24:ARG:NH1	2.39	0.56
28:2:46:THR:O	28:2:50:LYS:HG3	2.05	0.56
30:4:28:ASN:OD1	30:4:31:ASN:HB2	2.06	0.56
4:F:171:ALA:HA	4:F:174:ARG:HD3	1.88	0.56
9:K:75:TYR:N	9:K:75:TYR:CD1	2.73	0.56
12:N:12:GLN:HG3	12:N:73:PRO:HD2	1.88	0.56
23:Y:41:ARG:NH1	26:A:164:A:O3'	2.39	0.56
26:A:137:G:H21	26:A:1524:G:H1'	1.70	0.56
26:A:640:G:O2'	26:A:642:G:OP2	2.24	0.55
26:A:2509:C:H5	30:4:8:ARG:CZ	2.20	0.55
26:A:2873:U:O4	26:A:2895:A:N1	2.38	0.55
33:7:11:CYS:SG	33:7:14:CYS:N	2.80	0.55
1:C:65:ILE:HG13	1:C:104:TYR:HB3	1.88	0.55
9:K:8:ALA:HB2	26:A:625:A:O2'	2.07	0.55
9:K:15:TRP:CD1	9:K:15:TRP:N	2.73	0.55
19:U:4:ILE:HD11	24:Z:58:TYR:CE1	2.38	0.55
19:U:59:THR:HG23	19:U:80:LYS:HE3	1.86	0.55
21:W:6:ASN:HB2	21:W:138:LEU:C	2.26	0.55
25:B:60:G:C2'	25:B:61:C:O5'	2.53	0.55
25:B:86:U:O2	25:B:88:C:H2'	2.06	0.55
26:A:1563:A:C6	26:A:1565:A:C5	2.94	0.55
26:A:1649:C:N4	26:A:1790:A:OP2	2.35	0.55
26:A:2851:G:N2	26:A:3001:G:OP2	2.36	0.55
1:C:35:ARG:CD	1:C:36:PRO:HD3	2.35	0.55
1:C:256:ARG:O	1:C:257:THR:HB	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Q:74:PRO:HB2	15:Q:77:SER:HB2	1.87	0.55
26:A:1659:U:H2'	26:A:1660:A:H8	1.71	0.55
26:A:3017:C:N3	26:A:3025:G:O6	2.39	0.55
3:E:7:VAL:HG21	3:E:16:GLY:HA3	1.86	0.55
13:O:69:LYS:O	13:O:71:ARG:NH1	2.40	0.55
18:T:18:ARG:NH1	26:A:1436:C:C2'	2.69	0.55
25:B:19:G:C5'	25:B:19:G:C8	2.84	0.55
26:A:222:A:O2'	26:A:508:G:N3	2.40	0.55
26:A:263:G:O2'	26:A:517:A:N3	2.39	0.55
26:A:1573:U:C1'	26:A:1574:G:P	2.94	0.55
1:C:257:THR:HG23	26:A:2020:A:O3'	2.06	0.55
2:D:178:GLN:HE22	26:A:2995:U:HO2'	1.54	0.55
9:K:141:GLU:OE1	9:K:142:ILE:C	2.49	0.55
9:K:145:VAL:HG23	9:K:145:VAL:O	2.05	0.55
21:W:105:LYS:HZ3	21:W:136:GLU:CG	2.19	0.55
4:F:11:LEU:CD1	4:F:108:ASP:HB2	2.36	0.55
10:L:80:ASP:OD2	15:Q:61:ARG:NH2	2.40	0.55
13:O:81:ALA:O	13:O:85:PRO:HG2	2.05	0.55
19:U:69:THR:C	19:U:71:THR:N	2.64	0.55
20:V:10:LEU:HD23	20:V:20:LYS:HB3	1.88	0.55
21:W:40:HIS:C	21:W:42:THR:N	2.65	0.55
25:B:16:A:H2	25:B:68:G:H22	1.55	0.55
26:A:1593:U:O2	26:A:1593:U:H2'	2.07	0.55
11:M:12:ALA:HB3	11:M:15:GLU:HB2	1.87	0.55
18:T:11:THR:HG22	18:T:113:ILE:HG23	1.86	0.55
26:A:1586:C:O5'	26:A:1586:C:H6	1.89	0.55
30:4:15:CYS:C	30:4:20:HIS:CA	2.79	0.55
1:C:18:VAL:HG21	26:A:1785:C:H5''	1.88	0.55
12:N:34:ILE:HG23	12:N:104:PHE:H	1.71	0.55
26:A:1582:C:O5'	26:A:1582:C:H6	1.88	0.55
26:A:2644:C:OP1	32:6:34:GLU:HG3	2.06	0.55
1:C:256:ARG:CD	1:C:258:ARG:CD	2.85	0.55
2:D:7:LEU:HB2	2:D:34:ASN:HD21	1.71	0.55
22:X:43:THR:OG1	26:A:2560:A:N6	2.33	0.55
26:A:868:C:H5''	31:5:3:LYS:HE2	1.88	0.55
26:A:2691:C:OP1	33:7:8:LYS:NZ	2.39	0.55
6:H:23:ASP:O	6:H:27:ARG:HB3	2.07	0.55
13:O:29:PHE:HB2	13:O:79:LEU:HD12	1.68	0.55
16:R:89:GLU:OE1	17:S:8:LYS:NZ	2.37	0.55
21:W:131:ILE:HD11	21:W:162:ILE:HD12	1.87	0.55
26:A:351:G:O6	26:A:444:U:O2	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:45:MET:HE3	4:F:64:LEU:HG	1.89	0.54
12:N:22:SER:OG	12:N:23:GLY:N	2.40	0.54
13:O:94:TYR:O	13:O:116:VAL:HG22	2.07	0.54
26:A:1583:U:H2'	26:A:1584:U:C5	2.42	0.54
33:7:22:ARG:HB3	33:7:36:GLN:HB3	1.88	0.54
2:D:84:LEU:HD22	2:D:209:ARG:HD3	1.90	0.54
4:F:29:TYR:O	4:F:30:ALA:HB3	2.08	0.54
6:H:131:PRO:HA	6:H:145:SER:HA	1.89	0.54
20:V:28:PRO:CG	26:A:83:C:P	2.95	0.54
25:B:35:G:N2	25:B:36:U:C2	2.75	0.54
25:B:59:A:H2'	25:B:60:G:C8	2.42	0.54
26:A:1581:C:N4	26:A:1591:U:C6	2.76	0.54
1:C:24:ILE:HD13	1:C:84:TYR:HB2	1.88	0.54
1:C:66:ASP:OD2	1:C:103:ARG:NH1	2.41	0.54
4:F:50:ALA:O	4:F:51:ALA:HB3	2.06	0.54
4:F:118:ILE:H	4:F:118:ILE:CD1	1.96	0.54
5:G:154:ARG:NH1	26:A:2750:G:OP1	2.40	0.54
8:J:79:LYS:HD3	8:J:82:LEU:HD12	1.89	0.54
14:P:73:ILE:HG22	14:P:75:GLY:H	1.72	0.54
18:T:15:ARG:HG2	18:T:109:HIS:CD2	2.43	0.54
22:X:13:GLY:O	22:X:14:ARG:HG3	2.06	0.54
25:B:24:G:N7	25:B:56:C:H2'	2.21	0.54
25:B:57:U:C3'	25:B:58:A:C5'	2.86	0.54
26:A:1567:C:HO2'	26:A:1568:C:P	2.28	0.54
26:A:2490:A:N6	26:A:2497:A:OP2	2.39	0.54
30:4:55:ARG:HG3	30:4:55:ARG:O	2.08	0.54
1:C:35:ARG:CG	1:C:36:PRO:CD	2.85	0.54
1:C:156:ALA:HB2	1:C:163:ILE:HG13	1.89	0.54
4:F:55:LYS:HB2	4:F:55:LYS:HZ3	1.71	0.54
7:I:41:ARG:HH21	8:J:119:ASN:HA	1.72	0.54
11:M:90:GLY:HA2	11:M:122:VAL:HG22	1.90	0.54
13:O:43:ALA:HA	13:O:46:PRO:HD2	1.89	0.54
13:O:79:LEU:O	13:O:83:ILE:HG13	2.06	0.54
16:R:25:ARG:NH1	26:A:2245:C:OP1	2.41	0.54
20:V:86:ARG:NE	20:V:88:ASP:OD2	2.36	0.54
26:A:541:G:N2	26:A:546:G:OP2	2.40	0.54
26:A:737:A:N1	26:A:2593:A:O2'	2.41	0.54
26:A:1564:A:C3'	26:A:1565:A:C5'	2.86	0.54
26:A:2230:C:O2'	26:A:3044:A:N3	2.38	0.54
4:F:11:LEU:HD22	4:F:108:ASP:CA	2.37	0.54
8:J:107:VAL:O	8:J:111:ALA:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:134:ALA:O	9:K:135:GLN:HG2	2.08	0.54
19:U:69:THR:O	19:U:71:THR:N	2.40	0.54
31:5:9:GLN:HA	31:5:9:GLN:OE1	2.07	0.54
3:E:8:LYS:NZ	3:E:148:LEU:HB3	2.23	0.54
9:K:42:PRO:HB3	16:R:68:ALA:HB2	1.89	0.54
9:K:47:ASN:ND2	26:A:649:U:O2	2.40	0.54
13:O:20:LEU:CD2	13:O:24:LEU:CD1	2.85	0.54
17:S:6:ILE:C	17:S:7:VAL:CG2	2.78	0.54
19:U:30:THR:HG23	19:U:83:ILE:HG22	1.90	0.54
20:V:28:PRO:HG3	26:A:83:C:P	2.47	0.54
25:B:60:G:H2'	25:B:61:C:C5'	2.37	0.54
26:A:1578:G:H22	26:A:1592:G:C1'	2.21	0.54
26:A:1600:G:C3'	26:A:1601:G:C5'	2.86	0.54
26:A:2755:A:N6	26:A:2885:G:O6	2.41	0.54
1:C:97:TYR:HD2	1:C:101:GLU:HG3	1.72	0.54
4:F:79:LYS:HG2	4:F:80:SER:N	2.23	0.54
9:K:13:ARG:NE	9:K:121:LYS:NZ	2.53	0.54
14:P:104:ARG:HH12	26:A:2517:C:H5''	1.72	0.54
25:B:89:C:H6	25:B:89:C:P	2.30	0.54
3:E:170:ARG:NE	26:A:404:A:OP1	2.38	0.54
4:F:114:ALA:O	4:F:118:ILE:HD11	2.08	0.54
5:G:61:ARG:NH1	26:A:2981:A:O2'	2.40	0.54
12:N:85:SER:O	26:A:2500:G:OP2	2.26	0.54
13:O:90:ARG:HH12	13:O:118:GLU:HG3	1.72	0.54
21:W:6:ASN:CG	21:W:138:LEU:O	2.51	0.54
24:Z:13:LEU:HD12	24:Z:14:THR:H	1.72	0.54
25:B:19:G:C5	25:B:20:G:N7	2.75	0.54
25:B:60:G:H2'	25:B:61:C:O5'	2.07	0.54
26:A:270:U:O2	26:A:458:G:C6	2.61	0.54
20:V:79:LYS:HG3	20:V:79:LYS:O	2.07	0.54
26:A:2862:G:O2'	26:A:3002:A:N6	2.40	0.54
2:D:159:ARG:H	2:D:159:ARG:HD2	1.73	0.54
4:F:115:LEU:HD23	4:F:183:PRO:HG2	1.89	0.54
8:J:96:LYS:NZ	21:W:120:PRO:HB2	2.22	0.54
9:K:116:ARG:HH22	26:A:615:A:H5''	1.73	0.54
9:K:141:GLU:OE2	9:K:143:LYS:CD	2.56	0.54
12:N:85:SER:OG	22:X:8:SER:OG	2.25	0.54
12:N:103:LEU:HD11	12:N:127:ILE:HD11	1.90	0.54
22:X:83:VAL:CG1	22:X:85:ARG:HA	2.34	0.54
25:B:2:U:H3	25:B:115:A:N6	2.05	0.54
26:A:1580:A:C6	26:A:1591:U:N3	2.62	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:15:CYS:C	30:4:20:HIS:HB3	2.29	0.54
32:6:33:LEU:HD23	32:6:36:LYS:HD2	1.89	0.54
16:R:50:ARG:O	16:R:54:LYS:NZ	2.40	0.53
18:T:6:GLU:HA	18:T:117:ARG:NH1	2.23	0.53
22:X:83:VAL:O	22:X:84:ALA:HB3	2.07	0.53
24:Z:13:LEU:CG	24:Z:17:GLU:HB2	2.38	0.53
26:A:1561:C:C6	26:A:1562:C:C5	2.95	0.53
26:A:1572:G:O6	26:A:1600:G:C6	2.61	0.53
4:F:51:ALA:C	4:F:85:LYS:HZ2	1.87	0.53
5:G:116:ILE:HD11	5:G:152:LEU:HD11	1.90	0.53
7:I:9:ALA:HA	7:I:12:ASP:HB2	1.89	0.53
13:O:76:VAL:O	13:O:80:PHE:HB2	2.08	0.53
25:B:58:A:N7	25:B:59:A:N7	2.53	0.53
25:B:60:G:C8	25:B:60:G:C5'	2.85	0.53
26:A:444:U:H5'	26:A:446:G:H4'	1.90	0.53
26:A:944:A:N7	26:A:2471:A:O2'	2.42	0.53
26:A:1583:U:H2'	26:A:1584:U:C4	2.44	0.53
26:A:2337:A:N6	26:A:2342:A:N7	2.56	0.53
4:F:45:MET:HB3	4:F:94:ALA:H	1.74	0.53
12:N:10:ARG:HG3	12:N:90:PRO:HG3	1.91	0.53
25:B:23:G:H1	25:B:60:G:H1	1.56	0.53
25:B:94:G:N3	26:A:1033:A:H4'	2.23	0.53
4:F:168:THR:CG2	14:P:3:HIS:CE1	2.91	0.53
6:H:94:SER:HA	6:H:125:LYS:HD3	1.90	0.53
19:U:96:PHE:CD2	19:U:96:PHE:C	2.86	0.53
1:C:55:GLY:CA	1:C:218:ARG:HG3	2.38	0.53
2:D:154:CYS:HB3	26:A:2798:G:HO2'	1.70	0.53
4:F:8:LEU:HD22	4:F:16:ARG:HD2	1.90	0.53
4:F:31:ASN:OD1	25:B:57:U:O4'	2.26	0.53
12:N:118:LEU:O	12:N:122:ILE:HB	2.08	0.53
19:U:92:PRO:HG2	19:U:94:ASP:OD1	2.08	0.53
21:W:87:PRO:C	21:W:90:ARG:NH2	2.60	0.53
25:B:10:G:O6	25:B:107:A:N1	2.42	0.53
26:A:828:G:H22	26:A:832:G:H5''	1.74	0.53
3:E:55:ARG:NH2	26:A:788:C:OP1	2.42	0.53
16:R:6:ARG:NH1	26:A:1366:A:OP2	2.41	0.53
26:A:270:U:O2	26:A:458:G:O6	2.27	0.53
26:A:1567:C:O2'	26:A:1568:C:P	2.66	0.53
26:A:2224:C:O2'	26:A:2913:U:OP2	2.26	0.53
26:A:2348:G:O2'	26:A:2396:A:N6	2.41	0.53
3:E:118:ARG:HH22	3:E:189:LEU:HA	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:168:THR:HG21	14:P:3:HIS:ND1	2.23	0.53
5:G:16:ASP:HB2	5:G:27:LYS:HB3	1.90	0.53
8:J:107:VAL:O	8:J:111:ALA:CB	2.56	0.53
9:K:147:GLN:HG2	26:A:1131:G:H1'	1.90	0.53
12:N:70:PRO:HA	12:N:95:ALA:HB2	1.91	0.53
20:V:9:VAL:HB	20:V:71:VAL:HB	1.90	0.53
21:W:21:LYS:NZ	25:B:80:C:N4	2.46	0.53
25:B:87:U:O2'	25:B:88:C:H4'	2.08	0.53
26:A:189:A:N3	26:A:794:G:O2'	2.37	0.53
26:A:1589:G:O5'	26:A:1589:G:H8	1.91	0.53
1:C:35:ARG:HD2	1:C:36:PRO:CD	2.37	0.53
5:G:62:SER:O	5:G:66:HIS:HB2	2.08	0.53
9:K:98:THR:HG23	9:K:124:VAL:HB	1.90	0.53
13:O:90:ARG:HH22	13:O:118:GLU:HB3	1.68	0.53
21:W:9:ASN:HD22	21:W:57:VAL:CG1	2.17	0.53
23:Y:19:SER:OG	23:Y:20:HIS:N	2.37	0.53
26:A:384:G:H2'	26:A:385:G:H8	1.72	0.53
26:A:1921:G:H2'	26:A:1922:G:H8	1.73	0.53
9:K:112:ASN:ND2	26:A:650:G:H5''	2.24	0.53
10:L:28:SER:HA	26:A:2787:U:H4'	1.90	0.53
13:O:81:ALA:C	13:O:85:PRO:CD	2.74	0.53
24:Z:44:ASN:HD21	26:A:58:G:P	2.31	0.53
26:A:1603:G:H2'	26:A:1604:G:H8	1.74	0.53
28:2:42:HIS:O	28:2:46:THR:HG23	2.08	0.53
30:4:15:CYS:O	30:4:20:HIS:CA	2.54	0.53
1:C:256:ARG:O	26:A:2014:G:C4'	2.52	0.53
1:C:257:THR:CG2	26:A:2020:A:O3'	2.57	0.53
2:D:84:LEU:HD21	2:D:207:VAL:HG11	1.90	0.53
3:E:182:GLN:CD	26:A:706:G:C8	2.83	0.53
24:Z:45:ARG:O	24:Z:49:THR:OG1	2.27	0.53
25:B:89:C:H2'	25:B:90:G:C8	2.44	0.53
26:A:2747:G:O2'	26:A:2988:A:O2'	2.27	0.53
1:C:76:ASN:C	1:C:98:LEU:CD2	2.82	0.52
1:C:98:LEU:HD22	1:C:98:LEU:N	2.24	0.52
9:K:5:THR:HG21	26:A:624:G:H4'	1.91	0.52
13:O:80:PHE:C	13:O:80:PHE:CD2	2.85	0.52
21:W:62:GLY:O	21:W:63:THR:OG1	2.26	0.52
26:A:1627:U:H2'	26:A:1628:A:H2'	1.90	0.52
20:V:4:HIS:CE1	20:V:96:ARG:HH22	2.22	0.52
25:B:11:U:O2	25:B:11:U:H2'	2.08	0.52
25:B:34:G:H8	25:B:34:G:O5'	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:82:A:N1	25:B:91:G:C6	2.77	0.52
26:A:114:G:OP2	26:A:116:A:O2'	2.26	0.52
26:A:1566:A:C1'	26:A:1605:G:H1	2.21	0.52
6:H:44:GLU:O	6:H:48:GLU:CB	2.57	0.52
7:I:4:ALA:O	7:I:8:THR:OG1	2.23	0.52
19:U:19:LYS:NZ	26:A:1508:A:N1	2.53	0.52
26:A:1044:U:O2'	27:1:24:ARG:O	2.27	0.52
26:A:1540:U:O4	26:A:1632:G:O6	2.27	0.52
26:A:1565:A:C2'	26:A:1566:A:C8	2.85	0.52
26:A:1567:C:C2'	26:A:1568:C:OP2	2.57	0.52
26:A:1570:C:C4	26:A:1602:U:C2	2.84	0.52
26:A:1600:G:O2'	26:A:1601:G:H5''	2.09	0.52
26:A:1830:C:H5'	31:5:10:PRO:HG2	1.91	0.52
26:A:2356:G:H2'	26:A:2380:G:H1	1.74	0.52
1:C:14:ARG:NH2	26:A:1913:G:N7	2.55	0.52
4:F:6:LYS:CA	4:F:6:LYS:CE	2.87	0.52
4:F:46:GLY:O	4:F:47:VAL:HG13	2.09	0.52
4:F:113:ILE:O	4:F:116:PRO:HD2	2.09	0.52
19:U:67:LYS:HZ2	19:U:67:LYS:CB	2.23	0.52
20:V:43:LYS:NZ	20:V:43:LYS:CB	2.73	0.52
20:V:99:LYS:NZ	20:V:99:LYS:CB	2.73	0.52
26:A:239:U:OP1	26:A:684:G:N2	2.42	0.52
1:C:158:SER:OG	1:C:159:ALA:N	2.34	0.52
9:K:75:TYR:HD2	9:K:86:LYS:HG2	1.73	0.52
12:N:17:GLN:HB2	12:N:39:HIS:HB2	1.91	0.52
16:R:41:HIS:HE1	26:A:655:G:H4'	1.75	0.52
26:A:1544:U:H3	26:A:1626:G:H1	1.58	0.52
26:A:1604:G:C2	26:A:1605:G:C8	2.98	0.52
1:C:262:LYS:N	1:C:263:PRO:CD	2.73	0.52
5:G:127:GLU:OE1	5:G:131:LYS:NZ	2.42	0.52
10:L:109:LYS:HB3	10:L:110:LYS:HE2	1.92	0.52
26:A:1573:U:O2'	26:A:1573:U:O2	2.27	0.52
26:A:2315:U:OP1	26:A:2422:A:O2'	2.28	0.52
30:4:8:ARG:HH21	30:4:28:ASN:HB2	1.74	0.52
33:7:35:ARG:CG	33:7:36:GLN:H	2.21	0.52
11:M:81:GLY:HA2	11:M:84:ASN:HD22	1.75	0.52
11:M:106:LYS:NZ	26:A:714:U:O2'	2.43	0.52
25:B:25:G:C2'	25:B:26:A:H5'	2.40	0.52
26:A:1078:G:O6	34:8:8:LYS:NZ	2.43	0.52
26:A:1938:G:H21	26:A:1956:A:H62	1.58	0.52
26:A:2585:U:OP1	32:6:24:ARG:NH1	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:ARG:CG	1:C:81:HIS:CG	2.92	0.52
13:O:75:VAL:HG12	13:O:79:LEU:HD13	1.92	0.52
27:1:51:HIS:CD2	27:1:51:HIS:N	2.74	0.52
28:2:42:HIS:N	28:2:43:PRO:CD	2.72	0.52
5:G:4:ILE:HD13	26:A:2972:A:H5'	1.91	0.52
9:K:1:MET:N	9:K:2:PRO:CD	2.73	0.52
10:L:109:LYS:CD	10:L:110:LYS:NZ	2.73	0.52
22:X:16:SER:O	22:X:17:ALA:CB	2.58	0.52
30:4:38:ILE:HG22	30:4:40:LYS:HG2	1.92	0.52
14:P:22:HIS:HE1	25:B:9:G:OP2	1.93	0.52
18:T:35:SER:HA	18:T:77:VAL:HA	1.92	0.52
26:A:1533:U:O2	26:A:1803:A:O2'	2.25	0.52
26:A:1856:C:O3'	26:A:2933:G:N2	2.43	0.52
31:5:6:ARG:CB	31:5:6:ARG:CZ	2.87	0.52
1:C:34:VAL:HG22	1:C:63:ARG:HG2	1.91	0.51
1:C:256:ARG:CG	1:C:258:ARG:HD2	2.39	0.51
9:K:75:TYR:CD2	9:K:86:LYS:HG2	2.43	0.51
10:L:8:LEU:HD13	10:L:19:ILE:CG1	2.40	0.51
13:O:117:ARG:CD	13:O:118:GLU:N	2.73	0.51
19:U:77:LYS:HZ2	19:U:79:THR:HG22	1.73	0.51
25:B:5:C:H42	25:B:112:C:H42	1.57	0.51
25:B:86:U:H2'	25:B:88:C:H1'	1.90	0.51
26:A:1171:C:H2'	26:A:1172:A:H8	1.75	0.51
28:2:44:PHE:C	28:2:48:LYS:HE3	2.35	0.51
31:5:21:PHE:O	31:5:25:MET:HG2	2.09	0.51
1:C:145:VAL:HG11	1:C:175:LEU:HD11	1.92	0.51
1:C:259:LYS:HG2	26:A:2016:G:OP1	2.09	0.51
1:C:262:LYS:N	1:C:262:LYS:CD	2.73	0.51
3:E:5:VAL:HG12	3:E:18:VAL:O	2.10	0.51
8:J:128:LYS:HG2	26:A:1198:C:H4'	1.93	0.51
9:K:14:SER:N	9:K:52:ASP:OD1	2.31	0.51
11:M:24:ARG:NH1	26:A:1365:G:OP2	2.43	0.51
22:X:17:ALA:HB1	26:A:2485:C:OP1	2.10	0.51
22:X:46:HIS:HB2	22:X:77:THR:HG22	1.91	0.51
26:A:1564:A:H3'	26:A:1565:A:C5'	2.41	0.51
26:A:1589:G:C2'	26:A:1590:G:H5'	2.40	0.51
26:A:1589:G:H2'	26:A:1590:G:H5'	1.91	0.51
26:A:2340:A:H61	26:A:2389:U:H3	1.58	0.51
33:7:16:VAL:HG22	33:7:25:VAL:HG22	1.92	0.51
1:C:62:TYR:HE1	26:A:2033:U:H3'	1.75	0.51
1:C:256:ARG:CZ	1:C:258:ARG:NE	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:139:LYS:HE2	3:E:142:LYS:HD2	1.92	0.51
4:F:138:GLY:HA3	26:A:2529:A:C5'	2.27	0.51
13:O:16:HIS:HD2	26:A:1390:A:N7	2.04	0.51
20:V:96:ARG:NH2	20:V:96:ARG:CB	2.72	0.51
26:A:1755:A:O2'	26:A:1758:G:N2	2.36	0.51
26:A:2571:C:OP1	30:4:40:LYS:NZ	2.36	0.51
28:2:42:HIS:N	28:2:43:PRO:HD2	2.24	0.51
1:C:209:ALA:HB2	26:A:2007:C:O2'	2.10	0.51
4:F:9:PRO:HD2	4:F:12:LYS:HE3	1.91	0.51
13:O:35:LYS:HG3	13:O:112:VAL:HG22	1.93	0.51
19:U:59:THR:CG2	19:U:80:LYS:HE3	2.39	0.51
21:W:102:ARG:HH21	21:W:138:LEU:HD11	1.70	0.51
25:B:24:G:O6	25:B:60:G:C2	2.63	0.51
26:A:1174:G:N1	26:A:1220:C:OP2	2.44	0.51
26:A:1563:A:N7	26:A:1565:A:C5	2.78	0.51
26:A:1599:U:H3'	26:A:1599:U:OP2	2.09	0.51
30:4:9:PRO:HD3	30:4:27:LYS:O	2.09	0.51
1:C:25:THR:CG2	1:C:81:HIS:C	2.83	0.51
2:D:63:ILE:HG22	2:D:65:PRO:HD2	1.93	0.51
12:N:65:TRP:HZ3	26:A:989:G:O2'	1.93	0.51
21:W:87:PRO:HA	21:W:90:ARG:NH2	2.16	0.51
26:A:1584:U:H6	26:A:1584:U:H3'	1.75	0.51
26:A:1595:G:C5'	26:A:1596:C:OP2	2.59	0.51
26:A:1940:A:N6	26:A:1954:C:O2'	2.43	0.51
26:A:2142:A:O2'	26:A:2144:C:N4	2.43	0.51
28:2:44:PHE:O	28:2:48:LYS:CE	2.55	0.51
1:C:108:PRO:HG3	1:C:128:GLY:HA2	1.91	0.51
1:C:145:VAL:HG13	1:C:191:ALA:HB2	1.93	0.51
3:E:45:LYS:CG	26:A:709:U:C4	2.94	0.51
3:E:131:VAL:HG13	3:E:140:SER:HB2	1.91	0.51
3:E:201:LEU:HD23	3:E:201:LEU:C	2.36	0.51
19:U:5:THR:O	19:U:6:ASP:HB2	2.10	0.51
20:V:72:MET:CE	26:A:383:U:H5'	2.41	0.51
21:W:83:LEU:HD11	21:W:92:ILE:CG2	2.36	0.51
26:A:1597:G:N3	26:A:1598:U:H6	2.02	0.51
26:A:1601:G:H2'	26:A:1602:U:C6	2.46	0.51
8:J:114:LYS:O	8:J:118:LEU:N	2.40	0.51
16:R:48:ARG:NH1	16:R:49:ASP:OD1	2.44	0.51
20:V:2:LYS:HE3	20:V:83:VAL:HG12	1.92	0.51
23:Y:17:SER:HB2	23:Y:27:ARG:HD2	1.91	0.51
23:Y:33:ILE:HA	23:Y:52:CYS:HA	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:601:A:N3	26:A:673:C:O2'	2.39	0.51
9:K:141:GLU:OE2	9:K:143:LYS:HG3	2.01	0.51
18:T:75:THR:CB	18:T:118:PRO:HD3	2.32	0.51
26:A:1544:U:O4	26:A:1626:G:O6	2.29	0.51
26:A:2279:C:OP1	29:3:5:LYS:NZ	2.44	0.51
26:A:2764:C:O2'	26:A:2964:A:N3	2.34	0.51
28:2:38:CYS:CB	28:2:40:GLN:NE2	2.73	0.51
28:2:43:PRO:HA	28:2:46:THR:OG1	2.09	0.51
31:5:5:LYS:HB3	31:5:9:GLN:HE22	1.67	0.51
1:C:57:GLY:C	1:C:58:HIS:O	2.54	0.51
3:E:186:TYR:O	3:E:190:ASN:HB2	2.11	0.51
11:M:78:VAL:HG21	11:M:98:LEU:HD13	1.91	0.51
11:M:134:ARG:HH22	11:M:146:GLU:HG2	1.75	0.51
13:O:29:PHE:CE2	13:O:51:LEU:HD13	2.45	0.51
25:B:80:C:O2'	26:A:1033:A:H1'	2.10	0.51
26:A:242:G:OP2	32:6:3:LYS:HE2	2.10	0.51
26:A:854:A:H1'	26:A:855:C:H5	1.75	0.51
26:A:1127:A:N3	26:A:1272:C:O2'	2.39	0.51
28:2:38:CYS:SG	28:2:40:GLN:CD	2.94	0.51
1:C:37:LEU:HD23	1:C:62:TYR:CD1	2.45	0.51
1:C:261:ASN:C	1:C:262:LYS:HD3	2.36	0.51
4:F:62:ASN:O	4:F:65:ALA:O	2.28	0.51
20:V:2:LYS:HE2	20:V:85:TYR:CE2	2.46	0.51
21:W:81:LYS:HB2	21:W:96:ASP:O	2.10	0.51
22:X:54:GLY:N	22:X:58:THR:O	2.39	0.51
26:A:277:U:H2'	26:A:278:A:C8	2.46	0.51
26:A:1323:G:O2'	26:A:1352:A:N1	2.40	0.51
26:A:1577:C:C5	26:A:1594:G:O6	2.62	0.51
26:A:1598:U:C4	26:A:1601:G:C6	2.99	0.51
1:C:61:ALA:O	1:C:63:ARG:NH2	2.44	0.50
4:F:102:ARG:NH1	28:2:9:TYR:CE1	2.78	0.50
10:L:7:ARG:NH2	10:L:7:ARG:CG	2.73	0.50
4:F:71:LYS:HG3	28:2:5:ILE:HB	1.93	0.50
5:G:65:LEU:HD12	5:G:68:LEU:HD23	1.93	0.50
16:R:98:LEU:CD2	17:S:4:TYR:OH	2.59	0.50
18:T:75:THR:O	18:T:118:PRO:CD	2.59	0.50
24:Z:62:ARG:NH2	24:Z:66:LEU:HD11	2.26	0.50
1:C:26:ARG:HD3	1:C:81:HIS:CD2	2.38	0.50
11:M:84:ASN:HD21	11:M:118:LEU:HA	1.76	0.50
15:Q:93:ARG:HH21	26:A:1971:C:H5	1.60	0.50
25:B:24:G:HO2'	25:B:56:C:H41	1.48	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:34:G:O2'	25:B:35:G:N7	2.43	0.50
26:A:2211:C:H2'	26:A:2212:A:H8	1.76	0.50
26:A:2547:G:O6	26:A:2556:C:N3	2.44	0.50
4:F:11:LEU:HD22	4:F:108:ASP:CB	2.41	0.50
6:H:62:ILE:H	6:H:65:ALA:HB3	1.77	0.50
9:K:1:MET:H3	9:K:2:PRO:HD3	1.77	0.50
26:A:2380:G:N2	26:A:2381:A:N1	2.58	0.50
26:A:2756:G:O2'	26:A:2881:A:N1	2.40	0.50
28:2:63:LYS:O	28:2:65:TYR:HD2	1.94	0.50
10:L:31:ARG:NH2	26:A:2900:C:OP1	2.45	0.50
12:N:111:GLU:OE2	12:N:115:ARG:CD	2.59	0.50
20:V:42:LYS:HD2	26:A:586:U:C5'	2.36	0.50
26:A:1592:G:O2'	26:A:1593:U:C6	2.57	0.50
26:A:1673:A:O2'	26:A:2926:A:OP2	2.28	0.50
31:5:6:ARG:NH1	31:5:6:ARG:CB	2.72	0.50
3:E:51:SER:HB2	26:A:35:A:C4'	2.42	0.50
9:K:1:MET:CE	26:A:642:G:OP1	2.60	0.50
9:K:27:ARG:HH11	9:K:27:ARG:CG	2.25	0.50
13:O:16:HIS:CD2	26:A:1390:A:N7	2.78	0.50
25:B:34:G:C6	25:B:44:C:C6	2.99	0.50
26:A:247:G:OP2	26:A:249:C:N4	2.41	0.50
26:A:499:G:OP2	26:A:2630:A:O2'	2.27	0.50
31:5:6:ARG:C	31:5:7:THR:HG23	2.36	0.50
1:C:213:ARG:HH22	1:C:219:PRO:HD3	1.75	0.50
19:U:67:LYS:HE2	26:A:1451:A:OP2	2.10	0.50
22:X:50:ASN:HB2	22:X:80:ILE:HB	1.94	0.50
24:Z:62:ARG:HD2	24:Z:66:LEU:HD22	1.93	0.50
25:B:56:C:O2	25:B:56:C:O2'	2.22	0.50
26:A:813:C:O2'	26:A:849:A:N6	2.41	0.50
26:A:1665:U:H2'	26:A:1666:A:H8	1.77	0.50
33:7:25:VAL:HB	33:7:34:GLN:HG2	1.92	0.50
11:M:65:LYS:HD2	26:A:2640:G:H5''	1.92	0.50
26:A:1596:C:O2'	26:A:1597:G:C8	2.65	0.50
26:A:1606:G:H2'	26:A:1606:G:N3	2.27	0.50
2:D:178:GLN:NE2	26:A:2995:U:O2'	2.37	0.50
9:K:136:GLN:HA	9:K:136:GLN:OE1	2.12	0.50
18:T:7:PHE:O	18:T:7:PHE:HD1	1.95	0.50
25:B:85:C:H3'	25:B:85:C:H6	1.75	0.50
9:K:75:TYR:HB3	9:K:85:ARG:O	2.11	0.49
9:K:113:LYS:HD2	26:A:616:A:P	2.52	0.49
19:U:67:LYS:HB3	19:U:67:LYS:NZ	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:83:ILE:HD12	26:A:1456:G:N2	2.13	0.49
21:W:52:ARG:NH1	21:W:53:ASP:OD1	2.45	0.49
25:B:58:A:C8	25:B:58:A:C5'	2.86	0.49
26:A:1566:A:C4	26:A:1605:G:C6	3.00	0.49
1:C:34:VAL:HG22	1:C:63:ARG:CG	2.42	0.49
2:D:157:PRO:HD2	2:D:158:GLY:H	1.78	0.49
3:E:149:THR:C	3:E:150:GLU:CG	2.85	0.49
4:F:115:LEU:O	4:F:118:ILE:HD13	2.11	0.49
13:O:58:GLY:HA2	13:O:62:ASN:HB2	1.94	0.49
21:W:9:ASN:O	21:W:68:THR:N	2.30	0.49
26:A:217:G:H22	26:A:235:U:H4'	1.77	0.49
3:E:136:PRO:HB3	3:E:164:VAL:HA	1.94	0.49
4:F:78:ARG:O	4:F:88:GLU:OE1	2.30	0.49
4:F:158:GLY:HA3	26:A:2529:A:C2	2.47	0.49
7:I:27:GLU:HB3	7:I:104:VAL:HB	1.93	0.49
16:R:90:VAL:HG13	17:S:6:ILE:CD1	2.42	0.49
19:U:91:LYS:CG	19:U:92:PRO:HD3	2.40	0.49
21:W:62:GLY:HA2	21:W:65:ALA:HB2	1.95	0.49
26:A:218:A:N3	26:A:234:U:O2'	2.38	0.49
26:A:718:C:O2'	26:A:772:U:OP1	2.26	0.49
26:A:966:U:H2'	26:A:967:G:H8	1.77	0.49
26:A:1590:G:N3	26:A:1591:U:C6	2.79	0.49
28:2:60:ARG:C	28:2:60:ARG:CD	2.86	0.49
1:C:256:ARG:NH1	1:C:258:ARG:NH1	2.60	0.49
3:E:201:LEU:C	3:E:201:LEU:CD2	2.85	0.49
4:F:11:LEU:HD21	4:F:108:ASP:HA	1.95	0.49
4:F:47:VAL:HG23	4:F:48:GLY:N	2.26	0.49
18:T:13:LYS:HG2	18:T:111:THR:HG23	1.93	0.49
19:U:67:LYS:NZ	26:A:1451:A:OP2	2.45	0.49
21:W:46:HIS:HE1	25:B:74:A:O2'	1.96	0.49
21:W:81:LYS:N	21:W:96:ASP:O	2.43	0.49
26:A:2963:U:H2'	26:A:2964:A:H8	1.77	0.49
12:N:35:GLN:NE2	21:W:90:ARG:NH1	2.60	0.49
14:P:16:ASN:O	14:P:20:ARG:HB2	2.12	0.49
26:A:242:G:OP2	32:6:3:LYS:CE	2.61	0.49
26:A:280:G:H1	26:A:306:U:H3	1.60	0.49
3:E:118:ARG:HH22	3:E:189:LEU:HD23	1.77	0.49
4:F:32:VAL:CG2	25:B:55:G:H5''	2.43	0.49
4:F:147:GLU:HA	28:2:28:LYS:HD3	1.93	0.49
5:G:61:ARG:O	5:G:65:LEU:HB2	2.13	0.49
17:S:77:LYS:HD3	17:S:86:LYS:HE2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:223:A:OP2	26:A:507:G:N2	2.41	0.49
26:A:277:U:H2'	26:A:278:A:H8	1.77	0.49
26:A:403:U:O2'	26:A:422:A:N3	2.45	0.49
4:F:21:GLU:O	4:F:25:GLN:HG3	2.13	0.49
9:K:84:LEU:HD11	26:A:1250:U:H6	1.77	0.49
13:O:118:GLU:OE1	13:O:118:GLU:HA	2.11	0.49
15:Q:48:ARG:NH1	26:A:2909:G:OP1	2.43	0.49
20:V:81:THR:OG1	20:V:100:THR:HG23	2.12	0.49
26:A:567:A:H1'	26:A:568:A:H5''	1.94	0.49
26:A:1580:A:C5	26:A:1592:G:N3	2.80	0.49
1:C:256:ARG:NE	1:C:258:ARG:NE	2.60	0.49
4:F:11:LEU:CD2	4:F:108:ASP:CA	2.91	0.49
4:F:46:GLY:O	4:F:47:VAL:CG1	2.61	0.49
10:L:19:ILE:HG22	10:L:43:VAL:HA	1.95	0.49
13:O:33:ARG:CB	13:O:114:GLU:HG2	2.43	0.49
25:B:21:C:H2'	25:B:22:A:O5'	2.13	0.49
26:A:610:C:O2	26:A:646:U:O2'	2.31	0.49
26:A:1610:C:H2'	26:A:1611:A:C8	2.46	0.49
26:A:2375:G:H2'	26:A:2376:G:H8	1.77	0.49
26:A:2629:G:O2'	26:A:2635:A:N6	2.42	0.49
10:L:22:ILE:HD12	26:A:2176:A:C5	2.48	0.49
14:P:112:ARG:N	25:B:49:C:OP1	2.40	0.49
21:W:28:ARG:HH12	25:B:77:A:H5'	1.78	0.49
21:W:77:LEU:CG	21:W:100:VAL:HG21	2.43	0.49
25:B:55:G:H2'	25:B:56:C:H6	1.78	0.49
26:A:1543:A:N1	26:A:1628:A:O2'	2.44	0.49
26:A:1581:C:N4	26:A:1591:U:N1	2.61	0.49
26:A:1596:C:O2'	26:A:1597:G:C5'	2.60	0.49
31:5:21:PHE:HB2	31:5:46:THR:HG21	1.95	0.49
7:I:9:ALA:HB3	7:I:56:LEU:HD11	1.95	0.49
9:K:87:ARG:NH1	9:K:91:GLU:OE2	2.46	0.49
12:N:60:ARG:NH1	26:A:1193:C:C5'	2.71	0.49
13:O:38:GLU:O	13:O:42:ARG:HG3	2.13	0.49
19:U:33:VAL:HG11	19:U:42:ILE:HD11	1.93	0.49
19:U:67:LYS:CE	26:A:1451:A:OP2	2.61	0.49
26:A:799:G:OP1	31:5:19:HIS:HD2	1.96	0.49
26:A:1044:U:P	27:1:37:ARG:HH12	2.36	0.49
3:E:5:VAL:HG22	3:E:6:ASP:N	2.27	0.48
19:U:66:ARG:HA	19:U:75:LYS:CA	2.43	0.48
25:B:54:A:H2'	25:B:55:G:C8	2.48	0.48
26:A:805:C:O2'	26:A:895:G:OP1	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:ASP:O	26:A:1720:G:N2	2.23	0.48
2:D:162:LYS:HG2	26:A:2843:C:H5''	1.95	0.48
4:F:80:SER:OG	4:F:88:GLU:N	2.46	0.48
8:J:96:LYS:HE2	21:W:120:PRO:CB	2.37	0.48
10:L:19:ILE:HB	10:L:41:ALA:HB1	1.95	0.48
18:T:77:VAL:HG22	18:T:117:ARG:HG2	1.96	0.48
22:X:56:ASP:N	22:X:56:ASP:OD1	2.39	0.48
25:B:19:G:C6	25:B:20:G:C5	3.01	0.48
25:B:88:C:H3'	25:B:88:C:H6	1.79	0.48
26:A:1552:A:H1'	26:A:1618:C:H42	1.78	0.48
26:A:2509:C:C4	30:4:8:ARG:NH1	2.79	0.48
30:4:13:LEU:HA	30:4:53:GLU:HA	1.95	0.48
1:C:261:ASN:C	1:C:262:LYS:CD	2.86	0.48
3:E:144:PHE:CE1	3:E:148:LEU:CD1	2.97	0.48
4:F:8:LEU:CD2	4:F:16:ARG:HD2	2.43	0.48
17:S:16:VAL:HG12	17:S:22:VAL:HG21	1.96	0.48
20:V:76:SER:C	20:V:77:ASP:OD1	2.56	0.48
26:A:1563:A:N6	26:A:1565:A:C5	2.81	0.48
26:A:1564:A:C2'	26:A:1565:A:C5'	2.86	0.48
26:A:1564:A:H3'	26:A:1565:A:H5''	1.94	0.48
1:C:25:THR:CG2	1:C:81:HIS:ND1	2.77	0.48
3:E:6:ASP:HA	3:E:16:GLY:O	2.13	0.48
3:E:24:LEU:HD21	3:E:208:ASN:CG	2.38	0.48
3:E:180:PRO:HG3	3:E:200:ALA:HB1	1.94	0.48
4:F:46:GLY:HA3	26:A:2529:A:H61	1.79	0.48
19:U:6:ASP:OD2	24:Z:23:ARG:CG	2.60	0.48
19:U:67:LYS:CB	19:U:67:LYS:NZ	2.76	0.48
22:X:75:ARG:NH1	26:A:2557:A:OP1	2.45	0.48
24:Z:62:ARG:HH21	24:Z:66:LEU:CD1	2.26	0.48
25:B:19:G:C8	25:B:19:G:C4'	2.96	0.48
25:B:37:C:C5	25:B:38:C:C5	3.01	0.48
26:A:1590:G:C2	26:A:1591:U:C5	3.00	0.48
26:A:1637:G:O2'	26:A:1805:G:O2'	2.31	0.48
26:A:1882:A:N6	26:A:2220:C:H42	2.11	0.48
29:3:27:LEU:HB3	29:3:38:LYS:HB3	1.95	0.48
4:F:35:ILE:CG2	4:F:36:PRO:HD2	2.43	0.48
9:K:45:THR:OG1	16:R:64:ARG:NH2	2.46	0.48
10:L:8:LEU:HD12	10:L:19:ILE:O	2.14	0.48
12:N:60:ARG:NH2	12:N:60:ARG:CG	2.72	0.48
12:N:111:GLU:OE2	12:N:115:ARG:HB2	2.13	0.48
21:W:157:ILE:HB	21:W:179:VAL:HB	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:13:LEU:HD21	24:Z:17:GLU:O	2.14	0.48
25:B:86:U:O2'	25:B:87:U:H2'	2.14	0.48
26:A:1569:A:O2'	26:A:1570:C:C6	2.63	0.48
2:D:129:ARG:HG2	2:D:170:MET:HB3	1.96	0.48
3:E:154:VAL:HB	3:E:175:VAL:HG23	1.95	0.48
10:L:107:ARG:HD3	10:L:115:VAL:HG11	1.94	0.48
12:N:134:ARG:HD3	21:W:129:ASN:ND2	2.29	0.48
18:T:30:LEU:HD23	29:3:24:ALA:HB2	1.95	0.48
18:T:99:ARG:HD2	26:A:862:U:O2'	2.12	0.48
21:W:6:ASN:HD22	21:W:6:ASN:C	2.22	0.48
24:Z:62:ARG:NH2	24:Z:66:LEU:CD1	2.77	0.48
26:A:1171:C:H2'	26:A:1172:A:C8	2.49	0.48
26:A:2072:G:O6	26:A:2111:U:O4	2.31	0.48
4:F:45:MET:HE2	4:F:64:LEU:HD21	1.83	0.48
5:G:132:PHE:HZ	5:G:149:ILE:HG21	1.79	0.48
13:O:14:SER:C	13:O:15:SER:HG	2.14	0.48
13:O:20:LEU:HD23	13:O:24:LEU:HD12	1.95	0.48
24:Z:48:ARG:HG3	26:A:58:G:OP1	2.13	0.48
25:B:10:G:C6	25:B:11:U:H1'	2.47	0.48
33:7:35:ARG:CG	33:7:36:GLN:N	2.73	0.48
1:C:256:ARG:NH1	1:C:258:ARG:HH11	2.12	0.48
9:K:84:LEU:HD11	26:A:1250:U:C6	2.49	0.48
9:K:112:ASN:OD1	26:A:650:G:OP1	2.31	0.48
12:N:17:GLN:NE2	26:A:1075:U:H5	2.11	0.48
26:A:351:G:N2	26:A:444:U:O4	2.40	0.48
26:A:1411:G:OP1	26:A:2933:G:O2'	2.26	0.48
26:A:1571:C:O2'	26:A:1572:G:C5'	2.54	0.48
28:2:41:CYS:CB	28:2:44:PHE:CZ	2.86	0.48
10:L:77:ILE:HG12	15:Q:71:ARG:HD3	1.96	0.48
16:R:57:PHE:HZ	26:A:623:A:H4'	1.78	0.48
16:R:98:LEU:HD21	17:S:4:TYR:OH	2.14	0.48
20:V:2:LYS:CD	20:V:83:VAL:CB	2.91	0.48
26:A:79:G:N2	26:A:100:A:OP2	2.44	0.48
26:A:681:C:H2'	26:A:682:A:H8	1.79	0.48
26:A:1885:G:O2'	26:A:2215:U:O4	2.28	0.48
26:A:2374:U:H2'	26:A:2375:G:C8	2.49	0.48
1:C:76:ASN:CB	1:C:98:LEU:HD21	2.42	0.48
4:F:9:PRO:O	4:F:13:GLN:N	2.43	0.48
7:I:48:THR:HB	7:I:81:PHE:HB2	1.96	0.48
15:Q:33:GLU:OE1	15:Q:38:ARG:NH2	2.47	0.48
20:V:97:ILE:HD12	20:V:103:LYS:C	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:87:PRO:O	21:W:90:ARG:NH1	2.46	0.48
26:A:81:A:N1	26:A:96:G:O2'	2.34	0.48
26:A:265:A:N1	26:A:515:U:O2'	2.41	0.48
26:A:2081:U:OP1	26:A:2634:G:O2'	2.26	0.48
26:A:2745:C:O2'	26:A:2788:A:N3	2.39	0.48
1:C:5:LYS:HD2	1:C:17:SER:HB3	1.96	0.47
1:C:59:LYS:HG3	26:A:1788:G:H4'	1.96	0.47
1:C:76:ASN:O	1:C:98:LEU:HD23	2.11	0.47
4:F:70:GLN:OE1	4:F:96:VAL:CG2	2.62	0.47
12:N:59:LYS:NZ	12:N:59:LYS:CB	2.73	0.47
13:O:116:VAL:HG23	13:O:116:VAL:O	2.13	0.47
26:A:1581:C:H2'	26:A:1582:C:C5	2.44	0.47
26:A:2163:U:OP1	26:A:2828:U:O2'	2.29	0.47
4:F:73:GLU:HB3	25:B:42:C:C6	2.48	0.47
9:K:37:ARG:NH1	26:A:1125:C:OP1	2.46	0.47
10:L:73:ASP:OD1	10:L:73:ASP:N	2.46	0.47
20:V:46:ALA:HB2	26:A:572:C:P	2.54	0.47
21:W:79:LEU:N	21:W:98:LEU:O	2.48	0.47
26:A:292:G:H2'	26:A:293:G:H8	1.79	0.47
26:A:1554:U:C4	26:A:1617:C:N4	2.82	0.47
26:A:1568:C:H2'	26:A:1569:A:N7	2.29	0.47
26:A:1578:G:N9	26:A:1592:G:N1	2.57	0.47
26:A:2800:G:O2'	26:A:2803:C:OP2	2.28	0.47
33:7:21:GLY:C	33:7:22:ARG:HG3	2.39	0.47
1:C:79:VAL:HG23	1:C:114:GLY:H	1.78	0.47
1:C:108:PRO:HA	1:C:196:VAL:HA	1.96	0.47
1:C:256:ARG:CD	1:C:258:ARG:NE	2.76	0.47
4:F:23:LEU:HD22	4:F:36:PRO:HD2	1.95	0.47
11:M:51:GLU:HG3	32:6:57:ARG:HH11	1.70	0.47
19:U:69:THR:CG2	19:U:73:PHE:C	2.87	0.47
25:B:13:C:O2'	25:B:14:A:H3'	2.14	0.47
25:B:89:C:H2'	25:B:90:G:H8	1.79	0.47
26:A:1830:C:H4'	31:5:10:PRO:CD	2.44	0.47
26:A:1830:C:C5'	31:5:10:PRO:HG2	2.43	0.47
1:C:143:HIS:ND1	1:C:194:GLY:O	2.39	0.47
1:C:178:PRO:HG2	26:A:2016:G:O6	2.14	0.47
13:O:49:GLU:OE1	13:O:94:TYR:CD2	2.67	0.47
20:V:43:LYS:O	20:V:60:VAL:N	2.47	0.47
20:V:87:ILE:HG12	20:V:94:LYS:HG3	1.96	0.47
21:W:122:THR:HG23	21:W:181:VAL:HG13	1.96	0.47
22:X:83:VAL:CG1	22:X:85:ARG:CB	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:34:G:O6	25:B:44:C:C6	2.68	0.47
25:B:35:G:N1	25:B:36:U:C4	2.82	0.47
26:A:1551:U:O4	26:A:1619:U:O4	2.32	0.47
30:4:29:ARG:NH2	30:4:34:ASP:CG	2.72	0.47
4:F:102:ARG:NH1	28:2:9:TYR:CD1	2.82	0.47
9:K:1:MET:H2	9:K:2:PRO:CD	2.27	0.47
15:Q:55:SER:HB2	26:A:2907:C:H5'	1.97	0.47
20:V:11:VAL:HG21	20:V:38:VAL:HG11	1.96	0.47
20:V:27:TYR:HB3	20:V:30:ARG:HB2	1.96	0.47
24:Z:33:ARG:HA	24:Z:36:MET:HG2	1.95	0.47
25:B:58:A:C6	25:B:59:A:C8	2.99	0.47
25:B:59:A:C3'	25:B:60:G:H5'	2.45	0.47
26:A:103:C:H2'	26:A:104:G:H8	1.79	0.47
26:A:325:U:H2'	26:A:326:A:H8	1.79	0.47
26:A:534:G:H4'	26:A:535:A:H5'	1.97	0.47
26:A:2528:G:H22	26:A:2536:U:H3	1.62	0.47
3:E:181:ASP:OD1	3:E:181:ASP:N	2.43	0.47
25:B:4:A:C2	25:B:25:G:N1	2.82	0.47
26:A:1110:C:H2'	26:A:1111:G:H8	1.80	0.47
26:A:1588:G:H3'	26:A:1589:G:H8	1.79	0.47
1:C:67:PHE:HE1	1:C:106:ILE:HD11	1.80	0.47
1:C:262:LYS:N	1:C:263:PRO:HD3	2.30	0.47
4:F:23:LEU:HD21	4:F:29:TYR:OH	2.14	0.47
6:H:23:ASP:O	6:H:27:ARG:CB	2.62	0.47
10:L:107:ARG:HH21	10:L:115:VAL:HG11	1.80	0.47
14:P:50:GLN:NE2	25:B:7:G:N3	2.51	0.47
19:U:29:TYR:CE2	19:U:93:ILE:HB	2.50	0.47
21:W:94:HIS:CE1	25:B:75:U:O2	2.67	0.47
22:X:42:GLY:N	22:X:57:ASP:OD2	2.46	0.47
25:B:34:G:O6	25:B:44:C:H2'	2.13	0.47
26:A:451:U:H2'	26:A:452:G:C8	2.49	0.47
26:A:1414:G:N1	26:A:1858:A:OP2	2.36	0.47
26:A:1550:G:N2	26:A:1620:U:O2	2.35	0.47
26:A:1563:A:O2'	26:A:1564:A:OP2	2.28	0.47
26:A:1597:G:C4	26:A:1598:U:C6	2.96	0.47
26:A:2255:A:O2'	26:A:2678:G:N2	2.44	0.47
32:6:27:ALA:O	32:6:29:ARG:N	2.46	0.47
1:C:25:THR:CG2	1:C:81:HIS:HD1	2.28	0.47
4:F:44:ASN:C	4:F:44:ASN:ND2	2.73	0.47
4:F:115:LEU:HD23	4:F:183:PRO:CD	2.45	0.47
4:F:118:ILE:HB	4:F:121:PHE:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:I:27:GLU:HG3	7:I:76:PRO:HG2	1.97	0.47
16:R:124:PRO:HB3	26:A:1268:C:H4'	1.97	0.47
21:W:164:LEU:HD13	21:W:168:VAL:HG12	1.96	0.47
22:X:56:ASP:HA	26:A:2610:C:H4'	1.95	0.47
22:X:76:LYS:CE	26:A:973:G:OP1	2.63	0.47
26:A:1541:G:C6	26:A:1630:U:O4	2.68	0.47
26:A:1596:C:O2'	26:A:1597:G:P	2.73	0.47
30:4:35:ARG:HD3	30:4:35:ARG:HA	1.68	0.47
5:G:3:ARG:NH1	26:A:2975:G:OP2	2.43	0.47
9:K:114:LEU:HD12	26:A:650:G:H5'	1.97	0.47
12:N:74:LEU:HD22	26:A:1075:U:OP2	2.15	0.47
13:O:33:ARG:HD3	13:O:114:GLU:HG2	1.95	0.47
15:Q:1:MET:N	26:A:3096:U:O2	2.44	0.47
21:W:28:ARG:NH1	25:B:76:G:O3'	2.48	0.47
25:B:83:C:H5''	27:1:52:HIS:CE1	2.50	0.47
26:A:347:U:H2'	26:A:348:G:H8	1.80	0.47
26:A:1162:G:O2'	26:A:1229:A:N6	2.44	0.47
26:A:1596:C:O2'	26:A:1597:G:H5'	2.15	0.47
26:A:2644:C:OP1	32:6:34:GLU:CD	2.57	0.47
1:C:73:ASP:HB3	1:C:120:GLY:N	2.25	0.47
1:C:132:PRO:HD2	1:C:135:ASN:HD22	1.79	0.47
8:J:40:PHE:O	8:J:44:TYR:HB2	2.15	0.47
11:M:76:GLN:HE22	26:A:720:C:H42	1.63	0.47
15:Q:92:ARG:HG3	26:A:1970:G:H5''	1.95	0.47
20:V:31:ASN:O	20:V:68:VAL:HB	2.16	0.47
21:W:14:ASN:OD1	21:W:14:ASN:N	2.48	0.47
21:W:134:GLU:HB2	21:W:171:ILE:HD11	1.97	0.47
25:B:24:G:N9	25:B:56:C:C2	2.83	0.47
26:A:1535:C:H3'	26:A:1536:A:H8	1.79	0.47
26:A:1562:C:O2'	26:A:1563:A:OP2	2.32	0.47
26:A:1595:G:C8	26:A:1596:C:C5	2.88	0.47
26:A:1717:U:H5''	26:A:1718:C:H5	1.80	0.47
26:A:2753:G:O6	33:7:31:ARG:NH1	2.47	0.47
32:6:58:ILE:HD13	32:6:61:LEU:HD12	1.97	0.47
3:E:77:GLY:H	26:A:789:G:H5''	1.80	0.46
9:K:112:ASN:CG	9:K:113:LYS:N	2.73	0.46
13:O:14:SER:OG	26:A:2913:U:O2'	2.32	0.46
17:S:76:HIS:HE1	17:S:85:HIS:HD2	1.63	0.46
21:W:29:ARG:HH12	25:B:90:G:C4'	2.28	0.46
25:B:52:G:O2'	25:B:53:A:N7	2.45	0.46
34:8:6:ARG:O	34:8:10:ASP:HB2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:34:GLN:NE2	25:B:57:U:O2'	2.47	0.46
8:J:106:GLN:O	8:J:110:ILE:HB	2.15	0.46
9:K:142:ILE:HG22	9:K:143:LYS:H	1.80	0.46
10:L:35:ILE:HG21	10:L:103:GLY:HA3	1.98	0.46
11:M:35:ARG:NH1	11:M:41:LYS:O	2.47	0.46
20:V:46:ALA:CB	26:A:572:C:OP1	2.62	0.46
20:V:96:ARG:NH2	20:V:96:ARG:CG	2.72	0.46
25:B:84:C:C5	25:B:85:C:C4	3.03	0.46
26:A:1588:G:H3'	26:A:1589:G:C8	2.50	0.46
30:4:18:CYS:SG	30:4:19:LYS:HG2	2.55	0.46
3:E:145:LEU:HA	3:E:148:LEU:CD1	2.38	0.46
4:F:10:ARG:NH1	4:F:10:ARG:CG	2.72	0.46
20:V:79:LYS:HE3	20:V:79:LYS:HB2	1.70	0.46
21:W:77:LEU:HD13	21:W:100:VAL:HB	1.96	0.46
23:Y:34:GLN:NE2	26:A:2453:U:O2	2.43	0.46
25:B:15:U:H3'	25:B:16:A:H8	1.79	0.46
25:B:25:G:H2'	25:B:26:A:H5'	1.97	0.46
25:B:54:A:C2'	25:B:55:G:C5'	2.91	0.46
26:A:1530:G:N2	26:A:1805:G:H1	2.13	0.46
26:A:2154:G:O2'	26:A:2192:G:O6	2.28	0.46
31:5:6:ARG:CZ	31:5:6:ARG:HB3	2.44	0.46
1:C:49:ILE:N	26:A:894:U:OP1	2.33	0.46
2:D:7:LEU:HD11	2:D:82:ALA:HB3	1.97	0.46
3:E:7:VAL:CB	3:E:16:GLY:CA	2.84	0.46
5:G:159:LYS:HA	5:G:172:ARG:HH22	1.81	0.46
6:H:124:ILE:HG22	6:H:125:LYS:H	1.81	0.46
10:L:17:LYS:HB3	10:L:45:ASP:HB3	1.96	0.46
19:U:58:ASN:HB3	26:A:1456:G:H1'	1.97	0.46
25:B:5:C:OP1	25:B:61:C:O2'	2.23	0.46
25:B:59:A:H2'	25:B:60:G:H8	1.80	0.46
26:A:334:G:H2'	26:A:335:G:C8	2.50	0.46
26:A:2515:U:H2'	26:A:2516:U:C6	2.51	0.46
2:D:34:ASN:HD21	2:D:54:TYR:HB2	1.80	0.46
2:D:156:THR:CG2	26:A:2256:G:N2	2.75	0.46
2:D:159:ARG:NH1	2:D:159:ARG:HG2	2.30	0.46
3:E:8:LYS:HZ2	3:E:148:LEU:HB3	1.81	0.46
19:U:94:ASP:OD1	19:U:94:ASP:N	2.48	0.46
26:A:1189:G:H1'	26:A:1207:G:H2'	1.96	0.46
26:A:2509:C:OP2	30:4:28:ASN:ND2	2.48	0.46
30:4:16:GLU:HA	30:4:20:HIS:HB3	1.97	0.46
4:F:76:ARG:HG2	4:F:91:PRO:HA	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:99:ARG:HD3	25:B:45:G:H5'	1.98	0.46
14:P:43:SER:CB	25:B:28:A:OP1	2.63	0.46
16:R:90:VAL:HG13	17:S:6:ILE:HD13	1.97	0.46
21:W:36:VAL:HG22	21:W:94:HIS:CE1	2.50	0.46
22:X:76:LYS:HD3	26:A:973:G:OP1	2.16	0.46
26:A:1479:G:N2	26:A:1482:A:OP2	2.47	0.46
26:A:1612:U:H2'	26:A:1613:G:H8	1.81	0.46
3:E:131:VAL:O	3:E:133:GLY:N	2.49	0.46
3:E:208:ASN:N	3:E:208:ASN:HD22	2.13	0.46
4:F:114:ALA:HB1	4:F:144:MET:HE2	1.97	0.46
8:J:40:PHE:HZ	8:J:58:VAL:HG11	1.81	0.46
9:K:147:GLN:O	16:R:75:THR:HG21	2.16	0.46
25:B:54:A:H2'	25:B:55:G:H5'	1.93	0.46
26:A:747:A:H2	26:A:768:G:H21	1.63	0.46
26:A:1479:G:H4'	26:A:2025:C:H5	1.79	0.46
2:D:159:ARG:H	2:D:159:ARG:CD	2.28	0.46
9:K:14:SER:O	9:K:52:ASP:HB3	2.16	0.46
12:N:83:MET:HE2	12:N:83:MET:HB3	1.70	0.46
13:O:42:ARG:O	13:O:46:PRO:CD	2.63	0.46
13:O:106:ASP:OD1	13:O:106:ASP:N	2.48	0.46
16:R:77:ASN:HD22	26:A:1270:G:H21	1.64	0.46
22:X:83:VAL:O	22:X:85:ARG:HA	2.16	0.46
25:B:24:G:N9	25:B:56:C:N3	2.63	0.46
30:4:19:LYS:HD2	30:4:44:ASN:CG	2.39	0.46
4:F:64:LEU:HD12	4:F:72:PRO:CB	2.46	0.46
17:S:3:THR:CB	17:S:102:ILE:HD11	2.44	0.46
17:S:6:ILE:O	17:S:7:VAL:HG22	2.12	0.46
20:V:96:ARG:CZ	20:V:96:ARG:CB	2.94	0.46
26:A:2070:A:H2'	26:A:2071:A:C8	2.51	0.46
1:C:229:VAL:HB	26:A:899:G:O6	2.16	0.46
3:E:24:LEU:HD21	3:E:208:ASN:CB	2.46	0.46
4:F:185:LYS:HE2	4:F:185:LYS:C	2.40	0.46
7:I:49:TYR:HD1	7:I:80:ALA:HB2	1.81	0.46
14:P:43:SER:HB2	25:B:28:A:OP1	2.16	0.46
18:T:36:VAL:HG22	18:T:78:VAL:HG23	1.98	0.46
21:W:112:VAL:HG23	21:W:126:GLN:HE21	1.80	0.46
25:B:79:A:N1	25:B:94:G:O6	2.49	0.46
26:A:661:U:O2'	26:A:1101:A:N1	2.40	0.46
26:A:2394:A:O2'	26:A:2396:A:OP1	2.28	0.46
1:C:73:ASP:HA	1:C:119:SER:HB3	1.98	0.45
4:F:44:ASN:HD22	4:F:45:MET:N	2.13	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:99:ARG:HD3	25:B:45:G:O4'	2.16	0.45
10:L:75:SER:HB2	15:Q:71:ARG:HE	1.80	0.45
15:Q:58:PHE:HD1	15:Q:75:VAL:HG22	1.82	0.45
17:S:79:LYS:NZ	26:A:1108:A:N1	2.54	0.45
18:T:18:ARG:HH12	26:A:1436:C:C2'	2.28	0.45
21:W:83:LEU:HD12	21:W:92:ILE:HD12	1.95	0.45
26:A:2509:C:C5	30:4:8:ARG:CZ	2.94	0.45
1:C:37:LEU:CD2	1:C:62:TYR:HB2	2.37	0.45
3:E:150:GLU:OE1	3:E:193:ASP:CG	2.58	0.45
11:M:61:LEU:HD12	32:6:14:PHE:HZ	1.81	0.45
12:N:110:ASP:OD1	12:N:110:ASP:N	2.43	0.45
13:O:16:HIS:ND1	13:O:16:HIS:C	2.73	0.45
21:W:40:HIS:ND1	21:W:40:HIS:C	2.72	0.45
26:A:1595:G:OP2	26:A:1596:C:C5	2.68	0.45
3:E:140:SER:O	3:E:144:PHE:HB3	2.17	0.45
4:F:183:PRO:O	4:F:184:PHE:CE2	2.55	0.45
8:J:80:LEU:HD13	8:J:110:ILE:HG23	1.97	0.45
19:U:14:PRO:HA	19:U:31:PHE:HA	1.98	0.45
20:V:47:VAL:C	20:V:56:SER:CA	2.86	0.45
26:A:1040:U:H2'	26:A:1041:A:C8	2.52	0.45
1:C:58:HIS:CE1	26:A:1788:G:H21	2.28	0.45
1:C:221:VAL:HG21	26:A:897:A:C8	2.51	0.45
9:K:114:LEU:HD23	9:K:117:GLN:HE21	1.80	0.45
13:O:26:THR:CG2	13:O:75:VAL:HG21	2.46	0.45
25:B:83:C:C5'	27:1:52:HIS:CE1	2.99	0.45
26:A:273:A:H61	26:A:314:G:H1'	1.81	0.45
26:A:790:A:N3	26:A:2667:C:O2'	2.44	0.45
26:A:2059:G:H1	26:A:2122:U:H3	1.64	0.45
26:A:2288:C:H2'	26:A:2289:C:C6	2.52	0.45
26:A:2374:U:H2'	26:A:2375:G:H8	1.81	0.45
26:A:2527:G:H1	26:A:2537:C:H42	1.62	0.45
4:F:6:LYS:CE	4:F:6:LYS:N	2.80	0.45
4:F:45:MET:HE2	4:F:45:MET:CA	2.41	0.45
4:F:73:GLU:HG2	25:B:42:C:C4	2.43	0.45
4:F:154:ASP:OD1	4:F:155:ARG:N	2.48	0.45
5:G:165:TYR:HB2	5:G:168:GLU:HB2	1.98	0.45
21:W:78:ALA:HB1	21:W:97:LEU:HB3	1.99	0.45
26:A:314:G:O2'	26:A:321:G:O2'	2.35	0.45
26:A:377:C:H2'	26:A:378:G:H8	1.81	0.45
26:A:1573:U:OP1	26:A:1593:U:OP1	2.34	0.45
26:A:1754:G:C6	26:A:1759:A:N1	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:15:ALA:HB3	27:1:20:ARG:HG3	1.98	0.45
3:E:83:GLN:H	3:E:83:GLN:HG2	1.42	0.45
9:K:76:ARG:HG2	9:K:76:ARG:O	2.17	0.45
10:L:76:TYR:HB2	15:Q:72:THR:HB	1.98	0.45
10:L:120:GLU:OE1	15:Q:64:SER:HB3	2.15	0.45
13:O:38:GLU:OE2	13:O:99:LYS:NZ	2.50	0.45
13:O:46:PRO:HG2	13:O:47:TYR:N	2.32	0.45
19:U:13:ALA:O	19:U:32:VAL:N	2.38	0.45
1:C:71:ASP:OD1	1:C:71:ASP:N	2.30	0.45
3:E:7:VAL:O	3:E:14:THR:CA	2.55	0.45
3:E:151:ASN:O	3:E:152:LYS:CB	2.57	0.45
12:N:60:ARG:NH1	26:A:1194:C:OP2	2.49	0.45
12:N:124:LYS:HD2	26:A:2708:G:H1'	1.99	0.45
17:S:76:HIS:HE1	17:S:85:HIS:CD2	2.35	0.45
19:U:77:LYS:HE2	19:U:78:SER:C	2.41	0.45
20:V:83:VAL:CG1	20:V:96:ARG:CG	2.95	0.45
26:A:286:G:N2	26:A:287:A:H62	2.14	0.45
26:A:605:G:OP2	29:3:14:ARG:NH2	2.49	0.45
26:A:857:U:H2'	26:A:858:A:C8	2.51	0.45
1:C:97:TYR:CD2	1:C:101:GLU:HG3	2.51	0.45
1:C:261:ASN:C	1:C:263:PRO:HD3	2.41	0.45
4:F:170:ASP:OD1	4:F:170:ASP:N	2.41	0.45
8:J:114:LYS:HA	8:J:117:ASP:HB3	1.99	0.45
10:L:71:ARG:NH2	10:L:105:GLU:HG3	2.32	0.45
11:M:51:GLU:OE2	32:6:57:ARG:NE	2.49	0.45
12:N:60:ARG:NE	26:A:1194:C:P	2.89	0.45
12:N:108:TYR:CD2	12:N:110:ASP:OD1	2.70	0.45
19:U:77:LYS:CE	19:U:79:THR:HG22	2.45	0.45
20:V:4:HIS:ND1	20:V:96:ARG:CZ	2.67	0.45
22:X:72:LYS:HG3	22:X:73:ARG:H	1.80	0.45
25:B:22:A:C6	25:B:23:G:O6	2.70	0.45
26:A:1550:G:O6	26:A:1620:U:O4	2.34	0.45
1:C:168:LYS:HA	1:C:173:ALA:HA	1.97	0.45
4:F:70:GLN:HE21	25:B:43:C:H4'	1.80	0.45
13:O:20:LEU:HD23	13:O:20:LEU:O	2.17	0.45
13:O:33:ARG:CD	13:O:114:GLU:HG2	2.44	0.45
14:P:88:ILE:O	14:P:92:ALA:CB	2.65	0.45
19:U:83:ILE:HD13	26:A:1456:G:C4	2.51	0.45
21:W:37:LEU:HD21	21:W:99:VAL:CG2	2.47	0.45
24:Z:5:THR:HG23	24:Z:6:THR:N	2.25	0.45
26:A:159:A:N3	26:A:2431:C:O2'	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1379:G:OP1	29:3:16:ARG:NH2	2.47	0.45
26:A:1537:U:H2'	26:A:1538:G:H8	1.82	0.45
26:A:2375:G:H2'	26:A:2376:G:C8	2.52	0.45
3:E:9:THR:HG22	3:E:128:THR:CG2	2.47	0.45
4:F:11:LEU:CD2	4:F:108:ASP:N	2.80	0.45
12:N:39:HIS:HB3	12:N:99:PRO:HD3	1.99	0.45
13:O:9:ARG:CD	13:O:14:SER:HB3	2.47	0.45
15:Q:50:GLN:HB2	15:Q:57:THR:HG22	1.99	0.45
20:V:100:THR:O	20:V:101:ASN:HB2	2.17	0.45
21:W:38:TYR:O	21:W:38:TYR:CD1	2.69	0.45
21:W:98:LEU:C	21:W:98:LEU:CD2	2.90	0.45
21:W:124:VAL:HG12	21:W:181:VAL:HG22	1.99	0.45
26:A:249:C:OP2	26:A:2618:C:O2'	2.33	0.45
26:A:857:U:H2'	26:A:858:A:H8	1.81	0.45
26:A:1512:U:OP2	26:A:1513:C:N4	2.44	0.45
27:1:19:GLN:HG2	27:1:50:VAL:HG12	1.98	0.45
1:C:63:ARG:NH1	26:A:1788:G:OP2	2.50	0.44
2:D:60:ARG:HH22	26:A:3055:G:H5'	1.82	0.44
3:E:51:SER:OG	26:A:35:A:C5'	2.58	0.44
4:F:27:PHE:HB2	4:F:29:TYR:CE1	2.51	0.44
19:U:74:GLY:HA2	26:A:61:G:O2'	2.18	0.44
25:B:20:G:N1	25:B:63:U:C4	2.73	0.44
25:B:34:G:O2'	25:B:35:G:C5	2.70	0.44
25:B:58:A:H2'	25:B:59:A:O5'	2.17	0.44
26:A:130:C:H2'	26:A:131:A:C8	2.53	0.44
26:A:478:A:H4'	26:A:479:A:H5'	1.99	0.44
26:A:2238:A:H2'	26:A:2239:A:C8	2.53	0.44
27:1:8:GLN:HG2	27:1:31:ILE:HA	1.99	0.44
10:L:7:ARG:NH2	10:L:20:LEU:CD1	2.43	0.44
11:M:61:LEU:HD12	32:6:14:PHE:CZ	2.52	0.44
14:P:108:THR:CB	25:B:47:A:O2'	2.64	0.44
20:V:86:ARG:CB	20:V:97:ILE:CG1	2.89	0.44
22:X:83:VAL:HG13	22:X:85:ARG:CA	2.37	0.44
25:B:89:C:C5	25:B:89:C:OP2	2.70	0.44
26:A:681:C:H2'	26:A:682:A:C8	2.53	0.44
26:A:1580:A:C2	26:A:1592:G:C1'	2.87	0.44
28:2:41:CYS:CA	28:2:43:PRO:HD2	2.47	0.44
30:4:20:HIS:CD2	30:4:20:HIS:O	2.70	0.44
2:D:158:GLY:O	26:A:2276:G:N3	2.50	0.44
18:T:41:ASP:OD2	29:3:38:LYS:HB2	2.17	0.44
20:V:83:VAL:HG11	20:V:96:ARG:CG	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:97:ILE:HD13	20:V:103:LYS:O	2.16	0.44
26:A:944:A:C8	26:A:2472:C:H5'	2.52	0.44
26:A:1296:G:H2'	26:A:1297:G:C8	2.52	0.44
26:A:1515:C:N4	26:A:1516:G:O6	2.50	0.44
26:A:1532:G:O2'	26:A:1803:A:N1	2.48	0.44
26:A:2616:A:H5''	32:6:28:ASN:ND2	2.33	0.44
1:C:256:ARG:O	26:A:2014:G:O3'	2.34	0.44
3:E:14:THR:CG2	3:E:15:ASP:H	2.15	0.44
4:F:26:GLU:OE1	4:F:27:PHE:CE2	2.70	0.44
12:N:74:LEU:HD12	12:N:94:VAL:HG21	1.99	0.44
12:N:108:TYR:CE2	12:N:110:ASP:OD1	2.70	0.44
22:X:83:VAL:HG11	22:X:86:PRO:HD3	1.99	0.44
26:A:176:G:H3'	26:A:177:G:H8	1.83	0.44
26:A:1525:U:H2'	26:A:1526:A:H8	1.83	0.44
26:A:1576:C:O2	26:A:1577:C:C4	2.71	0.44
28:2:62:GLU:O	28:2:65:TYR:CD2	2.70	0.44
31:5:22:ARG:O	31:5:26:ARG:CD	2.58	0.44
1:C:51:THR:HG21	1:C:54:LYS:CE	2.46	0.44
2:D:154:CYS:CB	26:A:2798:G:HO2'	2.27	0.44
4:F:6:LYS:N	4:F:6:LYS:HE3	2.32	0.44
9:K:5:THR:CG2	26:A:624:G:H4'	2.47	0.44
13:O:52:ILE:HD12	13:O:94:TYR:CB	2.48	0.44
13:O:90:ARG:HH21	13:O:118:GLU:HB2	1.74	0.44
14:P:37:ARG:HD2	14:P:103:ASP:HB2	1.98	0.44
14:P:44:ALA:O	14:P:77:LYS:NZ	2.44	0.44
17:S:103:LYS:C	17:S:103:LYS:CD	2.86	0.44
19:U:74:GLY:O	26:A:61:G:O3'	2.35	0.44
26:A:1569:A:C8	26:A:1569:A:OP2	2.70	0.44
26:A:2323:G:H2'	26:A:2324:A:H8	1.83	0.44
26:A:3070:G:H4'	26:A:3071:A:H5'	1.99	0.44
30:4:19:LYS:O	30:4:20:HIS:CG	2.70	0.44
5:G:108:LEU:HD13	5:G:153:ARG:HG2	1.98	0.44
10:L:109:LYS:CD	10:L:110:LYS:HZ1	2.24	0.44
13:O:29:PHE:HE2	13:O:51:LEU:HD13	1.79	0.44
16:R:26:GLY:O	16:R:30:ARG:NH1	2.51	0.44
21:W:37:LEU:HD13	21:W:69:LEU:HD13	1.95	0.44
26:A:738:A:O2'	26:A:740:A:OP1	2.32	0.44
26:A:742:G:O2'	26:A:2575:G:OP1	2.36	0.44
26:A:947:U:H2'	26:A:948:G:C8	2.53	0.44
5:G:60:ARG:HA	5:G:63:ARG:HH21	1.82	0.44
13:O:72:ASP:O	13:O:76:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:102:ARG:HH21	21:W:138:LEU:CD2	2.22	0.44
26:A:947:U:H2'	26:A:948:G:H8	1.83	0.44
26:A:1562:C:O2'	26:A:1563:A:O4'	2.35	0.44
26:A:1586:C:H2'	26:A:1587:G:O4'	2.18	0.44
26:A:2339:G:H3'	26:A:2340:A:H8	1.83	0.44
30:4:19:LYS:O	30:4:21:ARG:NH2	2.51	0.44
9:K:18:ILE:HD13	9:K:18:ILE:HG21	1.80	0.44
13:O:33:ARG:HB2	13:O:114:GLU:HG2	2.00	0.44
14:P:43:SER:HB3	14:P:46:HIS:H	1.83	0.44
20:V:77:ASP:OD1	20:V:77:ASP:N	2.49	0.44
26:A:254:G:H4'	26:A:472:C:H4'	1.99	0.44
26:A:351:G:N1	26:A:444:U:N3	2.45	0.44
26:A:1159:C:H2'	26:A:1160:G:H8	1.82	0.44
28:2:41:CYS:HB2	28:2:44:PHE:HZ	1.74	0.44
30:4:15:CYS:HB3	30:4:20:HIS:H	1.81	0.44
31:5:40:LYS:O	31:5:40:LYS:HG3	2.18	0.44
4:F:120:ASP:O	4:F:122:ARG:HD3	2.17	0.44
7:I:57:VAL:HA	7:I:60:ALA:HB3	2.00	0.44
10:L:93:PRO:HD2	10:L:113:LYS:HD3	2.00	0.44
21:W:6:ASN:ND2	21:W:6:ASN:C	2.75	0.44
24:Z:48:ARG:HD2	26:A:58:G:OP1	2.18	0.44
25:B:89:C:P	25:B:89:C:C6	3.10	0.44
26:A:325:U:H2'	26:A:326:A:C8	2.52	0.44
26:A:325:U:O4	26:A:450:G:O6	2.36	0.44
26:A:569:G:O2'	26:A:594:U:O4	2.35	0.44
26:A:621:U:H2'	26:A:622:C:C6	2.53	0.44
26:A:1439:G:H3'	26:A:1440:C:H4'	2.00	0.44
26:A:1551:U:C4	26:A:1619:U:O4	2.71	0.44
26:A:1575:A:C8	26:A:1575:A:OP2	2.70	0.44
26:A:2325:U:O4	26:A:2410:A:N1	2.51	0.44
4:F:56:LEU:O	4:F:59:GLY:N	2.51	0.43
4:F:66:LEU:HD23	28:2:27:THR:HG22	1.81	0.43
10:L:4:GLN:HE22	26:A:2176:A:H61	1.66	0.43
18:T:7:PHE:N	18:T:8:PRO:CD	2.81	0.43
21:W:105:LYS:HZ3	21:W:136:GLU:HG3	1.83	0.43
25:B:27:A:H2'	25:B:28:A:H8	1.83	0.43
26:A:2:A:H2'	26:A:3:A:C8	2.52	0.43
26:A:406:A:N6	26:A:420:G:O2'	2.50	0.43
26:A:1551:U:H3'	26:A:1552:A:H8	1.83	0.43
3:E:14:THR:CG2	3:E:15:ASP:N	2.73	0.43
13:O:68:LYS:HB2	26:A:2932:G:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:21:LYS:HZ2	25:B:80:C:H42	1.61	0.43
24:Z:44:ASN:ND2	26:A:58:G:OP1	2.50	0.43
25:B:18:C:H2'	25:B:19:G:H5'	1.81	0.43
26:A:196:A:H2	26:A:2658:A:H62	1.66	0.43
26:A:922:U:O2'	26:A:2284:A:N1	2.48	0.43
26:A:1621:C:H2'	26:A:1622:G:H8	1.83	0.43
26:A:1668:C:O2'	26:A:1764:A:N3	2.41	0.43
26:A:1921:G:H2'	26:A:1922:G:C8	2.53	0.43
26:A:2585:U:P	32:6:24:ARG:HH12	2.36	0.43
5:G:61:ARG:O	5:G:65:LEU:CB	2.67	0.43
12:N:14:HIS:HA	12:N:15:PRO:HD2	1.80	0.43
13:O:56:LYS:CD	13:O:87:TYR:O	2.67	0.43
15:Q:49:ARG:NE	15:Q:56:GLU:OE2	2.50	0.43
17:S:26:LYS:NZ	26:A:1281:G:O3'	2.51	0.43
18:T:7:PHE:O	18:T:7:PHE:CD1	2.70	0.43
19:U:4:ILE:O	19:U:5:THR:HB	2.18	0.43
19:U:58:ASN:HB2	19:U:83:ILE:HG12	1.99	0.43
20:V:97:ILE:CD1	20:V:104:ASP:HA	2.49	0.43
23:Y:34:GLN:OE1	26:A:2452:G:N2	2.44	0.43
26:A:1381:G:O2'	26:A:2236:G:O6	2.27	0.43
26:A:1566:A:H1'	26:A:1605:G:N1	2.24	0.43
26:A:1595:G:H5'	26:A:1596:C:N1	2.32	0.43
28:2:41:CYS:O	28:2:44:PHE:CE2	2.70	0.43
2:D:151:ILE:HD11	2:D:166:MET:HE3	1.99	0.43
3:E:118:ARG:NH2	3:E:189:LEU:HA	2.34	0.43
3:E:121:ASN:ND2	11:M:3:VAL:HG23	2.33	0.43
3:E:171:ASN:ND2	3:E:171:ASN:O	2.51	0.43
4:F:40:LYS:HG2	4:F:164:VAL:HB	2.00	0.43
5:G:151:ARG:HH21	26:A:2968:G:H4'	1.84	0.43
7:I:51:VAL:N	26:A:1202:A:OP1	2.51	0.43
8:J:59:GLU:HB3	8:J:71:ALA:HB3	2.00	0.43
13:O:25:ALA:O	13:O:29:PHE:CD2	2.70	0.43
13:O:29:PHE:CZ	13:O:51:LEU:CD1	2.99	0.43
13:O:48:ALA:O	13:O:52:ILE:HG13	2.18	0.43
23:Y:48:ARG:NH2	26:A:2424:C:OP1	2.36	0.43
26:A:334:G:H2'	26:A:335:G:H8	1.84	0.43
26:A:1106:A:H3'	27:1:11:SER:HB2	2.00	0.43
26:A:1583:U:C2	26:A:1584:U:O4	2.71	0.43
26:A:1590:G:C6	26:A:1591:U:O4	2.70	0.43
26:A:1597:G:C2	26:A:1598:U:C6	3.01	0.43
26:A:1597:G:C5	26:A:1598:U:H5	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:23:LEU:HD11	27:1:53:LEU:HD22	2.00	0.43
2:D:27:THR:OG1	2:D:196:GLY:O	2.28	0.43
2:D:143:ALA:HB1	26:A:1875:U:H4'	2.00	0.43
9:K:1:MET:H2	9:K:2:PRO:HD3	1.80	0.43
9:K:5:THR:HG21	26:A:624:G:O3'	2.18	0.43
10:L:109:LYS:HE3	10:L:109:LYS:HB2	1.74	0.43
18:T:117:ARG:HA	18:T:117:ARG:HD2	1.78	0.43
19:U:73:PHE:CZ	31:5:43:ARG:NH2	2.80	0.43
21:W:100:VAL:HG11	21:W:137:ALA:CB	2.16	0.43
21:W:133:ILE:HD11	21:W:144:LEU:HD11	2.00	0.43
25:B:21:C:H6	25:B:21:C:C3'	2.29	0.43
26:A:1189:G:O2'	26:A:1207:G:OP2	2.35	0.43
26:A:1561:C:C3'	26:A:1562:C:H5'	2.48	0.43
26:A:1581:C:N4	26:A:1590:G:N3	2.66	0.43
26:A:1621:C:H2'	26:A:1622:G:C8	2.54	0.43
33:7:3:VAL:CG1	33:7:37:GLY:HA3	2.49	0.43
2:D:185:VAL:HG22	2:D:192:LEU:HG	2.01	0.43
3:E:77:GLY:N	26:A:789:G:H5''	2.33	0.43
3:E:124:ILE:H	3:E:124:ILE:HG13	1.48	0.43
4:F:185:LYS:O	4:F:185:LYS:HG3	2.18	0.43
12:N:111:GLU:C	12:N:111:GLU:CD	2.86	0.43
19:U:83:ILE:HD11	26:A:1456:G:H21	1.63	0.43
20:V:28:PRO:HG3	26:A:82:G:O3'	2.19	0.43
26:A:334:G:H1	26:A:347:U:H3	1.66	0.43
26:A:802:C:OP1	31:5:9:GLN:HG3	2.19	0.43
26:A:1525:U:H2'	26:A:1526:A:C8	2.53	0.43
26:A:1898:U:N3	26:A:1981:U:OP2	2.46	0.43
26:A:3022:G:H2'	26:A:3023:G:C8	2.53	0.43
3:E:103:PRO:HD2	3:E:106:MET:HE3	2.00	0.43
9:K:77:HIS:CD2	9:K:77:HIS:C	2.97	0.43
20:V:4:HIS:CD2	20:V:96:ARG:NH1	2.86	0.43
21:W:105:LYS:NZ	21:W:136:GLU:N	2.66	0.43
26:A:860:G:O2'	26:A:863:G:O2'	2.21	0.43
26:A:2693:A:N6	26:A:2705:G:O2'	2.51	0.43
30:4:19:LYS:HB2	30:4:21:ARG:CZ	2.48	0.43
5:G:35:LEU:HD13	5:G:76:LEU:HD22	2.00	0.43
11:M:49:MET:HB2	11:M:58:HIS:CE1	2.54	0.43
21:W:21:LYS:O	21:W:25:ARG:HG2	2.19	0.43
24:Z:44:ASN:O	24:Z:47:LEU:N	2.51	0.43
26:A:241:A:H61	26:A:255:A:H5''	1.83	0.43
26:A:286:G:H21	26:A:287:A:H62	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:895:G:O2'	26:A:898:A:N6	2.51	0.43
26:A:1118:A:OP2	26:A:1273:G:N1	2.37	0.43
26:A:1291:G:N2	26:A:1292:U:O3'	2.52	0.43
26:A:3012:U:O2'	26:A:3030:A:N3	2.39	0.43
7:I:57:VAL:O	7:I:61:ALA:N	2.51	0.43
9:K:15:TRP:H	9:K:15:TRP:HD1	1.64	0.43
9:K:15:TRP:CE3	9:K:55:ILE:HD11	2.54	0.43
10:L:67:LYS:HA	10:L:67:LYS:HD2	1.83	0.43
18:T:18:ARG:HH12	26:A:1436:C:H2'	1.84	0.43
25:B:84:C:C5	25:B:85:C:N3	2.86	0.43
26:A:1581:C:O2'	26:A:1582:C:H6	2.02	0.43
1:C:241:SER:N	26:A:2195:U:O2	2.52	0.43
4:F:9:PRO:HG2	4:F:12:LYS:HE3	2.00	0.43
4:F:146:HIS:CE1	28:2:35:VAL:HG23	2.53	0.43
18:T:35:SER:O	18:T:39:ALA:N	2.51	0.43
26:A:815:G:O2'	26:A:1850:A:N3	2.51	0.43
26:A:1567:C:O2'	26:A:1568:C:H5'	2.19	0.43
28:2:63:LYS:O	28:2:65:TYR:CD2	2.70	0.43
1:C:67:PHE:HB3	1:C:153:ALA:HB3	2.01	0.42
3:E:103:PRO:HG3	26:A:773:G:O2'	2.18	0.42
5:G:160:GLY:HA3	5:G:164:ARG:HH21	1.84	0.42
13:O:9:ARG:HG2	13:O:14:SER:HA	2.01	0.42
19:U:6:ASP:CG	24:Z:23:ARG:HG3	2.44	0.42
21:W:77:LEU:HD13	21:W:100:VAL:CB	2.49	0.42
26:A:721:A:N3	26:A:730:G:N2	2.63	0.42
26:A:832:G:H3'	26:A:833:A:H8	1.83	0.42
26:A:1573:U:C6	26:A:1573:U:OP2	2.72	0.42
26:A:2510:A:N6	30:4:25:THR:OG1	2.52	0.42
26:A:2539:G:H2'	26:A:2540:G:C8	2.54	0.42
26:A:2879:G:O2'	26:A:2888:G:O6	2.35	0.42
2:D:7:LEU:HG	2:D:207:VAL:HG22	2.01	0.42
4:F:45:MET:HB2	4:F:64:LEU:HD11	2.01	0.42
4:F:45:MET:HB3	4:F:94:ALA:O	2.15	0.42
13:O:4:PRO:HG2	26:A:3094:A:C2	2.51	0.42
20:V:99:LYS:HA	20:V:99:LYS:HD2	1.64	0.42
21:W:8:PRO:O	21:W:8:PRO:HG2	2.19	0.42
25:B:33:C:H2'	25:B:34:G:O4'	2.19	0.42
26:A:1574:G:C5'	26:A:1575:A:OP1	2.66	0.42
26:A:1665:U:H2'	26:A:1666:A:C8	2.54	0.42
26:A:2643:U:H4'	30:4:24:ILE:HD13	2.01	0.42
1:C:132:PRO:HD2	1:C:135:ASN:ND2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:121:PHE:CD2	4:F:121:PHE:O	2.72	0.42
9:K:65:SER:OG	26:A:1259:U:OP2	2.35	0.42
10:L:8:LEU:HD22	10:L:84:ALA:HB2	2.01	0.42
19:U:34:HIS:HA	19:U:35:PRO:HD3	1.86	0.42
24:Z:57:VAL:O	24:Z:61:LEU:HG	2.18	0.42
25:B:29:C:N4	25:B:55:G:H22	2.15	0.42
26:A:961:U:O2'	26:A:963:U:O4	2.32	0.42
26:A:1000:C:H2'	26:A:1001:C:H5''	2.00	0.42
26:A:1188:A:N7	26:A:1214:A:O2'	2.44	0.42
26:A:1601:G:C4	26:A:1602:U:C5	3.08	0.42
26:A:2814:A:H2'	26:A:2815:C:C6	2.55	0.42
10:L:108:GLU:CG	10:L:109:LYS:N	2.73	0.42
14:P:90:GLU:O	14:P:94:ALA:CB	2.68	0.42
21:W:38:TYR:CZ	21:W:96:ASP:OD2	2.65	0.42
21:W:38:TYR:OH	21:W:81:LYS:HD3	2.19	0.42
21:W:62:GLY:C	21:W:63:THR:HG23	2.44	0.42
21:W:80:THR:HG21	21:W:83:LEU:CD2	2.48	0.42
25:B:85:C:C6	25:B:85:C:C3'	3.02	0.42
25:B:85:C:O2	25:B:86:U:N3	2.52	0.42
26:A:13:G:H5''	29:3:14:ARG:HB3	2.00	0.42
26:A:760:U:H2'	26:A:761:G:C8	2.55	0.42
26:A:1174:G:H4'	26:A:1204:A:H8	1.84	0.42
26:A:1976:A:O2'	26:A:2938:G:O2'	2.32	0.42
26:A:2467:U:H2'	26:A:2468:U:C6	2.54	0.42
30:4:34:ASP:O	30:4:35:ARG:HB2	2.18	0.42
1:C:23:GLU:OE2	1:C:23:GLU:HA	2.18	0.42
2:D:51:GLN:HE21	2:D:81:VAL:HG11	1.84	0.42
3:E:76:GLN:HE22	3:E:83:GLN:NE2	2.18	0.42
9:K:73:PHE:CE1	9:K:88:THR:HG22	2.54	0.42
12:N:61:GLY:C	12:N:108:TYR:CE1	2.95	0.42
14:P:88:ILE:O	14:P:92:ALA:HB2	2.19	0.42
25:B:58:A:C8	25:B:58:A:C4'	3.02	0.42
26:A:1007:G:H2'	26:A:1008:G:H8	1.83	0.42
26:A:2482:U:O2'	26:A:2651:C:OP2	2.35	0.42
7:I:48:THR:N	7:I:81:PHE:O	2.47	0.42
13:O:67:MET:HE2	13:O:67:MET:HB3	1.80	0.42
19:U:74:GLY:HA2	26:A:61:G:H4'	2.02	0.42
20:V:89:ASP:O	20:V:91:THR:N	2.53	0.42
21:W:37:LEU:HD21	21:W:99:VAL:HG22	2.01	0.42
21:W:146:VAL:HG21	21:W:157:ILE:HG21	2.01	0.42
22:X:64:PRO:CB	26:A:759:G:H1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:83:VAL:O	22:X:83:VAL:HG22	2.19	0.42
26:A:1586:C:H2'	26:A:1587:G:C4'	2.50	0.42
26:A:1594:G:H8	26:A:1594:G:O5'	2.02	0.42
26:A:1791:A:H2'	26:A:1792:A:C8	2.54	0.42
26:A:2422:A:N1	26:A:2450:C:N4	2.64	0.42
28:2:41:CYS:O	28:2:44:PHE:CD2	2.73	0.42
28:2:62:GLU:O	28:2:65:TYR:CE2	2.73	0.42
3:E:24:LEU:HD21	3:E:208:ASN:HB3	2.01	0.42
4:F:56:LEU:N	4:F:56:LEU:HD23	2.34	0.42
4:F:64:LEU:HD12	4:F:72:PRO:HB2	2.00	0.42
12:N:108:TYR:HB3	12:N:114:ALA:HB2	2.01	0.42
16:R:97:GLU:O	16:R:101:SER:OG	2.35	0.42
19:U:77:LYS:HE2	19:U:79:THR:CA	2.49	0.42
21:W:36:VAL:HG21	25:B:74:A:C2	2.52	0.42
22:X:26:PHE:N	22:X:29:GLN:HE21	2.12	0.42
23:Y:37:ARG:HB3	23:Y:46:LYS:HD3	2.00	0.42
26:A:1690:A:H2'	26:A:1691:A:C8	2.55	0.42
1:C:125:ILE:HG23	1:C:193:VAL:HG11	2.01	0.42
3:E:3:LEU:O	3:E:4:LYS:HG3	2.20	0.42
3:E:9:THR:HG22	3:E:128:THR:HG23	2.01	0.42
18:T:7:PHE:N	18:T:8:PRO:HD3	2.34	0.42
25:B:59:A:H3'	25:B:60:G:C8	2.55	0.42
26:A:210:G:OP2	31:5:28:ARG:NH2	2.51	0.42
26:A:1586:C:O5'	26:A:1586:C:C6	2.70	0.42
26:A:2616:A:H5''	32:6:28:ASN:HD22	1.84	0.42
26:A:2665:C:OP2	26:A:2810:U:O2'	2.37	0.42
4:F:56:LEU:CD2	4:F:56:LEU:N	2.83	0.42
9:K:7:LYS:HG3	26:A:626:G:OP1	2.20	0.42
13:O:21:LEU:HD23	13:O:21:LEU:HA	1.89	0.42
19:U:45:ALA:O	19:U:49:ILE:HG12	2.20	0.42
21:W:54:PHE:HE2	21:W:92:ILE:HG21	1.84	0.42
22:X:75:ARG:NE	26:A:2558:C:N4	2.63	0.42
23:Y:28:ARG:NH1	23:Y:30:ASN:OD1	2.53	0.42
25:B:40:A:N6	28:2:1:MET:H3	1.98	0.42
26:A:1565:A:H2	26:A:1606:G:C4	2.35	0.42
31:5:15:ARG:NH1	31:5:47:ALA:HB1	2.35	0.42
1:C:37:LEU:HD23	1:C:62:TYR:CG	2.55	0.42
3:E:176:HIS:CE1	26:A:708:G:O6	2.73	0.42
3:E:189:LEU:HD13	11:M:9:LEU:HD11	2.02	0.42
12:N:21:ALA:HB2	12:N:98:LYS:HB2	2.02	0.42
15:Q:57:THR:OG1	15:Q:73:PHE:O	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:95:ARG:HG3	18:T:101:PHE:CD2	2.55	0.42
19:U:38:ASN:OD1	19:U:38:ASN:N	2.46	0.42
19:U:94:ASP:O	19:U:95:LEU:HB3	2.19	0.42
24:Z:48:ARG:CG	26:A:58:G:OP1	2.68	0.42
26:A:1678:U:H3	26:A:2926:A:H61	1.68	0.42
1:C:29:PRO:CB	1:C:34:VAL:CG2	2.84	0.41
1:C:177:MET:HE2	1:C:183:ARG:HB3	2.02	0.41
4:F:44:ASN:ND2	4:F:45:MET:O	2.53	0.41
20:V:30:ARG:HD2	20:V:32:LYS:HD2	2.02	0.41
20:V:72:MET:HE3	26:A:383:U:H5'	2.01	0.41
24:Z:62:ARG:HD3	24:Z:62:ARG:C	2.43	0.41
25:B:59:A:C2'	25:B:60:G:C5'	2.94	0.41
26:A:97:U:OP1	26:A:98:U:O2'	2.32	0.41
26:A:2457:U:H2'	26:A:2458:G:C8	2.55	0.41
3:E:176:HIS:HE1	26:A:708:G:O6	2.03	0.41
4:F:11:LEU:HD12	4:F:11:LEU:HA	1.88	0.41
4:F:47:VAL:HG23	4:F:92:ILE:HG22	2.02	0.41
13:O:79:LEU:C	13:O:79:LEU:CD2	2.85	0.41
20:V:2:LYS:CD	20:V:83:VAL:HB	2.49	0.41
21:W:63:THR:C	21:W:64:ASN:CG	2.87	0.41
22:X:15:ASP:CB	26:A:2487:C:N4	2.75	0.41
26:A:844:G:H5'	26:A:845:C:H5''	2.01	0.41
26:A:1567:C:C2	26:A:1603:G:O6	2.73	0.41
26:A:1882:A:H61	26:A:2220:C:N4	2.17	0.41
26:A:2364:C:H2'	26:A:2365:A:C8	2.55	0.41
26:A:2497:A:H2'	26:A:2498:A:C8	2.55	0.41
30:4:29:ARG:C	30:4:31:ASN:H	2.27	0.41
4:F:23:LEU:HD22	4:F:35:ILE:HG23	2.02	0.41
4:F:47:VAL:HG21	4:F:92:ILE:C	2.45	0.41
4:F:56:LEU:HD23	4:F:57:ILE:H	1.85	0.41
12:N:59:LYS:C	12:N:60:ARG:CG	2.90	0.41
12:N:134:ARG:HD3	21:W:129:ASN:HD21	1.85	0.41
14:P:77:LYS:HB3	14:P:112:ARG:HD3	2.01	0.41
17:S:92:GLN:HE22	26:A:1281:G:H21	1.67	0.41
21:W:118:ALA:HB1	21:W:122:THR:HG21	2.02	0.41
27:1:50:VAL:O	27:1:54:VAL:HG22	2.19	0.41
4:F:57:ILE:O	4:F:61:ILE:HG13	2.21	0.41
9:K:15:TRP:O	9:K:16:TYR:CD1	2.74	0.41
14:P:68:ALA:HA	14:P:71:ARG:HB2	2.01	0.41
26:A:150:C:H2'	26:A:151:A:C8	2.55	0.41
26:A:1243:G:OP1	33:7:22:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:26:SER:OG	28:2:27:THR:N	2.53	0.41
31:5:38:ARG:CA	31:5:45:LEU:HD21	2.50	0.41
32:6:48:THR:OG1	32:6:49:THR:N	2.48	0.41
1:C:98:LEU:HD22	1:C:98:LEU:H	1.84	0.41
6:H:24:GLY:O	6:H:28:ASN:HB2	2.21	0.41
8:J:90:GLY:HA2	8:J:99:VAL:HG11	2.01	0.41
9:K:1:MET:HE2	26:A:642:G:OP1	2.20	0.41
9:K:93:LEU:HG	9:K:100:VAL:HG21	2.01	0.41
25:B:27:A:H2'	25:B:28:A:C8	2.55	0.41
26:A:1499:A:O2'	26:A:1519:C:O2	2.39	0.41
26:A:1574:G:N2	26:A:1599:U:H5''	2.35	0.41
26:A:1584:U:C6	26:A:1584:U:C3'	3.03	0.41
26:A:1854:U:H2'	26:A:1855:A:H8	1.85	0.41
4:F:45:MET:CG	4:F:60:ALA:HB1	2.49	0.41
13:O:114:GLU:C	13:O:115:LEU:O	2.63	0.41
26:A:210:G:P	31:5:28:ARG:HH22	2.43	0.41
26:A:1597:G:O2'	26:A:1598:U:P	2.78	0.41
26:A:2781:G:H2'	26:A:2782:C:C6	2.56	0.41
1:C:118:GLU:O	1:C:129:ASN:HB2	2.20	0.41
3:E:155:LEU:HD11	3:E:178:ILE:HD11	2.01	0.41
8:J:16:GLN:HG2	8:J:55:VAL:HG12	2.02	0.41
10:L:9:LYS:O	10:L:83:ALA:HA	2.20	0.41
13:O:99:LYS:HE2	26:A:3037:C:H5''	2.03	0.41
19:U:83:ILE:CD1	26:A:1456:G:C4	2.97	0.41
19:U:94:ASP:C	19:U:96:PHE:H	2.21	0.41
25:B:24:G:H2'	25:B:56:C:C4	2.56	0.41
25:B:56:C:O2	25:B:56:C:C2'	2.69	0.41
25:B:96:A:C2	26:A:977:G:C2	2.91	0.41
26:A:442:U:H2'	26:A:443:C:C6	2.56	0.41
26:A:600:A:H2	26:A:674:U:H4'	1.86	0.41
26:A:1224:G:H2'	26:A:1225:G:H8	1.86	0.41
26:A:1562:C:O2'	26:A:1563:A:P	2.79	0.41
26:A:1569:A:N3	26:A:1570:C:H5	2.18	0.41
31:5:14:ARG:HH11	31:5:14:ARG:HD2	1.75	0.41
1:C:19:SER:O	1:C:21:PHE:CD2	2.74	0.41
9:K:27:ARG:CG	9:K:27:ARG:NH1	2.82	0.41
19:U:21:TYR:HA	19:U:24:ILE:HG12	2.00	0.41
21:W:37:LEU:HA	21:W:97:LEU:O	2.21	0.41
26:A:1026:A:N1	26:A:2501:G:O2'	2.49	0.41
26:A:1501:C:H2'	26:A:1502:G:C8	2.56	0.41
26:A:1551:U:O4	26:A:1618:C:N4	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1576:C:O2'	26:A:1577:C:P	2.79	0.41
26:A:1633:U:H2'	26:A:1634:C:C6	2.56	0.41
33:7:24:MET:HE3	33:7:24:MET:HB2	1.77	0.41
1:C:35:ARG:CD	1:C:36:PRO:CD	2.97	0.41
1:C:161:VAL:HG13	1:C:178:PRO:HB3	2.02	0.41
4:F:10:ARG:O	4:F:13:GLN:HB3	2.21	0.41
4:F:76:ARG:HH12	25:B:41:U:H3	1.68	0.41
4:F:182:PHE:HA	4:F:183:PRO:HD3	1.90	0.41
5:G:110:TYR:HD1	26:A:2891:C:H1'	1.85	0.41
12:N:17:GLN:HB3	12:N:96:ASN:HD21	1.86	0.41
13:O:87:TYR:OH	13:O:115:LEU:HB3	2.21	0.41
14:P:14:ARG:HH21	25:B:46:A:H5''	1.86	0.41
15:Q:28:HIS:ND1	15:Q:41:VAL:HG12	2.36	0.41
19:U:69:THR:HG21	19:U:73:PHE:C	2.45	0.41
19:U:69:THR:CB	19:U:73:PHE:O	2.68	0.41
21:W:40:HIS:O	21:W:41:GLY:C	2.62	0.41
21:W:140:ILE:HA	21:W:141:PRO:HD3	1.89	0.41
22:X:15:ASP:CA	26:A:2486:U:O4	2.68	0.41
25:B:34:G:N1	25:B:44:C:C4	2.88	0.41
25:B:79:A:N1	25:B:94:G:C6	2.88	0.41
26:A:176:G:OP2	26:A:176:G:N2	2.42	0.41
26:A:658:U:O2'	26:A:924:G:OP2	2.37	0.41
26:A:683:G:H1'	32:6:2:PRO:HD2	2.02	0.41
26:A:733:U:H2'	26:A:734:C:C6	2.56	0.41
26:A:1086:C:H2'	26:A:1087:G:H8	1.86	0.41
26:A:1565:A:H2	26:A:1606:G:N9	2.19	0.41
26:A:1579:C:O2'	26:A:1580:A:P	2.79	0.41
26:A:1590:G:N1	26:A:1591:U:C5	2.89	0.41
26:A:1602:U:C2'	26:A:1603:G:C8	2.96	0.41
26:A:1627:U:H2'	26:A:1628:A:H8	1.86	0.41
26:A:1704:U:H2'	26:A:1705:C:C6	2.56	0.41
26:A:2043:C:O2'	26:A:2195:U:OP2	2.38	0.41
26:A:2096:G:H2'	26:A:2097:G:H8	1.86	0.41
26:A:2106:A:H3'	26:A:2107:G:H5''	2.02	0.41
26:A:2593:A:H2'	26:A:2594:G:H8	1.84	0.41
27:1:49:THR:HG22	27:1:50:VAL:HG13	2.03	0.41
30:4:13:LEU:HD23	30:4:53:GLU:HB3	2.02	0.41
3:E:78:SER:OG	3:E:79:THR:N	2.53	0.41
11:M:31:LYS:HE3	11:M:31:LYS:HB3	1.94	0.41
19:U:94:ASP:C	19:U:96:PHE:N	2.75	0.41
21:W:29:ARG:HH12	25:B:90:G:H4'	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:83:VAL:CG1	22:X:85:ARG:HB2	2.42	0.41
26:A:181:A:N3	26:A:521:C:O2'	2.47	0.41
26:A:323:C:H42	26:A:453:U:H3	1.69	0.41
26:A:1591:U:O2	26:A:1591:U:C2'	2.69	0.41
26:A:3041:C:OP2	26:A:3042:A:N6	2.50	0.41
9:K:3:THR:HG21	26:A:1113:C:C2	2.46	0.40
9:K:109:LEU:HD23	9:K:109:LEU:HA	1.87	0.40
13:O:64:ARG:NH1	26:A:1675:U:O2	2.55	0.40
15:Q:99:LEU:HD11	15:Q:109:ILE:HD11	2.02	0.40
26:A:1688:G:N2	26:A:1748:A:H1'	2.36	0.40
26:A:1761:G:H2'	26:A:1762:C:C6	2.56	0.40
26:A:2701:U:O4	33:7:10:ILE:HG12	2.21	0.40
2:D:124:ALA:HB3	2:D:129:ARG:HG3	2.02	0.40
3:E:172:LEU:HD12	3:E:172:LEU:HA	1.93	0.40
6:H:43:ALA:O	6:H:47:ALA:CB	2.68	0.40
10:L:69:ARG:HD2	10:L:69:ARG:HA	1.91	0.40
12:N:60:ARG:HB2	12:N:61:GLY:H	1.62	0.40
18:T:54:VAL:HG22	18:T:110:ILE:HD13	2.03	0.40
19:U:67:LYS:NZ	26:A:1451:A:P	2.93	0.40
26:A:76:C:O2'	26:A:428:A:N3	2.48	0.40
26:A:1624:U:O2'	26:A:1625:G:H8	2.04	0.40
26:A:2350:G:H2'	26:A:2351:A:C8	2.56	0.40
26:A:2649:A:H4'	26:A:2650:A:H5''	2.03	0.40
26:A:2686:U:H2'	26:A:2687:U:C6	2.56	0.40
30:4:39:LYS:HA	30:4:50:PRO:HA	2.03	0.40
1:C:26:ARG:HD2	1:C:81:HIS:CE1	2.49	0.40
1:C:44:ASN:OD1	1:C:44:ASN:N	2.50	0.40
1:C:54:LYS:NZ	26:A:2032:A:P	2.94	0.40
2:D:157:PRO:CD	2:D:158:GLY:H	2.34	0.40
9:K:14:SER:O	9:K:52:ASP:CG	2.65	0.40
9:K:75:TYR:H	9:K:75:TYR:HD1	1.68	0.40
15:Q:48:ARG:NE	15:Q:59:THR:OG1	2.50	0.40
17:S:6:ILE:O	17:S:39:VAL:HG13	2.21	0.40
19:U:58:ASN:HD22	26:A:1456:G:N2	2.18	0.40
19:U:71:THR:HB	26:A:544:U:C2	2.56	0.40
21:W:99:VAL:HG12	21:W:101:GLN:H	1.86	0.40
25:B:20:G:C2	25:B:63:U:N3	2.68	0.40
25:B:20:G:C6	25:B:63:U:O4	2.74	0.40
25:B:88:C:C3'	25:B:88:C:C6	3.03	0.40
26:A:937:U:H2'	26:A:938:G:C8	2.56	0.40
26:A:937:U:H2'	26:A:938:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:153:GLY:O	2:D:155:ALA:N	2.55	0.40
3:E:4:LYS:CA	3:E:20:LEU:HD21	2.52	0.40
3:E:55:ARG:HD2	3:E:82:PRO:HD3	2.04	0.40
4:F:44:ASN:ND2	4:F:45:MET:N	2.70	0.40
13:O:96:ARG:CZ	13:O:116:VAL:HG12	2.48	0.40
18:T:6:GLU:O	18:T:7:PHE:CB	2.70	0.40
21:W:184:ALA:HA	21:W:185:PRO:HD3	1.94	0.40
26:A:845:C:OP1	26:A:1992:U:O2'	2.27	0.40
26:A:860:G:H21	26:A:865:A:H61	1.70	0.40
26:A:1805:G:H2'	26:A:1806:A:H8	1.85	0.40
26:A:1922:G:H2'	26:A:1923:G:H8	1.86	0.40
3:E:34:MET:HE3	3:E:189:LEU:HD11	2.04	0.40
4:F:35:ILE:HG23	4:F:36:PRO:HD2	2.03	0.40
9:K:134:ALA:O	9:K:135:GLN:CB	2.70	0.40
13:O:20:LEU:C	13:O:20:LEU:CD2	2.85	0.40
19:U:4:ILE:CG1	24:Z:58:TYR:HE1	2.34	0.40
25:B:79:A:H2	25:B:94:G:N1	2.10	0.40
26:A:55:G:O2'	26:A:70:A:N1	2.53	0.40
26:A:1105:C:O2'	26:A:1118:A:N3	2.44	0.40
26:A:1393:C:H2'	26:A:1394:A:H8	1.85	0.40
26:A:2176:A:N3	26:A:2784:C:O2'	2.46	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 PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	271/278 (98%)	233 (86%)	33 (12%)	5 (2%)	6	34
2	D	212/217 (98%)	199 (94%)	11 (5%)	2 (1%)	14	47
3	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	3	24
4	F	179/187 (96%)	162 (90%)	15 (8%)	2 (1%)	11	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
6	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	18	52
7	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
8	J	131/142 (92%)	118 (90%)	13 (10%)	0	100	100
9	K	145/147 (99%)	133 (92%)	9 (6%)	3 (2%)	5	31
10	L	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
11	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
12	N	132/138 (96%)	113 (86%)	19 (14%)	0	100	100
13	O	115/199 (58%)	102 (89%)	10 (9%)	3 (3%)	4	26
14	P	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
15	Q	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
16	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
17	S	100/103 (97%)	94 (94%)	5 (5%)	1 (1%)	12	45
18	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	4	25
19	U	92/100 (92%)	70 (76%)	16 (17%)	6 (6%)	1	8
20	V	93/105 (89%)	83 (89%)	8 (9%)	2 (2%)	5	29
21	W	186/215 (86%)	171 (92%)	10 (5%)	5 (3%)	4	25
22	X	80/88 (91%)	61 (76%)	13 (16%)	6 (8%)	1	5
23	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
24	Z	61/77 (79%)	59 (97%)	1 (2%)	1 (2%)	7	36
27	1	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
28	2	64/75 (85%)	61 (95%)	2 (3%)	1 (2%)	7	36
29	3	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
30	4	48/55 (87%)	37 (77%)	7 (15%)	4 (8%)	0	4
31	5	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
32	6	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
33	7	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	8	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	3623/3991 (91%)	3287 (91%)	285 (8%)	51 (1%)	11	39

All (51) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	58	HIS
1	C	145	VAL
1	C	262	LYS
3	E	94	LYS
3	E	152	LYS
4	F	47	VAL
9	K	142	ILE
18	T	7	PHE
18	T	118	PRO
21	W	41	GLY
21	W	83	LEU
24	Z	10	LEU
1	C	146	GLU
2	D	155	ALA
3	E	65	PRO
4	F	142	GLN
9	K	140	PHE
13	O	15	SER
13	O	115	LEU
19	U	68	ARG
21	W	63	THR
22	X	12	ASN
22	X	16	SER
22	X	17	ALA
1	C	36	PRO
9	K	2	PRO
19	U	70	ARG
19	U	75	LYS
21	W	85	VAL
22	X	85	ARG
30	4	34	ASP
3	E	4	LYS
3	E	93	PRO
6	H	125	LYS
13	O	60	LEU
18	T	8	PRO
19	U	6	ASP
20	V	90	GLU
20	V	101	ASN
21	W	87	PRO
22	X	84	ALA
30	4	7	VAL
2	D	157	PRO

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Mol	Chain	Res	Type
3	E	132	GLU
19	U	5	THR
17	S	7	VAL
19	U	10	ILE
22	X	83	VAL
28	2	42	HIS
30	4	33	PRO
30	4	9	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	214/218 (98%)	204 (95%)	10 (5%)	23	57
2	D	160/163 (98%)	157 (98%)	3 (2%)	50	73
3	E	167/173 (96%)	158 (95%)	9 (5%)	20	53
4	F	150/156 (96%)	138 (92%)	12 (8%)	11	40
5	G	148/150 (99%)	147 (99%)	1 (1%)	76	83
6	H	90/116 (78%)	90 (100%)	0	100	100
7	I	89/120 (74%)	89 (100%)	0	100	100
8	J	102/108 (94%)	102 (100%)	0	100	100
9	K	120/120 (100%)	116 (97%)	4 (3%)	33	65
10	L	99/100 (99%)	98 (99%)	1 (1%)	68	80
11	M	112/114 (98%)	111 (99%)	1 (1%)	70	81
12	N	112/116 (97%)	107 (96%)	5 (4%)	24	58
13	O	96/158 (61%)	90 (94%)	6 (6%)	16	48
14	P	93/94 (99%)	93 (100%)	0	100	100
15	Q	100/100 (100%)	99 (99%)	1 (1%)	68	80
16	R	97/99 (98%)	97 (100%)	0	100	100
17	S	82/83 (99%)	81 (99%)	1 (1%)	63	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	T	90/117 (77%)	88 (98%)	2 (2%)	45	71
19	U	82/85 (96%)	71 (87%)	11 (13%)	4	19
20	V	81/86 (94%)	71 (88%)	10 (12%)	4	22
21	W	154/168 (92%)	137 (89%)	17 (11%)	6	26
22	X	59/63 (94%)	56 (95%)	3 (5%)	21	54
23	Y	50/51 (98%)	50 (100%)	0	100	100
24	Z	58/66 (88%)	55 (95%)	3 (5%)	21	54
27	1	53/54 (98%)	52 (98%)	1 (2%)	50	73
28	2	57/63 (90%)	54 (95%)	3 (5%)	20	53
29	3	43/46 (94%)	43 (100%)	0	100	100
30	4	48/52 (92%)	40 (83%)	8 (17%)	2	11
31	5	35/36 (97%)	34 (97%)	1 (3%)	37	67
32	6	53/54 (98%)	53 (100%)	0	100	100
33	7	35/35 (100%)	33 (94%)	2 (6%)	18	51
34	8	18/19 (95%)	18 (100%)	0	100	100
All	All	2947/3183 (93%)	2832 (96%)	115 (4%)	30	62

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

Mol	Chain	Res	Type
1	C	31	LYS
1	C	35	ARG
1	C	36	PRO
1	C	37	LEU
1	C	71	ASP
1	C	73	ASP
1	C	106	ILE
1	C	225	VAL
1	C	247	VAL
1	C	258	ARG
2	D	156	THR
2	D	159	ARG
2	D	160	VAL
3	E	4	LYS
3	E	31	ILE
3	E	33	LEU
3	E	124	ILE

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Mol	Chain	Res	Type
3	E	130	LEU
3	E	150	GLU
3	E	177	VAL
3	E	178	ILE
3	E	201	LEU
4	F	6	LYS
4	F	10	ARG
4	F	11	LEU
4	F	44	ASN
4	F	55	LYS
4	F	92	ILE
4	F	96	VAL
4	F	108	ASP
4	F	110	LEU
4	F	118	ILE
4	F	185	LYS
4	F	186	GLU
5	G	90	ILE
9	K	75	TYR
9	K	76	ARG
9	K	113	LYS
9	K	141	GLU
10	L	8	LEU
11	M	57	ILE
12	N	34	ILE
12	N	59	LYS
12	N	60	ARG
12	N	92	TRP
12	N	122	ILE
13	O	5	THR
13	O	14	SER
13	O	16	HIS
13	O	54	HIS
13	O	79	LEU
13	O	117	ARG
15	Q	32	ILE
17	S	103	LYS
18	T	6	GLU
18	T	118	PRO
19	U	9	ASP
19	U	10	ILE
19	U	12	LEU

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Mol	Chain	Res	Type
19	U	59	THR
19	U	66	ARG
19	U	67	LYS
19	U	69	THR
19	U	75	LYS
19	U	94	ASP
19	U	95	LEU
19	U	96	PHE
20	V	10	LEU
20	V	20	LYS
20	V	22	LYS
20	V	30	ARG
20	V	41	ILE
20	V	77	ASP
20	V	89	ASP
20	V	95	VAL
20	V	96	ARG
20	V	99	LYS
21	W	6	ASN
21	W	7	ILE
21	W	36	VAL
21	W	40	HIS
21	W	64	ASN
21	W	83	LEU
21	W	100	VAL
21	W	101	GLN
21	W	102	ARG
21	W	112	VAL
21	W	114	VAL
21	W	119	THR
21	W	131	ILE
21	W	139	SER
21	W	146	VAL
21	W	158	THR
21	W	172	SER
22	X	14	ARG
22	X	15	ASP
22	X	38	VAL
24	Z	5	THR
24	Z	14	THR
24	Z	47	LEU
27	1	51	HIS

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Mol	Chain	Res	Type
28	2	38	CYS
28	2	44	PHE
28	2	60	ARG
30	4	22	ASN
30	4	23	TYR
30	4	26	LYS
30	4	27	LYS
30	4	30	ARG
30	4	36	LEU
30	4	37	GLU
30	4	42	CYS
31	5	27	THR
33	7	20	HIS
33	7	36	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (87) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	38	HIS
1	C	53	HIS
1	C	58	HIS
1	C	96	HIS
1	C	130	ASN
1	C	135	ASN
1	C	205	ASN
2	D	34	ASN
2	D	80	HIS
2	D	142	GLN
3	E	35	HIS
3	E	41	GLN
3	E	83	GLN
3	E	121	ASN
3	E	184	ASN
3	E	202	ASN
4	F	28	ASN
4	F	31	ASN
4	F	34	GLN
4	F	44	ASN
4	F	134	ASN
4	F	142	GLN
4	F	146	HIS
4	F	169	ASN

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Mol	Chain	Res	Type
5	G	22	GLN
5	G	66	HIS
6	H	118	GLN
6	H	137	HIS
7	I	16	GLN
8	J	33	HIS
8	J	119	ASN
9	K	47	ASN
9	K	96	HIS
9	K	103	ASN
9	K	132	HIS
9	K	135	GLN
10	L	4	GLN
11	M	58	HIS
11	M	76	GLN
11	M	127	ASN
12	N	96	ASN
12	N	123	HIS
13	O	16	HIS
13	O	77	HIS
14	P	3	HIS
14	P	41	ASN
14	P	50	GLN
16	R	39	GLN
16	R	41	HIS
17	S	67	HIS
17	S	76	HIS
17	S	85	HIS
17	S	90	HIS
17	S	92	GLN
18	T	67	ASN
18	T	68	ASN
19	U	27	ASN
19	U	58	ASN
21	W	6	ASN
21	W	46	HIS
21	W	91	ASN
21	W	126	GLN
21	W	161	GLN
22	X	29	GLN
22	X	46	HIS
22	X	79	ASN

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Mol	Chain	Res	Type
23	Y	22	HIS
23	Y	45	ASN
24	Z	44	ASN
24	Z	52	GLN
27	1	8	GLN
27	1	42	GLN
27	1	48	ASN
27	1	51	HIS
28	2	20	HIS
28	2	40	GLN
30	4	48	HIS
30	4	49	GLN
31	5	11	ASN
31	5	19	HIS
32	6	7	HIS
32	6	28	ASN
32	6	31	HIS
32	6	35	HIS
33	7	20	HIS
33	7	34	GLN
34	8	17	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	B	116/118 (98%)	42 (36%)	3 (2%)
26	A	3096/3120 (99%)	788 (25%)	44 (1%)
All	All	3212/3238 (99%)	830 (25%)	47 (1%)

All (830) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	B	4	A
25	B	5	C
25	B	7	G
25	B	10	G
25	B	12	C
25	B	13	C
25	B	14	A
25	B	15	U
25	B	19	G

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Mol	Chain	Res	Type
25	B	21	C
25	B	22	A
25	B	23	G
25	B	24	G
25	B	25	G
25	B	26	A
25	B	30	G
25	B	34	G
25	B	35	G
25	B	37	C
25	B	40	A
25	B	41	U
25	B	44	C
25	B	45	G
25	B	47	A
25	B	52	G
25	B	53	A
25	B	55	G
25	B	56	C
25	B	57	U
25	B	58	A
25	B	59	A
25	B	60	G
25	B	66	C
25	B	67	A
25	B	68	G
25	B	85	C
25	B	86	U
25	B	88	C
25	B	90	G
25	B	102	A
25	B	106	C
25	B	113	G
26	A	7	U
26	A	11	A
26	A	12	G
26	A	20	G
26	A	29	C
26	A	31	U
26	A	32	G
26	A	33	G
26	A	52	G

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Mol	Chain	Res	Type
26	A	58	G
26	A	59	G
26	A	60	A
26	A	68	A
26	A	71	A
26	A	72	G
26	A	77	G
26	A	80	G
26	A	81	A
26	A	88	A
26	A	89	A
26	A	90	C
26	A	93	A
26	A	94	G
26	A	98	U
26	A	99	G
26	A	115	A
26	A	117	U
26	A	122	A
26	A	125	C
26	A	128	G
26	A	136	U
26	A	143	G
26	A	161	U
26	A	164	A
26	A	173	U
26	A	175	G
26	A	180	A
26	A	186	G
26	A	195	A
26	A	198	A
26	A	203	A
26	A	205	U
26	A	212	A
26	A	214	G
26	A	215	A
26	A	220	A
26	A	221	A
26	A	227	A
26	A	229	U
26	A	230	G
26	A	231	U

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Mol	Chain	Res	Type
26	A	237	C
26	A	245	G
26	A	248	G
26	A	250	G
26	A	264	G
26	A	265	A
26	A	272	A
26	A	274	C
26	A	275	C
26	A	279	U
26	A	283	U
26	A	285	U
26	A	286	G
26	A	287	A
26	A	288	U
26	A	291	C
26	A	292	G
26	A	296	A
26	A	297	G
26	A	299	G
26	A	300	G
26	A	301	U
26	A	302	U
26	A	303	G
26	A	305	G
26	A	309	G
26	A	314	G
26	A	315	U
26	A	317	G
26	A	318	U
26	A	319	G
26	A	322	A
26	A	323	C
26	A	326	A
26	A	327	U
26	A	329	U
26	A	330	U
26	A	331	U
26	A	336	C
26	A	337	U
26	A	338	C
26	A	346	C

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Mol	Chain	Res	Type
26	A	351	G
26	A	352	G
26	A	357	U
26	A	358	G
26	A	361	A
26	A	364	A
26	A	366	G
26	A	370	U
26	A	384	G
26	A	393	U
26	A	404	A
26	A	412	A
26	A	416	C
26	A	417	C
26	A	424	G
26	A	425	U
26	A	427	A
26	A	434	G
26	A	438	U
26	A	445	U
26	A	446	G
26	A	449	G
26	A	450	G
26	A	452	G
26	A	453	U
26	A	454	U
26	A	459	A
26	A	460	G
26	A	468	G
26	A	471	C
26	A	472	C
26	A	474	G
26	A	489	A
26	A	491	U
26	A	493	U
26	A	498	G
26	A	505	C
26	A	509	U
26	A	512	G
26	A	530	G
26	A	543	U
26	A	544	U

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Mol	Chain	Res	Type
26	A	547	U
26	A	555	G
26	A	561	G
26	A	562	G
26	A	566	A
26	A	567	A
26	A	568	A
26	A	569	G
26	A	585	G
26	A	589	A
26	A	591	G
26	A	592	A
26	A	594	U
26	A	595	A
26	A	596	C
26	A	605	G
26	A	617	U
26	A	618	C
26	A	619	C
26	A	620	G
26	A	639	C
26	A	640	G
26	A	641	U
26	A	642	G
26	A	643	G
26	A	644	G
26	A	647	G
26	A	649	U
26	A	655	G
26	A	665	G
26	A	666	A
26	A	667	A
26	A	678	A
26	A	679	G
26	A	684	G
26	A	685	G
26	A	689	U
26	A	696	A
26	A	706	G
26	A	707	G
26	A	708	G
26	A	709	U

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Mol	Chain	Res	Type
26	A	712	G
26	A	721	A
26	A	725	A
26	A	728	G
26	A	730	G
26	A	731	A
26	A	740	A
26	A	747	A
26	A	753	A
26	A	757	G
26	A	758	A
26	A	760	U
26	A	763	G
26	A	765	G
26	A	766	G
26	A	768	G
26	A	769	U
26	A	770	A
26	A	774	G
26	A	784	G
26	A	785	A
26	A	794	G
26	A	801	U
26	A	830	A
26	A	832	G
26	A	838	G
26	A	845	C
26	A	862	U
26	A	863	G
26	A	868	C
26	A	871	A
26	A	872	G
26	A	878	G
26	A	879	A
26	A	880	G
26	A	890	G
26	A	891	G
26	A	897	A
26	A	899	G
26	A	904	A
26	A	908	A
26	A	915	U

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Mol	Chain	Res	Type
26	A	917	A
26	A	919	A
26	A	920	G
26	A	921	C
26	A	927	C
26	A	942	U
26	A	944	A
26	A	945	G
26	A	960	G
26	A	961	U
26	A	966	U
26	A	971	G
26	A	973	G
26	A	974	G
26	A	975	U
26	A	981	U
26	A	982	A
26	A	994	A
26	A	995	U
26	A	996	G
26	A	1001	C
26	A	1002	C
26	A	1003	A
26	A	1007	G
26	A	1009	U
26	A	1011	A
26	A	1012	C
26	A	1013	U
26	A	1014	G
26	A	1016	C
26	A	1022	C
26	A	1025	A
26	A	1029	C
26	A	1030	C
26	A	1042	A
26	A	1044	U
26	A	1046	C
26	A	1047	A
26	A	1048	A
26	A	1049	G
26	A	1058	A
26	A	1062	A

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Mol	Chain	Res	Type
26	A	1063	G
26	A	1068	C
26	A	1070	G
26	A	1074	A
26	A	1076	A
26	A	1078	G
26	A	1085	G
26	A	1091	A
26	A	1092	G
26	A	1098	A
26	A	1100	C
26	A	1101	A
26	A	1107	G
26	A	1114	G
26	A	1130	C
26	A	1131	G
26	A	1140	G
26	A	1141	U
26	A	1143	G
26	A	1144	A
26	A	1151	U
26	A	1163	A
26	A	1164	A
26	A	1169	A
26	A	1171	C
26	A	1173	G
26	A	1175	A
26	A	1178	U
26	A	1181	G
26	A	1184	U
26	A	1185	A
26	A	1186	G
26	A	1187	A
26	A	1188	A
26	A	1189	G
26	A	1190	C
26	A	1191	A
26	A	1192	G
26	A	1201	G
26	A	1202	A
26	A	1205	G
26	A	1206	A

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Mol	Chain	Res	Type
26	A	1207	G
26	A	1209	G
26	A	1212	U
26	A	1213	A
26	A	1215	U
26	A	1216	A
26	A	1224	G
26	A	1229	A
26	A	1230	G
26	A	1232	G
26	A	1233	A
26	A	1237	U
26	A	1238	G
26	A	1239	C
26	A	1240	G
26	A	1244	A
26	A	1246	A
26	A	1250	U
26	A	1251	A
26	A	1253	C
26	A	1260	C
26	A	1261	A
26	A	1270	G
26	A	1275	A
26	A	1292	U
26	A	1293	G
26	A	1303	U
26	A	1325	U
26	A	1332	G
26	A	1335	G
26	A	1343	G
26	A	1344	A
26	A	1345	G
26	A	1347	G
26	A	1353	G
26	A	1362	A
26	A	1363	G
26	A	1365	G
26	A	1368	A
26	A	1369	A
26	A	1371	G
26	A	1372	C

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Mol	Chain	Res	Type
26	A	1386	G
26	A	1389	U
26	A	1404	C
26	A	1409	C
26	A	1415	A
26	A	1416	A
26	A	1417	A
26	A	1440	C
26	A	1444	U
26	A	1448	C
26	A	1456	G
26	A	1462	G
26	A	1465	C
26	A	1467	U
26	A	1480	A
26	A	1493	A
26	A	1494	U
26	A	1499	A
26	A	1501	C
26	A	1507	G
26	A	1510	A
26	A	1521	C
26	A	1522	G
26	A	1529	U
26	A	1531	C
26	A	1532	G
26	A	1533	U
26	A	1534	C
26	A	1539	A
26	A	1540	U
26	A	1546	A
26	A	1549	G
26	A	1550	G
26	A	1551	U
26	A	1552	A
26	A	1553	C
26	A	1554	U
26	A	1555	A
26	A	1556	A
26	A	1562	C
26	A	1563	A
26	A	1564	A

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Mol	Chain	Res	Type
26	A	1565	A
26	A	1566	A
26	A	1567	C
26	A	1568	C
26	A	1569	A
26	A	1570	C
26	A	1571	C
26	A	1572	G
26	A	1574	G
26	A	1575	A
26	A	1576	C
26	A	1577	C
26	A	1578	G
26	A	1579	C
26	A	1580	A
26	A	1581	C
26	A	1582	C
26	A	1584	U
26	A	1585	U
26	A	1586	C
26	A	1587	G
26	A	1588	G
26	A	1589	G
26	A	1590	G
26	A	1591	U
26	A	1592	G
26	A	1593	U
26	A	1594	G
26	A	1595	G
26	A	1596	C
26	A	1597	G
26	A	1598	U
26	A	1599	U
26	A	1600	G
26	A	1601	G
26	A	1602	U
26	A	1603	G
26	A	1605	G
26	A	1606	G
26	A	1625	G
26	A	1629	G
26	A	1630	U

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Mol	Chain	Res	Type
26	A	1632	G
26	A	1633	U
26	A	1636	A
26	A	1637	G
26	A	1638	C
26	A	1639	G
26	A	1640	A
26	A	1641	U
26	A	1642	G
26	A	1648	A
26	A	1649	C
26	A	1654	G
26	A	1658	G
26	A	1672	C
26	A	1674	G
26	A	1676	G
26	A	1678	U
26	A	1679	A
26	A	1680	A
26	A	1681	U
26	A	1688	G
26	A	1703	G
26	A	1710	A
26	A	1711	G
26	A	1713	U
26	A	1715	A
26	A	1717	U
26	A	1721	U
26	A	1724	G
26	A	1727	A
26	A	1728	U
26	A	1731	A
26	A	1737	A
26	A	1744	A
26	A	1748	A
26	A	1753	C
26	A	1754	G
26	A	1767	U
26	A	1768	C
26	A	1769	G
26	A	1774	U
26	A	1778	A

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Mol	Chain	Res	Type
26	A	1780	G
26	A	1786	G
26	A	1787	A
26	A	1789	A
26	A	1792	A
26	A	1798	U
26	A	1803	A
26	A	1813	C
26	A	1826	A
26	A	1836	A
26	A	1837	G
26	A	1845	G
26	A	1852	A
26	A	1863	G
26	A	1864	U
26	A	1866	C
26	A	1869	G
26	A	1870	U
26	A	1871	G
26	A	1872	A
26	A	1878	G
26	A	1887	A
26	A	1892	G
26	A	1893	C
26	A	1903	C
26	A	1906	U
26	A	1916	A
26	A	1917	G
26	A	1933	G
26	A	1958	C
26	A	1967	G
26	A	1973	C
26	A	1974	A
26	A	1975	A
26	A	1981	U
26	A	1990	A
26	A	1998	C
26	A	1999	U
26	A	2017	C
26	A	2018	G
26	A	2026	A
26	A	2028	G

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Mol	Chain	Res	Type
26	A	2033	U
26	A	2046	A
26	A	2052	G
26	A	2062	G
26	A	2064	A
26	A	2074	G
26	A	2075	G
26	A	2083	A
26	A	2085	C
26	A	2086	U
26	A	2088	C
26	A	2089	C
26	A	2090	U
26	A	2091	U
26	A	2092	U
26	A	2093	G
26	A	2094	G
26	A	2095	G
26	A	2096	G
26	A	2106	A
26	A	2107	G
26	A	2111	U
26	A	2112	U
26	A	2118	C
26	A	2120	A
26	A	2130	G
26	A	2131	G
26	A	2137	A
26	A	2138	C
26	A	2140	A
26	A	2142	A
26	A	2151	A
26	A	2153	G
26	A	2154	G
26	A	2160	A
26	A	2161	A
26	A	2163	U
26	A	2167	U
26	A	2179	U
26	A	2190	A
26	A	2191	C
26	A	2194	A

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Mol	Chain	Res	Type
26	A	2195	U
26	A	2196	G
26	A	2206	C
26	A	2215	U
26	A	2217	U
26	A	2221	A
26	A	2244	A
26	A	2247	A
26	A	2251	G
26	A	2255	A
26	A	2256	G
26	A	2257	A
26	A	2263	G
26	A	2267	C
26	A	2276	G
26	A	2279	C
26	A	2280	G
26	A	2284	A
26	A	2285	G
26	A	2286	A
26	A	2299	C
26	A	2315	U
26	A	2316	G
26	A	2317	G
26	A	2319	G
26	A	2320	C
26	A	2322	C
26	A	2323	G
26	A	2325	U
26	A	2328	G
26	A	2334	U
26	A	2335	G
26	A	2337	A
26	A	2338	G
26	A	2339	G
26	A	2340	A
26	A	2341	U
26	A	2342	A
26	A	2343	G
26	A	2346	G
26	A	2348	G
26	A	2349	A

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Mol	Chain	Res	Type
26	A	2351	A
26	A	2353	U
26	A	2354	G
26	A	2355	U
26	A	2356	G
26	A	2357	A
26	A	2362	C
26	A	2368	C
26	A	2371	G
26	A	2380	G
26	A	2382	G
26	A	2383	U
26	A	2384	C
26	A	2385	G
26	A	2386	U
26	A	2387	U
26	A	2388	G
26	A	2390	U
26	A	2392	A
26	A	2393	A
26	A	2394	A
26	A	2395	U
26	A	2396	A
26	A	2404	G
26	A	2407	C
26	A	2408	G
26	A	2409	U
26	A	2410	A
26	A	2411	U
26	A	2413	G
26	A	2414	G
26	A	2418	U
26	A	2421	A
26	A	2427	G
26	A	2433	U
26	A	2434	A
26	A	2436	A
26	A	2446	G
26	A	2449	A
26	A	2462	G
26	A	2463	G
26	A	2467	U

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Mol	Chain	Res	Type
26	A	2473	U
26	A	2476	G
26	A	2490	A
26	A	2502	A
26	A	2506	G
26	A	2507	C
26	A	2510	A
26	A	2511	A
26	A	2512	A
26	A	2529	A
26	A	2531	G
26	A	2532	G
26	A	2545	G
26	A	2546	A
26	A	2549	G
26	A	2551	A
26	A	2558	C
26	A	2559	A
26	A	2567	U
26	A	2571	C
26	A	2574	C
26	A	2578	A
26	A	2582	A
26	A	2585	U
26	A	2586	G
26	A	2596	G
26	A	2601	A
26	A	2607	G
26	A	2608	G
26	A	2609	A
26	A	2612	A
26	A	2614	U
26	A	2615	G
26	A	2616	A
26	A	2626	U
26	A	2627	C
26	A	2630	A
26	A	2631	G
26	A	2640	G
26	A	2643	U
26	A	2647	U
26	A	2648	C

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Mol	Chain	Res	Type
26	A	2649	A
26	A	2650	A
26	A	2651	C
26	A	2653	G
26	A	2654	A
26	A	2655	U
26	A	2659	A
26	A	2665	C
26	A	2669	G
26	A	2671	G
26	A	2672	A
26	A	2673	U
26	A	2676	C
26	A	2677	A
26	A	2682	G
26	A	2694	G
26	A	2698	C
26	A	2700	A
26	A	2702	A
26	A	2705	G
26	A	2715	U
26	A	2718	G
26	A	2726	G
26	A	2729	G
26	A	2737	G
26	A	2742	A
26	A	2744	C
26	A	2753	G
26	A	2758	A
26	A	2759	G
26	A	2786	U
26	A	2788	A
26	A	2790	A
26	A	2791	G
26	A	2793	G
26	A	2796	A
26	A	2797	C
26	A	2802	G
26	A	2810	U
26	A	2826	A
26	A	2827	G
26	A	2833	U

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Mol	Chain	Res	Type
26	A	2837	U
26	A	2839	U
26	A	2853	C
26	A	2860	U
26	A	2865	G
26	A	2866	A
26	A	2870	C
26	A	2876	C
26	A	2878	A
26	A	2887	G
26	A	2893	G
26	A	2897	G
26	A	2906	U
26	A	2908	U
26	A	2913	U
26	A	2915	C
26	A	2926	A
26	A	2936	C
26	A	2938	G
26	A	2942	G
26	A	2950	C
26	A	2956	G
26	A	2957	A
26	A	2963	U
26	A	2968	G
26	A	2972	A
26	A	2975	G
26	A	2976	C
26	A	2977	A
26	A	2982	A
26	A	2985	G
26	A	2989	A
26	A	2990	A
26	A	2993	U
26	A	3002	A
26	A	3004	C
26	A	3005	A
26	A	3009	U
26	A	3011	C
26	A	3014	A
26	A	3015	C
26	A	3021	A

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Mol	Chain	Res	Type
26	A	3022	G
26	A	3023	G
26	A	3029	U
26	A	3039	C
26	A	3042	A
26	A	3045	C
26	A	3047	A
26	A	3056	A
26	A	3057	U
26	A	3070	G
26	A	3082	U
26	A	3088	C
26	A	3093	A
26	A	3094	A
26	A	3095	C
26	A	3101	C
26	A	3105	C
26	A	3106	C
26	A	3107	G
26	A	3112	A
26	A	3113	A
26	A	3114	A
26	A	3115	A

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	B	12	C
25	B	60	G
25	B	66	C
26	A	89	A
26	A	97	U
26	A	316	U
26	A	336	C
26	A	357	U
26	A	445	U
26	A	567	A
26	A	974	G
26	A	980	C
26	A	981	U
26	A	1002	C
26	A	1010	U

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Mol	Chain	Res	Type
26	A	1084	U
26	A	1186	G
26	A	1562	C
26	A	1563	A
26	A	1564	A
26	A	1565	A
26	A	1566	A
26	A	1567	C
26	A	1568	C
26	A	1569	A
26	A	1570	C
26	A	1571	C
26	A	1573	U
26	A	1575	A
26	A	1576	C
26	A	1577	C
26	A	1578	G
26	A	1579	C
26	A	1580	A
26	A	1581	C
26	A	1590	G
26	A	1591	U
26	A	1596	C
26	A	1597	G
26	A	1598	U
26	A	1730	U
26	A	2085	C
26	A	2088	C
26	A	2094	G
26	A	2350	G
26	A	2381	A
26	A	2435	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

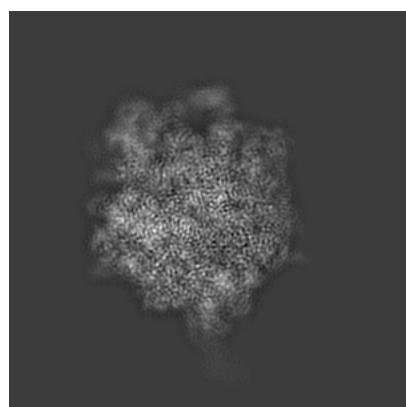
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6922. These allow visual inspection of the internal detail of the map and identification of artifacts.

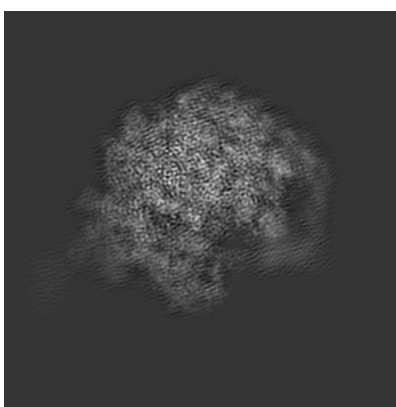
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

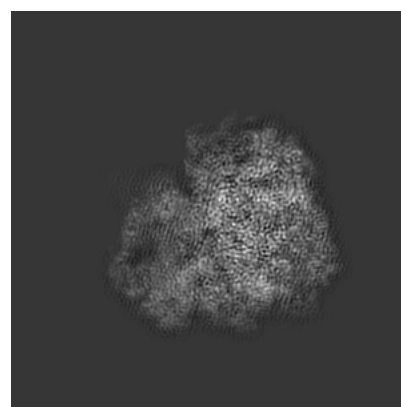
6.1.1 Primary map



X



Y

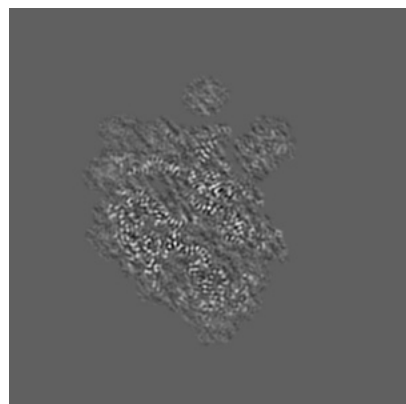


Z

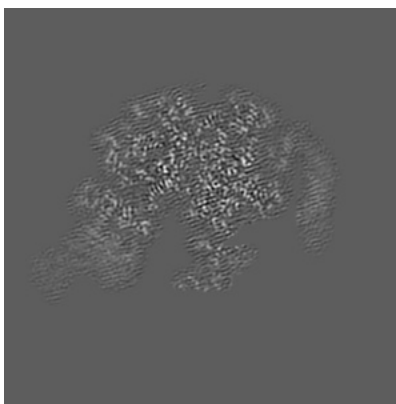
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

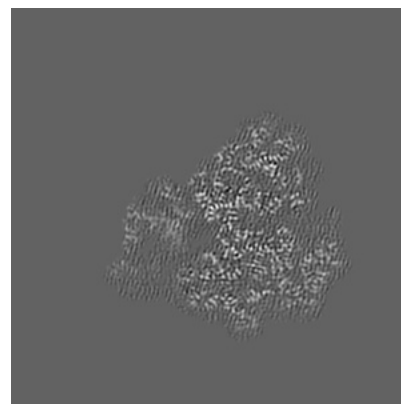
6.2.1 Primary map



X Index: 172



Y Index: 172

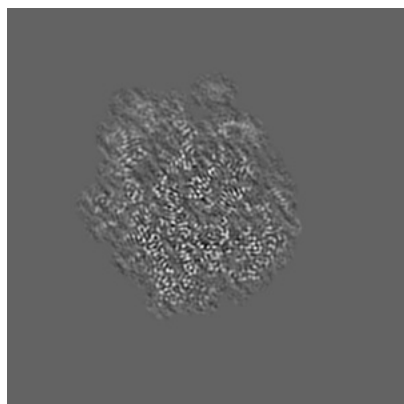


Z Index: 172

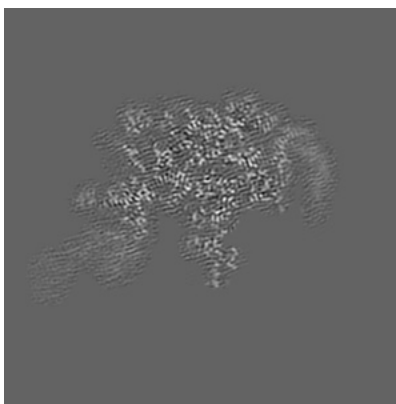
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

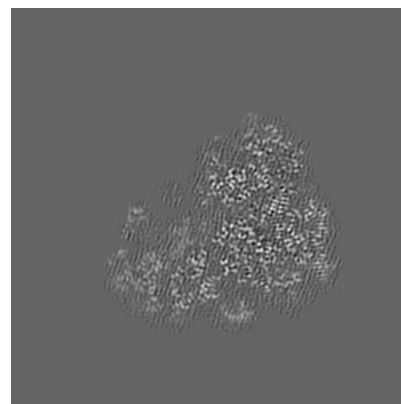
6.3.1 Primary map



X Index: 205



Y Index: 181

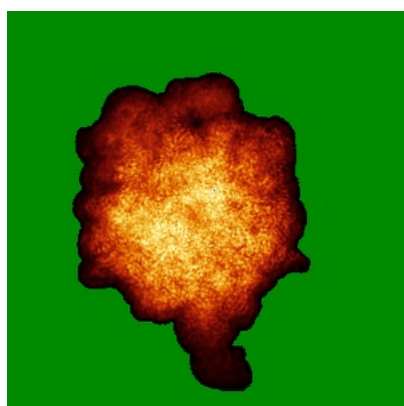


Z Index: 154

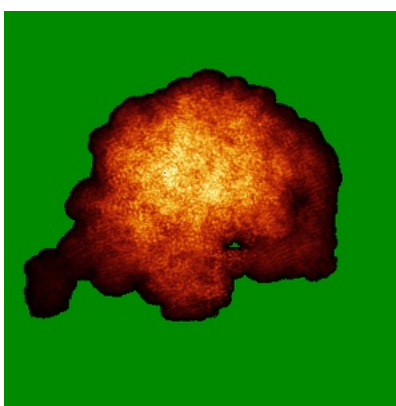
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

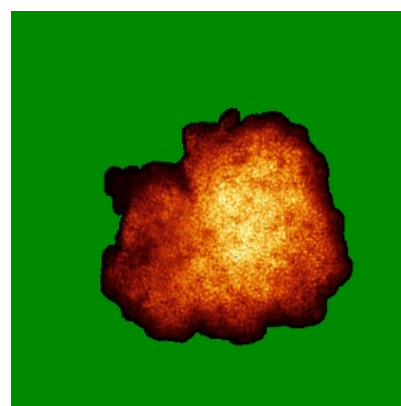
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

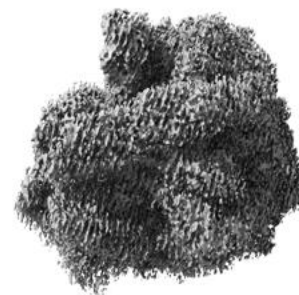
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

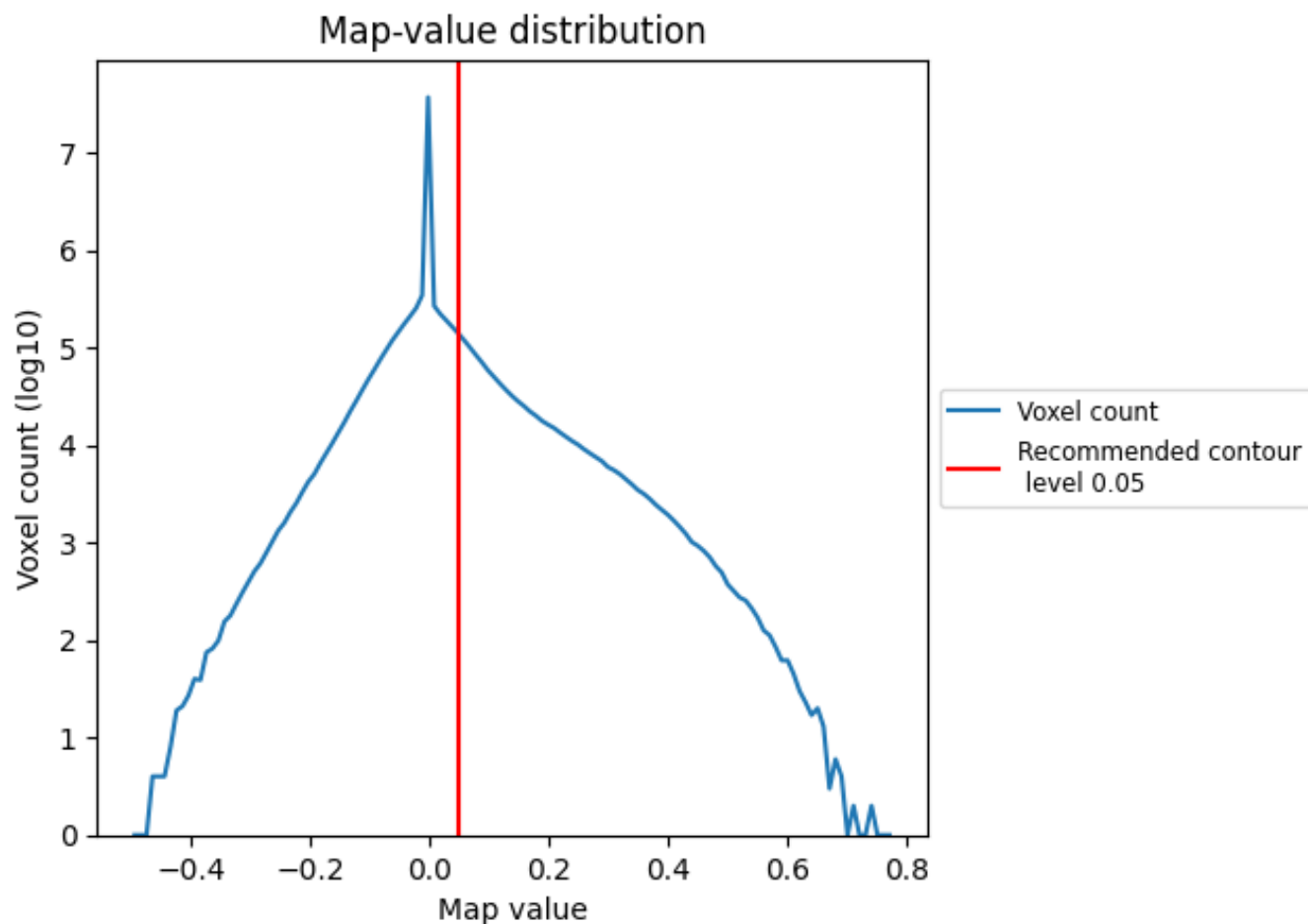
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

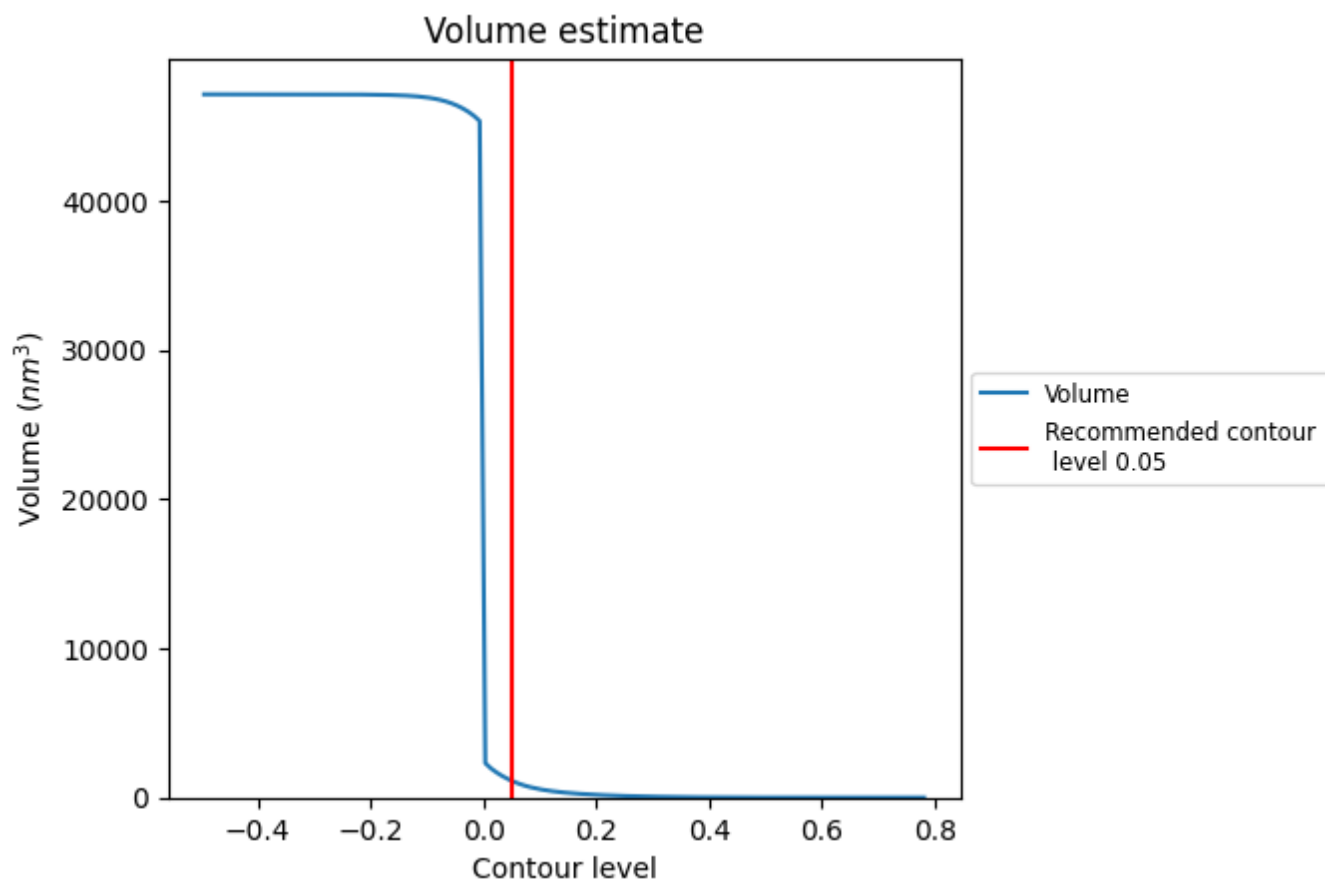
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

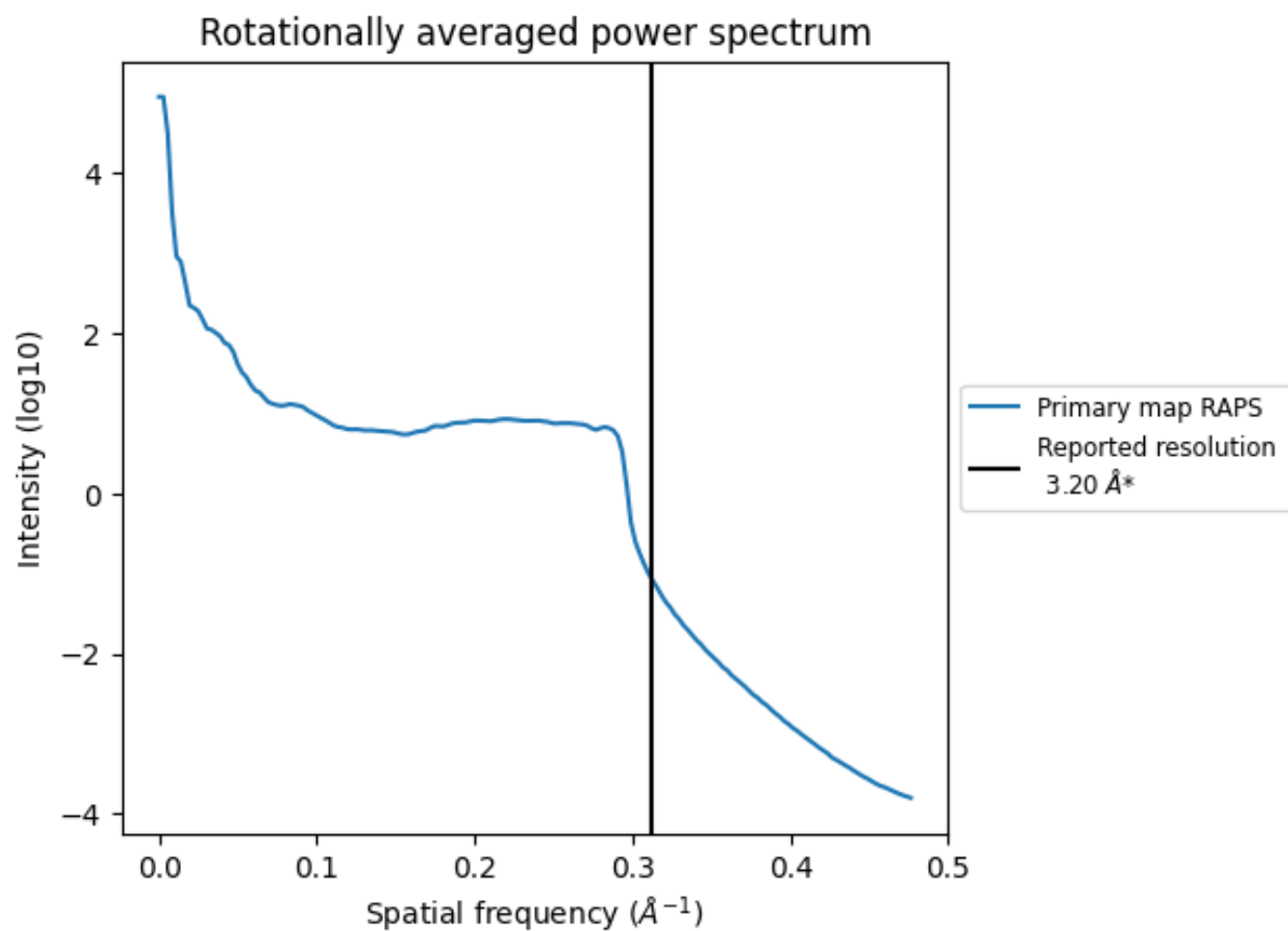
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1134 nm³; this corresponds to an approximate mass of 1024 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

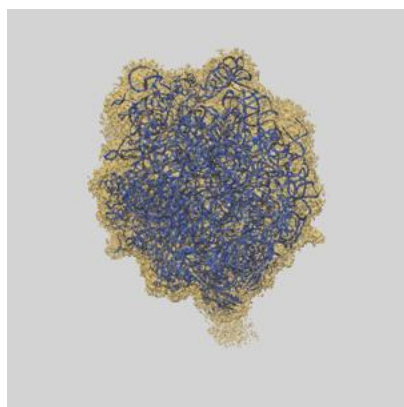
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

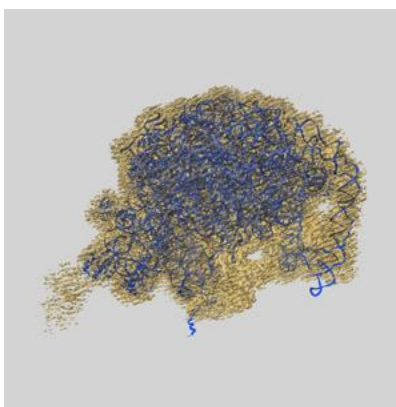
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6922 and PDB model 5ZET. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

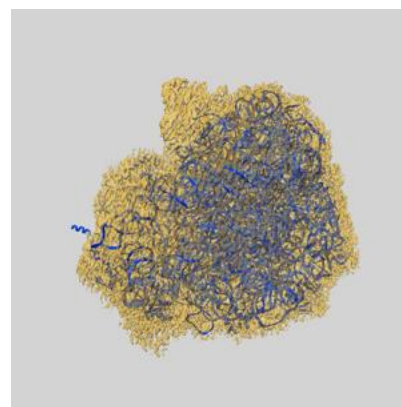
9.1 Map-model overlay [i](#)



X



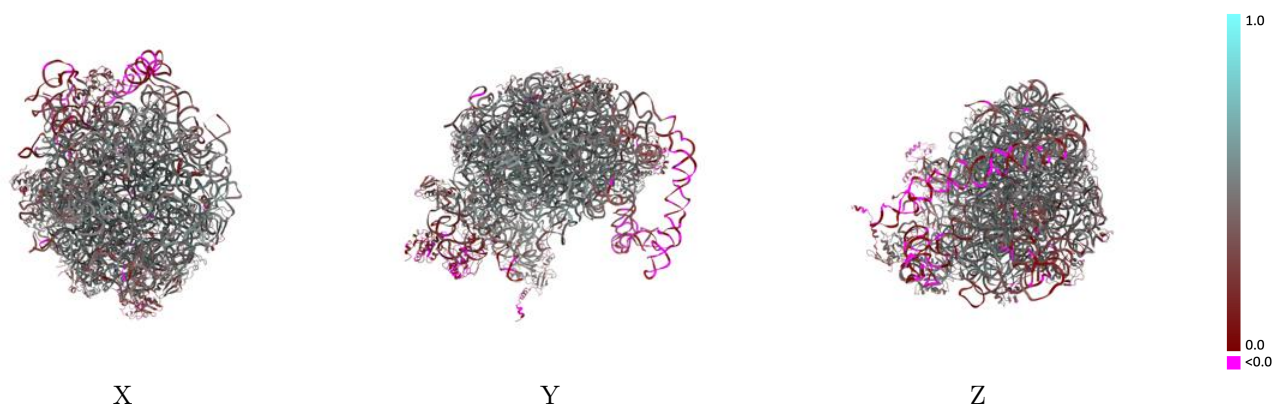
Y



Z

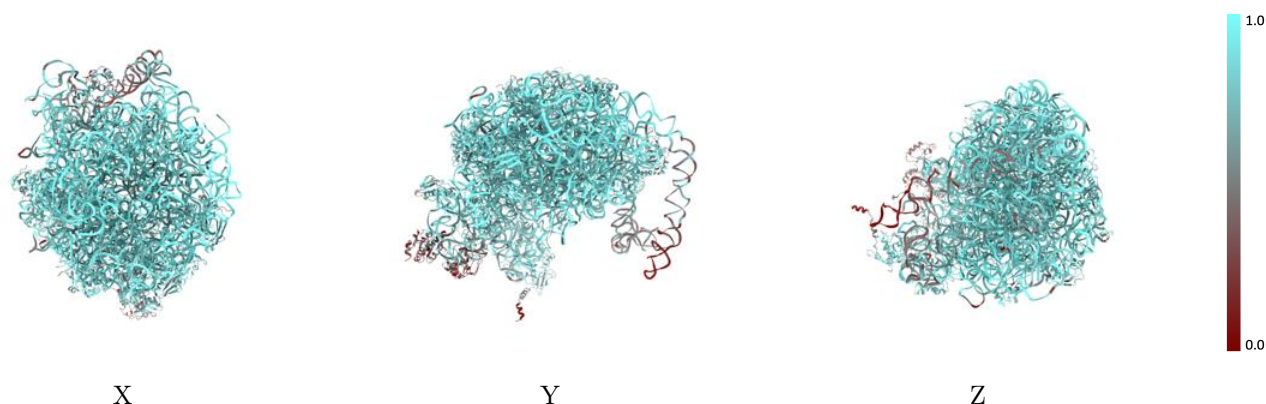
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



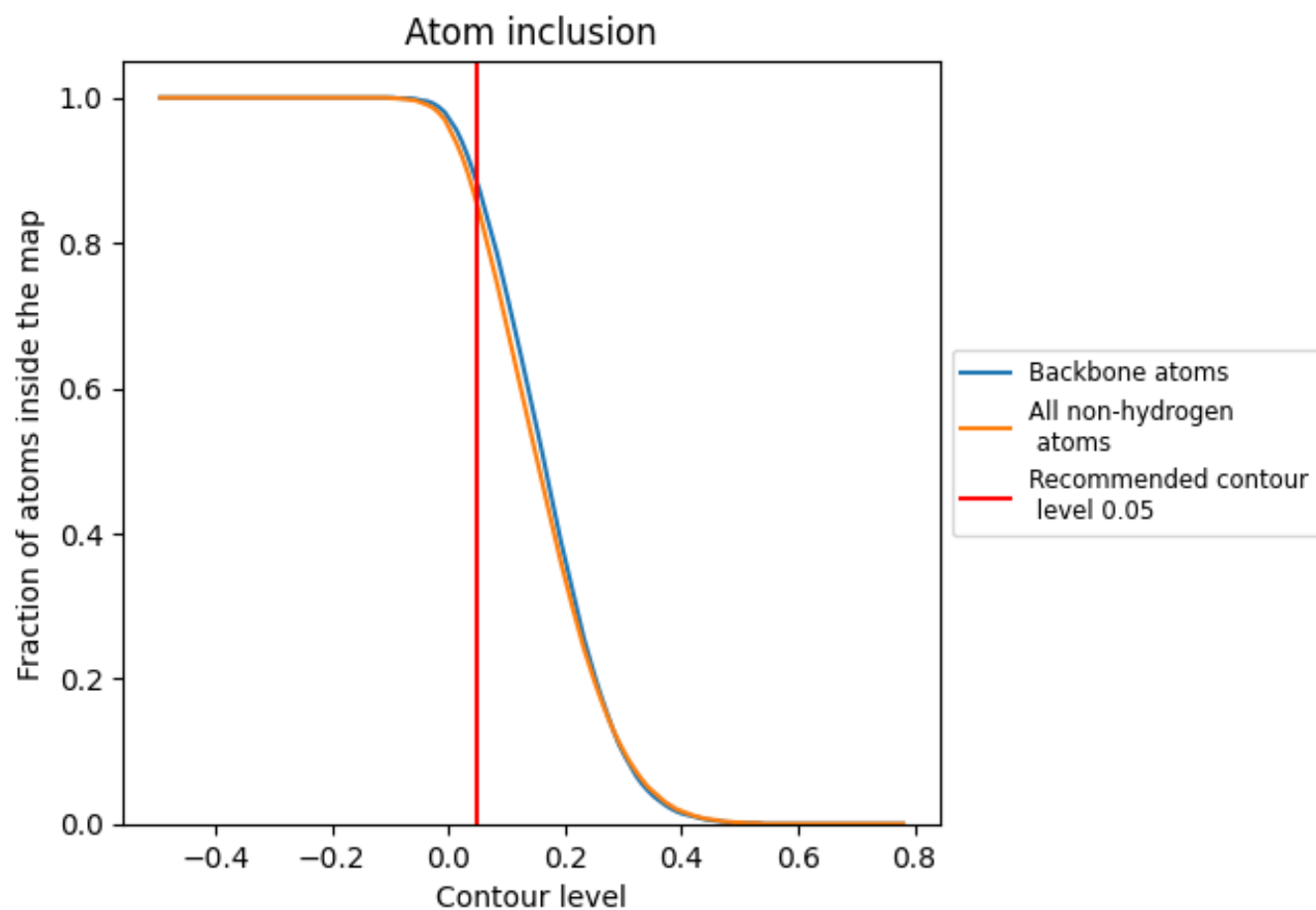
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.4220
1	 0.8210	 0.4500
2	 0.5390	 0.1850
3	 0.8360	 0.4500
4	 0.8040	 0.3790
5	 0.8610	 0.4740
6	 0.8690	 0.4850
7	 0.8810	 0.4790
8	 0.7930	 0.4410
A	 0.8820	 0.4320
B	 0.8620	 0.3920
C	 0.8530	 0.4810
D	 0.8520	 0.4720
E	 0.8200	 0.4230
F	 0.7930	 0.3790
G	 0.7670	 0.3570
H	 0.6300	 0.3000
I	 0.3450	 0.1310
J	 0.3720	 0.0990
K	 0.8400	 0.4650
L	 0.8260	 0.4500
M	 0.8220	 0.4320
N	 0.8410	 0.4600
O	 0.8220	 0.4380
P	 0.8330	 0.4300
Q	 0.8040	 0.4390
R	 0.8670	 0.4750
S	 0.8390	 0.4340
T	 0.8120	 0.4440
U	 0.7910	 0.4080
V	 0.7680	 0.3650
W	 0.6950	 0.3140
X	 0.8340	 0.4650
Y	 0.8370	 0.4520
Z	 0.8180	 0.4000

