



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 06:46 AM UTC

PDB ID : 5UYL / pdb_00005uyL
EMDB ID : EMD-8616
Title : 70S ribosome bound with cognate ternary complex base-paired to A site codon (Structure II)
Authors : Loveland, A.B.; Demo, G.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2017-02-24
Resolution : 3.60 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

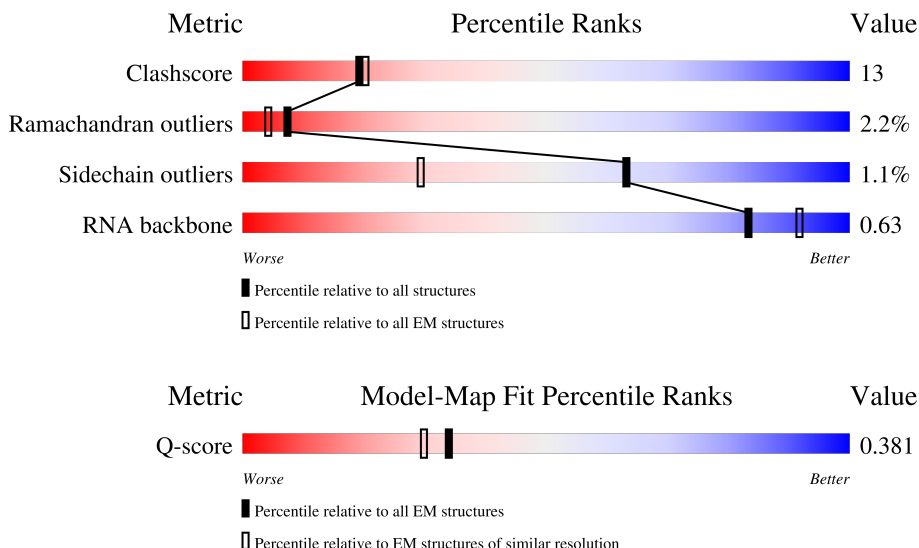
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.



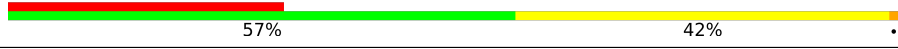
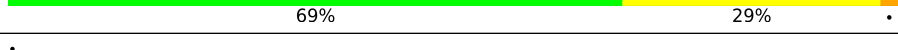
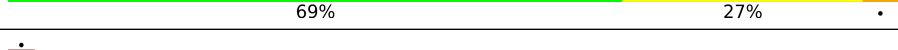
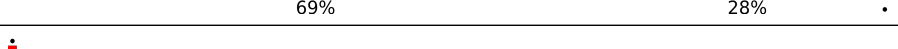
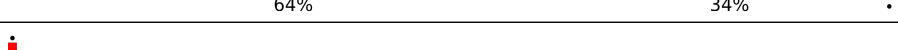
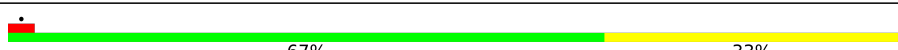
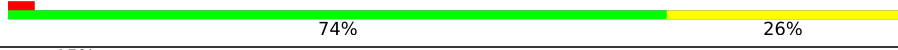
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	04	271	
2	05	209	
3	06	201	

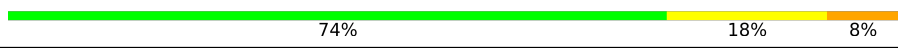
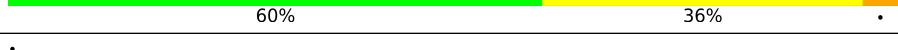
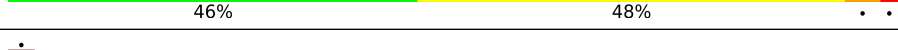
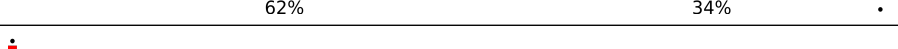
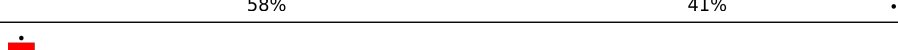
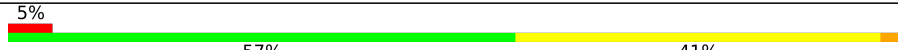
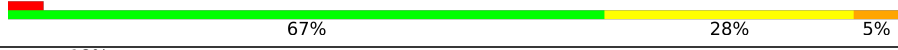
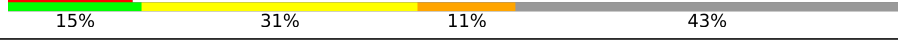
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Mol	Chain	Length	Quality of chain
4	07	177	
5	08	176	
6	09	149	
7	10	131	
8	11	141	
9	12	142	
10	13	122	
11	14	143	
12	15	136	
13	16	120	
14	17	116	
15	18	114	
16	19	117	
17	20	103	
18	21	110	
19	22	93	
20	23	102	
21	24	94	
22	25	75	
23	26	77	
24	27	63	
25	28	58	
26	29	66	
27	30	56	
28	31	50	

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Mol	Chain	Length	Quality of chain
29	32	46	
30	33	64	
31	34	38	
32	B	218	
33	C	206	
34	D	205	
35	E	157	
36	F	100	
37	G	151	
38	H	129	
39	I	127	
40	J	98	
41	K	116	
42	L	123	
43	M	114	
44	N	100	
45	O	88	
46	P	82	
47	Q	80	
48	R	65	
49	S	79	
50	T	85	
51	U	65	
52	03	234	
53	A	1539	

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Mol	Chain	Length	Quality of chain
54	01	2903	
55	02	120	
56	W	77	
56	X	77	
57	V	18	
58	Y	76	
59	Z	392	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 153753 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	04	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	07	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	10	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	13	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	16	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	17	116	Total	C	N	O	0	0
			892	552	178	162		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
15	18	114	Total	C	N	O	S	0
			917	574	179	163	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	19	117	Total	C	N	O		0
			947	604	192	151		0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	20	103	Total	C	N	O	S	0
			816	516	153	145	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	21	110	Total	C	N	O	S	0
			857	532	166	156	3	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	22	93	Total	C	N	O	S	0
			739	466	139	132	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	23	102	Total	C	N	O		0
			780	492	146	142		0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	29	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	31	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	03	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	01	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	747	C	U	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	02	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

- Molecule 56 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
56	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	V	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 58 is a RNA chain called tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Y	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 59 is a protein called Elongation factor Tu 2.

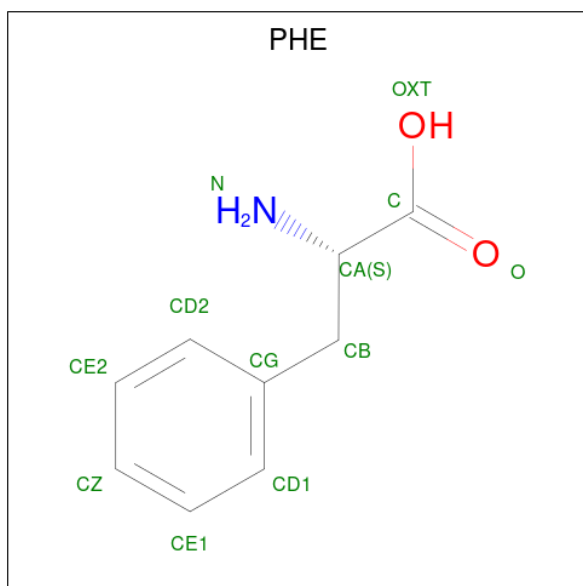
Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	392	Total	C	N	O	S	0	0
			3029	1915	521	580	13		

- Molecule 60 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



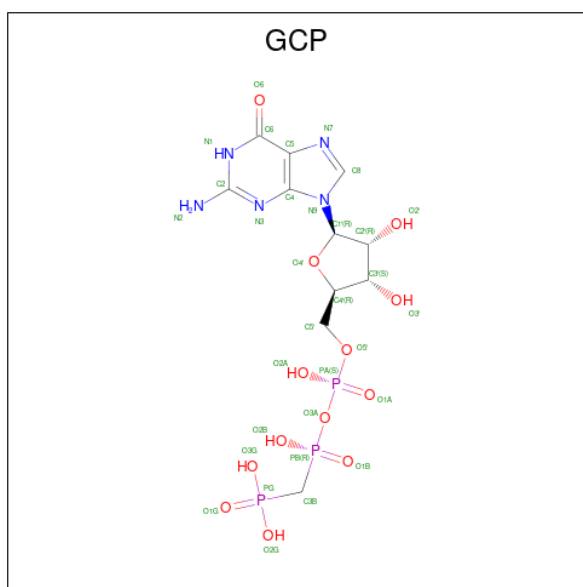
Mol	Chain	Residues	Atoms					AltConf
60	W	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 61 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms					AltConf
61	Y	1	Total	C	N	O		0
			11	9	1	1		

- Molecule 62 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

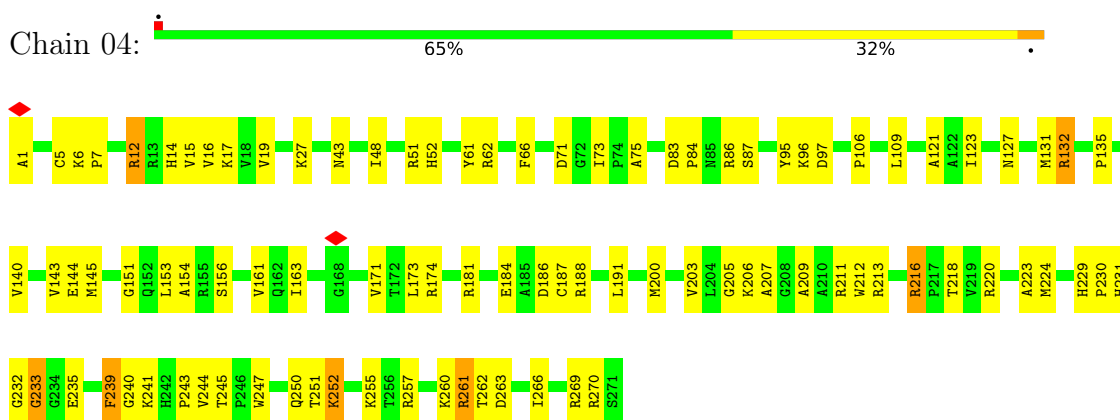


Mol	Chain	Residues	Atoms					AltConf
62	Z	1	Total	C	N	O	P	0
			32	11	5	13	3	

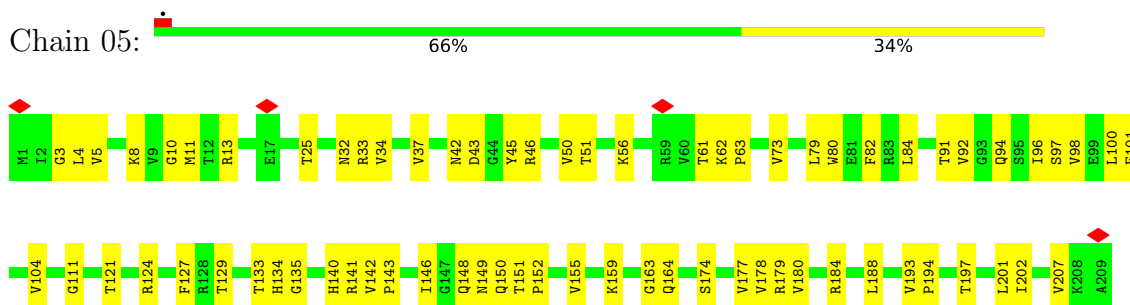
3 Residue-property plots

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.

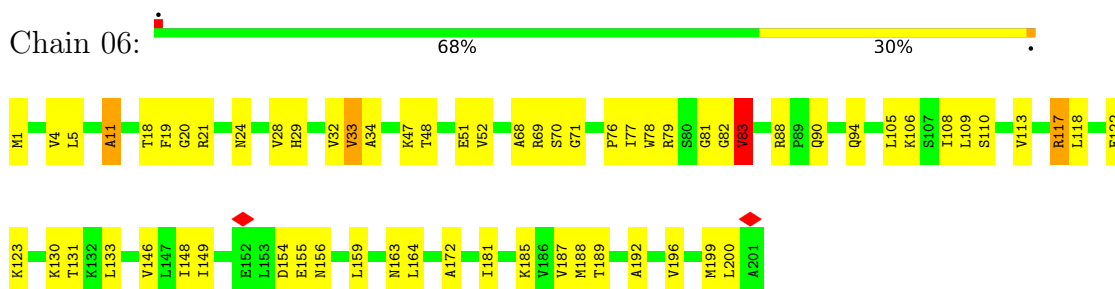
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

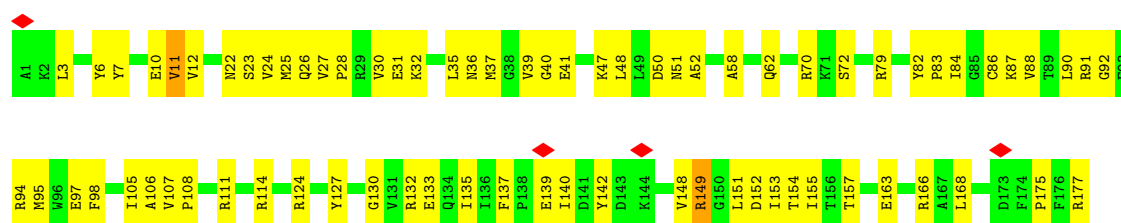


• Molecule 3: 50S ribosomal protein L4



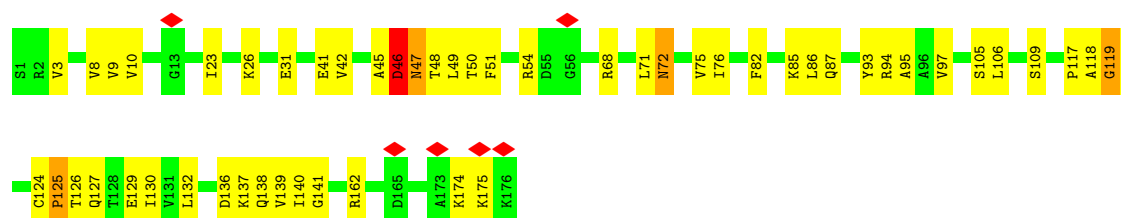
• Molecule 4: 50S ribosomal protein L5

Chain 07:  58% 41%



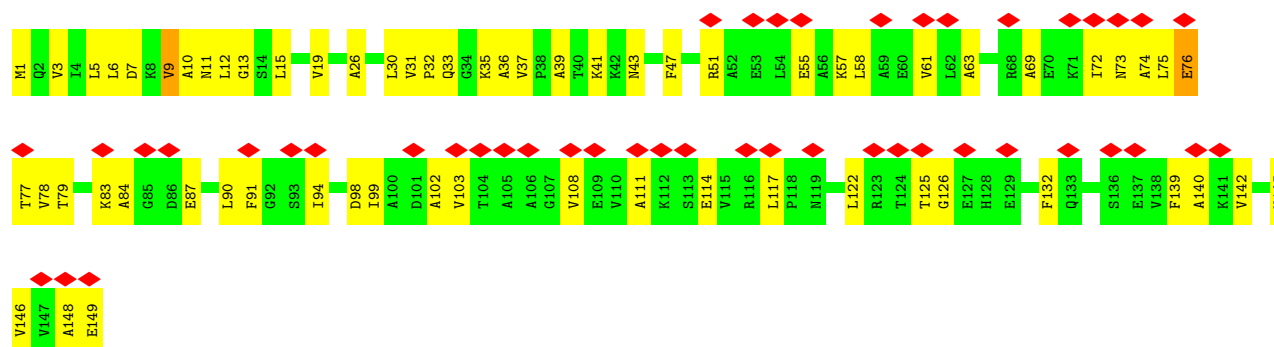
• Molecule 5: 50S ribosomal protein L6

Chain 08:  70% 27%



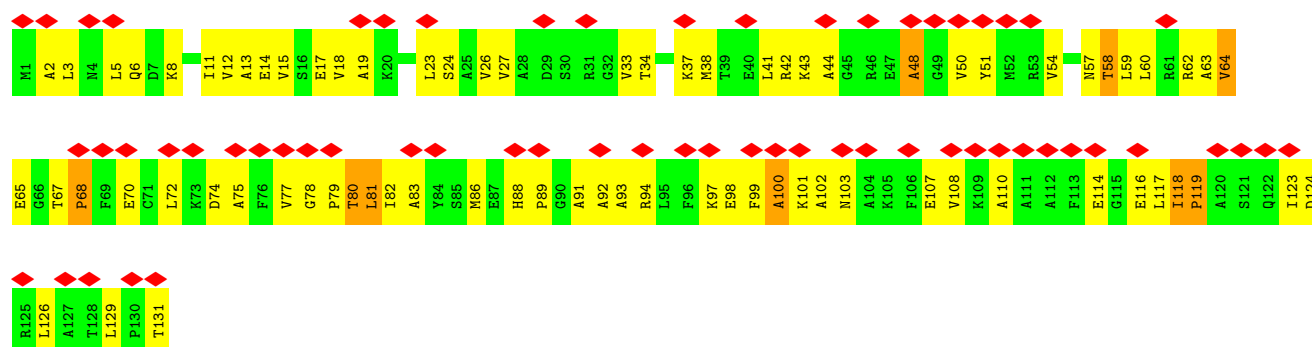
• Molecule 6: 50S ribosomal protein L9

Chain 09:  31% 57% 42%

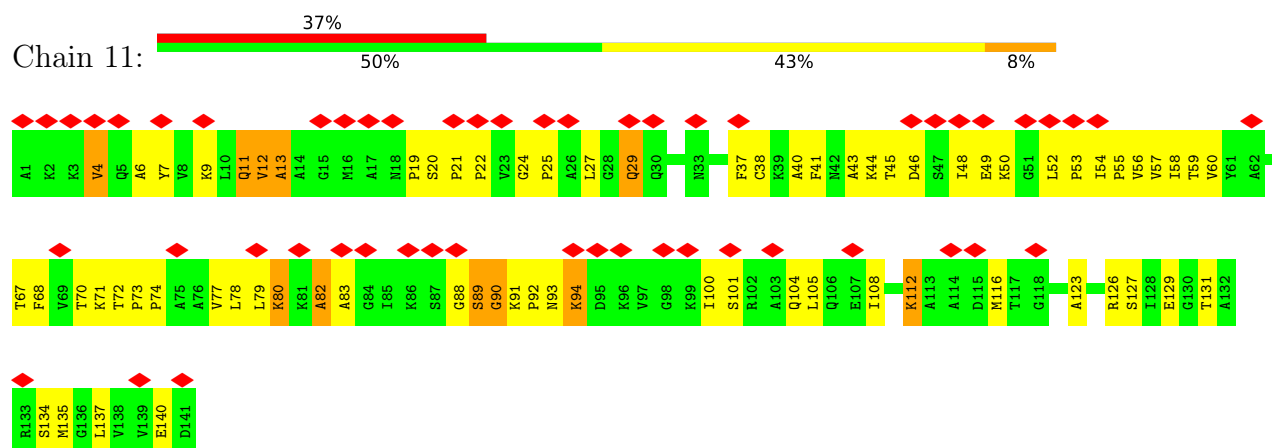


• Molecule 7: 50S ribosomal protein L10

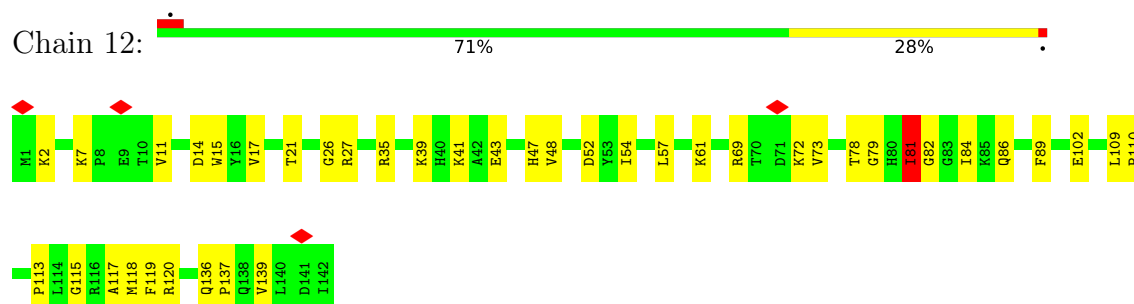
Chain 10:  47% 41% 52% 7%



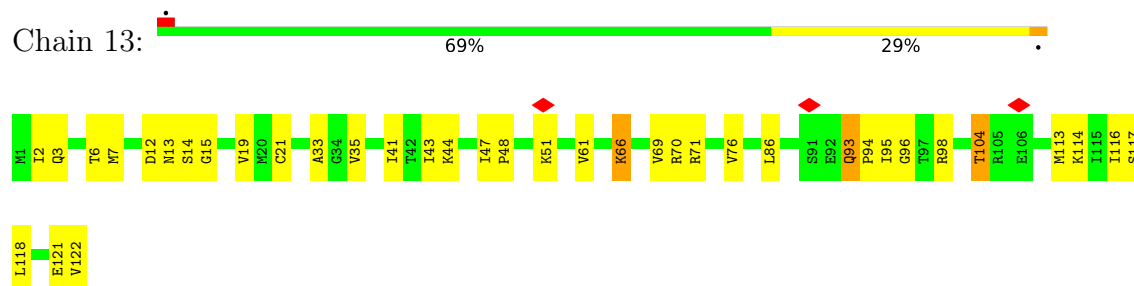
- Molecule 8: 50S ribosomal protein L11



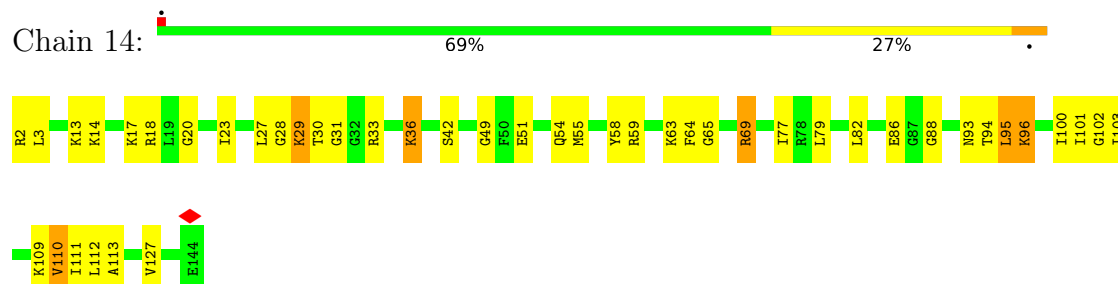
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14

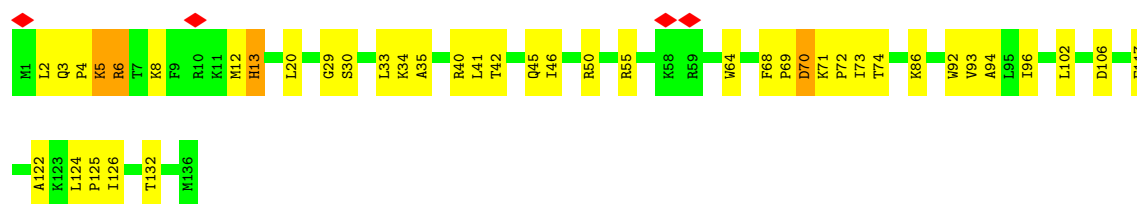


- Molecule 11: 50S ribosomal protein L15

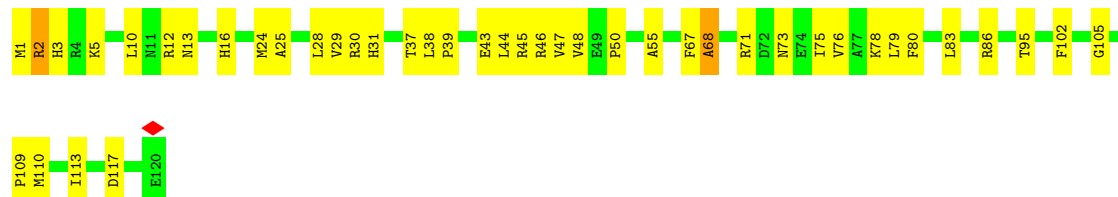


- Molecule 12: 50S ribosomal protein L16





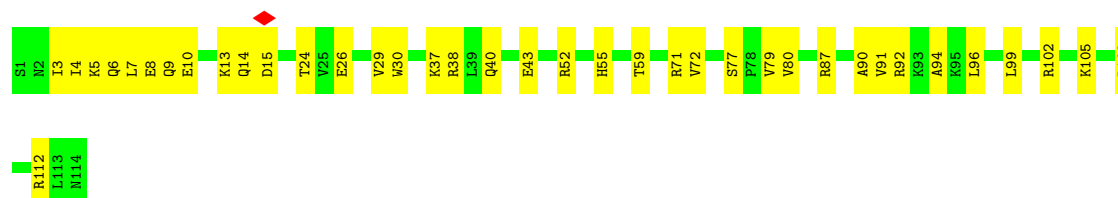
- Molecule 13: 50S ribosomal protein L17



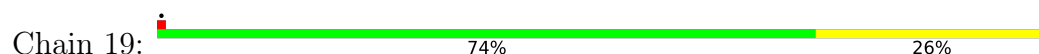
- Molecule 14: 50S ribosomal protein L18



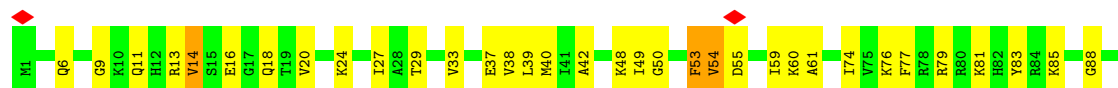
- Molecule 15: 50S ribosomal protein L19

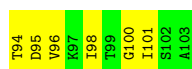


- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21





- Molecule 18: 50S ribosomal protein L22

Chain 21: 66% 32%



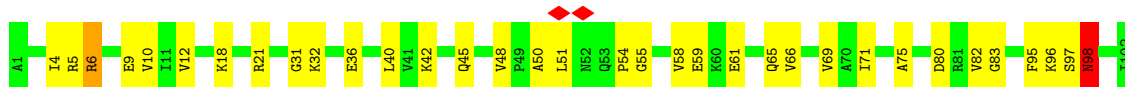
- Molecule 19: 50S ribosomal protein L23

Chain 22: 67% 33%



- Molecule 20: 50S ribosomal protein L24

Chain 23: 67% 31%



- Molecule 21: 50S ribosomal protein L25

Chain 24: 64% 35%



- Molecule 22: 50S ribosomal protein L27

Chain 25: 75% 25%

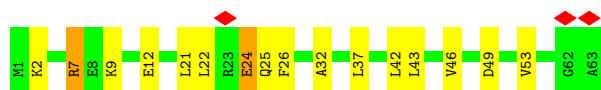
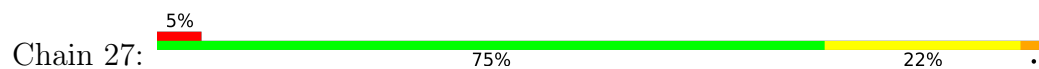


- Molecule 23: 50S ribosomal protein L28

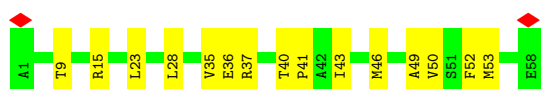
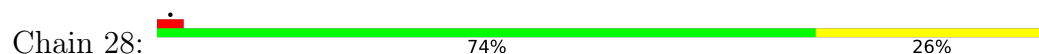
Chain 26: 57% 42%



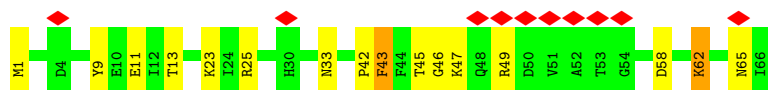
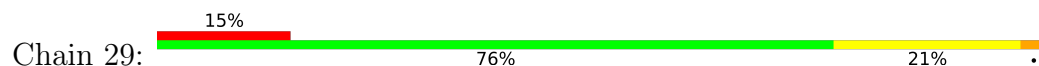
- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



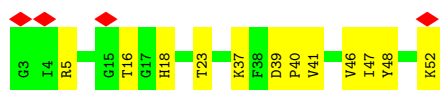
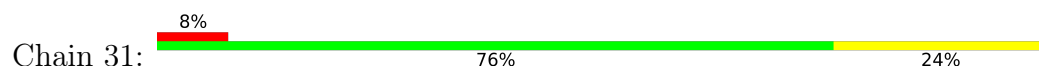
- Molecule 26: 50S ribosomal protein L31



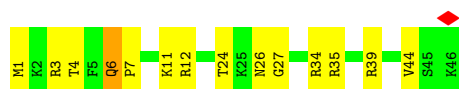
- Molecule 27: 50S ribosomal protein L32



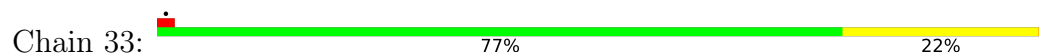
- Molecule 28: 50S ribosomal protein L33

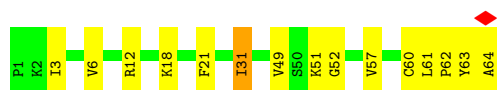


- Molecule 29: 50S ribosomal protein L34

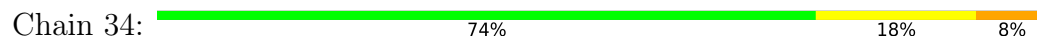


- Molecule 30: 50S ribosomal protein L35

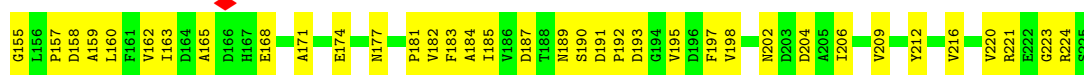
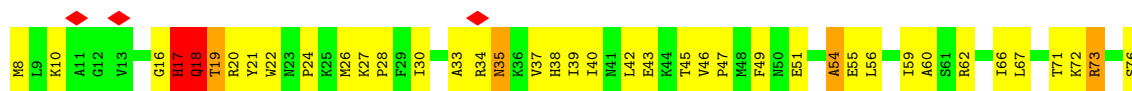




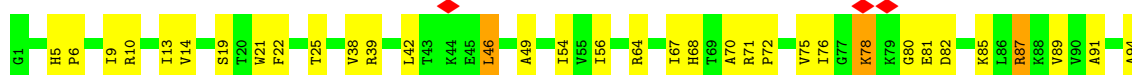
- Molecule 31: 50S ribosomal protein L36



- Molecule 32: 30S ribosomal protein S2



- Molecule 33: 30S ribosomal protein S3

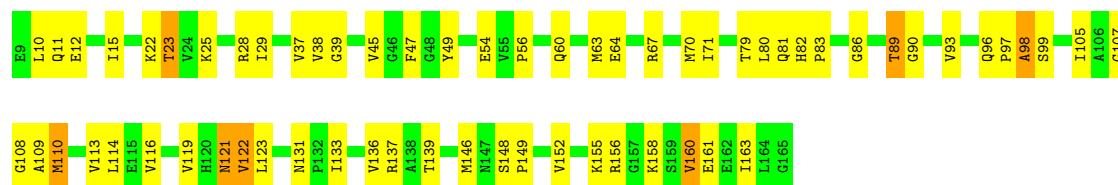


- Molecule 34: 30S ribosomal protein S4

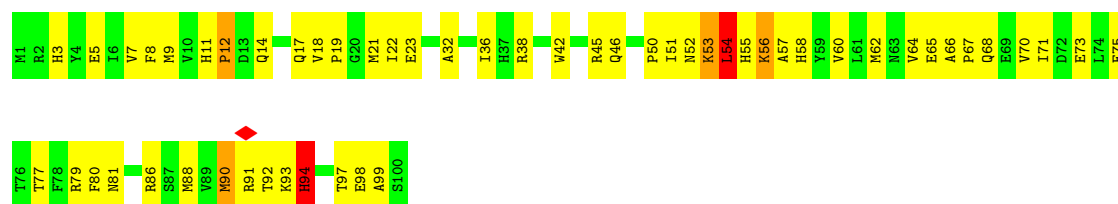




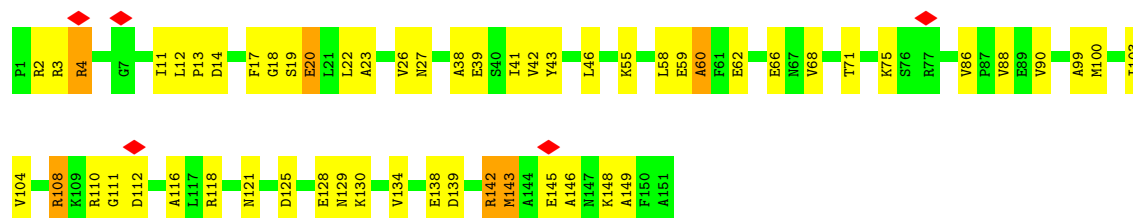
• Molecule 35: 30S ribosomal protein S5



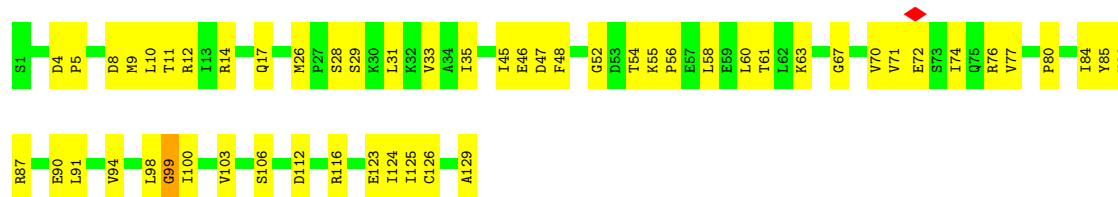
• Molecule 36: 30S ribosomal protein S6



• Molecule 37: 30S ribosomal protein S7

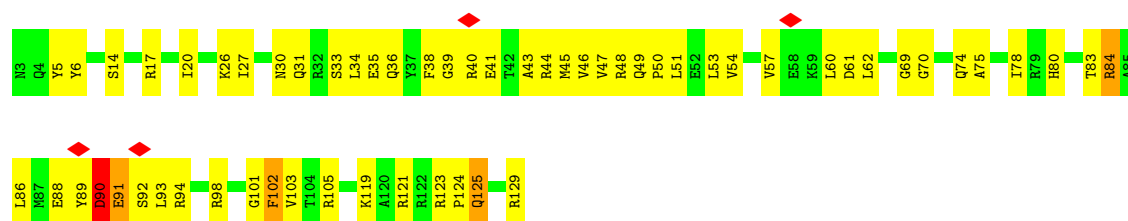


• Molecule 38: 30S ribosomal protein S8

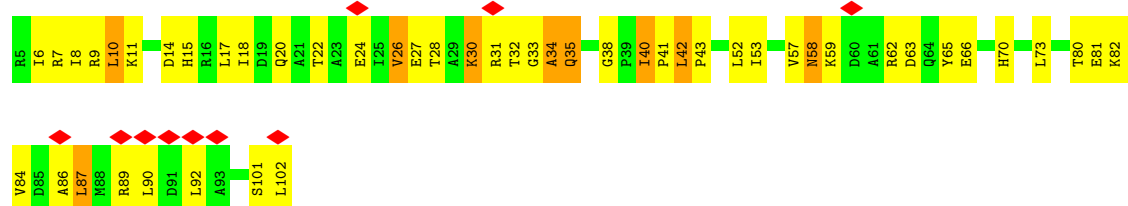


• Molecule 39: 30S ribosomal protein S9

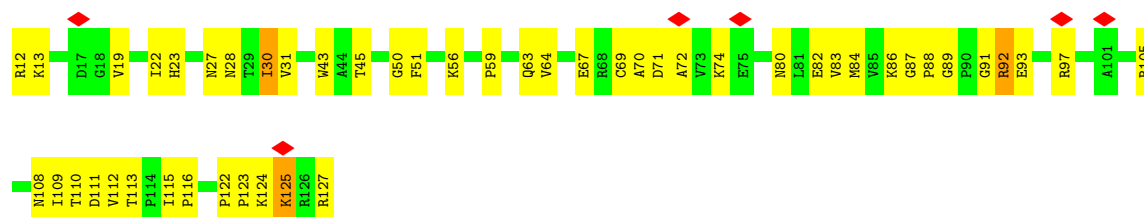




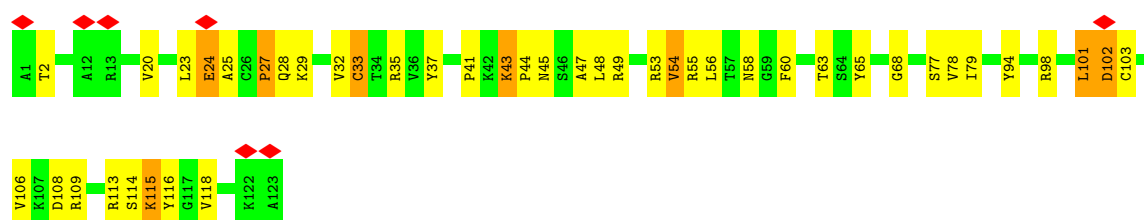
- Molecule 40: 30S ribosomal protein S10



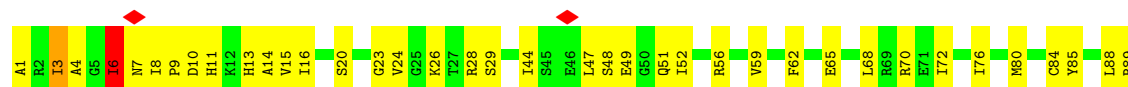
- Molecule 41: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S12

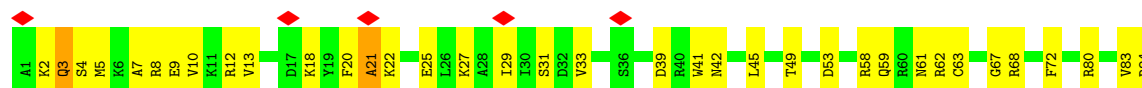


- Molecule 43: 30S ribosomal protein S13

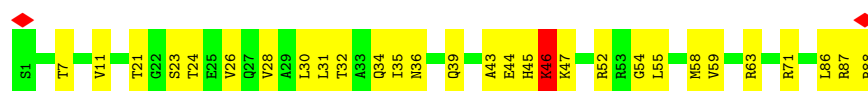




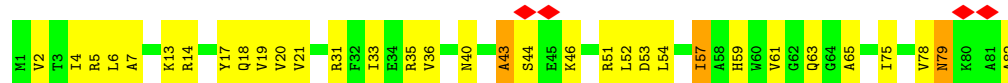
- Molecule 44: 30S ribosomal protein S14



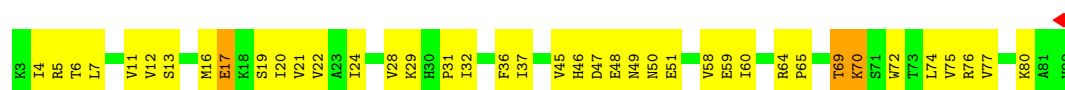
- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

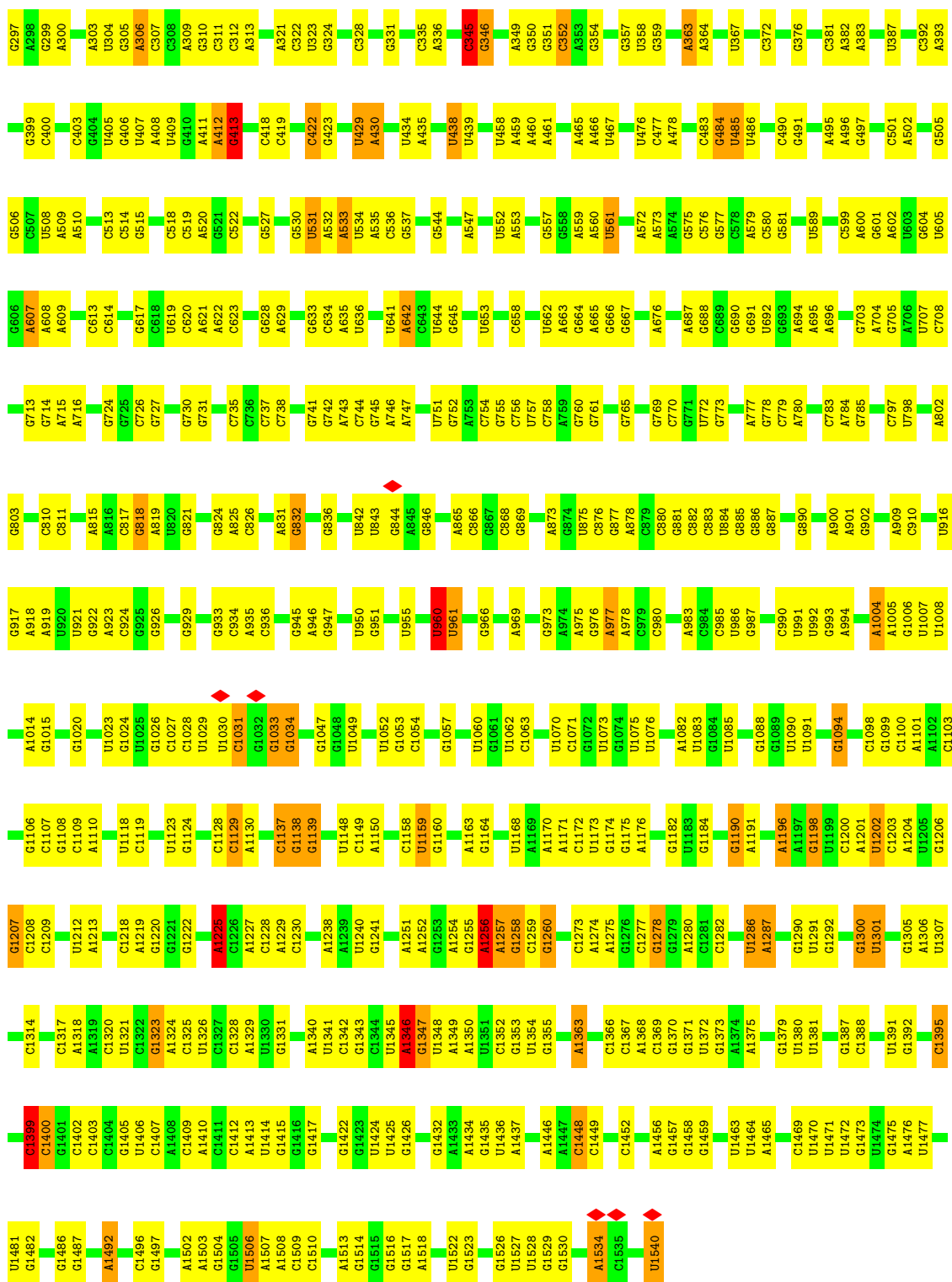


- Molecule 48: 30S ribosomal protein S18



- Molecule 49: 30S ribosomal protein S19



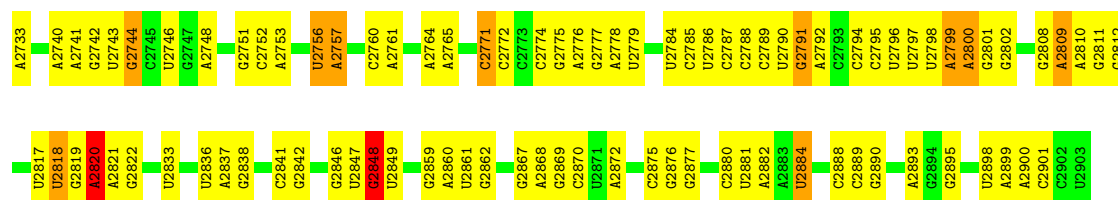


• Molecule 54: 23S ribosomal RNA



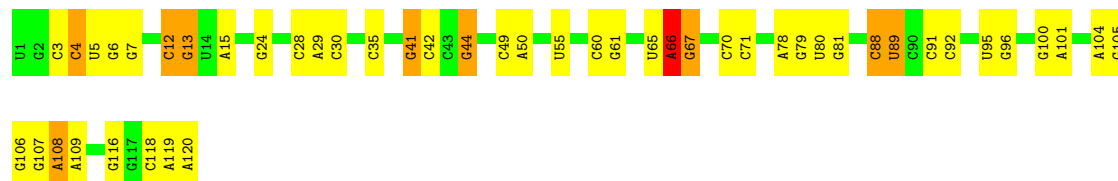


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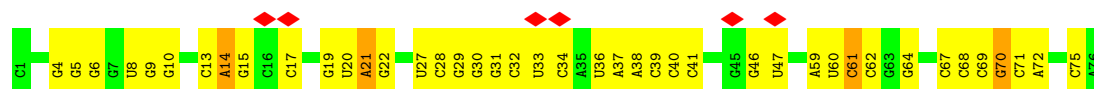
• Molecule 55: 5S ribosomal RNA

Chain 02: 60% 32% 8%



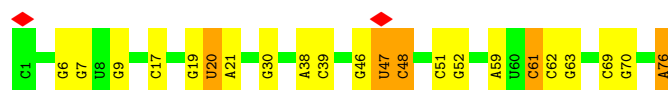
• Molecule 56: tRNA^{fMet}

Chain X: 8% 45% 49% 5%



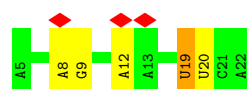
• Molecule 56: tRNA^{fMet}

Chain W: 71% 22% 6%



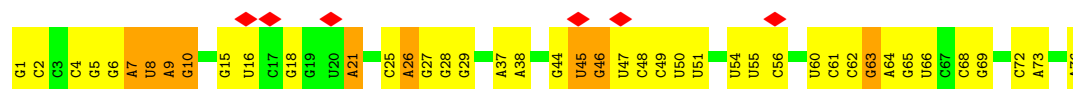
• Molecule 57: mRNA

Chain V: 17% 72% 22% 6%



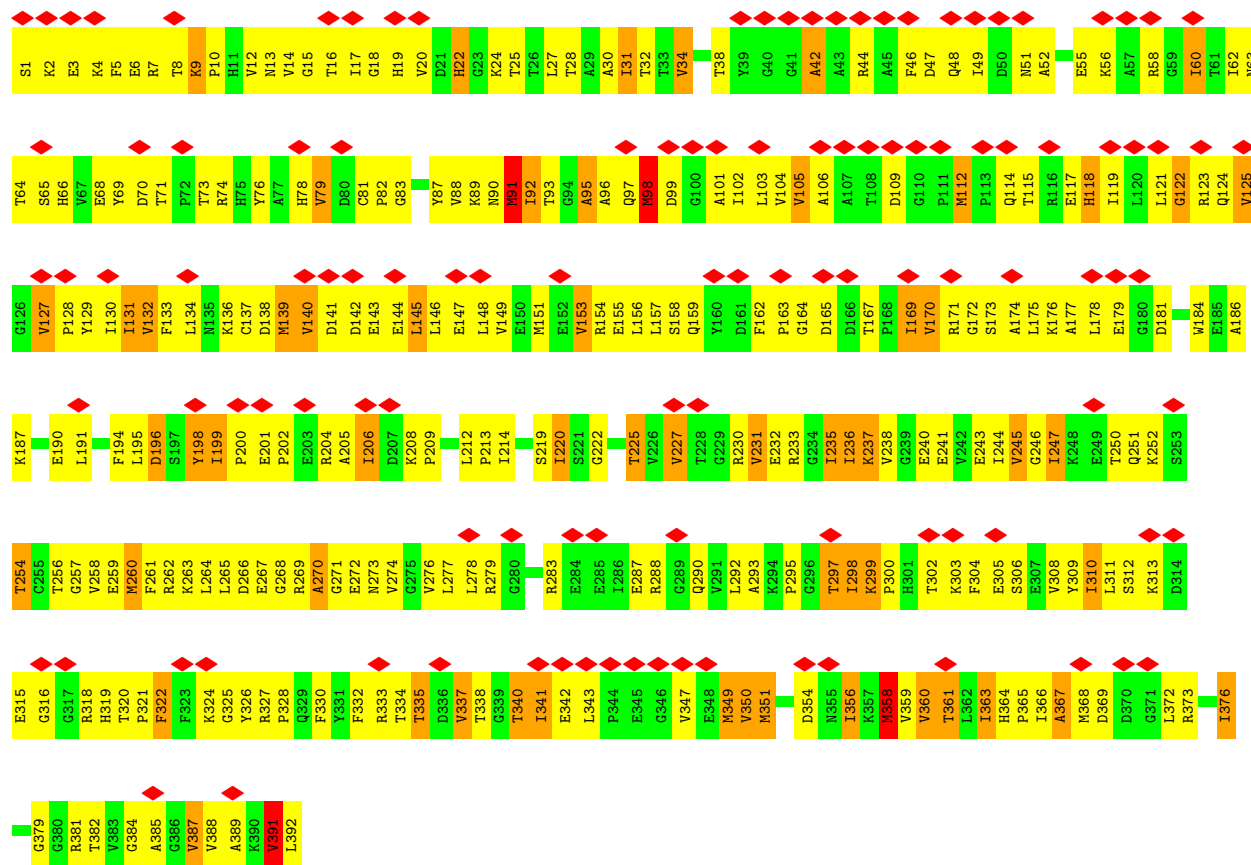
• Molecule 58: tRNA^{Phe}

Chain Y: 8% 43% 45% 12%



• Molecule 59: Elongation factor Tu 2

Chain Z: 29% 29% 55% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10431	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTFFIND3 was used to determine CTF values. FREALIGN applied CTF correction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	60976	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	16.901	Depositor
Minimum map value	-5.858	Depositor
Average map value	-0.407	Depositor
Map value standard deviation	1.298	Depositor
Recommended contour level	3.49	Depositor
Map size ($\text{\AA}$)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, FME

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	04	0.37	0/2122	0.92	9/2852 (0.3%)
2	05	0.37	0/1586	0.88	1/2134 (0.0%)
3	06	0.36	0/1571	0.90	6/2113 (0.3%)
4	07	0.36	0/1435	0.89	6/1926 (0.3%)
5	08	0.36	0/1343	0.87	5/1816 (0.3%)
6	09	0.43	0/1122	1.04	6/1515 (0.4%)
7	10	0.51	0/1002	1.18	9/1350 (0.7%)
8	11	0.51	0/1046	1.10	7/1410 (0.5%)
9	12	0.37	0/1152	0.88	3/1551 (0.2%)
10	13	0.35	0/948	0.92	1/1268 (0.1%)
11	14	0.36	0/1054	1.00	3/1403 (0.2%)
12	15	0.39	0/1093	0.84	2/1460 (0.1%)
13	16	0.36	0/974	0.91	3/1301 (0.2%)
14	17	0.34	0/902	0.92	3/1209 (0.2%)
15	18	0.34	0/929	0.89	3/1242 (0.2%)
16	19	0.36	0/960	0.93	4/1278 (0.3%)
17	20	0.36	0/829	0.92	3/1107 (0.3%)
18	21	0.36	0/864	0.96	2/1156 (0.2%)
19	22	0.35	0/745	0.82	0/994
20	23	0.35	0/788	0.94	2/1051 (0.2%)
21	24	0.35	0/766	0.82	2/1025 (0.2%)
22	25	0.34	0/582	0.86	0/769
23	26	0.35	0/635	0.90	1/848 (0.1%)
24	27	0.35	0/510	0.94	2/677 (0.3%)
25	28	0.36	0/453	0.83	0/605
26	29	0.41	0/532	0.92	3/709 (0.4%)
27	30	0.34	0/450	0.74	0/599
28	31	0.38	0/417	0.75	1/554 (0.2%)
29	32	0.42	0/380	0.96	3/498 (0.6%)
30	33	0.35	0/513	0.89	0/676
31	34	0.34	0/303	0.83	1/397 (0.3%)
32	B	0.45	1/1736 (0.1%)	1.06	15/2338 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.39	0/1652	0.96	6/2225 (0.3%)
34	D	0.37	0/1665	0.99	7/2227 (0.3%)
35	E	0.38	0/1170	0.96	4/1573 (0.3%)
36	F	0.40	0/836	1.06	5/1128 (0.4%)
37	G	0.36	0/1196	1.03	9/1602 (0.6%)
38	H	0.36	0/989	0.99	3/1326 (0.2%)
39	I	0.38	0/1034	1.01	6/1375 (0.4%)
40	J	0.42	0/797	1.02	4/1077 (0.4%)
41	K	0.38	0/886	0.98	4/1195 (0.3%)
42	L	0.40	0/969	1.09	8/1300 (0.6%)
43	M	0.36	0/893	0.94	0/1193
44	N	0.36	0/817	0.92	4/1088 (0.4%)
45	O	0.36	0/722	0.93	3/964 (0.3%)
46	P	0.37	0/659	0.96	4/884 (0.5%)
47	Q	0.38	0/658	0.98	3/881 (0.3%)
48	R	0.42	0/545	0.99	4/731 (0.5%)
49	S	0.39	0/653	0.91	1/877 (0.1%)
50	T	0.35	0/671	1.02	6/888 (0.7%)
51	U	0.43	0/551	1.04	5/728 (0.7%)
52	03	2.12	24/1033 (2.3%)	1.24	10/1387 (0.7%)
53	A	0.46	0/36963	0.55	16/57662 (0.0%)
54	01	0.47	0/69796	0.56	19/108888 (0.0%)
55	02	0.45	0/2872	0.58	3/4479 (0.1%)
56	W	0.47	0/1832	0.53	0/2855
56	X	0.53	0/1832	0.59	1/2855 (0.0%)
57	V	0.51	0/436	0.58	0/679
58	Y	0.53	0/1809	0.58	1/2819 (0.0%)
59	Z	2.06	62/3085 (2.0%)	1.10	15/4173 (0.4%)
All	All	0.55	87/166763 (0.1%)	0.70	257/248890 (0.1%)

All (87) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Z	91	MET	SD-CE	12.16	2.10	1.79
59	Z	260	MET	SD-CE	11.22	2.07	1.79
52	03	218	MET	SD-CE	10.52	2.05	1.79
59	Z	358	MET	SD-CE	10.20	2.05	1.79
32	B	160	LEU	C-N	9.90	1.47	1.33
52	03	161	VAL	CA-CB	9.19	1.64	1.54
59	Z	112	MET	SD-CE	9.09	2.02	1.79
52	03	8	MET	SD-CE	8.61	2.01	1.79
59	Z	368	MET	SD-CE	8.59	2.01	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Z	98	MET	SD-CE	8.00	1.99	1.79
59	Z	351	MET	SD-CE	7.78	1.99	1.79
52	03	15	VAL	CA-CB	7.70	1.64	1.54
52	03	11	ILE	CA-CB	7.58	1.63	1.54
59	Z	139	MET	SD-CE	7.47	1.98	1.79
59	Z	361	THR	CA-CB	7.28	1.63	1.53
59	Z	310	ILE	CA-CB	7.17	1.62	1.54
59	Z	206	ILE	CA-CB	7.16	1.64	1.54
59	Z	71	THR	CA-CB	7.08	1.63	1.53
59	Z	169	ILE	CA-CB	7.03	1.61	1.53
59	Z	302	THR	CA-CB	7.01	1.63	1.53
59	Z	151	MET	SD-CE	6.84	1.96	1.79
52	03	178	VAL	CA-CB	6.81	1.62	1.54
52	03	23	ILE	CA-CB	6.75	1.61	1.54
59	Z	387	VAL	CA-CB	6.71	1.62	1.55
52	03	222	VAL	CA-CB	6.66	1.62	1.54
59	Z	347	VAL	CA-CB	6.45	1.64	1.54
59	Z	247	ILE	CA-CB	6.42	1.62	1.54
59	Z	302	THR	CA-C	6.38	1.57	1.52
59	Z	376	ILE	CA-CB	6.36	1.61	1.54
59	Z	34	VAL	CA-CB	6.29	1.62	1.54
52	03	42	VAL	CA-CB	6.28	1.62	1.53
52	03	175	ILE	CA-CB	6.25	1.61	1.54
59	Z	391	VAL	CA-CB	6.20	1.62	1.54
59	Z	227	VAL	CA-CB	6.19	1.61	1.54
59	Z	341	ILE	CA-CB	6.15	1.61	1.54
59	Z	127	VAL	CA-CB	6.14	1.62	1.54
59	Z	20	VAL	CA-CB	6.11	1.60	1.54
59	Z	350	VAL	CA-CB	6.05	1.61	1.53
59	Z	131	ILE	CA-CB	6.03	1.62	1.54
59	Z	205	ALA	CA-CB	6.03	1.61	1.53
59	Z	231	VAL	CA-CB	5.99	1.60	1.54
59	Z	245	VAL	CA-CB	5.97	1.61	1.54
59	Z	199	ILE	CA-CB	5.97	1.61	1.54
59	Z	349	MET	SD-CE	5.95	1.94	1.79
59	Z	42	ALA	CA-CB	5.92	1.62	1.53
59	Z	360	VAL	CA-CB	5.92	1.62	1.54
52	03	63	THR	CA-CB	5.87	1.62	1.53
59	Z	60	ILE	CA-CB	5.86	1.63	1.54
59	Z	130	ILE	CA-CB	5.81	1.61	1.54
59	Z	105	VAL	CA-CB	5.80	1.61	1.53
59	Z	140	VAL	CA-CB	5.77	1.63	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Z	337	VAL	CA-CB	5.77	1.63	1.54
59	Z	102	ILE	CA-CB	5.75	1.61	1.54
59	Z	170	VAL	CA-CB	5.73	1.61	1.54
59	Z	363	ILE	CA-CB	5.72	1.63	1.54
59	Z	92	ILE	CA-CB	5.72	1.60	1.54
59	Z	79	VAL	CA-CB	5.68	1.60	1.53
59	Z	297	THR	CA-CB	5.67	1.62	1.53
52	03	59	VAL	CA-CB	5.67	1.61	1.54
52	03	50	ILE	CA-CB	5.65	1.62	1.54
52	03	27	ILE	CA-CB	5.64	1.61	1.54
59	Z	335	THR	CA-CB	5.62	1.62	1.53
52	03	202	THR	CA-CB	5.58	1.62	1.53
59	Z	31	ILE	CA-CB	5.50	1.60	1.54
59	Z	163	PRO	CA-C	5.48	1.58	1.53
59	Z	42	ALA	CA-C	5.46	1.56	1.52
52	03	5	THR	CA-CB	5.45	1.64	1.53
52	03	209	ILE	CA-CB	5.45	1.61	1.54
59	Z	235	ILE	CA-CB	5.43	1.63	1.55
59	Z	356	ILE	CA-CB	5.41	1.62	1.54
59	Z	125	VAL	CA-CB	5.41	1.61	1.54
59	Z	340	THR	CA-CB	5.36	1.59	1.53
59	Z	95	ALA	CA-CB	5.30	1.61	1.53
52	03	18	THR	CA-CB	5.28	1.61	1.53
59	Z	298	ILE	CA-CB	5.26	1.61	1.54
59	Z	38	THR	CA-CB	5.25	1.61	1.53
52	03	35	THR	CA-CB	5.25	1.60	1.53
52	03	10	VAL	CA-CB	5.23	1.61	1.54
59	Z	153	VAL	CA-CB	5.22	1.60	1.54
59	Z	254	THR	CA-CB	5.19	1.59	1.53
52	03	214	ILE	CA-CB	5.18	1.60	1.54
59	Z	270	ALA	CA-CB	5.10	1.61	1.53
52	03	207	VAL	CA-CB	5.09	1.61	1.54
52	03	39	VAL	CA-CB	5.07	1.61	1.54
52	03	170	ILE	CA-CB	5.05	1.60	1.54
59	Z	349	MET	CG-SD	5.04	1.93	1.80
59	Z	132	VAL	CA-CB	5.01	1.60	1.54

All (257) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	H	67	GLY	N-CA-C	-12.41	98.10	114.85
36	F	91	ARG	N-CA-C	10.26	123.03	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	10	117	LEU	N-CA-C	9.73	125.86	107.75
59	Z	99	ASP	N-CA-C	-9.48	100.03	111.69
8	11	12	VAL	N-CA-C	-9.46	99.52	110.21
32	B	160	LEU	O-C-N	-9.42	108.92	122.87
42	L	114	SER	N-CA-C	-8.79	101.64	111.14
18	21	66	ILE	N-CA-C	-8.68	104.19	111.91
59	Z	196	ASP	N-CA-C	-8.66	102.84	112.72
11	14	95	LEU	N-CA-C	-8.49	101.54	112.23
52	03	23	ILE	N-CA-C	8.45	119.23	110.36
53	A	438	U	C2'-C3'-O3'	8.07	121.60	109.50
59	Z	9	LYS	N-CA-C	8.03	120.83	110.39
8	11	94	LYS	N-CA-C	-8.02	103.29	113.23
37	G	149	ALA	N-CA-C	-7.81	103.54	113.23
53	A	1190	G	C2'-C3'-O3'	7.78	121.16	109.50
33	C	99	GLN	N-CA-C	-7.75	100.94	111.55
51	U	29	ALA	N-CA-C	-7.73	103.41	112.92
39	I	88	GLU	N-CA-C	-7.72	103.31	112.89
52	03	180	PHE	N-CA-C	-7.66	97.54	109.25
1	04	223	ALA	N-CA-C	-7.65	104.47	113.88
16	19	50	ARG	N-CA-C	-7.64	104.08	113.41
42	L	108	ASP	N-CA-C	7.61	120.53	111.02
37	G	60	ALA	N-CA-C	-7.58	102.97	112.90
7	10	42	ARG	N-CA-C	-7.50	104.25	113.41
23	26	57	VAL	N-CA-C	-7.50	103.15	110.72
37	G	143	MET	N-CA-C	-7.41	103.70	112.89
45	O	43	ALA	N-CA-C	-7.40	103.14	111.14
46	P	75	ILE	N-CA-C	-7.37	101.57	111.44
50	T	70	LYS	N-CA-C	-7.26	103.44	111.36
8	11	27	LEU	N-CA-C	-7.24	104.25	113.23
59	Z	22	HIS	N-CA-C	-7.20	105.41	114.56
44	N	21	ALA	N-CA-C	-7.20	102.56	113.51
52	03	179	ASP	N-CA-C	-7.19	103.52	111.36
17	20	53	PHE	N-CA-C	-7.06	101.64	111.52
32	B	160	LEU	CA-C-N	7.04	131.38	121.24
32	B	160	LEU	C-N-CA	7.04	131.38	121.24
34	D	168	THR	N-CA-C	7.03	120.31	111.24
37	G	142	ARG	N-CA-C	-7.02	104.86	113.50
8	11	29	GLN	N-CA-C	-7.00	103.58	111.14
9	12	79	GLY	N-CA-C	-6.98	105.69	115.32
17	20	50	GLY	N-CA-C	-6.90	96.82	113.18
49	S	9	PHE	N-CA-C	6.88	120.46	110.28
59	Z	308	VAL	N-CA-C	6.84	117.69	108.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	14	113	ALA	N-CA-C	-6.80	104.62	113.12
40	J	26	VAL	N-CA-C	-6.75	102.40	111.44
53	A	1301	U	N1-C1'-C2'	6.73	122.09	112.00
6	09	72	ILE	N-CA-C	-6.72	103.68	111.00
8	11	80	LYS	N-CA-C	-6.70	104.59	112.89
59	Z	322	PHE	N-CA-C	6.68	117.40	108.38
42	L	43	LYS	N-CA-C	6.66	124.53	109.81
54	01	1070	A	C2'-C3'-O3'	6.64	119.46	109.50
51	U	10	PRO	N-CA-C	6.64	126.14	112.47
59	Z	299	LYS	N-CA-C	-6.58	101.50	109.72
34	D	165	GLU	N-CA-C	6.57	118.10	111.07
13	16	68	ALA	N-CA-C	-6.56	104.21	111.82
52	03	6	LYS	N-CA-C	6.55	122.18	111.37
7	10	80	THR	N-CA-C	6.55	124.74	110.80
7	10	44	ALA	N-CA-C	-6.53	104.25	111.36
26	29	43	PHE	N-CA-C	-6.51	105.97	114.04
42	L	25	ALA	N-CA-C	6.51	120.40	111.54
26	29	62	LYS	N-CA-C	-6.50	104.93	112.92
7	10	64	VAL	N-CA-C	-6.49	103.47	112.50
7	10	65	GLU	N-CA-C	-6.45	104.89	112.89
37	G	23	ALA	N-CA-C	-6.45	104.34	111.82
52	03	202	THR	N-CA-C	-6.42	104.92	112.89
44	N	49	THR	N-CA-C	-6.41	104.37	111.36
36	F	11	HIS	CA-C-N	6.39	127.83	119.84
36	F	11	HIS	C-N-CA	6.39	127.83	119.84
14	17	116	GLN	N-CA-C	6.37	119.19	108.23
59	Z	361	THR	N-CA-C	-6.34	98.88	108.96
52	03	32	GLU	N-CA-C	-6.33	103.68	111.40
8	11	89	SER	N-CA-C	-6.32	104.08	110.97
24	27	22	LEU	N-CA-C	-6.31	104.40	111.28
6	09	69	ALA	N-CA-C	-6.31	104.84	112.54
5	08	46	ASP	N-CA-C	6.27	124.16	110.80
54	01	1020	A	C2'-C3'-O3'	6.23	118.85	109.50
50	T	84	LYS	N-CA-C	-6.21	104.59	111.36
45	O	46	LYS	N-CA-C	6.20	124.00	110.80
5	08	72	ASN	N-CA-C	-6.19	104.07	111.69
1	04	12	ARG	N-CA-C	-6.19	106.70	114.56
42	L	54	VAL	N-CA-C	6.18	118.26	108.87
33	C	87	ARG	N-CA-C	-6.17	105.23	112.89
32	B	135	MET	N-CA-C	6.17	117.67	111.07
37	G	108	ARG	N-CA-C	-6.15	104.66	111.36
32	B	18	GLN	N-CA-C	6.14	123.89	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	Z	247	ILE	N-CA-C	6.13	116.88	110.62
53	A	1346	A	N9-C1'-C2'	6.12	121.18	112.00
53	A	1256	A	N9-C1'-C2'	6.12	121.17	112.00
3	06	79	ARG	N-CA-C	-6.11	101.47	110.52
7	10	100	ALA	N-CA-C	-6.11	104.73	111.82
15	18	14	GLN	N-CA-C	6.11	118.02	111.36
38	H	45	ILE	N-CA-C	6.10	116.65	108.11
54	01	1818	U	N1-C1'-C2'	6.10	121.14	112.00
55	02	66	A	C2'-C3'-O3'	-6.08	104.58	113.70
59	Z	145	LEU	N-CA-C	-6.08	104.73	111.36
37	G	146	ALA	N-CA-C	-6.08	104.00	112.45
52	03	37	LYS	N-CA-C	6.07	123.74	110.80
54	01	2287	A	N9-C1'-C2'	6.05	121.08	112.00
7	10	43	LYS	N-CA-C	-6.05	104.80	111.82
12	15	126	ILE	N-CA-C	6.04	117.83	109.80
32	B	133	ALA	N-CA-C	-6.02	104.83	111.82
54	01	1320	C	N1-C1'-C2'	6.01	121.02	112.00
6	09	75	LEU	N-CA-C	-6.01	104.73	111.28
32	B	80	LYS	N-CA-C	-6.01	104.81	111.36
42	L	115	LYS	N-CA-C	-6.01	102.44	110.55
35	E	160	VAL	N-CA-C	5.94	116.60	110.36
34	D	8	LEU	N-CA-C	-5.94	107.02	114.56
15	18	94	ALA	N-CA-C	5.93	118.26	111.02
13	16	2	ARG	N-CA-C	5.91	119.34	111.30
6	09	63	ALA	N-CA-C	-5.89	104.44	111.69
53	A	1399	C	C4'-C3'-O3'	5.89	118.23	109.40
37	G	4	ARG	N-CA-C	5.88	118.76	110.23
39	I	90	ASP	N-CA-C	5.88	123.31	110.80
44	N	33	VAL	N-CA-C	5.87	118.38	111.05
54	01	2820	A	N9-C1'-C2'	5.86	120.80	112.00
9	12	81	ILE	N-CA-C	5.86	121.52	109.34
54	01	100	U	N1-C1'-C2'	5.84	120.76	112.00
50	T	7	LYS	N-CA-C	-5.84	106.12	113.18
53	A	1300	G	N9-C1'-C2'	5.83	120.74	112.00
33	C	80	GLY	N-CA-C	-5.81	107.24	115.43
10	13	66	LYS	N-CA-C	-5.80	106.25	113.38
5	08	119	GLY	N-CA-C	5.79	126.91	113.18
3	06	81	GLY	N-CA-C	-5.79	99.46	113.18
34	D	166	LYS	CA-C-N	5.79	127.07	119.84
34	D	166	LYS	C-N-CA	5.79	127.07	119.84
28	31	41	VAL	N-CA-C	-5.78	107.05	111.62
1	04	87	SER	N-CA-C	-5.78	106.57	113.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	P	54	LEU	N-CA-C	5.78	119.14	111.75
32	B	62	ARG	N-CA-C	-5.77	104.95	112.23
53	A	1540	U	N1-C1'-C2'	5.75	120.63	112.00
32	B	17	HIS	N-CA-C	5.75	123.04	110.80
54	01	669	G	N9-C1'-C2'	5.74	120.61	112.00
34	D	88	ASN	N-CA-C	-5.74	105.77	112.89
14	17	113	ALA	N-CA-C	-5.73	105.95	113.12
46	P	57	ILE	N-CA-C	-5.73	104.93	110.72
52	03	200	LYS	N-CA-C	5.73	117.73	109.48
44	N	18	LYS	N-CA-C	-5.72	106.84	113.88
48	R	26	ALA	N-CA-C	-5.72	103.86	111.24
59	Z	96	ALA	N-CA-C	5.71	119.06	111.75
41	K	69	CYS	N-CA-C	-5.70	106.49	113.50
7	10	75	ALA	N-CA-C	-5.69	105.83	112.89
59	Z	245	VAL	N-CA-C	5.69	116.14	108.17
12	15	13	HIS	N-CA-C	5.68	117.88	110.43
17	20	14	VAL	N-CA-C	5.68	116.06	108.11
36	F	54	LEU	N-CA-C	5.68	122.89	110.80
53	A	818	G	N9-C1'-C2'	5.67	120.51	112.00
4	07	137	PHE	CA-C-N	5.66	126.91	119.84
4	07	137	PHE	C-N-CA	5.66	126.91	119.84
35	E	110	MET	N-CA-C	-5.65	106.43	113.55
59	Z	141	ASP	N-CA-C	-5.64	106.06	113.17
59	Z	220	ILE	N-CA-C	5.62	116.67	109.30
54	01	2324	U	N1-C1'-C2'	5.62	120.43	112.00
5	08	109	SER	N-CA-C	-5.59	106.41	113.18
54	01	2212	A	N9-C1'-C2'	5.59	120.38	112.00
58	Y	9	A	N9-C1'-C2'	5.57	120.36	112.00
39	I	119	LYS	N-CA-C	5.57	116.51	107.32
32	B	88	GLN	N-CA-C	5.56	122.65	110.80
16	19	70	GLN	N-CA-C	-5.56	105.37	111.82
24	27	24	GLU	N-CA-C	5.56	122.65	110.80
50	T	79	THR	N-CA-C	-5.56	105.14	111.14
3	06	189	THR	N-CA-C	-5.55	101.49	110.32
53	A	1225	A	N9-C1'-C2'	5.55	120.32	112.00
4	07	148	VAL	N-CA-C	-5.55	106.97	111.91
54	01	1178	C	N1-C1'-C2'	5.53	120.30	112.00
32	B	30	ILE	N-CA-C	5.52	116.66	108.65
51	U	24	LYS	N-CA-C	5.52	122.56	110.80
55	02	41	G	N9-C1'-C2'	5.52	120.28	112.00
42	L	45	ASN	N-CA-C	5.52	118.36	111.24
47	Q	69	THR	N-CA-C	-5.52	101.07	108.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	19	101	ASP	N-CA-C	5.51	117.63	108.20
42	L	24	GLU	N-CA-C	5.51	122.54	110.80
39	I	53	LEU	N-CA-C	-5.51	105.82	112.54
55	02	44	G	N9-C1'-C2'	5.50	120.25	112.00
41	K	125	LYS	N-CA-C	5.47	122.45	110.80
3	06	33	VAL	N-CA-C	-5.47	105.39	110.53
26	29	65	ASN	N-CA-C	5.47	119.78	113.38
37	G	86	VAL	N-CA-C	5.45	113.88	107.77
48	R	15	GLU	N-CA-C	-5.39	106.71	113.72
34	D	194	ILE	N-CA-C	-5.39	100.61	108.97
21	24	80	HIS	N-CA-C	-5.39	103.14	110.36
54	01	301	G	N9-C1'-C2'	5.38	122.07	114.00
50	T	82	ILE	N-CA-C	5.38	116.86	111.00
40	J	87	LEU	N-CA-C	-5.37	105.59	111.82
47	Q	32	ILE	N-CA-C	5.37	116.15	110.72
1	04	132	ARG	N-CA-C	-5.37	104.71	113.19
6	09	76	GLU	N-CA-C	5.35	118.78	111.39
5	08	125	PRO	N-CA-C	-5.35	107.17	113.86
11	14	69	ARG	N-CA-C	-5.35	106.60	113.23
50	T	10	ALA	N-CA-C	-5.33	104.36	111.24
36	F	90	MET	N-CA-C	5.33	117.96	109.65
20	23	75	ALA	N-CA-C	-5.33	106.95	113.50
46	P	43	ALA	N-CA-C	-5.31	106.57	112.57
54	01	1930	G	N9-C1'-C2'	5.31	119.97	112.00
32	B	111	LYS	N-CA-C	-5.31	105.66	111.82
51	U	44	ARG	N-CA-C	-5.31	105.16	111.69
14	17	20	GLU	N-CA-C	-5.30	107.36	113.88
15	18	15	ASP	N-CA-C	5.29	118.10	107.41
31	34	37	GLN	N-CA-C	5.29	117.12	110.24
53	A	345	C	N1-C1'-C2'	5.29	119.93	112.00
33	C	25	THR	N-CA-C	5.26	117.70	111.33
4	07	10	GLU	N-CA-C	5.24	117.80	111.40
21	24	45	ASP	N-CA-C	5.24	117.41	111.02
41	K	97	ARG	N-CA-C	-5.22	106.41	112.89
38	H	99	GLY	N-CA-C	-5.22	102.59	112.10
54	01	1730	C	N1-C1'-C2'	5.22	119.83	112.00
8	11	82	ALA	N-CA-C	-5.21	105.75	112.68
16	19	10	ARG	N-CA-C	-5.21	105.69	111.36
54	01	1329	U	N1-C1'-C2'	5.20	119.80	112.00
47	Q	37	ILE	N-CA-C	5.19	115.79	108.36
53	A	1196	A	N9-C1'-C2'	5.19	119.78	112.00
20	23	98	ASN	N-CA-C	-5.18	99.76	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B	198	VAL	N-CA-C	5.18	115.77	109.30
18	21	29	VAL	N-CA-C	5.17	115.79	110.36
40	J	40	ILE	CA-C-N	5.17	126.30	119.84
40	J	40	ILE	C-N-CA	5.17	126.30	119.84
3	06	117	ARG	N-CA-C	-5.17	106.66	113.17
32	B	54	ALA	N-CA-C	-5.16	106.50	112.89
4	07	124	ARG	N-CA-C	-5.15	107.65	114.04
59	Z	118	HIS	N-CA-C	-5.15	105.79	111.71
53	A	413	G	N9-C1'-C2'	5.14	119.71	112.00
54	01	858	G	C2'-C3'-O3'	-5.14	105.99	113.70
9	12	139	VAL	N-CA-C	5.13	116.30	109.37
4	07	11	VAL	N-CA-C	5.13	115.75	110.36
6	09	7	ASP	N-CA-C	5.13	117.33	109.95
41	K	50	GLY	N-CA-C	-5.13	103.60	111.24
54	01	1395	A	N9-C1'-C2'	5.13	119.69	112.00
51	U	9	GLU	N-CA-C	5.12	121.14	109.81
53	A	1256	A	C4'-C3'-O3'	-5.12	105.32	113.00
54	01	2848	G	N9-C1'-C2'	5.12	119.68	112.00
3	06	5	LEU	N-CA-C	-5.11	101.94	110.17
2	05	174	SER	N-CA-C	5.11	118.64	111.90
33	C	89	VAL	N-CA-C	5.11	116.44	110.62
48	R	22	TYR	N-CA-C	5.11	119.27	113.19
52	03	194	VAL	N-CA-C	-5.10	105.73	110.53
13	16	67	PHE	N-CA-C	-5.09	107.61	113.88
45	O	39	GLN	N-CA-C	-5.09	105.64	111.14
39	I	84	ARG	N-CA-C	-5.09	105.92	111.82
29	32	35	ARG	N-CA-C	-5.08	106.93	113.23
48	R	45	GLY	N-CA-C	5.08	125.21	113.18
1	04	97	ASP	N-CA-C	5.07	119.22	113.19
54	01	2286	G	N9-C1'-C2'	5.07	119.60	112.00
39	I	6	TYR	N-CA-C	5.07	116.94	108.99
1	04	216	ARG	CA-C-N	5.05	126.16	119.84
1	04	216	ARG	C-N-CA	5.05	126.16	119.84
53	A	1363	A	N9-C1'-C2'	5.05	119.58	112.00
35	E	131	ASN	CA-C-N	5.04	124.48	119.24
35	E	131	ASN	C-N-CA	5.04	124.48	119.24
52	03	11	ILE	N-CA-C	-5.02	105.81	110.53
53	A	960	U	C4'-C3'-O3'	5.02	116.93	109.40
1	04	27	LYS	CA-C-N	5.01	125.28	119.92
1	04	27	LYS	C-N-CA	5.01	125.28	119.92
32	B	43	GLU	N-CA-C	-5.01	106.43	112.54
33	C	170	GLY	N-CA-C	5.00	116.61	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	32	6	GLN	CA-C-N	5.00	126.09	119.84
29	32	6	GLN	C-N-CA	5.00	126.09	119.84
56	X	67	C	N1-C1'-C2'	5.00	119.50	112.00

There are no chirality outliers.

There are no planarity outliers.

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	04	2083	0	2157	80	0
2	05	1565	0	1616	48	0
3	06	1552	0	1619	51	0
4	07	1411	0	1447	64	0
5	08	1323	0	1374	34	0
6	09	1111	0	1148	40	0
7	10	989	0	1025	61	0
8	11	1032	0	1088	65	0
9	12	1129	0	1162	32	0
10	13	939	0	1012	29	0
11	14	1045	0	1117	35	0
12	15	1074	0	1157	40	0
13	16	961	0	1000	32	0
14	17	892	0	923	20	0
15	18	917	0	965	32	0
16	19	947	0	1022	31	0
17	20	816	0	839	31	0
18	21	857	0	922	24	0
19	22	739	0	807	21	0
20	23	780	0	834	22	0
21	24	753	0	780	30	0
22	25	575	0	592	19	0
23	26	625	0	655	21	0
24	27	509	0	543	9	0
25	28	449	0	491	16	0
26	29	523	0	524	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	30	444	0	461	22	0
28	31	410	0	440	7	0
29	32	377	0	418	13	0
30	33	504	0	574	13	0
31	34	302	0	343	9	0
32	B	1705	0	1732	93	0
33	C	1625	0	1699	51	0
34	D	1643	0	1710	51	0
35	E	1157	0	1199	51	0
36	F	818	0	808	43	0
37	G	1182	0	1240	41	0
38	H	979	0	1034	47	0
39	I	1022	0	1070	39	0
40	J	787	0	828	44	0
41	K	870	0	878	38	0
42	L	955	0	1019	26	0
43	M	884	0	944	35	0
44	N	805	0	847	36	0
45	O	714	0	737	18	0
46	P	649	0	666	26	0
47	Q	649	0	691	29	0
48	R	536	0	552	23	0
49	S	638	0	665	33	0
50	T	665	0	714	20	0
51	U	545	0	579	46	0
52	03	1026	0	1092	123	0
53	A	33012	0	16618	454	0
54	01	62317	0	31346	853	0
55	02	2568	0	1303	34	0
56	W	1640	0	836	15	0
56	X	1640	0	837	28	0
57	V	388	0	196	4	0
58	Y	1619	0	821	38	0
59	Z	3029	0	3043	303	0
60	W	10	0	10	3	0
61	Y	11	0	8	3	0
62	Z	32	0	14	0	0
All	All	153753	0	104791	3282	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 13.

All (3282) 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)
59:Z:112:MET:CE	59:Z:112:MET:SD	2.02	1.47
59:Z:358:MET:SD	59:Z:358:MET:CE	2.05	1.45
52:03:218:MET:CE	52:03:218:MET:SD	2.05	1.44
56:W:76:A:O3'	60:W:101:FME:C	1.63	1.43
59:Z:260:MET:CE	59:Z:260:MET:SD	2.07	1.43
59:Z:91:MET:CE	59:Z:91:MET:SD	2.10	1.39
54:01:45:G:H5''	54:01:46:G:H5'	1.32	1.12
51:U:9:GLU:HG2	51:U:10:PRO:HD3	1.10	1.08
52:03:51:ASP:HB3	52:03:57:GLN:HG3	1.39	1.04
35:E:80:LEU:HD13	35:E:122:VAL:HG11	1.39	1.03
7:10:57:ASN:HB2	7:10:62:ARG:HD2	1.39	1.02
54:01:2277:G:H2'	54:01:2278:A:H5''	1.43	0.99
7:10:118:ILE:H	7:10:119:PRO:CD	1.71	0.98
36:F:12:PRO:HD2	36:F:54:LEU:HD21	1.43	0.98
54:01:507:A:H5''	54:01:508:A:H5''	1.46	0.97
40:J:42:LEU:HD11	40:J:73:LEU:HG	1.42	0.97
59:Z:303:LYS:HG2	59:Z:361:THR:HG22	1.46	0.97
59:Z:369:ASP:HB2	59:Z:372:LEU:HB2	1.48	0.96
7:10:118:ILE:H	7:10:119:PRO:HD2	1.30	0.96
8:11:55:PRO:HG2	8:11:71:LYS:HB2	1.46	0.96
51:U:9:GLU:HG2	51:U:10:PRO:CD	1.96	0.95
48:R:70:THR:HG23	48:R:71:ASP:H	1.31	0.95
52:03:200:LYS:HD2	52:03:201:PRO:HD2	1.45	0.95
59:Z:7:ARG:HH22	59:Z:269:ARG:HE	1.12	0.94
55:02:3:C:H2'	55:02:4:C:H5''	1.46	0.94
36:F:38:ARG:HD3	36:F:97:THR:HA	1.49	0.93
52:03:46:VAL:HG22	52:03:212:VAL:HA	1.48	0.93
59:Z:256:THR:HG21	59:Z:279:ARG:HD3	1.52	0.92
1:04:48:ILE:HD11	1:04:51:ARG:HA	1.52	0.91
59:Z:214:ILE:HD12	59:Z:290:GLN:HB3	1.51	0.90
9:12:109:LEU:HD13	9:12:118:MET:HG3	1.49	0.90
1:04:106:PRO:HD2	1:04:109:LEU:HD22	1.52	0.89
3:06:34:ALA:HA	3:06:94:GLN:HE21	1.35	0.89
54:01:1597:A:H5''	54:01:1598:A:H5'	1.53	0.89
11:14:95:LEU:HD22	11:14:100:ILE:HD11	1.52	0.89
8:11:91:LYS:HG3	8:11:94:LYS:HE2	1.53	0.89
32:B:112:ARG:HH12	32:B:116:LEU:HD13	1.36	0.88
59:Z:206:ILE:HG22	59:Z:270:ALA:H	1.39	0.88
12:15:33:LEU:HD13	12:15:117:PHE:HB3	1.56	0.88
7:10:88:HIS:HB2	7:10:89:PRO:HD3	1.56	0.88
58:Y:6:G:H3'	58:Y:7:A:H5''	1.56	0.87
8:11:48:ILE:HG13	8:11:49:GLU:H	1.39	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:10:PRO:HB2	59:Z:74:ARG:HD3	1.57	0.87
8:11:123:ALA:HB1	54:01:1081:U:H4'	1.56	0.86
51:U:16:ARG:HB2	51:U:19:LYS:HD3	1.57	0.86
59:Z:6:GLU:HG2	59:Z:8:THR:HG23	1.54	0.86
38:H:46:GLU:HB3	38:H:61:THR:HB	1.56	0.86
56:W:76:A:C3'	60:W:101:FME:C	2.53	0.86
21:24:72:VAL:HG12	21:24:93:ARG:HA	1.58	0.85
59:Z:58:ARG:HG3	59:Z:60:ILE:HG12	1.57	0.85
53:A:1259:C:H3'	53:A:1260:G:H5''	1.57	0.85
59:Z:246:GLY:HA3	59:Z:290:GLN:HG3	1.57	0.85
8:11:20:SER:HB3	8:11:21:PRO:HD3	1.57	0.85
46:P:31:ARG:HH21	53:A:230:G:H5''	1.40	0.85
52:03:31:LYS:HA	52:03:34:ALA:HB3	1.59	0.85
7:10:118:ILE:HG22	7:10:119:PRO:HD3	1.59	0.84
59:Z:14:VAL:HG11	59:Z:195:LEU:HD21	1.58	0.84
43:M:15:VAL:HG23	43:M:16:ILE:HD12	1.57	0.84
59:Z:119:ILE:HD12	59:Z:156:LEU:HG	1.57	0.84
35:E:107:GLY:HA3	53:A:9:G:H5'	1.60	0.84
53:A:1029:U:H2'	53:A:1031:C:H1'	1.58	0.84
49:S:5:LYS:HG3	49:S:6:LYS:HG2	1.59	0.84
49:S:29:PRO:HG2	49:S:31:ARG:HH12	1.42	0.83
52:03:4:LEU:HD12	52:03:9:ARG:HG2	1.58	0.83
12:15:45:GLN:HE21	54:01:2485:G:H5''	1.43	0.83
7:10:18:VAL:HA	7:10:86:MET:HE2	1.61	0.82
42:L:109:ARG:HH12	53:A:537:G:H5''	1.42	0.82
54:01:2800:A:H3'	54:01:2801:G:H5'	1.61	0.82
53:A:112:G:H21	53:A:354:G:H5'	1.42	0.82
50:T:70:LYS:HA	50:T:73:ARG:HE	1.42	0.82
59:Z:154:ARG:HD3	59:Z:165:ASP:HA	1.61	0.82
59:Z:326:TYR:O	59:Z:341:ILE:HG12	1.80	0.82
10:13:21:CYS:HA	10:13:41:ILE:HG22	1.62	0.82
7:10:19:ALA:HA	7:10:70:GLU:HG3	1.60	0.81
36:F:52:ASN:O	36:F:53:LYS:HG3	1.79	0.81
54:01:121:G:H4'	54:01:149:A:H5'	1.62	0.81
2:05:155:VAL:HG21	54:01:2618:G:H21	1.45	0.81
54:01:2452:C:H42	54:01:2504:U:H3	1.29	0.81
52:03:4:LEU:HB3	52:03:9:ARG:HE	1.44	0.81
1:04:257:ARG:HH21	1:04:266:ILE:HD12	1.45	0.81
40:J:17:LEU:HG	40:J:20:GLN:HE21	1.46	0.80
37:G:128:GLU:HG3	37:G:130:LYS:HE2	1.64	0.80
8:11:29:GLN:HE22	54:01:1096:A:H61	1.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:89:LYS:HD3	59:Z:288:ARG:HH22	1.46	0.80
59:Z:260:MET:HE2	59:Z:272:GLU:HB3	1.64	0.80
59:Z:245:VAL:HG13	59:Z:250:THR:HG21	1.63	0.80
39:I:83:THR:HG21	39:I:102:PHE:HB3	1.64	0.79
56:X:13:C:H2'	56:X:14:A:H5''	1.64	0.79
20:23:42:LYS:HE2	54:01:499:U:H5''	1.64	0.79
35:E:155:LYS:HB3	38:H:70:VAL:HG13	1.64	0.79
35:E:152:VAL:HG11	38:H:98:LEU:HD13	1.65	0.79
59:Z:105:VAL:HB	59:Z:134:LEU:HD23	1.64	0.79
59:Z:309:TYR:HE2	59:Z:311:LEU:HD13	1.48	0.79
59:Z:184:TRP:HA	59:Z:187:LYS:HD3	1.66	0.78
53:A:405:U:H3'	53:A:406:G:H5'	1.65	0.78
10:13:121:GLU:HG2	10:13:122:VAL:HG23	1.64	0.78
30:33:18:LYS:HG3	54:01:651:G:H5'	1.64	0.78
51:U:66:ARG:HG3	53:A:1099:G:H4'	1.64	0.78
32:B:18:GLN:HG3	32:B:187:ASP:OD2	1.84	0.78
6:09:1:MET:HB3	6:09:3:VAL:HG23	1.65	0.78
54:01:189:G:H2'	54:01:205:G:H22	1.48	0.78
39:I:20:ILE:HD11	39:I:60:LEU:HD22	1.65	0.77
46:P:20:VAL:HG23	46:P:35:ARG:HA	1.66	0.77
10:13:13:ASN:HD21	10:13:98:ARG:HB2	1.50	0.76
52:03:41:SER:HA	52:03:177:LYS:HA	1.67	0.76
2:05:33:ARG:HD3	2:05:73:VAL:HB	1.67	0.76
59:Z:93:THR:HG23	59:Z:334:THR:HA	1.67	0.76
59:Z:63:ASN:HA	59:Z:90:ASN:ND2	1.99	0.76
9:12:117:ALA:HA	9:12:120:ARG:HH21	1.50	0.76
47:Q:45:VAL:HG21	47:Q:60:ILE:HD13	1.67	0.76
42:L:32:VAL:HB	42:L:55:ARG:HB3	1.67	0.76
8:11:38:CYS:HA	8:11:41:PHE:HB3	1.68	0.76
46:P:4:ILE:HG12	46:P:21:VAL:HG22	1.67	0.76
8:11:101:SER:HB3	8:11:104:GLN:HG3	1.66	0.76
33:C:116:ALA:HB3	33:C:184:ASN:HD22	1.47	0.76
8:11:126:ARG:HA	8:11:129:GLU:HG3	1.68	0.75
44:N:25:GLU:HB2	44:N:29:ILE:HD12	1.68	0.75
48:R:11:ARG:HG3	48:R:14:ALA:HB3	1.68	0.75
8:11:11:GLN:HB2	8:11:56:VAL:HG12	1.69	0.75
54:01:2114:A:H61	54:01:2117:A:H62	1.32	0.75
54:01:2799:A:H2'	54:01:2800:A:H5'	1.68	0.75
41:K:124:LYS:HE2	53:A:1523:G:H5''	1.67	0.75
54:01:1053:C:H2'	54:01:1054:A:H5''	1.66	0.75
54:01:1645:G:H5''	54:01:1646:C:H5'	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:73:ARG:HH22	32:B:94:ARG:HH22	1.31	0.75
38:H:77:VAL:HG12	38:H:84:ILE:HD12	1.67	0.75
54:01:2162:G:H2'	54:01:2163:A:H8	1.51	0.75
35:E:54:GLU:HG2	35:E:56:PRO:HD2	1.68	0.75
54:01:265:A:H4'	54:01:266:G:OP1	1.85	0.75
52:03:57:GLN:HE22	52:03:203:GLN:HB3	1.52	0.75
32:B:71:THR:HG22	32:B:72:LYS:H	1.52	0.75
13:16:37:THR:HG22	13:16:39:PRO:HD2	1.67	0.74
36:F:66:ALA:HB1	36:F:67:PRO:HD2	1.69	0.74
51:U:28:LEU:HA	51:U:31:VAL:HG12	1.69	0.74
22:25:36:GLN:NE2	22:25:39:THR:HA	2.01	0.74
42:L:79:ILE:HG22	42:L:103:CYS:HB2	1.67	0.74
15:18:52:ARG:NH2	54:01:2720:U:H5''	2.01	0.74
59:Z:260:MET:HB2	59:Z:274:VAL:HG12	1.68	0.74
3:06:105:LEU:HD23	3:06:108:ILE:HD11	1.69	0.74
53:A:1206:G:H2'	53:A:1207:G:H5''	1.68	0.74
12:15:12:MET:HA	54:01:910:A:H62	1.52	0.74
17:20:40:MET:HE3	17:20:42:ALA:HB2	1.70	0.74
21:24:77:VAL:HG23	21:24:89:ILE:HG12	1.68	0.74
59:Z:305:GLU:HA	59:Z:359:VAL:HG22	1.70	0.73
21:24:86:LEU:HD13	21:24:89:ILE:HD11	1.68	0.73
39:I:123:ARG:HD3	39:I:124:PRO:HD2	1.69	0.73
54:01:528:A:N1	54:01:2042:A:H2'	2.03	0.73
7:10:103:ASN:ND2	7:10:110:ALA:HB3	2.02	0.73
43:M:28:ARG:HH21	43:M:62:PHE:HB2	1.52	0.73
44:N:68:ARG:HG3	53:A:1202:U:H4'	1.70	0.73
37:G:12:LEU:HD12	37:G:13:PRO:HD2	1.69	0.73
51:U:16:ARG:HH21	51:U:19:LYS:HG2	1.54	0.73
53:A:1137:C:H5'	53:A:1138:G:H5'	1.71	0.73
59:Z:343:LEU:HA	59:Z:358:MET:HB2	1.70	0.73
13:16:78:LYS:HE2	13:16:83:LEU:HD21	1.71	0.73
53:A:1414:U:H2'	53:A:1415:G:H8	1.54	0.73
52:03:193:LEU:HD23	52:03:196:LEU:HD22	1.70	0.72
41:K:30:ILE:HB	41:K:45:THR:HG22	1.72	0.72
10:13:71:ARG:HH12	15:18:71:ARG:HH21	1.37	0.72
32:B:183:PHE:HB3	32:B:197:PHE:HB2	1.71	0.72
59:Z:237:LYS:H	59:Z:237:LYS:HD2	1.52	0.72
8:11:72:THR:HG21	8:11:112:LYS:HG3	1.72	0.72
11:14:96:LYS:HE3	11:14:103:ILE:HA	1.72	0.72
55:02:3:C:C2'	55:02:4:C:H5''	2.18	0.72
59:Z:88:VAL:O	59:Z:92:ILE:HG13	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:20:14:VAL:HG23	17:20:18:GLN:HE21	1.53	0.72
32:B:118:THR:HA	32:B:121:GLN:HE21	1.55	0.72
59:Z:313:LYS:HD3	59:Z:319:HIS:O	1.89	0.72
21:24:42:LEU:HD13	21:24:47:VAL:HG21	1.72	0.72
53:A:1033:G:H3'	53:A:1034:G:H5''	1.72	0.72
32:B:16:GLY:O	32:B:17:HIS:HB2	1.89	0.72
51:U:66:ARG:HG3	53:A:1099:G:C4'	2.20	0.72
4:07:22:ASN:HB2	4:07:26:GLN:HE22	1.55	0.72
2:05:13:ARG:HH11	15:18:55:HIS:HA	1.53	0.71
5:08:138:GLN:HE22	54:01:2746:U:H1'	1.54	0.71
59:Z:49:ILE:HG23	59:Z:65:SER:HB3	1.72	0.71
10:13:76:VAL:H	15:18:72:VAL:HG22	1.55	0.71
32:B:165:ALA:HB3	32:B:190:SER:HB3	1.72	0.71
19:22:2:ILE:HD11	54:01:144:A:H4'	1.71	0.71
39:I:91:GLU:HA	39:I:94:ARG:HB2	1.72	0.71
8:11:45:THR:HG22	8:11:50:LYS:HG2	1.72	0.71
54:01:2591:C:H2'	54:01:2592:G:C8	2.26	0.71
34:D:144:ILE:HD13	34:D:177:MET:HB3	1.71	0.71
37:G:111:GLY:HA2	37:G:118:ARG:HH11	1.56	0.71
41:K:124:LYS:HE3	53:A:780:A:H5''	1.72	0.71
49:S:14:LEU:O	49:S:18:VAL:HG23	1.91	0.71
54:01:885:C:H2'	54:01:886:A:H5'	1.72	0.71
7:10:27:VAL:HG13	7:10:83:ALA:HB3	1.73	0.70
54:01:2277:G:C2'	54:01:2278:A:H5''	2.18	0.70
59:Z:139:MET:HE2	59:Z:139:MET:HA	1.71	0.70
10:13:13:ASN:ND2	10:13:98:ARG:HB2	2.06	0.70
59:Z:149:VAL:O	59:Z:153:VAL:HG23	1.92	0.70
34:D:97:LEU:HB2	34:D:134:TYR:HB3	1.74	0.70
54:01:2141:G:H22	54:01:2151:U:H1'	1.56	0.70
53:A:484:G:H4'	53:A:485:U:H5''	1.73	0.70
32:B:18:GLN:O	32:B:19:THR:HB	1.89	0.70
56:X:69:C:H2'	56:X:70:G:H5'	1.73	0.70
59:Z:260:MET:O	59:Z:263:LYS:HB2	1.92	0.70
11:14:101:ILE:HG13	11:14:102:GLY:H	1.56	0.70
53:A:960:U:H4'	53:A:961:U:O5'	1.91	0.70
29:32:34:ARG:HH21	29:32:39:ARG:HD2	1.56	0.70
54:01:1055:G:H1'	54:01:1084:A:H61	1.57	0.70
20:23:36:GLU:HA	20:23:61:GLU:HG2	1.74	0.69
22:25:39:THR:H	54:01:2331:G:H4'	1.56	0.69
33:C:116:ALA:HB3	33:C:184:ASN:ND2	2.07	0.69
39:I:35:GLU:HA	39:I:39:GLY:HA3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:275:C:H2'	54:01:276:U:H4'	1.72	0.69
39:I:48:ARG:HA	39:I:51:LEU:HD12	1.73	0.69
43:M:23:GLY:HA2	43:M:68:LEU:HD22	1.75	0.69
46:P:5:ARG:HB2	53:A:376:G:H5''	1.74	0.69
38:H:9:MET:HG3	38:H:26:MET:SD	2.32	0.69
5:08:87:GLN:HE21	5:08:162:ARG:HD2	1.57	0.69
32:B:16:GLY:HA2	32:B:40:ILE:HG13	1.73	0.69
54:01:118:A:H5'	54:01:119:A:C8	2.27	0.69
59:Z:206:ILE:HG22	59:Z:270:ALA:N	2.06	0.69
32:B:182:VAL:HG23	32:B:195:VAL:HA	1.72	0.69
46:P:43:ALA:HA	46:P:46:LYS:HE3	1.73	0.69
16:19:49:ARG:HD2	54:01:993:G:OP1	1.93	0.69
23:26:5:GLN:HG2	23:26:49:ARG:HB2	1.73	0.69
40:J:57:VAL:O	40:J:58:ASN:HB2	1.93	0.69
43:M:13:HIS:HB2	43:M:16:ILE:HD13	1.75	0.69
8:11:79:LEU:HD13	8:11:137:LEU:HD13	1.74	0.69
59:Z:237:LYS:HD3	59:Z:240:GLU:HB2	1.75	0.69
59:Z:364:HIS:HB3	59:Z:365:PRO:HD2	1.75	0.69
19:22:35:ALA:HB3	19:22:38:ALA:HB2	1.74	0.68
20:23:10:VAL:HG12	20:23:71:ILE:HA	1.75	0.68
33:C:82:ASP:HA	33:C:85:LYS:HE3	1.75	0.68
52:03:193:LEU:HA	52:03:196:LEU:HB2	1.75	0.68
54:01:2106:U:H2'	54:01:2107:G:H8	1.58	0.68
21:24:25:LYS:HG2	21:24:43:ASP:HA	1.75	0.68
36:F:64:VAL:HG22	36:F:65:GLU:H	1.56	0.68
53:A:1218:C:H2'	53:A:1219:A:C8	2.28	0.68
59:Z:212:LEU:HD12	59:Z:231:VAL:HG22	1.75	0.68
38:H:9:MET:HE1	38:H:35:ILE:HB	1.75	0.68
52:03:27:ILE:HB	52:03:182:ALA:HB1	1.76	0.68
54:01:2296:U:H5''	54:01:2297:A:OP1	1.93	0.68
2:05:4:LEU:HD23	2:05:32:ASN:HD22	1.57	0.68
34:D:131:ILE:H	34:D:131:ILE:HD12	1.57	0.68
33:C:5:HIS:HB3	44:N:88:MET:HE3	1.75	0.68
39:I:27:ILE:HG21	39:I:34:LEU:HD22	1.75	0.68
41:K:19:VAL:HG13	41:K:82:GLU:HB2	1.75	0.68
7:10:23:LEU:HD13	7:10:118:ILE:HB	1.74	0.68
16:19:105:PHE:O	16:19:109:VAL:HG23	1.94	0.68
34:D:172:VAL:HG22	34:D:174:ALA:H	1.58	0.68
4:07:127:TYR:HB3	4:07:155:ILE:HB	1.75	0.68
54:01:876:C:H42	54:01:901:C:H42	1.42	0.68
59:Z:63:ASN:HD22	59:Z:90:ASN:HD21	1.42	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:83:GLY:HA2	59:Z:118:HIS:NE2	2.09	0.68
37:G:148:LYS:O	37:G:148:LYS:HD3	1.93	0.68
56:X:39:C:H2'	56:X:40:C:C6	2.28	0.68
32:B:33:ALA:HB2	32:B:39:ILE:HG13	1.76	0.68
39:I:89:TYR:HB3	39:I:93:LEU:HD12	1.75	0.68
59:Z:129:TYR:HB3	59:Z:199:ILE:HD13	1.76	0.67
59:Z:231:VAL:HG21	59:Z:236:ILE:HD11	1.75	0.67
54:01:2699:C:H2'	54:01:2700:A:H8	1.59	0.67
59:Z:19:HIS:HB3	59:Z:22:HIS:CE1	2.29	0.67
29:32:24:THR:HG23	29:32:27:GLY:H	1.58	0.67
48:R:48:ALA:O	48:R:52:ARG:HG3	1.94	0.67
50:T:83:ASN:HA	50:T:86:ALA:HB3	1.77	0.67
54:01:534:U:H2'	54:01:535:G:H8	1.58	0.67
4:07:58:ALA:O	4:07:139:GLU:HG2	1.94	0.67
54:01:322:A:H5'	54:01:340:A:H1'	1.76	0.67
54:01:2267:A:H5''	54:01:2268:A:H5'	1.76	0.67
1:04:261:ARG:HD3	1:04:262:THR:HG23	1.77	0.67
4:07:87:LYS:HD2	54:01:2313:C:H5''	1.74	0.67
52:03:34:ALA:HB1	52:03:178:VAL:HG11	1.76	0.67
54:01:677:A:O2'	54:01:2071:A:H5'	1.94	0.67
8:11:48:ILE:HG13	8:11:49:GLU:N	2.10	0.67
46:P:13:LYS:HE3	53:A:392:C:H4'	1.75	0.67
54:01:742:A:H2'	54:01:743:A:C8	2.30	0.67
32:B:66:ILE:CD1	32:B:159:ALA:HB3	2.25	0.67
59:Z:237:LYS:HB3	59:Z:267:GLU:OE2	1.95	0.67
11:14:111:ILE:H	11:14:111:ILE:HD12	1.58	0.67
34:D:84:ASN:HB3	34:D:87:GLU:HB2	1.77	0.67
6:09:84:ALA:HA	6:09:91:PHE:H	1.59	0.67
9:12:7:LYS:HG2	54:01:538:A:H4'	1.77	0.67
53:A:769:G:H4'	53:A:1513:A:H4'	1.77	0.67
59:Z:97:GLN:NE2	59:Z:230:ARG:H	1.93	0.67
36:F:68:GLN:NE2	53:A:738:C:H5''	2.09	0.66
43:M:47:LEU:HD21	43:M:51:GLN:HB2	1.77	0.66
54:01:118:A:H5'	54:01:119:A:H8	1.61	0.66
54:01:1790:C:H2'	54:01:1791:A:C5	2.30	0.66
50:T:73:ARG:HH22	53:A:263:A:P	2.18	0.66
18:21:83:LYS:HG2	18:21:95:ARG:HH12	1.61	0.66
45:O:87:ARG:HE	45:O:88:ARG:H	1.41	0.66
59:Z:112:MET:H	59:Z:115:THR:HB	1.60	0.66
59:Z:332:PHE:H	59:Z:335:THR:HB	1.59	0.66
6:09:9:VAL:HB	6:09:13:GLY:HA3	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:P:7:ALA:HB3	46:P:18:GLN:HB2	1.78	0.66
53:A:225:C:H2'	53:A:226:G:H5''	1.77	0.66
6:09:12:LEU:HD13	6:09:19:VAL:HG21	1.76	0.66
9:12:117:ALA:HA	9:12:120:ARG:NH2	2.11	0.66
23:26:70:LEU:HD23	23:26:73:ARG:HH21	1.59	0.66
47:Q:64:ARG:HD2	53:A:264:C:H4'	1.77	0.66
54:01:1394:U:H4'	54:01:1603:A:H4'	1.77	0.66
54:01:2118:U:H5	54:01:2149:U:H1'	1.59	0.66
32:B:96:LEU:H	32:B:99:MET:HE3	1.60	0.66
59:Z:19:HIS:HA	59:Z:83:GLY:HA3	1.76	0.66
59:Z:212:LEU:HG	59:Z:231:VAL:HA	1.77	0.66
3:06:146:VAL:HG12	3:06:185:LYS:HB2	1.78	0.66
12:15:41:LEU:HG	12:15:96:ILE:HG13	1.77	0.66
42:L:78:VAL:O	42:L:102:ASP:HB2	1.94	0.66
54:01:2553:G:H3'	54:01:2554:U:H5''	1.77	0.66
59:Z:186:ALA:O	59:Z:190:GLU:HG3	1.96	0.66
7:10:118:ILE:N	7:10:119:PRO:CD	2.51	0.65
17:20:49:ILE:HG22	17:20:54:VAL:HA	1.78	0.65
54:01:2771:C:H2'	54:01:2772:C:C6	2.32	0.65
20:23:4:ILE:HD12	20:23:4:ILE:H	1.61	0.65
34:D:100:VAL:HG21	34:D:136:VAL:HG21	1.77	0.65
9:12:7:LYS:O	9:12:11:VAL:HG23	1.96	0.65
52:03:37:LYS:HD2	54:01:2127:G:H5'	1.78	0.65
4:07:28:PRO:HB2	4:07:168:LEU:HD22	1.78	0.65
5:08:8:VAL:HB	5:08:49:LEU:HB2	1.77	0.65
33:C:46:LEU:HB3	33:C:49:ALA:HB3	1.79	0.65
53:A:664:G:H22	53:A:741:G:H1	1.45	0.65
54:01:858:G:H5'	54:01:859:G:OP2	1.96	0.65
59:Z:322:PHE:CE1	59:Z:350:VAL:HB	2.32	0.65
32:B:137:THR:O	32:B:141:GLU:HG3	1.97	0.65
52:03:57:GLN:NE2	52:03:203:GLN:HB3	2.12	0.65
53:A:202:G:H21	53:A:466:A:H61	1.45	0.65
54:01:639:U:H2'	54:01:640:C:C6	2.31	0.65
2:05:151:THR:HB	2:05:152:PRO:HD3	1.78	0.65
11:14:30:THR:O	11:14:33:ARG:HG2	1.97	0.65
12:15:45:GLN:NE2	54:01:2485:G:H5''	2.11	0.65
32:B:129:THR:HB	32:B:132:GLU:HG2	1.79	0.65
34:D:94:GLU:HA	34:D:99:ASN:ND2	2.11	0.65
4:07:47:LYS:HA	4:07:50:ASP:OD2	1.96	0.65
52:03:165:ASN:HB3	52:03:171:ILE:HB	1.77	0.65
54:01:780:G:H2'	54:01:782:A:N7	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2467:C:H2'	54:01:2468:A:O4'	1.96	0.65
44:N:92:ILE:H	44:N:92:ILE:HD12	1.61	0.64
10:13:69:VAL:HG21	10:13:104:THR:HG21	1.80	0.64
42:L:101:LEU:O	42:L:103:CYS:N	2.30	0.64
53:A:212:G:H2'	53:A:213:G:H8	1.61	0.64
5:08:94:ARG:HB2	5:08:105:SER:HB2	1.78	0.64
14:17:80:GLU:O	14:17:84:GLU:HG3	1.97	0.64
8:11:53:PRO:HG2	8:11:77:VAL:HG11	1.79	0.64
15:18:38:ARG:HH22	15:18:40:GLN:HB3	1.61	0.64
53:A:352:C:H4'	53:A:354:G:OP1	1.96	0.64
11:14:63:LYS:HA	30:33:12:ARG:HG2	1.79	0.64
21:24:80:HIS:ND1	21:24:81:PRO:HD2	2.12	0.64
34:D:96:ARG:O	34:D:100:VAL:HG23	1.97	0.64
50:T:79:THR:HG22	50:T:83:ASN:ND2	2.13	0.64
53:A:112:G:N2	53:A:354:G:H5'	2.12	0.64
1:04:144:GLU:HG3	1:04:188:ARG:O	1.98	0.64
32:B:174:GLU:HA	32:B:177:ASN:ND2	2.13	0.64
33:C:87:ARG:HG3	33:C:98:ALA:HB3	1.79	0.64
42:L:41:PRO:HD2	42:L:47:ALA:H	1.62	0.64
1:04:145:MET:HE1	1:04:181:ARG:HH12	1.61	0.64
13:16:38:LEU:HB3	13:16:39:PRO:HD3	1.79	0.64
59:Z:5:PHE:HB2	59:Z:263:LYS:HB3	1.79	0.64
59:Z:140:VAL:HG23	59:Z:142:ASP:H	1.63	0.64
1:04:144:GLU:HB2	1:04:187:CYS:HB3	1.80	0.64
40:J:52:LEU:HD21	40:J:59:LYS:HD2	1.80	0.64
32:B:129:THR:HG22	32:B:131:LYS:H	1.63	0.64
38:H:29:SER:O	38:H:33:VAL:HG23	1.98	0.64
43:M:24:VAL:HG23	43:M:28:ARG:HB3	1.80	0.64
46:P:57:ILE:O	46:P:61:VAL:HG23	1.98	0.64
58:Y:25:C:H3'	58:Y:26:A:H5''	1.80	0.64
17:20:38:VAL:HG13	17:20:54:VAL:HG23	1.80	0.63
35:E:10:LEU:HD22	35:E:67:ARG:HH22	1.61	0.63
49:S:5:LYS:HD2	49:S:6:LYS:HE3	1.79	0.63
53:A:1412:C:H2'	53:A:1413:A:C8	2.33	0.63
54:01:189:G:H2'	54:01:205:G:N2	2.11	0.63
55:02:88:C:H5''	55:02:89:U:OP1	1.97	0.63
58:Y:7:A:H3'	58:Y:8:U:H5''	1.80	0.63
48:R:49:LYS:O	48:R:53:GLN:HG3	1.98	0.63
7:10:8:LYS:O	7:10:12:VAL:HG23	1.98	0.63
45:O:45:HIS:O	45:O:47:LYS:N	2.31	0.63
18:21:29:VAL:HG21	18:21:69:LEU:HD23	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2799:A:C2'	54:01:2800:A:H5'	2.29	0.63
59:Z:300:PRO:HG2	59:Z:365:PRO:HB2	1.81	0.63
49:S:62:THR:HG22	49:S:63:ASP:H	1.64	0.63
3:06:69:ARG:HH22	54:01:2445:G:P	2.22	0.63
54:01:554:U:H2'	54:01:555:G:O4'	1.98	0.63
54:01:839:U:H2'	54:01:840:C:C6	2.34	0.63
59:Z:88:VAL:HG13	59:Z:92:ILE:HD11	1.81	0.63
53:A:129:A:H1'	53:A:130:A:N7	2.14	0.63
59:Z:63:ASN:ND2	59:Z:90:ASN:HD21	1.95	0.63
36:F:12:PRO:HG3	36:F:57:ALA:HA	1.80	0.63
54:01:1386:C:H2'	54:01:1387:A:C8	2.33	0.63
54:01:2141:G:H2'	54:01:2142:A:H8	1.64	0.63
6:09:94:ILE:HG23	6:09:98:ASP:HB2	1.81	0.63
8:11:77:VAL:HA	8:11:80:LYS:HG3	1.81	0.63
19:22:58:VAL:HG13	19:22:85:VAL:HG22	1.80	0.63
20:23:12:VAL:HA	20:23:69:VAL:HG12	1.79	0.63
29:32:34:ARG:HD3	54:01:467:G:OP2	1.99	0.63
59:Z:27:LEU:O	59:Z:31:ILE:HG13	1.99	0.63
44:N:7:ALA:HA	44:N:10:VAL:HG12	1.80	0.62
52:03:207:VAL:HB	52:03:210:LYS:HG3	1.80	0.62
59:Z:191:LEU:HA	59:Z:194:PHE:CD2	2.34	0.62
12:15:3:GLN:HE21	12:15:92:TRP:NE1	1.97	0.62
52:03:27:ILE:HA	52:03:30:LEU:CD2	2.29	0.62
52:03:40:GLU:HB2	52:03:217:THR:OG1	1.98	0.62
42:L:109:ARG:NH1	53:A:537:G:H5''	2.13	0.62
59:Z:297:THR:HG23	59:Z:298:ILE:HD12	1.81	0.62
8:11:74:PRO:HG2	8:11:77:VAL:HG22	1.82	0.62
36:F:3:HIS:O	36:F:92:THR:HG22	1.99	0.62
54:01:1173:U:H2'	54:01:1174:U:H4'	1.81	0.62
59:Z:138:ASP:O	59:Z:139:MET:HE2	1.99	0.62
1:04:16:VAL:HB	1:04:203:VAL:HG22	1.81	0.62
13:16:24:MET:HE3	13:16:44:LEU:HD22	1.82	0.62
34:D:127:ARG:HH21	53:A:619:U:H4'	1.64	0.62
43:M:52:ILE:HG22	43:M:56:ARG:NH1	2.15	0.62
59:Z:129:TYR:HB3	59:Z:199:ILE:CD1	2.29	0.62
59:Z:231:VAL:HB	59:Z:270:ALA:HA	1.81	0.62
13:16:2:ARG:HG2	54:01:1653:G:H3'	1.82	0.62
14:17:56:LYS:O	14:17:60:GLU:HG3	2.00	0.62
25:28:37:ARG:HH21	54:01:929:U:H4'	1.65	0.62
54:01:1509:A:H2'	54:01:1510:G:C8	2.34	0.62
52:03:65:LEU:HD22	52:03:188:ASN:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Y:25:C:C3'	58:Y:26:A:H5''	2.29	0.62
59:Z:89:LYS:HD3	59:Z:288:ARG:NH2	2.14	0.62
3:06:122:GLU:HG3	3:06:123:LYS:H	1.65	0.62
32:B:216:VAL:O	32:B:220:VAL:HG23	1.98	0.62
37:G:112:ASP:H	37:G:118:ARG:HD3	1.63	0.62
44:N:85:GLU:HG3	44:N:89:ARG:HH22	1.63	0.62
52:03:31:LYS:HE3	52:03:181:ASP:HA	1.82	0.62
53:A:81:A:H2	53:A:88:U:H3	1.46	0.62
56:W:47:U:H3'	56:W:48:C:H5'	1.81	0.62
17:20:24:LYS:HA	17:20:94:THR:OG1	1.99	0.62
32:B:22:TRP:CZ3	32:B:24:PRO:HA	2.35	0.62
43:M:52:ILE:HG22	43:M:56:ARG:HH12	1.64	0.62
53:A:552:U:H2'	53:A:553:A:C8	2.34	0.62
54:01:1869:G:H3'	54:01:1870:C:C5'	2.30	0.62
59:Z:213:PRO:HD3	59:Z:232:GLU:HB2	1.81	0.62
54:01:310:A:C2'	54:01:311:A:H5''	2.30	0.62
59:Z:14:VAL:CG1	59:Z:195:LEU:HD21	2.29	0.62
2:05:135:GLY:HA2	54:01:743:A:OP1	1.99	0.61
53:A:1129:C:H2'	53:A:1139:G:N7	2.15	0.61
37:G:22:LEU:O	37:G:26:VAL:HG23	1.99	0.61
54:01:296:U:H2'	54:01:297:G:C8	2.36	0.61
54:01:2800:A:C2	54:01:2895:G:H1'	2.35	0.61
59:Z:7:ARG:NH2	59:Z:269:ARG:HE	1.93	0.61
59:Z:9:LYS:HB3	59:Z:74:ARG:HA	1.83	0.61
59:Z:155:GLU:HA	59:Z:158:SER:HB2	1.82	0.61
4:07:114:ARG:HG3	4:07:177:ARG:HE	1.65	0.61
49:S:3:SER:HA	53:A:1314:C:H41	1.65	0.61
59:Z:259:GLU:HG3	59:Z:263:LYS:C	2.25	0.61
8:11:89:SER:HB2	8:11:92:PRO:HG3	1.82	0.61
16:19:24:TYR:HE1	54:01:17:G:H4'	1.66	0.61
20:23:80:ASP:OD2	20:23:95:PHE:HB3	2.00	0.61
33:C:39:ARG:HG3	33:C:54:ILE:HD11	1.83	0.61
40:J:40:ILE:HB	40:J:73:LEU:HB2	1.80	0.61
59:Z:7:ARG:HH12	59:Z:272:GLU:HG3	1.64	0.61
3:06:154:ASP:OD2	3:06:156:ASN:HB3	2.01	0.61
6:09:47:PHE:HA	6:09:51:ARG:HD2	1.81	0.61
26:29:11:GLU:HA	26:29:25:ARG:HA	1.83	0.61
45:O:23:SER:HB3	45:O:26:VAL:HG23	1.82	0.61
54:01:296:U:H2'	54:01:297:G:H8	1.64	0.61
54:01:1068:G:H21	54:01:1096:A:H5'	1.65	0.61
59:Z:106:ALA:HB3	59:Z:109:ASP:OD2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Y:51:U:H4'	59:Z:325:GLY:O	2.00	0.61
36:F:64:VAL:HG22	36:F:65:GLU:N	2.16	0.61
47:Q:12:VAL:HB	47:Q:21:VAL:HG13	1.83	0.61
53:A:513:C:H2'	53:A:514:C:C6	2.36	0.61
9:12:17:VAL:HG23	9:12:137:PRO:HB2	1.83	0.61
15:18:4:ILE:O	15:18:8:GLU:HG3	2.01	0.61
18:21:88:ARG:HG3	18:21:94:ASP:OD2	2.01	0.61
59:Z:24:LYS:HG2	59:Z:104:VAL:HG21	1.81	0.61
44:N:53:ASP:HA	44:N:58:ARG:HD3	1.82	0.61
52:03:193:LEU:CD2	52:03:196:LEU:HD22	2.30	0.61
54:01:594:U:H2'	54:01:595:C:C6	2.35	0.61
4:07:40:GLY:HA3	54:01:2307:G:O6	2.00	0.60
8:11:52:LEU:O	8:11:54:ILE:HD12	2.01	0.60
54:01:2130:U:H5'	54:01:2159:G:N2	2.16	0.60
51:U:25:ALA:HB1	57:V:9:G:H4'	1.82	0.60
54:01:1683:U:H2'	54:01:1684:G:C8	2.36	0.60
59:Z:299:LYS:HD3	59:Z:300:PRO:O	2.01	0.60
5:08:95:ALA:HB1	5:08:130:ILE:HD11	1.82	0.60
22:25:33:ILE:HD11	22:25:78:ILE:HD11	1.83	0.60
37:G:41:ILE:HG23	37:G:116:ALA:HA	1.83	0.60
44:N:39:ASP:HA	44:N:42:ASN:HD22	1.67	0.60
56:X:14:A:H2'	56:X:15:G:O4'	2.00	0.60
61:Y:101:PHE:O	59:Z:261:PHE:HA	2.01	0.60
3:06:71:GLY:N	54:01:674:G:H5''	2.16	0.60
9:12:41:LYS:HB3	9:12:43:GLU:OE1	2.01	0.60
12:15:3:GLN:HE21	12:15:92:TRP:HE1	1.50	0.60
18:21:66:ILE:HD12	18:21:66:ILE:N	2.15	0.60
33:C:9:ILE:HG23	33:C:10:ARG:HG3	1.81	0.60
54:01:1077:A:H2'	54:01:1078:U:H5'	1.83	0.60
59:Z:27:LEU:HD21	59:Z:104:VAL:HG21	1.84	0.60
59:Z:82:PRO:HD2	59:Z:91:MET:HB2	1.83	0.60
12:15:40:ARG:NH1	12:15:73:ILE:HG13	2.17	0.60
53:A:1259:C:H3'	53:A:1260:G:C5'	2.31	0.60
53:A:1513:A:H2'	53:A:1514:G:H8	1.66	0.60
54:01:878:A:H3'	54:01:879:G:H8	1.66	0.60
54:01:1026:G:H2'	54:01:1027:A:H8	1.65	0.60
54:01:1055:G:H2'	54:01:1056:G:O4'	2.00	0.60
54:01:1807:G:H2'	54:01:1808:A:H5'	1.84	0.60
59:Z:19:HIS:HD2	59:Z:114:GLN:HB2	1.67	0.60
17:20:60:LYS:HB2	17:20:100:GLY:HA3	1.84	0.60
21:24:28:ALA:HB3	21:24:40:ILE:HB	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:56:LEU:HD12	42:L:60:PHE:HB2	1.82	0.60
59:Z:343:LEU:HA	59:Z:358:MET:CB	2.30	0.60
10:13:3:GLN:NE2	54:01:1666:G:H1'	2.16	0.60
15:18:7:LEU:HA	15:18:10:GLU:OE2	2.02	0.60
34:D:7:LYS:HG2	53:A:430:A:OP2	2.01	0.60
54:01:1056:G:H4'	54:01:1086:A:H8	1.67	0.60
54:01:2172:U:H4'	54:01:2174:C:H5	1.65	0.60
53:A:552:U:H2'	53:A:553:A:H8	1.66	0.60
59:Z:1:SER:HB2	59:Z:2:LYS:HD2	1.83	0.60
7:10:78:GLY:N	7:10:79:PRO:HD2	2.16	0.60
35:E:82:HIS:HB2	35:E:83:PRO:HD2	1.82	0.60
41:K:63:GLN:O	41:K:67:GLU:HG3	2.02	0.60
42:L:48:LEU:HB3	53:A:520:A:OP1	2.01	0.60
53:A:695:A:H2'	53:A:696:A:C8	2.36	0.60
55:02:66:A:H5''	55:02:67:G:OP1	2.01	0.60
56:X:21:A:H61	56:X:46:G:H2'	1.66	0.60
2:05:124:ARG:NH1	2:05:163:GLY:HA3	2.17	0.60
16:19:16:ILE:HG13	16:19:31:TYR:HE1	1.65	0.60
21:24:47:VAL:O	21:24:51:GLN:HG2	2.01	0.60
25:28:35:VAL:HG22	25:28:36:GLU:H	1.66	0.60
39:I:33:SER:H	39:I:36:GLN:HE21	1.49	0.60
45:O:71:ARG:NH2	53:A:754:C:H5'	2.16	0.60
47:Q:58:VAL:HG23	47:Q:77:VAL:HA	1.83	0.60
54:01:2817:U:H3'	54:01:2818:U:H5''	1.83	0.60
53:A:219:U:H2'	53:A:220:G:H8	1.67	0.59
53:A:399:G:H2'	53:A:400:C:C6	2.37	0.59
54:01:310:A:O2'	54:01:311:A:H5''	2.01	0.59
54:01:1068:G:N2	54:01:1096:A:H5'	2.16	0.59
54:01:1251:C:O2'	54:01:1252:G:H3'	2.02	0.59
54:01:1386:C:H2'	54:01:1387:A:H8	1.66	0.59
18:21:66:ILE:HD12	18:21:66:ILE:H	1.68	0.59
21:24:4:ILE:HD13	21:24:47:VAL:HG22	1.83	0.59
31:34:32:LYS:HE3	54:01:2478:A:H5'	1.84	0.59
45:O:32:THR:HG22	45:O:36:ASN:HD21	1.67	0.59
51:U:66:ARG:CG	53:A:1099:G:H4'	2.31	0.59
54:01:215:G:H4'	54:01:216:A:H4'	1.83	0.59
59:Z:6:GLU:CG	59:Z:8:THR:HG23	2.31	0.59
32:B:22:TRP:HA	32:B:189:ASN:HB3	1.84	0.59
32:B:96:LEU:N	32:B:99:MET:HE3	2.16	0.59
37:G:142:ARG:HB3	56:X:41:C:H4'	1.84	0.59
43:M:94:LEU:HB3	43:M:95:PRO:HD2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:1425:U:H2'	53:A:1426:G:H8	1.68	0.59
58:Y:28:G:H2'	58:Y:29:G:H8	1.67	0.59
11:14:101:ILE:HG13	11:14:102:GLY:N	2.16	0.59
59:Z:321:PRO:HG2	59:Z:349:MET:HE3	1.84	0.59
5:08:41:GLU:HG3	5:08:54:ARG:HH21	1.66	0.59
14:17:43:ASN:ND2	14:17:45:SER:HB3	2.17	0.59
33:C:67:ILE:HD11	33:C:100:ILE:HD11	1.84	0.59
35:E:133:ILE:HD12	35:E:133:ILE:H	1.67	0.59
51:U:32:ARG:HG3	51:U:33:ARG:HG3	1.84	0.59
59:Z:277:LEU:HD12	59:Z:278:LEU:N	2.18	0.59
1:04:6:LYS:HD2	54:01:705:A:H4'	1.85	0.59
4:07:175:PRO:HB3	26:29:47:LYS:NZ	2.17	0.59
5:08:137:LYS:HE2	54:01:2746:U:H5''	1.84	0.59
6:09:39:ALA:HA	6:09:43:ASN:HB2	1.84	0.59
52:03:65:LEU:HD11	52:03:175:ILE:HG22	1.84	0.59
48:R:17:VAL:HG22	48:R:18:GLN:H	1.68	0.59
54:01:2512:C:H2'	54:01:2513:A:O4'	2.03	0.59
1:04:144:GLU:HA	1:04:151:GLY:HA2	1.85	0.59
1:04:153:LEU:HD11	1:04:181:ARG:NH2	2.18	0.59
4:07:111:ARG:HD3	43:M:6:ILE:HG23	1.84	0.59
8:11:89:SER:O	8:11:91:LYS:N	2.35	0.59
32:B:221:ARG:HH11	32:B:224:ARG:HH11	1.49	0.59
33:C:113:LYS:HA	33:C:184:ASN:ND2	2.17	0.59
40:J:53:ILE:HD12	40:J:63:ASP:OD2	2.03	0.59
48:R:70:THR:HG23	48:R:71:ASP:N	2.12	0.59
53:A:235:C:H2'	53:A:236:A:C8	2.37	0.59
53:A:1206:G:C2'	53:A:1207:G:H5''	2.31	0.59
59:Z:60:ILE:HG13	59:Z:62:ILE:HG23	1.84	0.59
59:Z:128:PRO:HA	59:Z:162:PHE:HE1	1.68	0.59
59:Z:243:GLU:HG2	59:Z:245:VAL:HG22	1.85	0.59
41:K:88:PRO:HD3	51:U:28:LEU:HD22	1.85	0.59
53:A:695:A:H2'	53:A:696:A:H8	1.68	0.59
53:A:760:G:H2'	53:A:761:G:H5'	1.83	0.59
54:01:2760:C:O2'	54:01:2761:A:H5'	2.03	0.59
1:04:52:HIS:NE2	1:04:218:THR:HG23	2.18	0.59
54:01:1020:A:H1'	54:01:1021:A:OP2	2.03	0.59
59:Z:227:VAL:HG13	59:Z:276:VAL:HB	1.85	0.59
1:04:239:PHE:HZ	54:01:1826:G:H4'	1.68	0.58
10:13:113:MET:SD	10:13:116:ILE:HD11	2.43	0.58
54:01:1713:A:H61	54:01:1745:A:H61	1.51	0.58
59:Z:208:LYS:HB3	59:Z:233:ARG:NH2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:10:14:GLU:O	7:10:18:VAL:HG23	2.03	0.58
23:26:37:PHE:HE1	23:26:55:MET:HE3	1.68	0.58
39:I:98:ARG:HG3	39:I:103:VAL:HG21	1.85	0.58
59:Z:133:PHE:HD1	59:Z:170:VAL:HG23	1.67	0.58
9:12:81:ILE:HG23	9:12:82:GLY:N	2.18	0.58
48:R:59:LYS:HD3	53:A:735:C:H5'	1.83	0.58
53:A:1170:A:H2'	53:A:1171:A:O4'	2.03	0.58
54:01:45:G:H5''	54:01:46:G:C5'	2.21	0.58
54:01:1857:G:H2'	54:01:1884:G:N2	2.18	0.58
6:09:30:LEU:HB3	6:09:36:ALA:HB3	1.85	0.58
15:18:5:LYS:O	15:18:9:GLN:HG2	2.03	0.58
35:E:158:LYS:HZ1	38:H:63:LYS:HE3	1.67	0.58
40:J:10:LEU:HD12	40:J:10:LEU:O	2.03	0.58
44:N:9:GLU:O	44:N:13:VAL:HG23	2.03	0.58
53:A:1005:A:H2'	53:A:1006:G:O4'	2.03	0.58
54:01:2452:C:N4	54:01:2504:U:H3	1.98	0.58
18:21:55:ILE:O	18:21:59:GLU:HG2	2.03	0.58
22:25:36:GLN:HE22	22:25:39:THR:HA	1.65	0.58
38:H:54:THR:HG23	38:H:55:LYS:HG3	1.84	0.58
54:01:1222:U:H2'	54:01:1223:G:C8	2.38	0.58
59:Z:244:ILE:HG23	59:Z:244:ILE:O	2.03	0.58
52:03:5:THR:HB	54:01:2129:C:H5'	1.86	0.58
54:01:720:U:H2'	54:01:721:A:H8	1.69	0.58
59:Z:258:VAL:HG22	59:Z:276:VAL:HG22	1.86	0.58
1:04:163:ILE:HA	1:04:173:LEU:HD23	1.85	0.58
32:B:16:GLY:O	32:B:17:HIS:CB	2.51	0.58
32:B:35:ASN:HB3	32:B:37:VAL:HG12	1.84	0.58
52:03:9:ARG:O	52:03:13:GLU:HG3	2.04	0.58
54:01:1801:A:H5''	54:01:2203:U:H2'	1.85	0.58
54:01:2699:C:H2'	54:01:2700:A:C8	2.38	0.58
8:11:105:LEU:HD23	8:11:108:ILE:HD12	1.86	0.58
15:18:59:THR:HG22	15:18:72:VAL:HG12	1.85	0.58
21:24:30:ILE:HG13	21:24:40:ILE:HG13	1.86	0.58
33:C:13:ILE:HG22	33:C:14:VAL:HG23	1.86	0.58
52:03:19:LYS:HD3	52:03:21:TYR:HE1	1.69	0.58
54:01:2208:C:H2'	54:01:2209:G:C8	2.39	0.58
58:Y:62:C:H2'	58:Y:63:G:O4'	2.03	0.58
8:11:59:THR:HB	8:11:67:THR:HG23	1.85	0.58
16:19:43:GLN:HE21	17:20:77:PHE:HB3	1.69	0.58
38:H:85:TYR:CE1	38:H:123:GLU:HB2	2.39	0.58
39:I:17:ARG:HH22	53:A:1129:C:H5''	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:69:THR:HG22	52:03:161:VAL:HG12	1.86	0.58
53:A:662:U:H2'	53:A:663:A:C8	2.38	0.58
54:01:1437:C:H2'	54:01:1438:U:C6	2.39	0.58
54:01:1440:U:H2'	54:01:1441:G:C8	2.39	0.58
54:01:2537:U:H2'	54:01:2538:C:C6	2.39	0.58
1:04:145:MET:HE1	1:04:181:ARG:NH1	2.19	0.58
2:05:179:ARG:HB3	2:05:188:LEU:HD12	1.86	0.58
41:K:23:HIS:HB3	41:K:30:ILE:HG23	1.85	0.58
41:K:111:ASP:HB3	51:U:3:ILE:HG23	1.85	0.58
23:26:17:ARG:HE	23:26:23:ALA:HB2	1.69	0.57
51:U:65:ARG:HH12	53:A:1088:G:H5'	1.68	0.57
54:01:2514:U:H2'	54:01:2515:C:C6	2.39	0.57
16:19:43:GLN:NE2	17:20:77:PHE:HB3	2.19	0.57
47:Q:69:THR:HG22	47:Q:70:LYS:H	1.68	0.57
56:X:32:C:H2'	56:X:33:U:C2	2.39	0.57
58:Y:25:C:H2'	58:Y:26:A:H5''	1.85	0.57
36:F:73:GLU:O	36:F:77:THR:HG23	2.04	0.57
51:U:4:LYS:HD3	51:U:6:ARG:NH1	2.19	0.57
53:A:70:U:H5''	53:A:71:A:OP1	2.05	0.57
53:A:580:C:H2'	53:A:581:G:O4'	2.04	0.57
54:01:1440:U:H2'	54:01:1441:G:H8	1.68	0.57
35:E:93:VAL:HG11	35:E:139:THR:HG22	1.86	0.57
38:H:12:ARG:NH2	53:A:826:C:H5'	2.20	0.57
52:03:33:LEU:HD13	52:03:220:ALA:H	1.68	0.57
54:01:1053:C:C2'	54:01:1054:A:H5''	2.33	0.57
54:01:2287:A:O2'	54:01:2288:A:H2'	2.04	0.57
32:B:20:ARG:HG3	32:B:21:TYR:N	2.17	0.57
54:01:640:C:H2'	54:01:641:U:H6	1.69	0.57
6:09:76:GLU:HB3	6:09:142:VAL:HG22	1.85	0.57
43:M:24:VAL:HA	53:A:1329:A:H5''	1.87	0.57
54:01:1675:C:H2'	54:01:1676:A:O4'	2.04	0.57
59:Z:191:LEU:HA	59:Z:194:PHE:HD2	1.68	0.57
2:05:3:GLY:C	2:05:4:LEU:HD12	2.30	0.57
4:07:139:GLU:H	4:07:139:GLU:CD	2.12	0.57
32:B:56:LEU:HD21	32:B:183:PHE:HZ	1.69	0.57
46:P:36:VAL:HG23	46:P:53:ASP:HB3	1.87	0.57
54:01:2074:U:H2'	54:01:2075:U:C6	2.39	0.57
54:01:2629:U:O2'	54:01:2630:G:H5''	2.05	0.57
55:02:104:A:H2'	55:02:105:G:O4'	2.04	0.57
2:05:91:THR:HG23	2:05:94:GLN:HB2	1.87	0.57
10:13:3:GLN:HE22	54:01:1666:G:H1'	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:15:6:ARG:O	12:15:6:ARG:HD3	2.05	0.57
35:E:113:VAL:HG13	35:E:114:LEU:HD12	1.86	0.57
56:X:31:G:H2'	56:X:32:C:H5'	1.86	0.57
59:Z:97:GLN:HB2	59:Z:98:MET:HE3	1.86	0.57
40:J:20:GLN:O	40:J:24:GLU:HG3	2.04	0.57
46:P:46:LYS:HD2	53:A:617:G:H4'	1.86	0.57
54:01:703:U:H2'	54:01:704:G:O4'	2.05	0.57
54:01:1539:U:H2'	54:01:1540:G:H8	1.70	0.57
54:01:2818:U:H2'	54:01:2819:G:H8	1.70	0.57
59:Z:14:VAL:HG21	59:Z:69:TYR:OH	2.05	0.57
13:16:110:MET:HE2	13:16:110:MET:HA	1.86	0.57
32:B:174:GLU:HA	32:B:177:ASN:HD22	1.68	0.57
36:F:5:GLU:O	36:F:7:VAL:HG23	2.05	0.57
37:G:58:LEU:HD12	37:G:59:GLU:N	2.20	0.57
37:G:129:ASN:HB2	37:G:134:VAL:HG11	1.87	0.57
53:A:80:A:H62	53:A:86:G:H21	1.53	0.57
53:A:737:C:H2'	53:A:738:C:C6	2.40	0.57
53:A:1417:G:H2'	53:A:1482:G:N2	2.20	0.57
54:01:161:A:H3'	54:01:162:U:H5''	1.86	0.57
54:01:609:A:H2'	54:01:610:C:O4'	2.05	0.57
33:C:134:LYS:O	33:C:138:GLN:HG3	2.05	0.56
41:K:110:THR:HB	48:R:72:ARG:HH12	1.69	0.56
46:P:6:LEU:HD22	46:P:17:TYR:HB3	1.86	0.56
3:06:155:GLU:HG2	3:06:159:LEU:HG	1.86	0.56
26:29:58:ASP:O	26:29:62:LYS:HG3	2.05	0.56
49:S:28:LYS:HE3	49:S:29:PRO:HD2	1.87	0.56
53:A:1052:U:H2'	53:A:1200:C:H41	1.70	0.56
53:A:1070:U:H2'	53:A:1071:C:C6	2.40	0.56
54:01:1060:U:H5'	54:01:1062:G:H5'	1.86	0.56
54:01:1367:A:H2'	54:01:1368:G:H5'	1.86	0.56
54:01:2070:A:H2'	54:01:2071:A:C8	2.40	0.56
7:10:26:VAL:HB	7:10:82:ILE:HD12	1.87	0.56
8:11:11:GLN:HB3	8:11:55:PRO:HA	1.87	0.56
10:13:76:VAL:H	15:18:72:VAL:CG2	2.19	0.56
16:19:108:LEU:HA	17:20:48:LYS:HE2	1.88	0.56
32:B:8:MET:HE2	32:B:10:LYS:HG2	1.86	0.56
35:E:156:ARG:NH1	35:E:163:ILE:HB	2.20	0.56
38:H:28:SER:HB3	38:H:56:PRO:HB2	1.87	0.56
39:I:80:HIS:HE1	39:I:84:ARG:HH11	1.53	0.56
45:O:44:GLU:C	45:O:46:LYS:H	2.12	0.56
52:03:7:ARG:HD2	52:03:7:ARG:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:19:LYS:HD3	52:03:21:TYR:CE1	2.41	0.56
53:A:1342:C:H2'	53:A:1343:G:C8	2.41	0.56
54:01:1532:A:H1'	54:01:1540:G:N2	2.21	0.56
54:01:1880:U:H2'	54:01:1881:C:C6	2.41	0.56
59:Z:106:ALA:HB2	59:Z:136:LYS:HD3	1.86	0.56
2:05:46:ARG:HG2	2:05:84:LEU:HD12	1.88	0.56
35:E:96:GLN:HG2	35:E:98:ALA:H	1.70	0.56
41:K:51:PHE:CE2	41:K:64:VAL:HG11	2.41	0.56
46:P:36:VAL:HG21	46:P:57:ILE:HG13	1.86	0.56
52:03:4:LEU:HB3	52:03:9:ARG:NE	2.16	0.56
58:Y:26:A:H61	58:Y:45:U:H3	1.51	0.56
59:Z:147:GLU:HA	59:Z:171:ARG:HH22	1.68	0.56
1:04:15:VAL:HG22	1:04:205:GLY:HA3	1.87	0.56
4:07:107:VAL:HB	4:07:108:PRO:HD3	1.88	0.56
19:22:59:ASN:HD22	54:01:1342:A:H5''	1.69	0.56
22:25:66:GLU:HB3	22:25:68:LYS:HG3	1.87	0.56
24:27:49:ASP:O	24:27:53:VAL:HG23	2.05	0.56
31:34:4:ARG:O	31:34:37:GLN:HB3	2.06	0.56
43:M:3:ILE:HG13	43:M:7:ASN:HB3	1.87	0.56
45:O:7:THR:O	45:O:11:VAL:HG23	2.06	0.56
51:U:17:ARG:HA	51:U:20:ARG:NH1	2.21	0.56
53:A:663:A:H5'	53:A:836:G:OP1	2.05	0.56
54:01:1326:U:H2'	54:01:1327:A:H8	1.71	0.56
54:01:2170:A:H2'	54:01:2171:A:O4'	2.05	0.56
54:01:2698:U:H2'	54:01:2699:C:C6	2.40	0.56
54:01:581:C:H2'	54:01:582:A:C8	2.41	0.56
54:01:2785:C:H2'	54:01:2786:U:C6	2.41	0.56
59:Z:28:THR:HG23	59:Z:78:HIS:HD2	1.69	0.56
2:05:10:GLY:H	2:05:197:THR:HG23	1.70	0.56
11:14:64:PHE:HB2	54:01:2416:C:OP1	2.05	0.56
40:J:22:THR:O	40:J:26:VAL:HG23	2.06	0.56
53:A:714:G:H2'	53:A:715:A:C8	2.41	0.56
59:Z:219:SER:HB2	59:Z:283:ARG:HD2	1.87	0.56
7:10:34:THR:O	7:10:38:MET:HG3	2.06	0.56
9:12:14:ASP:CG	9:12:15:TRP:H	2.13	0.56
9:12:78:THR:HG22	54:01:2641:G:H5''	1.88	0.56
18:21:42:LYS:HB2	54:01:2010:G:H5''	1.87	0.56
54:01:704:G:H2'	54:01:726:G:N2	2.21	0.56
54:01:2121:G:H2'	54:01:2122:U:O4'	2.06	0.56
59:Z:132:VAL:HB	59:Z:169:ILE:HD12	1.87	0.56
59:Z:167:THR:HG22	59:Z:169:ILE:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:17:43:ASN:HD21	14:17:46:GLU:HG2	1.70	0.56
15:18:24:THR:HB	15:18:87:ARG:H	1.71	0.56
32:B:89:PHE:HE1	32:B:152:ASP:HB2	1.70	0.56
32:B:212:TYR:O	32:B:216:VAL:HG23	2.06	0.56
54:01:1936:A:H2	54:01:1943:U:H3	1.54	0.56
59:Z:4:LYS:HG2	59:Z:264:LEU:HB2	1.87	0.56
3:06:149:ILE:HD11	3:06:172:ALA:HA	1.88	0.56
10:13:12:ASP:HB2	10:13:96:GLY:HA3	1.88	0.56
12:15:20:LEU:HD23	21:24:81:PRO:HG2	1.87	0.56
12:15:29:GLY:HA2	12:15:106:ASP:HB2	1.88	0.56
15:18:38:ARG:NH2	15:18:40:GLN:HB3	2.21	0.56
32:B:89:PHE:HB3	32:B:149:GLY:O	2.05	0.56
53:A:304:U:H2'	53:A:305:G:C8	2.41	0.56
53:A:1352:C:H2'	53:A:1353:G:C8	2.41	0.56
3:06:4:VAL:HG12	3:06:11:ALA:HB2	1.88	0.55
3:06:24:ASN:O	3:06:28:VAL:HG23	2.06	0.55
6:09:79:THR:HG23	6:09:145:ASN:O	2.06	0.55
10:13:14:SER:OG	10:13:86:LEU:HD12	2.06	0.55
14:17:52:SER:OG	14:17:54:VAL:HG12	2.06	0.55
19:22:21:SER:O	19:22:25:GLU:HG2	2.05	0.55
27:30:30:ASP:HB3	27:30:34:GLY:H	1.70	0.55
31:34:15:LYS:HB2	31:34:15:LYS:NZ	2.21	0.55
34:D:61:ARG:HH21	34:D:67:LEU:HA	1.71	0.55
53:A:797:C:H2'	53:A:798:U:C6	2.41	0.55
54:01:640:C:H2'	54:01:641:U:C6	2.41	0.55
54:01:2875:C:H2'	54:01:2876:G:H8	1.71	0.55
59:Z:322:PHE:CZ	59:Z:350:VAL:HB	2.41	0.55
2:05:148:GLN:HB2	2:05:152:PRO:HG2	1.88	0.55
3:06:181:ILE:HG23	11:14:2:ARG:HG3	1.88	0.55
4:07:97:GLU:HG2	26:29:25:ARG:HB3	1.88	0.55
16:19:36:GLN:HE21	54:01:1252:G:H1	1.54	0.55
24:27:9:LYS:HB3	24:27:12:GLU:HB2	1.88	0.55
25:28:23:LEU:HD22	25:28:28:LEU:HD12	1.86	0.55
32:B:27:LYS:HB3	32:B:28:PRO:HD3	1.89	0.55
41:K:71:ASP:HA	41:K:74:LYS:HE2	1.88	0.55
42:L:33:CYS:HA	42:L:54:VAL:HA	1.88	0.55
52:03:193:LEU:O	52:03:197:LYS:HG3	2.06	0.55
53:A:935:A:H2'	53:A:936:C:C6	2.42	0.55
53:A:1286:U:H2'	53:A:1287:A:H5'	1.88	0.55
54:01:275:C:H3'	54:01:276:U:H5''	1.88	0.55
54:01:833:A:H2'	54:01:834:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:214:ILE:CD1	59:Z:290:GLN:HB3	2.31	0.55
59:Z:300:PRO:HB2	59:Z:366:ILE:N	2.21	0.55
1:04:71:ASP:O	1:04:73:ILE:HG13	2.06	0.55
5:08:136:ASP:OD2	5:08:139:VAL:HG23	2.06	0.55
52:03:214:ILE:CD1	52:03:222:VAL:HB	2.36	0.55
53:A:666:G:H2'	53:A:667:G:H8	1.72	0.55
54:01:1796:U:H2'	54:01:1797:G:H8	1.71	0.55
59:Z:306:SER:HB3	59:Z:358:MET:CE	2.37	0.55
8:11:91:LYS:HG3	8:11:94:LYS:CE	2.32	0.55
12:15:3:GLN:NE2	12:15:92:TRP:HE1	2.04	0.55
23:26:61:LYS:HE3	54:01:372:G:OP1	2.06	0.55
38:H:17:GLN:HE21	38:H:71:VAL:H	1.54	0.55
49:S:77:ARG:HD2	53:A:1225:A:H1'	1.88	0.55
53:A:1412:C:H2'	53:A:1413:A:H8	1.70	0.55
54:01:481:G:H2'	54:01:507:A:N1	2.20	0.55
54:01:1837:C:H2'	54:01:1899:A:H61	1.71	0.55
59:Z:243:GLU:HG3	59:Z:251:GLN:O	2.07	0.55
8:11:72:THR:HG22	8:11:116:MET:HE3	1.89	0.55
32:B:45:THR:HG22	32:B:49:PHE:HD1	1.70	0.55
51:U:49:ALA:O	51:U:53:LYS:HG3	2.06	0.55
54:01:100:U:H4'	54:01:101:A:O4'	2.07	0.55
1:04:257:ARG:HH11	1:04:257:ARG:HG2	1.71	0.55
6:09:132:PHE:O	6:09:139:PHE:HB3	2.07	0.55
38:H:76:ARG:NH1	38:H:125:ILE:HG23	2.21	0.55
41:K:88:PRO:HG2	41:K:89:GLY:H	1.71	0.55
52:03:222:VAL:HG12	52:03:224:VAL:HG13	1.89	0.55
53:A:123:U:H5''	53:A:311:C:O2'	2.06	0.55
53:A:909:A:H2'	53:A:910:C:O4'	2.07	0.55
53:A:1342:C:H2'	53:A:1343:G:H8	1.72	0.55
54:01:1170:C:H2'	54:01:1171:G:C8	2.42	0.55
59:Z:238:VAL:HG13	59:Z:257:GLY:N	2.21	0.55
6:09:6:LEU:HD11	6:09:37:VAL:HG23	1.88	0.55
14:17:76:LYS:O	14:17:80:GLU:HG3	2.07	0.55
17:20:83:TYR:CZ	54:01:1187:G:H5''	2.42	0.55
54:01:1278:C:H2'	54:01:1279:G:H8	1.71	0.55
59:Z:173:SER:N	59:Z:184:TRP:CE3	2.73	0.55
1:04:140:VAL:HG12	1:04:191:LEU:HD23	1.88	0.55
12:15:5:LYS:O	12:15:6:ARG:HG3	2.07	0.55
18:21:86:MET:HE3	18:21:87:PRO:O	2.05	0.55
25:28:15:ARG:HE	25:28:52:PHE:HE2	1.55	0.55
32:B:183:PHE:CB	32:B:197:PHE:HB2	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:86:LYS:HD2	38:H:90:GLU:HG2	1.88	0.55
53:A:20:U:H2'	53:A:21:G:O4'	2.07	0.55
30:33:6:VAL:HG21	30:33:60:CYS:HB2	1.87	0.55
33:C:13:ILE:H	33:C:13:ILE:HD12	1.72	0.55
42:L:49:ARG:HB3	42:L:65:TYR:HE1	1.72	0.55
49:S:16:LYS:NZ	49:S:16:LYS:HB3	2.22	0.55
52:03:5:THR:O	52:03:9:ARG:HG3	2.06	0.55
53:A:181:A:N6	53:A:194:C:H2'	2.22	0.55
53:A:1513:A:H2'	53:A:1514:G:C8	2.42	0.55
54:01:685:A:H5''	54:01:788:A:H62	1.72	0.55
59:Z:7:ARG:NH1	59:Z:272:GLU:HG3	2.22	0.55
59:Z:155:GLU:O	59:Z:159:GLN:HG2	2.07	0.55
1:04:240:GLY:HA3	54:01:2597:G:C5'	2.36	0.55
2:05:82:PHE:HE1	2:05:202:ILE:HG23	1.71	0.55
15:18:105:LYS:O	15:18:108:ARG:HG2	2.06	0.55
28:31:18:HIS:HB3	28:31:39:ASP:OD1	2.06	0.55
54:01:2185:U:H2'	54:01:2186:G:H8	1.72	0.55
54:01:2233:U:H2'	54:01:2234:G:H8	1.72	0.55
59:Z:213:PRO:HB2	59:Z:334:THR:HG21	1.88	0.55
4:07:70:ARG:HG2	4:07:70:ARG:HH21	1.71	0.54
6:09:84:ALA:HB2	6:09:90:LEU:HD12	1.89	0.54
12:15:42:THR:OG1	12:15:45:GLN:HG3	2.07	0.54
19:22:56:GLU:OE2	19:22:88:LYS:HG2	2.07	0.54
22:25:39:THR:HG21	54:01:2336:A:H61	1.71	0.54
46:P:2:VAL:HG23	46:P:65:ALA:HA	1.88	0.54
53:A:312:C:H2'	53:A:313:A:H8	1.72	0.54
53:A:1206:G:C3'	53:A:1207:G:H5''	2.36	0.54
54:01:414:C:H2'	54:01:415:A:C8	2.41	0.54
54:01:2286:G:H5''	54:01:2287:A:OP1	2.07	0.54
59:Z:332:PHE:HB3	59:Z:372:LEU:HD21	1.89	0.54
7:10:124:ASP:HB3	7:10:126:LEU:HG	1.89	0.54
8:11:46:ASP:OD1	8:11:50:LYS:HD3	2.07	0.54
52:03:14:LYS:HD2	52:03:33:LEU:HD23	1.89	0.54
52:03:177:LYS:H	52:03:180:PHE:HD2	1.53	0.54
59:Z:170:VAL:HG21	59:Z:191:LEU:HB2	1.89	0.54
59:Z:176:LYS:HD3	59:Z:184:TRP:NE1	2.22	0.54
40:J:15:HIS:HB3	40:J:70:HIS:NE2	2.22	0.54
47:Q:48:GLU:HB2	47:Q:51:GLU:OE2	2.07	0.54
51:U:18:PHE:HA	51:U:21:SER:HB3	1.89	0.54
53:A:1062:U:H2'	53:A:1063:C:C6	2.42	0.54
54:01:2286:G:H5'	54:01:2287:A:H1'	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:V:19:U:H2'	57:V:20:U:H6	1.71	0.54
8:11:56:VAL:HG23	8:11:70:THR:HA	1.88	0.54
39:I:125:GLN:HE22	53:A:1342:C:H1'	1.71	0.54
41:K:80:ASN:HB3	41:K:105:ARG:HH11	1.72	0.54
44:N:20:PHE:O	44:N:21:ALA:HB3	2.07	0.54
47:Q:13:SER:H	47:Q:21:VAL:HG13	1.73	0.54
52:03:26:ALA:O	52:03:29:LEU:HG	2.08	0.54
53:A:335:C:H2'	53:A:336:A:C8	2.42	0.54
53:A:918:A:H2'	53:A:919:A:C8	2.42	0.54
54:01:460:A:H2'	54:01:461:C:O4'	2.07	0.54
54:01:1872:A:H2'	54:01:1873:G:O4'	2.08	0.54
54:01:2105:U:H2'	54:01:2106:U:O4'	2.07	0.54
54:01:2432:A:H1'	56:X:75:C:H5'	1.88	0.54
54:01:2636:C:H2'	54:01:2637:U:C6	2.42	0.54
55:02:5:U:H2'	55:02:6:G:C8	2.43	0.54
12:15:122:ALA:HB1	54:01:2467:C:H1'	1.90	0.54
13:16:39:PRO:HG2	54:01:1651:G:H4'	1.90	0.54
21:24:75:GLN:HB2	21:24:92:VAL:HG23	1.89	0.54
37:G:125:ASP:HA	37:G:128:GLU:OE2	2.08	0.54
50:T:30:PHE:HB3	50:T:53:MET:HB3	1.89	0.54
53:A:1448:C:H2'	53:A:1449:C:H6	1.72	0.54
54:01:873:C:H2'	54:01:874:G:H8	1.73	0.54
54:01:2159:G:H2'	54:01:2160:C:O4'	2.07	0.54
54:01:2573:C:H5''	54:01:2574:G:H5''	1.89	0.54
59:Z:12:VAL:HB	59:Z:76:TYR:CE1	2.43	0.54
1:04:12:ARG:HH21	54:01:728:G:H4'	1.71	0.54
7:10:59:LEU:HB2	7:10:62:ARG:HB2	1.90	0.54
18:21:20:VAL:HG21	18:21:43:ALA:HB3	1.88	0.54
36:F:18:VAL:HB	36:F:19:PRO:HD3	1.89	0.54
53:A:1448:C:H2'	53:A:1449:C:C6	2.42	0.54
54:01:144:A:H2'	54:01:145:C:C6	2.43	0.54
54:01:1213:A:N6	54:01:1236:G:H1'	2.23	0.54
7:10:77:VAL:C	7:10:79:PRO:HD2	2.33	0.54
12:15:4:PRO:HG2	12:15:70:ASP:HA	1.90	0.54
15:18:99:LEU:O	15:18:99:LEU:HD23	2.08	0.54
22:25:22:PHE:CD2	54:01:922:C:H1'	2.43	0.54
36:F:9:MET:HE3	36:F:86:ARG:HB3	1.88	0.54
41:K:30:ILE:HD11	41:K:43:TRP:HB2	1.90	0.54
51:U:39:LYS:O	51:U:43:GLU:HG2	2.08	0.54
53:A:392:C:H2'	53:A:393:A:H8	1.72	0.54
54:01:2123:G:H2'	54:01:2124:G:O4'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2233:U:H2'	54:01:2234:G:C8	2.43	0.54
4:07:175:PRO:HB3	26:29:47:LYS:HZ1	1.73	0.54
13:16:2:ARG:O	13:16:2:ARG:HD3	2.08	0.54
27:30:24:VAL:HG13	27:30:25:THR:H	1.73	0.54
51:U:33:ARG:O	51:U:33:ARG:HD2	2.08	0.54
54:01:155:A:H2'	54:01:156:A:C8	2.43	0.54
54:01:2788:C:H2'	54:01:2789:C:C6	2.42	0.54
1:04:207:ALA:HB2	54:01:1790:C:O2'	2.07	0.54
4:07:37:MET:HB3	4:07:86:CYS:SG	2.48	0.54
7:10:99:PHE:HA	7:10:102:ALA:HB3	1.90	0.54
10:13:48:PRO:HB3	53:A:1422:G:H5'	1.90	0.54
23:26:63:ILE:O	23:26:67:LEU:HD13	2.08	0.54
34:D:59:LYS:O	34:D:63:ILE:HG13	2.08	0.54
54:01:27:G:N2	54:01:512:G:H1'	2.23	0.54
59:Z:63:ASN:HD22	59:Z:90:ASN:ND2	2.06	0.54
1:04:229:HIS:ND1	1:04:230:PRO:HD2	2.23	0.54
4:07:90:LEU:HD13	4:07:95:MET:HA	1.89	0.54
7:10:94:ARG:HD3	7:10:131:THR:HG22	1.90	0.54
8:11:126:ARG:HA	8:11:129:GLU:CG	2.38	0.54
13:16:29:VAL:HG11	13:16:75:ILE:HG23	1.89	0.54
32:B:66:ILE:HD12	32:B:159:ALA:HB3	1.89	0.54
36:F:32:ALA:HB2	36:F:70:VAL:HG21	1.89	0.54
48:R:56:ARG:HB3	48:R:60:ARG:NH1	2.23	0.54
52:03:21:TYR:HD2	52:03:222:VAL:HG13	1.71	0.54
53:A:935:A:H2'	53:A:936:C:H6	1.71	0.54
53:A:1207:G:H2'	53:A:1208:C:O4'	2.07	0.54
54:01:828:U:H2'	54:01:829:A:C8	2.43	0.54
59:Z:259:GLU:CD	59:Z:262:ARG:HA	2.33	0.54
59:Z:304:PHE:CD2	59:Z:388:VAL:HG13	2.43	0.54
59:Z:341:ILE:HA	59:Z:360:VAL:HG22	1.89	0.54
10:13:15:GLY:O	10:13:47:ILE:HG12	2.07	0.53
24:27:2:LYS:HE2	54:01:102:U:H1'	1.89	0.53
24:27:21:LEU:HA	24:27:25:GLN:HB3	1.90	0.53
36:F:19:PRO:O	36:F:23:GLU:HG3	2.08	0.53
47:Q:11:VAL:CG1	47:Q:20:ILE:HD11	2.38	0.53
53:A:82:G:H2'	53:A:83:C:O4'	2.08	0.53
53:A:1118:U:H2'	53:A:1119:C:C6	2.42	0.53
54:01:2875:C:H2'	54:01:2876:G:C8	2.43	0.53
5:08:71:LEU:O	5:08:75:VAL:HG23	2.08	0.53
7:10:37:LYS:HG2	7:10:41:LEU:HD12	1.91	0.53
7:10:64:VAL:O	7:10:68:PRO:HD3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:33:57:VAL:HA	30:33:60:CYS:SG	2.48	0.53
53:A:412:A:H5''	53:A:413:G:OP2	2.08	0.53
54:01:1141:U:H4'	54:01:1142:A:O4'	2.08	0.53
54:01:2358:A:H2'	54:01:2359:C:O4'	2.08	0.53
59:Z:287:GLU:HG3	59:Z:290:GLN:HB2	1.88	0.53
33:C:156:LEU:HD11	33:C:163:ARG:HE	1.73	0.53
36:F:46:GLN:HA	36:F:56:LYS:HA	1.91	0.53
53:A:784:A:H2'	53:A:785:G:C8	2.43	0.53
53:A:825:A:H2'	53:A:826:C:C6	2.43	0.53
53:A:1395:C:H6	53:A:1395:C:H5'	1.72	0.53
54:01:239:C:H2'	54:01:240:C:O4'	2.08	0.53
54:01:362:A:H3'	54:01:363:G:H8	1.73	0.53
54:01:2597:G:H2'	54:01:2598:A:C8	2.44	0.53
54:01:2808:G:H2'	54:01:2890:G:C6	2.43	0.53
5:08:126:THR:HG22	5:08:127:GLN:H	1.74	0.53
19:22:39:THR:OG1	19:22:42:GLU:HG3	2.09	0.53
20:23:12:VAL:HB	20:23:18:LYS:HA	1.90	0.53
27:30:14:MET:SD	54:01:2045:C:H5''	2.49	0.53
33:C:19:SER:HB3	33:C:21:TRP:NE1	2.24	0.53
33:C:120:THR:HG23	33:C:188:ALA:HB2	1.88	0.53
41:K:27:ASN:HB3	41:K:56:LYS:HZ1	1.73	0.53
52:03:38:PHE:CE1	54:01:2127:G:H4'	2.43	0.53
53:A:10:A:H2'	53:A:11:G:H8	1.73	0.53
53:A:1070:U:H2'	53:A:1071:C:H6	1.74	0.53
54:01:2281:A:O2'	54:01:2282:G:H5'	2.08	0.53
54:01:2328:A:H2'	54:01:2329:U:C6	2.43	0.53
54:01:2339:C:H2'	54:01:2340:A:C8	2.44	0.53
56:X:36:U:H2'	56:X:37:A:O4'	2.08	0.53
58:Y:4:C:H2'	58:Y:5:G:C8	2.43	0.53
59:Z:332:PHE:HB2	59:Z:335:THR:OG1	2.09	0.53
3:06:48:THR:O	3:06:52:VAL:HG23	2.08	0.53
8:11:44:LYS:O	8:11:48:ILE:HG12	2.07	0.53
18:21:82:MET:HB2	18:21:98:LYS:HB2	1.90	0.53
35:E:38:VAL:HG23	35:E:70:MET:HE2	1.91	0.53
54:01:1664:A:H61	54:01:1996:C:H42	1.57	0.53
54:01:1794:A:H2'	54:01:1795:C:C6	2.44	0.53
55:02:95:U:H2'	55:02:96:G:C8	2.43	0.53
56:X:13:C:C2'	56:X:14:A:H5''	2.37	0.53
59:Z:98:MET:HG2	59:Z:101:ALA:HB2	1.89	0.53
59:Z:209:PRO:HD2	59:Z:233:ARG:NH2	2.23	0.53
59:Z:305:GLU:HB3	59:Z:389:ALA:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:62:ARG:NH1	1:04:84:PRO:HD2	2.24	0.53
4:07:24:VAL:O	4:07:27:VAL:HG12	2.07	0.53
16:19:47:ARG:HG2	16:19:47:ARG:HH21	1.74	0.53
26:29:9:TYR:O	26:29:25:ARG:HD2	2.09	0.53
32:B:20:ARG:NH1	53:A:831:A:H5''	2.24	0.53
42:L:113:ARG:HD2	42:L:118:VAL:O	2.09	0.53
56:X:28:C:H2'	56:X:29:G:H8	1.73	0.53
5:08:97:VAL:HG23	5:08:124:CYS:SG	2.49	0.53
12:15:55:ARG:HD3	54:01:2469:A:H4'	1.91	0.53
22:25:22:PHE:HD2	54:01:922:C:H1'	1.72	0.53
27:30:54:ILE:HG23	27:30:56:LYS:H	1.74	0.53
39:I:47:VAL:HG12	39:I:78:ILE:HB	1.89	0.53
45:O:24:THR:O	45:O:28:VAL:HG23	2.09	0.53
51:U:36:PHE:C	51:U:38:GLU:H	2.17	0.53
54:01:1932:A:H2'	54:01:1933:G:O4'	2.09	0.53
54:01:2246:G:H2'	54:01:2247:A:C8	2.44	0.53
59:Z:16:THR:HG22	59:Z:24:LYS:HD2	1.91	0.53
59:Z:122:GLY:O	59:Z:125:VAL:HG12	2.08	0.53
59:Z:230:ARG:HB3	59:Z:273:ASN:HA	1.91	0.53
3:06:109:LEU:O	3:06:113:VAL:HG23	2.09	0.53
4:07:133:GLU:HB3	4:07:135:ILE:HG13	1.90	0.53
8:11:79:LEU:O	8:11:83:ALA:HB3	2.07	0.53
13:16:43:GLU:OE2	13:16:46:ARG:HD3	2.09	0.53
22:25:17:LEU:HD11	22:25:37:ARG:HH21	1.73	0.53
23:26:58:ILE:HG12	23:26:66:VAL:HG21	1.90	0.53
27:30:10:SER:O	27:30:14:MET:HG3	2.08	0.53
53:A:1273:C:H2'	53:A:1274:A:O4'	2.08	0.53
54:01:2533:U:H2'	54:01:2534:A:O4'	2.08	0.53
9:12:115:GLY:HA2	9:12:118:MET:HE3	1.91	0.53
14:17:15:ARG:O	14:17:19:GLN:HG2	2.08	0.53
17:20:9:GLY:O	54:01:996:A:H1'	2.08	0.53
18:21:4:ILE:HG22	18:21:106:VAL:HG22	1.91	0.53
31:34:1:MET:HE2	31:34:36:ARG:N	2.24	0.53
41:K:109:ILE:HG21	51:U:16:ARG:NH1	2.24	0.53
45:O:63:ARG:HH12	45:O:87:ARG:HH22	1.56	0.53
49:S:30:LEU:H	49:S:48:ILE:HG22	1.74	0.53
54:01:517:C:H2'	54:01:518:G:O4'	2.09	0.53
54:01:1038:G:H2'	54:01:1039:A:C8	2.43	0.53
54:01:1047:G:H2'	54:01:1110:G:C2	2.44	0.53
54:01:2480:C:H2'	54:01:2481:G:O4'	2.09	0.53
59:Z:243:GLU:HG3	59:Z:251:GLN:C	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:19:49:ARG:NH1	16:19:49:ARG:HB3	2.23	0.53
37:G:27:ASN:HB3	53:A:1375:A:H5'	1.91	0.53
48:R:56:ARG:HB3	48:R:60:ARG:HH12	1.74	0.53
52:03:4:LEU:HB3	52:03:9:ARG:HH21	1.74	0.53
54:01:996:A:H2'	54:01:997:G:H8	1.74	0.53
54:01:1035:U:H2'	54:01:1036:G:H8	1.74	0.53
54:01:2623:G:H2'	54:01:2624:G:H8	1.73	0.53
55:02:65:U:H3'	55:02:108:A:N6	2.24	0.53
59:Z:124:GLN:HG3	59:Z:385:ALA:HB1	1.91	0.53
59:Z:143:GLU:O	59:Z:147:GLU:HG3	2.09	0.53
59:Z:269:ARG:HD2	59:Z:272:GLU:HG2	1.89	0.53
20:23:4:ILE:HD12	20:23:4:ILE:N	2.23	0.52
31:34:19:ARG:HB2	31:34:24:ARG:HD2	1.91	0.52
35:E:149:PRO:HA	35:E:152:VAL:HG22	1.91	0.52
41:K:83:VAL:C	41:K:84:MET:HE2	2.34	0.52
53:A:235:C:H2'	53:A:236:A:H8	1.74	0.52
53:A:797:C:H2'	53:A:798:U:H6	1.74	0.52
53:A:1379:G:O2'	53:A:1380:U:H5'	2.10	0.52
54:01:1683:U:H2'	54:01:1684:G:H8	1.74	0.52
54:01:1709:U:H2'	54:01:1710:G:C8	2.44	0.52
54:01:1830:C:H2'	54:01:1831:G:H8	1.74	0.52
58:Y:25:C:C2'	58:Y:26:A:H5''	2.39	0.52
59:Z:79:VAL:HG12	59:Z:81:CYS:SG	2.49	0.52
9:12:113:PRO:HD2	54:01:558:U:P	2.48	0.52
24:27:32:ALA:HB2	24:27:37:LEU:HD23	1.92	0.52
33:C:81:GLU:OE2	33:C:85:LYS:HB2	2.09	0.52
37:G:19:SER:O	37:G:22:LEU:HG	2.09	0.52
40:J:81:GLU:HA	40:J:84:VAL:HG12	1.91	0.52
41:K:108:ASN:HB3	51:U:6:ARG:HG2	1.90	0.52
53:A:225:C:C3'	53:A:226:G:H5''	2.39	0.52
53:A:381:C:H2'	53:A:382:A:O4'	2.09	0.52
54:01:742:A:H2'	54:01:743:A:H8	1.74	0.52
54:01:2339:C:H2'	54:01:2340:A:H8	1.73	0.52
54:01:2632:A:H2'	54:01:2633:G:H8	1.75	0.52
56:X:28:C:H2'	56:X:29:G:C8	2.44	0.52
59:Z:309:TYR:CE2	59:Z:311:LEU:HA	2.44	0.52
1:04:260:LYS:HA	1:04:263:ASP:OD2	2.09	0.52
2:05:4:LEU:HD21	2:05:96:ILE:HG22	1.91	0.52
12:15:69:PRO:HA	12:15:94:ALA:HB2	1.90	0.52
29:32:3:ARG:HD3	29:32:4:THR:H	1.74	0.52
32:B:18:GLN:O	32:B:19:THR:CB	2.55	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B:60:ALA:CB	32:B:223:GLY:HA3	2.39	0.52
40:J:17:LEU:HG	40:J:20:GLN:NE2	2.21	0.52
49:S:19:GLU:O	49:S:23:GLU:HG2	2.10	0.52
52:03:180:PHE:HB2	52:03:185:LEU:HD21	1.92	0.52
53:A:560:A:H4'	53:A:561:U:H5'	1.90	0.52
2:05:8:LYS:HB2	2:05:201:LEU:CD1	2.39	0.52
10:13:114:LYS:HE3	10:13:118:LEU:HD11	1.91	0.52
16:19:5:ARG:NH2	16:19:5:ARG:HG3	2.24	0.52
22:25:36:GLN:HE21	22:25:53:HIS:HB3	1.73	0.52
29:32:4:THR:HG22	54:01:687:C:H1'	1.92	0.52
30:33:3:ILE:HG21	30:33:62:PRO:HG2	1.92	0.52
53:A:225:C:C2'	53:A:226:G:H5''	2.38	0.52
53:A:312:C:H2'	53:A:313:A:C8	2.44	0.52
54:01:634:C:H2'	54:01:635:C:C6	2.44	0.52
54:01:2106:U:H2'	54:01:2107:G:C8	2.42	0.52
54:01:2554:U:H2'	54:01:2555:U:C6	2.44	0.52
56:W:20:U:H3'	56:W:21:A:H5'	1.90	0.52
59:Z:245:VAL:HA	59:Z:250:THR:HG22	1.91	0.52
16:19:50:ARG:HG2	54:01:1156:A:C8	2.45	0.52
19:22:13:ALA:HB1	19:22:14:PRO:HD2	1.92	0.52
40:J:57:VAL:O	40:J:58:ASN:CB	2.57	0.52
44:N:63:CYS:HB3	44:N:67:GLY:H	1.75	0.52
51:U:33:ARG:O	51:U:34:ARG:HB2	2.08	0.52
58:Y:45:U:H3'	58:Y:46:G:H5''	1.91	0.52
4:07:90:LEU:HD12	4:07:90:LEU:O	2.10	0.52
12:15:8:LYS:HD2	54:01:869:G:H1'	1.90	0.52
27:30:39:ARG:CZ	54:01:2884:U:H3	2.23	0.52
32:B:83:ALA:HB3	32:B:90:PHE:HB3	1.91	0.52
33:C:19:SER:HB3	33:C:21:TRP:HE1	1.73	0.52
34:D:27:ILE:HD12	34:D:27:ILE:N	2.24	0.52
35:E:133:ILE:O	35:E:136:VAL:HG12	2.08	0.52
53:A:1527:U:H2'	53:A:1528:U:C6	2.44	0.52
54:01:1139:G:O2'	54:01:1140:C:H5'	2.09	0.52
54:01:2774:C:H2'	54:01:2775:G:O4'	2.09	0.52
54:01:2811:G:H2'	54:01:2812:G:C8	2.43	0.52
55:02:41:G:H2'	55:02:41:G:N3	2.25	0.52
59:Z:142:ASP:OD2	59:Z:145:LEU:HB2	2.09	0.52
3:06:192:ALA:O	3:06:196:VAL:HG23	2.09	0.52
7:10:27:VAL:CG1	7:10:83:ALA:HB3	2.38	0.52
12:15:74:THR:HG21	12:15:86:LYS:HE2	1.90	0.52
21:24:80:HIS:CE1	21:24:81:PRO:HD2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:33:61:LEU:HD12	30:33:61:LEU:O	2.10	0.52
36:F:17:GLN:O	36:F:21:MET:HG3	2.10	0.52
40:J:52:LEU:HB2	44:N:80:ARG:HD2	1.91	0.52
44:N:45:LEU:HG	49:S:12:LEU:HD21	1.91	0.52
53:A:212:G:H2'	53:A:213:G:C8	2.42	0.52
54:01:528:A:C2	54:01:2042:A:H2'	2.45	0.52
54:01:1857:G:H2'	54:01:1884:G:H22	1.74	0.52
54:01:2388:A:H5'	54:01:2389:G:OP2	2.10	0.52
59:Z:330:PHE:CE2	59:Z:360:VAL:HG11	2.44	0.52
5:08:23:ILE:HD11	5:08:42:VAL:HG11	1.91	0.52
10:13:7:MET:HE1	10:13:44:LYS:HG3	1.90	0.52
10:13:71:ARG:HH12	15:18:71:ARG:NH2	2.05	0.52
38:H:106:SER:HA	53:A:642:A:C8	2.45	0.52
50:T:34:VAL:HG21	50:T:78:LEU:HD21	1.91	0.52
53:A:1409:C:H2'	53:A:1410:A:C8	2.45	0.52
1:04:17:LYS:NZ	1:04:17:LYS:HB2	2.25	0.52
5:08:51:PHE:CE2	5:08:68:ARG:HA	2.45	0.52
9:12:81:ILE:HG23	9:12:82:GLY:H	1.74	0.52
33:C:175:HIS:ND1	53:A:1108:G:H5'	2.25	0.52
35:E:148:SER:HB2	35:E:149:PRO:HD2	1.92	0.52
38:H:77:VAL:HG23	38:H:126:CYS:HA	1.92	0.52
50:T:8:LYS:HE3	50:T:12:GLN:OE1	2.09	0.52
51:U:9:GLU:CG	51:U:10:PRO:HD3	2.06	0.52
52:03:53:ARG:HB3	56:X:62:C:H4'	1.90	0.52
53:A:52:C:H2'	53:A:53:A:C8	2.45	0.52
53:A:78:A:H2'	53:A:79:G:O4'	2.10	0.52
53:A:802:A:H2'	53:A:803:G:O4'	2.10	0.52
54:01:176:A:O2'	54:01:177:G:H5'	2.10	0.52
54:01:441:U:H2'	54:01:442:G:C8	2.45	0.52
54:01:662:G:H2'	54:01:663:G:H8	1.75	0.52
54:01:1056:G:H4'	54:01:1086:A:C8	2.43	0.52
54:01:1357:C:H2'	54:01:1358:G:O4'	2.10	0.52
54:01:1869:G:H3'	54:01:1870:C:H5''	1.92	0.52
54:01:2297:A:N1	54:01:2321:U:H5	2.07	0.52
58:Y:54:U:OP1	59:Z:320:THR:HG21	2.10	0.52
59:Z:300:PRO:CG	59:Z:365:PRO:HB2	2.40	0.52
2:05:34:VAL:HG22	2:05:50:VAL:HG12	1.92	0.52
3:06:76:PRO:HA	3:06:82:GLY:HA2	1.92	0.52
25:28:9:THR:HG22	25:28:53:MET:C	2.35	0.52
53:A:1399:C:H4'	53:A:1400:C:O5'	2.09	0.52
54:01:1297:C:OP1	54:01:2710:C:H4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2130:U:H4'	54:01:2134:A:H4'	1.92	0.52
54:01:2710:C:H2'	54:01:2711:A:C8	2.45	0.52
11:14:93:ASN:O	11:14:94:THR:HB	2.10	0.51
30:33:63:TYR:CE2	54:01:242:G:H5''	2.45	0.51
33:C:133:MET:HE3	33:C:167:TYR:HB2	1.92	0.51
36:F:3:HIS:HB2	36:F:92:THR:HA	1.92	0.51
52:03:184:LYS:HA	52:03:187:GLU:OE1	2.10	0.51
53:A:304:U:H2'	53:A:305:G:H8	1.73	0.51
53:A:868:C:H2'	53:A:869:G:O4'	2.10	0.51
53:A:1414:U:H2'	53:A:1415:G:C8	2.41	0.51
54:01:749:A:H4'	54:01:1271:G:N3	2.25	0.51
54:01:817:C:H2'	54:01:818:G:O4'	2.09	0.51
54:01:833:A:H2'	54:01:834:G:C8	2.45	0.51
54:01:848:C:H2'	54:01:849:A:C8	2.45	0.51
54:01:1268:A:H2'	54:01:1269:A:O4'	2.10	0.51
54:01:1796:U:H2'	54:01:1797:G:C8	2.45	0.51
54:01:2514:U:H2'	54:01:2515:C:H6	1.75	0.51
56:X:69:C:C2'	56:X:70:G:H5'	2.38	0.51
56:W:76:A:H3'	60:W:101:FME:C	2.39	0.51
4:07:22:ASN:HB2	4:07:26:GLN:NE2	2.24	0.51
15:18:52:ARG:HH22	54:01:2720:U:H5''	1.74	0.51
32:B:76:SER:HA	32:B:79:VAL:HG23	1.91	0.51
33:C:72:PRO:O	33:C:76:ILE:HG12	2.11	0.51
52:03:51:ASP:OD1	52:03:53:ARG:HB2	2.10	0.51
52:03:56:ASP:OD1	52:03:57:GLN:HG2	2.11	0.51
53:A:110:C:H2'	53:A:111:G:O4'	2.10	0.51
53:A:1256:A:H1'	53:A:1258:G:C4	2.45	0.51
53:A:1354:U:H2'	53:A:1355:G:H8	1.74	0.51
54:01:1098:A:H2'	54:01:1099:G:H5'	1.91	0.51
58:Y:10:G:C2	58:Y:26:A:H1'	2.45	0.51
52:03:30:LEU:HD12	52:03:31:LYS:N	2.26	0.51
53:A:1198:G:H5'	53:A:1198:G:H8	1.76	0.51
54:01:71:A:H5'	54:01:71:A:N3	2.25	0.51
59:Z:91:MET:HE3	59:Z:118:HIS:CD2	2.45	0.51
59:Z:306:SER:HB3	59:Z:358:MET:HE3	1.91	0.51
17:20:33:VAL:HG23	17:20:61:ALA:HB3	1.91	0.51
32:B:183:PHE:HA	32:B:195:VAL:HG13	1.91	0.51
35:E:49:TYR:HE1	35:E:133:ILE:HG12	1.75	0.51
53:A:434:U:H2'	53:A:435:A:C8	2.44	0.51
54:01:2801:G:H2'	54:01:2802:G:H8	1.75	0.51
59:Z:140:VAL:HG23	59:Z:142:ASP:N	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:324:LYS:HE3	59:Z:342:GLU:HA	1.92	0.51
1:04:224:MET:SD	1:04:229:HIS:HB2	2.51	0.51
52:03:27:ILE:HA	52:03:30:LEU:HD21	1.92	0.51
52:03:214:ILE:HD12	52:03:222:VAL:HB	1.92	0.51
53:A:309:A:H2'	53:A:310:G:H8	1.75	0.51
53:A:1506:U:O2'	53:A:1507:A:H5'	2.10	0.51
54:01:2646:C:H2'	54:01:2647:U:O4'	2.11	0.51
55:02:28:C:H2'	55:02:29:A:C8	2.45	0.51
56:W:21:A:H61	56:W:46:G:H2'	1.75	0.51
59:Z:309:TYR:CE2	59:Z:311:LEU:HD13	2.36	0.51
1:04:153:LEU:HD11	1:04:181:ARG:HH21	1.75	0.51
3:06:34:ALA:CA	3:06:94:GLN:HE21	2.17	0.51
4:07:105:ILE:C	4:07:108:PRO:HD2	2.36	0.51
16:19:24:TYR:CE1	54:01:17:G:H4'	2.46	0.51
25:28:40:THR:HG23	25:28:43:ILE:H	1.76	0.51
32:B:46:VAL:HB	32:B:47:PRO:HD3	1.93	0.51
38:H:28:SER:HB2	38:H:58:LEU:HB2	1.91	0.51
47:Q:6:THR:C	47:Q:7:LEU:HD12	2.35	0.51
53:A:514:C:H2'	53:A:515:G:H8	1.76	0.51
54:01:182:A:O2'	54:01:183:C:H5'	2.11	0.51
54:01:969:G:H2'	54:01:970:U:C6	2.45	0.51
54:01:1777:U:O2'	54:01:1778:U:H5'	2.11	0.51
59:Z:16:THR:OG1	59:Z:78:HIS:NE2	2.44	0.51
59:Z:206:ILE:HB	59:Z:235:ILE:HG23	1.92	0.51
14:17:29:HIS:CD2	55:02:7:G:H5''	2.46	0.51
32:B:45:THR:HG22	32:B:49:PHE:CD1	2.46	0.51
36:F:51:ILE:C	36:F:53:LYS:H	2.17	0.51
40:J:27:GLU:OE2	40:J:31:ARG:HD2	2.11	0.51
53:A:880:C:H2'	53:A:881:G:H8	1.76	0.51
54:01:2570:G:H2'	54:01:2571:U:O4'	2.11	0.51
54:01:2884:U:O2	54:01:2884:U:H3'	2.11	0.51
58:Y:1:G:H1'	59:Z:63:ASN:HD21	1.76	0.51
59:Z:237:LYS:HE3	59:Z:267:GLU:OE2	2.10	0.51
6:09:76:GLU:O	6:09:142:VAL:HG13	2.10	0.51
11:14:3:LEU:HD23	54:01:1203:U:H5'	1.93	0.51
35:E:108:GLY:O	35:E:109:ALA:HB3	2.11	0.51
39:I:49:GLN:N	39:I:50:PRO:HD2	2.25	0.51
53:A:17:U:H2'	53:A:18:C:C6	2.46	0.51
54:01:2684:U:H2'	54:01:2685:G:O4'	2.11	0.51
55:02:95:U:H2'	55:02:96:G:H8	1.76	0.51
56:W:62:C:H2'	56:W:63:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:49:ILE:HG23	59:Z:65:SER:CB	2.39	0.51
59:Z:147:GLU:HA	59:Z:171:ARG:NH2	2.26	0.51
4:07:114:ARG:HG3	4:07:177:ARG:NE	2.25	0.51
6:09:125:THR:HG21	6:09:148:ALA:HB2	1.93	0.51
40:J:83:THR:O	40:J:87:LEU:HG	2.10	0.51
49:S:38:THR:HG22	49:S:69:LYS:HG2	1.91	0.51
52:03:44:VAL:HG11	52:03:192:LEU:HD23	1.92	0.51
53:A:29:U:O2'	53:A:30:U:H5'	2.11	0.51
53:A:219:U:H2'	53:A:220:G:C8	2.46	0.51
53:A:224:U:H2'	53:A:225:C:C6	2.46	0.51
53:A:1258:G:H2'	53:A:1259:C:C6	2.45	0.51
54:01:2487:G:H2'	54:01:2488:G:C8	2.46	0.51
59:Z:157:LEU:HB3	59:Z:164:GLY:HA3	1.93	0.51
59:Z:324:LYS:HE3	59:Z:343:LEU:N	2.25	0.51
3:06:199:MET:HE2	3:06:200:LEU:HD12	1.92	0.51
16:19:54:ARG:O	16:19:58:GLN:HG2	2.11	0.51
21:24:20:LEU:HD11	21:24:41:GLU:HG3	1.92	0.51
52:03:191:ALA:O	52:03:194:VAL:HB	2.10	0.51
53:A:824:G:H2'	53:A:825:A:H8	1.76	0.51
53:A:1227:A:H2'	53:A:1228:C:H5'	1.92	0.51
54:01:807:U:H2'	54:01:808:G:C8	2.46	0.51
54:01:1370:C:H2'	54:01:1371:G:O4'	2.11	0.51
54:01:2795:C:H2'	54:01:2796:U:O4'	2.11	0.51
54:01:2818:U:H2'	54:01:2819:G:C8	2.46	0.51
54:01:2848:G:O2'	54:01:2849:U:H5'	2.11	0.51
59:Z:27:LEU:HD12	59:Z:28:THR:N	2.25	0.51
59:Z:287:GLU:CG	59:Z:290:GLN:HB2	2.40	0.51
3:06:131:THR:HB	3:06:164:LEU:HD11	1.94	0.50
7:10:74:ASP:HA	7:10:77:VAL:HG23	1.92	0.50
15:18:3:ILE:N	15:18:3:ILE:HD12	2.26	0.50
34:D:56:GLU:HG2	34:D:198:LEU:HB2	1.93	0.50
37:G:111:GLY:HA2	37:G:118:ARG:HD3	1.93	0.50
51:U:11:PHE:C	51:U:13:VAL:H	2.19	0.50
52:03:47:ASN:HB3	52:03:211:LYS:H	1.76	0.50
53:A:726:C:H2'	53:A:727:G:C8	2.46	0.50
54:01:74:A:H4'	54:01:75:G:O5'	2.11	0.50
54:01:579:G:H4'	54:01:2018:G:H5''	1.92	0.50
54:01:1837:C:H2'	54:01:1899:A:N6	2.26	0.50
54:01:1856:U:H2'	54:01:1857:G:O4'	2.11	0.50
56:X:5:G:H2'	56:X:6:G:C8	2.46	0.50
4:07:31:GLU:H	4:07:157:THR:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:09:77:THR:HA	6:09:142:VAL:HG13	1.93	0.50
7:10:24:SER:HB3	7:10:86:MET:SD	2.52	0.50
21:24:48:MET:CE	21:24:51:GLN:HE21	2.24	0.50
38:H:17:GLN:HG3	38:H:71:VAL:HB	1.93	0.50
43:M:10:ASP:O	43:M:11:HIS:HB2	2.11	0.50
43:M:28:ARG:HG2	43:M:62:PHE:CE2	2.46	0.50
53:A:67:C:H2'	53:A:68:G:C8	2.45	0.50
53:A:80:A:N6	53:A:86:G:H21	2.08	0.50
55:02:13:G:O2'	55:02:15:A:H2'	2.11	0.50
59:Z:137:CYS:HB3	59:Z:184:TRP:CZ3	2.47	0.50
5:08:42:VAL:HG23	5:08:50:THR:O	2.12	0.50
7:10:23:LEU:HD22	7:10:118:ILE:HG21	1.92	0.50
23:26:53:LYS:O	23:26:57:VAL:HG23	2.11	0.50
25:28:35:VAL:HG22	25:28:36:GLU:N	2.26	0.50
25:28:40:THR:OG1	25:28:41:PRO:HD2	2.11	0.50
47:Q:58:VAL:HG21	47:Q:74:LEU:HD11	1.93	0.50
53:A:744:C:H2'	53:A:745:G:C8	2.47	0.50
53:A:1228:C:H2'	53:A:1229:A:H8	1.76	0.50
53:A:1402:C:H2'	53:A:1403:C:O4'	2.10	0.50
54:01:655:A:H4'	54:01:656:G:H5'	1.93	0.50
2:05:184:ARG:HE	15:18:6:GLN:NE2	2.09	0.50
4:07:35:LEU:HD11	4:07:98:PHE:CE2	2.46	0.50
4:07:114:ARG:HH11	43:M:70:ARG:CZ	2.25	0.50
7:10:62:ARG:HG3	54:01:1046:A:O2'	2.12	0.50
11:14:20:GLY:HA2	11:14:28:GLY:HA2	1.92	0.50
15:18:92:ARG:HD3	54:01:1753:G:H5''	1.93	0.50
29:32:12:ARG:HH11	29:32:44:VAL:HG21	1.76	0.50
34:D:205:LYS:HB3	53:A:8:A:C5	2.46	0.50
37:G:110:ARG:HH22	37:G:121:ASN:HB3	1.76	0.50
45:O:55:LEU:O	45:O:59:VAL:HG23	2.11	0.50
54:01:310:A:H2'	54:01:311:A:H5''	1.91	0.50
54:01:676:A:H62	54:01:802:A:H61	1.60	0.50
54:01:720:U:H2'	54:01:721:A:C8	2.46	0.50
54:01:2176:A:H2'	54:01:2177:C:C6	2.47	0.50
55:02:29:A:H2'	55:02:30:C:O4'	2.12	0.50
56:X:21:A:N6	56:X:46:G:H2'	2.26	0.50
59:Z:206:ILE:HB	59:Z:235:ILE:CG2	2.42	0.50
59:Z:312:SER:HB2	59:Z:315:GLU:HG3	1.93	0.50
5:08:138:GLN:NE2	54:01:2746:U:H1'	2.22	0.50
16:19:5:ARG:HG3	16:19:5:ARG:HH21	1.76	0.50
16:19:93:ILE:HD12	17:20:13:ARG:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:T:42:ASP:HB3	50:T:45:ALA:HB3	1.93	0.50
52:03:11:ILE:HG22	52:03:220:ALA:HB2	1.94	0.50
52:03:27:ILE:O	52:03:31:LYS:HG3	2.11	0.50
52:03:221:GLY:HA3	54:01:2176:A:H5''	1.93	0.50
53:A:216:U:H2'	53:A:217:C:C6	2.46	0.50
53:A:884:U:H4'	53:A:885:G:H5''	1.93	0.50
54:01:2088:A:H2'	54:01:2089:C:C6	2.47	0.50
55:02:70:C:H2'	55:02:71:C:H6	1.77	0.50
59:Z:237:LYS:HB3	59:Z:267:GLU:CD	2.37	0.50
59:Z:269:ARG:CZ	59:Z:272:GLU:HG2	2.41	0.50
4:07:72:SER:OG	4:07:79:ARG:HA	2.10	0.50
7:10:18:VAL:HG12	7:10:70:GLU:HB2	1.93	0.50
10:13:41:ILE:C	10:13:41:ILE:HD12	2.37	0.50
16:19:93:ILE:O	16:19:97:ILE:HG13	2.12	0.50
25:28:50:VAL:HB	25:28:53:MET:HG2	1.94	0.50
35:E:39:GLY:HA3	35:E:45:VAL:HG12	1.93	0.50
39:I:26:LYS:C	39:I:27:ILE:HD12	2.36	0.50
44:N:5:MET:HE3	44:N:62:ARG:HH21	1.77	0.50
46:P:33:ILE:N	46:P:33:ILE:HD12	2.26	0.50
53:A:950:U:H2'	53:A:951:G:H8	1.76	0.50
54:01:546:U:H2'	54:01:547:A:O4'	2.10	0.50
54:01:1548:A:H2'	54:01:1549:A:C8	2.46	0.50
54:01:2487:G:H2'	54:01:2488:G:H8	1.77	0.50
54:01:2705:A:H2'	54:01:2706:A:O4'	2.11	0.50
59:Z:129:TYR:CD2	59:Z:199:ILE:HG23	2.46	0.50
3:06:149:ILE:CG2	3:06:188:MET:HG2	2.41	0.50
22:25:38:GLY:HA2	54:01:2330:G:H21	1.77	0.50
37:G:62:GLU:O	37:G:66:GLU:HG2	2.12	0.50
40:J:7:ARG:H	40:J:101:SER:HB2	1.77	0.50
53:A:1014:A:H2'	53:A:1015:G:O4'	2.12	0.50
54:01:172:A:H2'	54:01:173:A:C8	2.46	0.50
54:01:582:A:H2'	54:01:583:G:C8	2.47	0.50
59:Z:30:ALA:O	59:Z:34:VAL:HG23	2.11	0.50
59:Z:170:VAL:HG13	59:Z:194:PHE:HE2	1.76	0.50
7:10:81:LEU:HD12	54:01:1107:G:H1'	1.92	0.50
13:16:47:VAL:C	13:16:50:PRO:HD2	2.36	0.50
34:D:36:ALA:N	34:D:37:PRO:HD3	2.27	0.50
34:D:100:VAL:O	34:D:104:MET:HG2	2.12	0.50
36:F:18:VAL:O	36:F:22:ILE:HG13	2.12	0.50
39:I:43:ALA:O	39:I:46:VAL:HG22	2.12	0.50
52:03:62:ALA:C	52:03:160:GLN:HE22	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:69:THR:HG23	52:03:159:GLY:C	2.37	0.50
53:A:382:A:H2'	53:A:383:A:C8	2.47	0.50
53:A:407:U:H2'	53:A:408:A:C8	2.46	0.50
53:A:513:C:H2'	53:A:514:C:H6	1.74	0.50
53:A:613:C:H2'	53:A:614:C:C6	2.47	0.50
54:01:644:A:H2'	54:01:645:C:C4'	2.42	0.50
54:01:2450:A:OP1	54:01:2497:A:H2'	2.12	0.50
54:01:2810:A:H2'	54:01:2811:G:O4'	2.12	0.50
57:V:19:U:H2'	57:V:20:U:C6	2.47	0.50
59:Z:243:GLU:HG2	59:Z:245:VAL:CG2	2.42	0.50
7:10:59:LEU:HB2	7:10:62:ARG:CB	2.42	0.50
27:30:39:ARG:NH1	54:01:2884:U:H3	2.10	0.50
32:B:73:ARG:HH22	32:B:94:ARG:NH2	2.05	0.50
33:C:156:LEU:HD12	33:C:156:LEU:O	2.11	0.50
34:D:187:ARG:HD2	34:D:190:LEU:HD11	1.94	0.50
35:E:23:THR:HA	35:E:28:ARG:HA	1.94	0.50
52:03:175:ILE:HB	52:03:188:ASN:HB3	1.93	0.50
54:01:2185:U:H2'	54:01:2186:G:C8	2.47	0.50
54:01:2248:C:H2'	54:01:2249:U:H5'	1.93	0.50
58:Y:37:A:H2'	58:Y:38:A:O4'	2.12	0.50
1:04:123:ILE:HG21	36:F:80:PHE:CZ	2.47	0.49
10:13:19:VAL:HG12	10:13:43:ILE:HA	1.94	0.49
17:20:76:LYS:HB2	17:20:85:LYS:HB3	1.93	0.49
25:28:40:THR:CG2	25:28:43:ILE:HG12	2.42	0.49
33:C:111:ASP:O	33:C:115:VAL:HG23	2.11	0.49
40:J:84:VAL:HA	40:J:87:LEU:HD12	1.94	0.49
52:03:54:LYS:HB2	56:X:62:C:O2'	2.12	0.49
53:A:1148:U:H2'	53:A:1149:C:O4'	2.11	0.49
53:A:1458:G:H2'	53:A:1459:G:C8	2.47	0.49
54:01:886:A:H2'	54:01:886:A:N3	2.26	0.49
54:01:971:G:H2'	54:01:972:A:O4'	2.12	0.49
54:01:2556:C:H2'	54:01:2557:G:O4'	2.12	0.49
56:X:59:A:H2'	56:X:60:U:O4'	2.12	0.49
56:W:17:C:H5'	56:W:61:C:OP1	2.11	0.49
1:04:83:ASP:HB3	1:04:86:ARG:HB2	1.94	0.49
2:05:56:LYS:HB2	2:05:56:LYS:NZ	2.27	0.49
11:14:13:LYS:HE2	54:01:1245:G:OP1	2.12	0.49
34:D:10:LEU:HD13	34:D:62:ARG:HG3	1.94	0.49
35:E:105:ILE:HD11	35:E:123:LEU:HD22	1.93	0.49
53:A:916:U:H2'	53:A:917:G:H8	1.77	0.49
54:01:979:A:H2'	54:01:982:C:H42	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1447:C:H2'	54:01:1448:G:H8	1.77	0.49
54:01:1506:U:H2'	54:01:1507:C:C6	2.47	0.49
54:01:2156:G:H2'	54:01:2157:G:H5'	1.93	0.49
54:01:2158:A:H4'	54:01:2159:G:O4'	2.12	0.49
54:01:2286:G:H5'	54:01:2287:A:C1'	2.42	0.49
54:01:2286:G:H4'	54:01:2287:A:O4'	2.12	0.49
1:04:5:CYS:SG	1:04:17:LYS:HE3	2.52	0.49
3:06:149:ILE:HG23	3:06:188:MET:HG2	1.94	0.49
17:20:16:GLU:HB2	17:20:101:ILE:HG13	1.94	0.49
33:C:38:VAL:O	33:C:42:LEU:HD13	2.12	0.49
34:D:149:LYS:HZ2	34:D:177:MET:HB2	1.75	0.49
34:D:158:LEU:HD23	34:D:158:LEU:O	2.12	0.49
46:P:36:VAL:HG13	46:P:36:VAL:O	2.12	0.49
53:A:601:G:H2'	53:A:602:A:C8	2.47	0.49
53:A:1256:A:O2'	53:A:1257:A:H5''	2.12	0.49
54:01:2584:U:H2'	54:01:2585:U:H2'	1.94	0.49
59:Z:176:LYS:NZ	59:Z:184:TRP:HE1	2.10	0.49
3:06:117:ARG:HH12	11:14:2:ARG:HG2	1.77	0.49
5:08:82:PHE:CE2	5:08:137:LYS:HB2	2.47	0.49
9:12:84:ILE:HG23	9:12:84:ILE:O	2.13	0.49
13:16:45:ARG:HG2	13:16:95:THR:HG21	1.94	0.49
18:21:8:ARG:HA	18:21:102:HIS:ND1	2.27	0.49
52:03:29:LEU:HD12	52:03:30:LEU:N	2.27	0.49
53:A:1082:A:H2'	53:A:1083:U:O4'	2.13	0.49
54:01:329:G:O4'	54:01:477:A:H1'	2.13	0.49
54:01:372:G:H2'	54:01:400:G:O6	2.13	0.49
54:01:873:C:H2'	54:01:874:G:C8	2.47	0.49
54:01:1810:A:H2'	54:01:1811:G:O4'	2.12	0.49
54:01:2186:G:H2'	54:01:2187:U:O4'	2.11	0.49
54:01:2801:G:H2'	54:01:2802:G:C8	2.48	0.49
54:01:2881:U:H2'	54:01:2882:A:C8	2.48	0.49
59:Z:47:ASP:HA	59:Z:56:LYS:HE3	1.94	0.49
3:06:148:ILE:HD13	3:06:187:VAL:HG11	1.93	0.49
12:15:30:SER:O	12:15:132:THR:HG23	2.12	0.49
27:30:24:VAL:HG13	27:30:25:THR:N	2.27	0.49
29:32:11:LYS:HE3	54:01:686:U:H5''	1.93	0.49
33:C:39:ARG:HH21	33:C:56:ILE:HG13	1.77	0.49
38:H:72:GLU:HB3	38:H:129:ALA:HB3	1.93	0.49
46:P:5:ARG:HD2	53:A:376:G:H4'	1.94	0.49
47:Q:59:GLU:HB2	47:Q:76:ARG:H	1.77	0.49
52:03:67:HIS:HB2	52:03:188:ASN:OD1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:200:LYS:HD3	52:03:208:TYR:CD2	2.48	0.49
53:A:501:C:H2'	53:A:502:A:C8	2.47	0.49
53:A:533:A:O2'	53:A:534:U:H5''	2.12	0.49
53:A:1228:C:H2'	53:A:1229:A:C8	2.48	0.49
54:01:2270:A:H2'	54:01:2271:G:O4'	2.13	0.49
54:01:2837:A:H2'	54:01:2838:G:H8	1.77	0.49
56:W:38:A:H2'	56:W:39:C:O4'	2.12	0.49
59:Z:144:GLU:HA	59:Z:147:GLU:CG	2.42	0.49
59:Z:316:GLY:O	59:Z:381:ARG:HG3	2.12	0.49
7:10:13:ALA:O	7:10:17:GLU:HG3	2.13	0.49
10:13:51:LYS:HD2	10:13:95:ILE:HG22	1.95	0.49
32:B:153:MET:CE	32:B:157:PRO:HG3	2.43	0.49
37:G:2:ARG:HB3	53:A:933:G:OP2	2.12	0.49
41:K:86:LYS:HB2	41:K:112:VAL:HG23	1.95	0.49
44:N:3:GLN:HG3	53:A:1047:G:H5''	1.94	0.49
51:U:33:ARG:O	51:U:34:ARG:CB	2.61	0.49
53:A:56:U:H2'	53:A:57:G:H8	1.78	0.49
53:A:129:A:H1'	53:A:130:A:C8	2.48	0.49
54:01:233:A:H2'	54:01:234:U:O4'	2.13	0.49
54:01:437:U:H2'	54:01:438:G:C8	2.47	0.49
54:01:540:C:H2'	54:01:541:A:H8	1.78	0.49
54:01:2141:G:N2	54:01:2151:U:H1'	2.26	0.49
2:05:43:ASP:HB3	2:05:45:TYR:CE1	2.48	0.49
16:19:2:ARG:HB2	54:01:1248:G:C5	2.48	0.49
20:23:31:GLY:O	20:23:66:VAL:HG23	2.12	0.49
20:23:83:GLY:HA3	20:23:96:LYS:HE3	1.94	0.49
37:G:38:ALA:O	37:G:42:VAL:HG23	2.13	0.49
51:U:65:ARG:NE	51:U:65:ARG:HA	2.28	0.49
53:A:460:A:H2'	53:A:461:A:H8	1.77	0.49
53:A:1372:U:H2'	53:A:1373:G:O4'	2.12	0.49
54:01:598:U:H2'	54:01:599:A:H8	1.78	0.49
54:01:1611:C:H5'	54:01:1611:C:H6	1.75	0.49
59:Z:98:MET:O	59:Z:127:VAL:HG22	2.12	0.49
59:Z:175:LEU:O	59:Z:179:GLU:HG3	2.12	0.49
4:07:7:TYR:HA	4:07:11:VAL:CG2	2.43	0.49
8:11:55:PRO:HG3	54:01:1060:U:OP2	2.12	0.49
23:26:11:PRO:HG3	23:26:30:PRO:HD2	1.94	0.49
33:C:71:ARG:O	33:C:75:VAL:HG23	2.12	0.49
33:C:78:LYS:HB2	33:C:78:LYS:NZ	2.28	0.49
36:F:68:GLN:HA	36:F:71:ILE:HG22	1.94	0.49
39:I:5:TYR:HB2	39:I:20:ILE:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:67:C:H2'	53:A:68:G:H8	1.77	0.49
54:01:2498:C:O2'	54:01:2499:C:H5'	2.12	0.49
58:Y:49:C:H2'	58:Y:50:U:C6	2.47	0.49
59:Z:17:ILE:C	59:Z:17:ILE:HD12	2.37	0.49
2:05:149:ASN:CG	2:05:150:GLN:H	2.21	0.49
7:10:48:ALA:HB3	7:10:51:TYR:CE1	2.47	0.49
19:22:80:TRP:CZ3	19:22:82:LYS:HB3	2.48	0.49
47:Q:28:VAL:HG22	47:Q:29:LYS:N	2.28	0.49
51:U:29:ALA:HA	51:U:32:ARG:HD3	1.94	0.49
51:U:64:ALA:HA	51:U:66:ARG:HH22	1.78	0.49
53:A:286:C:H2'	53:A:287:U:C6	2.48	0.49
53:A:604:G:H2'	53:A:605:U:O4'	2.13	0.49
53:A:1007:U:H2'	53:A:1008:U:C6	2.48	0.49
54:01:1443:U:H2'	54:01:1444:G:C8	2.48	0.49
54:01:1447:C:H2'	54:01:1448:G:C8	2.47	0.49
54:01:1866:A:H2'	54:01:1867:G:O4'	2.12	0.49
54:01:2163:A:H2'	54:01:2163:A:N3	2.27	0.49
54:01:2231:U:H2'	54:01:2232:C:C6	2.48	0.49
54:01:2811:G:H2'	54:01:2812:G:H8	1.77	0.49
59:Z:176:LYS:HE2	59:Z:181:ASP:OD2	2.11	0.49
59:Z:304:PHE:HD2	59:Z:388:VAL:HG13	1.75	0.49
16:19:49:ARG:HB3	16:19:49:ARG:HH11	1.78	0.49
32:B:98:GLY:O	32:B:102:ASN:HB3	2.13	0.49
41:K:19:VAL:HG22	41:K:82:GLU:OE1	2.13	0.49
49:S:62:THR:H	49:S:65:MET:HE3	1.78	0.49
53:A:1456:A:H2'	53:A:1457:G:O4'	2.11	0.49
54:01:1524:G:H2'	54:01:1525:A:H8	1.78	0.49
59:Z:30:ALA:HB2	59:Z:178:LEU:HB2	1.94	0.49
59:Z:74:ARG:HH12	59:Z:201:GLU:HA	1.78	0.49
59:Z:391:VAL:C	59:Z:392:LEU:HD22	2.38	0.49
5:08:9:VAL:HA	5:08:48:THR:HA	1.94	0.48
5:08:118:ALA:O	5:08:120:ILE:N	2.46	0.48
5:08:174:LYS:HE3	54:01:2529:G:H4'	1.94	0.48
13:16:102:PHE:HE1	13:16:109:PRO:HG3	1.77	0.48
25:28:40:THR:HG22	25:28:43:ILE:HG12	1.94	0.48
35:E:47:PHE:CZ	35:E:137:ARG:HG2	2.47	0.48
49:S:52:ASN:CG	49:S:53:GLY:H	2.21	0.48
52:03:15:VAL:HG23	52:03:21:TYR:OH	2.13	0.48
52:03:64:VAL:HG22	52:03:160:GLN:HG2	1.94	0.48
53:A:70:U:H4'	53:A:71:A:H8	1.77	0.48
53:A:505:G:P	53:A:535:A:H5'	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:694:A:H2'	53:A:695:A:O4'	2.13	0.48
53:A:946:A:H2'	53:A:947:G:C8	2.48	0.48
53:A:1004:A:H2'	53:A:1005:A:O4'	2.12	0.48
55:02:3:C:C3'	55:02:4:C:H5''	2.43	0.48
59:Z:19:HIS:NE2	59:Z:112:MET:HE2	2.28	0.48
18:21:31:GLN:O	18:21:35:ILE:HG13	2.11	0.48
41:K:92:ARG:HE	51:U:24:LYS:NZ	2.10	0.48
44:N:92:ILE:HD12	44:N:92:ILE:N	2.27	0.48
46:P:31:ARG:NH2	53:A:230:G:H5''	2.18	0.48
49:S:27:LYS:HG2	49:S:28:LYS:H	1.78	0.48
52:03:8:MET:O	52:03:12:ARG:HB2	2.12	0.48
53:A:1340:A:H2'	53:A:1341:U:O4'	2.13	0.48
1:04:235:GLU:HG2	54:01:2599:G:C8	2.47	0.48
6:09:55:GLU:HA	6:09:58:LEU:HD12	1.95	0.48
6:09:126:GLY:H	6:09:146:VAL:HB	1.79	0.48
12:15:41:LEU:HA	12:15:45:GLN:OE1	2.13	0.48
13:16:102:PHE:CE1	13:16:109:PRO:HG3	2.48	0.48
15:18:3:ILE:HD12	15:18:3:ILE:H	1.77	0.48
19:22:49:LYS:C	19:22:50:LEU:HD12	2.39	0.48
22:25:45:ALA:O	22:25:47:VAL:HG23	2.13	0.48
39:I:121:ARG:HD2	53:A:1348:U:H4'	1.95	0.48
40:J:14:ASP:HB3	40:J:17:LEU:HB3	1.94	0.48
40:J:59:LYS:HE2	40:J:62:ARG:HH21	1.78	0.48
52:03:62:ALA:HB1	52:03:160:GLN:HE22	1.77	0.48
52:03:207:VAL:HB	52:03:210:LYS:CG	2.42	0.48
53:A:253:A:H2'	53:A:254:G:C8	2.48	0.48
53:A:299:G:H2'	53:A:300:A:C8	2.48	0.48
54:01:215:G:C4'	54:01:216:A:H4'	2.44	0.48
54:01:1547:C:H2'	54:01:1548:A:H8	1.78	0.48
12:15:41:LEU:HD22	12:15:125:PRO:HD2	1.95	0.48
17:20:37:GLU:HA	17:20:53:PHE:CD1	2.48	0.48
32:B:80:LYS:HB2	32:B:92:ASN:HD22	1.78	0.48
35:E:12:GLU:HB2	35:E:63:MET:HE1	1.95	0.48
35:E:98:ALA:HB2	35:E:123:LEU:HG	1.96	0.48
36:F:66:ALA:HB1	36:F:67:PRO:CD	2.43	0.48
39:I:121:ARG:NH1	53:A:1345:U:H5''	2.29	0.48
42:L:98:ARG:HB2	42:L:116:TYR:HA	1.94	0.48
44:N:61:ASN:HB3	44:N:72:PHE:CE2	2.48	0.48
52:03:43:ASP:OD2	52:03:217:THR:HG22	2.13	0.48
52:03:46:VAL:O	52:03:171:ILE:HG22	2.14	0.48
53:A:52:C:H2'	53:A:53:A:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:265:G:H2'	53:A:267:C:H5	1.78	0.48
53:A:297:G:H4'	53:A:557:G:H4'	1.94	0.48
53:A:530:G:H3'	53:A:531:U:C5'	2.44	0.48
54:01:1316:U:H2'	54:01:1317:G:C8	2.48	0.48
59:Z:304:PHE:CE2	59:Z:306:SER:HB2	2.48	0.48
4:07:140:ILE:HG22	4:07:142:TYR:H	1.79	0.48
7:10:41:LEU:HD13	54:01:1083:U:O5'	2.12	0.48
11:14:77:ILE:N	11:14:77:ILE:HD12	2.29	0.48
23:26:56:ARG:HA	23:26:59:ASP:HB2	1.96	0.48
27:30:8:THR:HG21	54:01:2020:A:H5'	1.95	0.48
32:B:153:MET:HE1	32:B:157:PRO:HG3	1.94	0.48
38:H:116:ARG:HG3	38:H:116:ARG:HH11	1.79	0.48
39:I:70:GLY:O	39:I:74:GLN:HG3	2.13	0.48
39:I:90:ASP:O	39:I:92:SER:N	2.46	0.48
53:A:1202:U:H2'	53:A:1203:C:O4'	2.14	0.48
53:A:1406:U:H2'	53:A:1407:C:O4'	2.13	0.48
53:A:1458:G:H2'	53:A:1459:G:H8	1.78	0.48
54:01:1507:C:H2'	54:01:1508:A:O4'	2.13	0.48
54:01:2637:U:H2'	54:01:2638:G:O4'	2.12	0.48
54:01:2785:C:H2'	54:01:2786:U:H6	1.77	0.48
1:04:240:GLY:HA3	54:01:2597:G:H5''	1.95	0.48
1:04:252:LYS:HB2	1:04:252:LYS:NZ	2.29	0.48
5:08:46:ASP:O	5:08:48:THR:N	2.46	0.48
6:09:55:GLU:HA	6:09:58:LEU:HB2	1.94	0.48
21:24:79:ARG:HG3	21:24:86:LEU:HD23	1.96	0.48
28:31:47:ILE:HD12	28:31:47:ILE:N	2.28	0.48
32:B:114:LYS:HB2	32:B:114:LYS:NZ	2.29	0.48
36:F:18:VAL:HG21	36:F:58:HIS:CD2	2.48	0.48
40:J:6:ILE:HG22	40:J:8:ILE:HG13	1.94	0.48
52:03:170:ILE:HG21	54:01:2177:C:O2	2.13	0.48
54:01:364:C:H2'	54:01:365:U:C6	2.49	0.48
54:01:2898:U:H2'	54:01:2899:A:C8	2.49	0.48
59:Z:125:VAL:HG13	59:Z:127:VAL:HG23	1.95	0.48
6:09:99:ILE:O	6:09:103:VAL:HG23	2.13	0.48
12:15:2:LEU:HB3	12:15:68:PHE:CE1	2.49	0.48
17:20:6:GLN:HG2	17:20:11:GLN:HG3	1.95	0.48
38:H:12:ARG:HD3	38:H:26:MET:HB3	1.96	0.48
40:J:30:LYS:HB3	40:J:30:LYS:NZ	2.29	0.48
43:M:47:LEU:CD2	43:M:51:GLN:HB2	2.41	0.48
52:03:50:ILE:CD1	52:03:52:ALA:HB2	2.44	0.48
52:03:54:LYS:HE3	52:03:56:ASP:CG	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:77:A:H2'	53:A:78:A:H8	1.79	0.48
53:A:195:A:H2'	53:A:196:A:C8	2.48	0.48
53:A:810:C:H2'	53:A:811:C:O4'	2.13	0.48
54:01:119:A:H4'	54:01:120:U:H5'	1.95	0.48
54:01:248:G:H5'	54:01:249:C:H5'	1.95	0.48
54:01:560:C:H2'	54:01:561:G:O4'	2.14	0.48
54:01:889:C:H2'	54:01:890:C:H5'	1.95	0.48
55:02:78:A:H2'	55:02:79:G:O4'	2.14	0.48
59:Z:73:THR:HG21	59:Z:196:ASP:HB3	1.95	0.48
59:Z:241:GLU:HA	59:Z:254:THR:HA	1.96	0.48
59:Z:245:VAL:HA	59:Z:250:THR:CG2	2.44	0.48
3:06:117:ARG:HA	3:06:185:LYS:HD3	1.94	0.48
7:10:59:LEU:HD22	7:10:62:ARG:HB2	1.95	0.48
10:13:2:ILE:HD12	10:13:6:THR:HG21	1.95	0.48
10:13:116:ILE:HD12	10:13:117:SER:N	2.29	0.48
13:16:55:ALA:HA	13:16:80:PHE:CE1	2.48	0.48
17:20:79:ARG:O	17:20:81:LYS:HG2	2.14	0.48
27:30:11:LYS:HA	27:30:14:MET:CE	2.44	0.48
29:32:12:ARG:NH1	29:32:44:VAL:HG21	2.28	0.48
32:B:66:ILE:HD13	32:B:159:ALA:HB3	1.93	0.48
34:D:37:PRO:HD2	34:D:41:GLY:HA3	1.96	0.48
34:D:120:LYS:HG2	34:D:130:ASN:HD21	1.78	0.48
34:D:131:ILE:HG22	34:D:133:SER:H	1.79	0.48
36:F:77:THR:O	36:F:81:ASN:HB2	2.14	0.48
53:A:977:A:H2'	53:A:978:A:H5''	1.95	0.48
53:A:1123:U:O2'	53:A:1124:G:H5'	2.14	0.48
54:01:181:A:H2'	54:01:182:A:C8	2.49	0.48
54:01:832:U:H2'	54:01:833:A:C8	2.49	0.48
54:01:1035:U:H2'	54:01:1036:G:C8	2.49	0.48
54:01:1043:C:H2'	54:01:1044:C:O4'	2.14	0.48
54:01:1354:A:H2'	54:01:1355:G:O4'	2.13	0.48
54:01:1536:C:H4'	54:01:1537:G:C2	2.49	0.48
54:01:1736:U:H2'	54:01:1737:G:O4'	2.13	0.48
54:01:1775:U:H2'	54:01:1776:G:O4'	2.13	0.48
54:01:2082:A:H2'	54:01:2083:G:O4'	2.13	0.48
54:01:2207:C:H2'	54:01:2208:C:C6	2.48	0.48
1:04:239:PHE:HB2	54:01:1903:G:OP1	2.13	0.48
8:11:79:LEU:HA	8:11:82:ALA:HB3	1.96	0.48
9:12:21:THR:HG23	9:12:61:LYS:HB3	1.96	0.48
11:14:79:LEU:HD12	11:14:112:LEU:HD12	1.96	0.48
13:16:73:ASN:HA	13:16:76:VAL:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:32:1:MET:HE1	29:32:3:ARG:CZ	2.43	0.48
32:B:37:VAL:HG22	32:B:38:HIS:N	2.28	0.48
32:B:158:ASP:O	32:B:181:PRO:HD2	2.14	0.48
33:C:64:ARG:HG3	33:C:99:GLN:O	2.13	0.48
34:D:8:LEU:HD21	34:D:31:CYS:HB3	1.96	0.48
41:K:71:ASP:O	41:K:72:ALA:HB3	2.14	0.48
47:Q:4:ILE:HD12	47:Q:4:ILE:O	2.13	0.48
51:U:17:ARG:HA	51:U:20:ARG:HH11	1.78	0.48
52:03:50:ILE:HD11	52:03:52:ALA:HB2	1.95	0.48
53:A:10:A:H2'	53:A:11:G:C8	2.47	0.48
54:01:1078:U:H4'	54:01:1079:C:H5''	1.96	0.48
54:01:1524:G:H2'	54:01:1525:A:C8	2.49	0.48
54:01:2317:A:H2'	54:01:2318:G:O4'	2.14	0.48
4:07:62:GLN:NE2	4:07:90:LEU:HB3	2.29	0.48
8:11:37:PHE:HE1	8:11:58:ILE:HG13	1.79	0.48
32:B:162:VAL:HB	32:B:184:ALA:CB	2.43	0.48
43:M:6:ILE:HG13	43:M:7:ASN:H	1.79	0.48
43:M:7:ASN:ND2	43:M:20:SER:HB2	2.29	0.48
50:T:77:ASN:O	50:T:81:GLN:HG2	2.14	0.48
52:03:31:LYS:HD2	52:03:182:ALA:H	1.77	0.48
53:A:1106:G:H2'	53:A:1107:C:C6	2.49	0.48
54:01:168:G:H2'	54:01:169:G:H8	1.79	0.48
54:01:226:A:H5''	54:01:257:C:O2'	2.14	0.48
54:01:464:U:H2'	54:01:465:G:O4'	2.14	0.48
54:01:575:A:O2'	54:01:576:U:H5'	2.13	0.48
54:01:669:G:H2'	54:01:669:G:N3	2.28	0.48
54:01:2743:U:C3'	54:01:2744:G:H5''	2.44	0.48
59:Z:89:LYS:HA	59:Z:92:ILE:HD12	1.95	0.48
59:Z:117:GLU:HB2	59:Z:382:THR:OG1	2.14	0.48
3:06:71:GLY:H	54:01:674:G:H5''	1.79	0.47
5:08:8:VAL:O	5:08:49:LEU:N	2.47	0.47
5:08:72:ASN:O	5:08:76:ILE:HG12	2.14	0.47
20:23:32:LYS:HG2	20:23:65:GLN:OE1	2.14	0.47
25:28:23:LEU:HD21	25:28:53:MET:SD	2.54	0.47
26:29:11:GLU:HB2	26:29:25:ARG:HE	1.79	0.47
46:P:59:HIS:O	46:P:63:GLN:HG2	2.13	0.47
53:A:24:U:H2'	53:A:25:C:C6	2.49	0.47
53:A:831:A:H2'	53:A:832:G:O4'	2.14	0.47
55:02:4:C:H6	55:02:4:C:H5'	1.79	0.47
59:Z:260:MET:HG2	59:Z:261:PHE:HD2	1.80	0.47
2:05:127:PHE:CD1	54:01:2512:C:H5''	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:102:GLU:HG2	9:12:119:PHE:HZ	1.79	0.47
15:18:77:SER:OG	15:18:79:VAL:HG12	2.13	0.47
18:21:20:VAL:HA	27:30:21:LEU:HD12	1.95	0.47
34:D:144:ILE:HB	34:D:149:LYS:NZ	2.28	0.47
52:03:41:SER:C	52:03:217:THR:HG23	2.39	0.47
53:A:151:A:H2'	53:A:152:A:O4'	2.13	0.47
53:A:921:U:H2'	53:A:922:G:O4'	2.14	0.47
54:01:264:C:O3'	54:01:265:A:H2'	2.14	0.47
54:01:282:A:H2'	54:01:283:G:C8	2.49	0.47
54:01:1990:C:H2'	54:01:1991:U:C6	2.49	0.47
54:01:2134:A:C6	54:01:2157:G:H4'	2.49	0.47
7:10:27:VAL:HG12	7:10:83:ALA:O	2.15	0.47
12:15:50:ARG:HH21	12:15:50:ARG:HG2	1.79	0.47
13:16:28:LEU:HD23	13:16:48:VAL:HG21	1.96	0.47
25:28:37:ARG:NH2	54:01:929:U:H4'	2.30	0.47
34:D:170:LEU:HA	34:D:182:LYS:HE2	1.96	0.47
36:F:88:MET:HG3	36:F:90:MET:HE2	1.96	0.47
39:I:101:GLY:O	39:I:103:VAL:HG22	2.14	0.47
46:P:20:VAL:HG22	46:P:21:VAL:N	2.29	0.47
52:03:51:ASP:C	52:03:53:ARG:H	2.20	0.47
52:03:190:GLU:O	52:03:194:VAL:N	2.47	0.47
53:A:59:A:H3'	53:A:331:G:H22	1.80	0.47
53:A:929:G:H5''	53:A:1534:A:H1'	1.96	0.47
53:A:946:A:H2'	53:A:947:G:H8	1.79	0.47
53:A:1175:G:H2'	53:A:1176:A:C8	2.50	0.47
53:A:1409:C:H2'	53:A:1410:A:H8	1.79	0.47
53:A:1492:A:H2'	54:01:1913:A:C2	2.49	0.47
54:01:537:G:H22	54:01:555:G:H2'	1.79	0.47
54:01:813:U:H2'	54:01:814:C:C6	2.50	0.47
54:01:1258:U:H2'	54:01:1259:G:C8	2.50	0.47
54:01:1430:G:H2'	54:01:1431:A:O4'	2.14	0.47
54:01:2577:A:H5''	54:01:2578:G:H5'	1.94	0.47
54:01:2648:G:H2'	54:01:2649:C:O4'	2.14	0.47
59:Z:144:GLU:HA	59:Z:147:GLU:HG3	1.96	0.47
59:Z:172:GLY:HA2	59:Z:184:TRP:CZ3	2.49	0.47
59:Z:305:GLU:HA	59:Z:359:VAL:CG2	2.43	0.47
1:04:121:ALA:HB1	1:04:127:ASN:HB3	1.96	0.47
1:04:220:ARG:HG3	54:01:1789:A:OP1	2.14	0.47
2:05:61:THR:HB	2:05:63:PRO:HD2	1.97	0.47
3:06:155:GLU:OE2	3:06:159:LEU:HD11	2.14	0.47
8:11:4:VAL:HA	8:11:7:TYR:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:39:LYS:NZ	9:12:39:LYS:HB3	2.29	0.47
17:20:14:VAL:HG21	17:20:98:ILE:HG13	1.96	0.47
18:21:57:ASN:HD22	18:21:61:ASN:HD22	1.61	0.47
33:C:19:SER:HB3	33:C:21:TRP:CD1	2.49	0.47
37:G:41:ILE:HD11	53:A:1240:U:O4'	2.15	0.47
39:I:45:MET:O	39:I:49:GLN:HG3	2.14	0.47
42:L:33:CYS:HB2	42:L:54:VAL:HG22	1.95	0.47
52:03:163:TYR:HB2	52:03:171:ILE:HD11	1.96	0.47
54:01:704:G:H2'	54:01:726:G:H22	1.78	0.47
54:01:1388:G:H2'	54:01:1389:G:C8	2.50	0.47
59:Z:24:LYS:HA	59:Z:27:LEU:HD21	1.96	0.47
8:11:72:THR:OG1	8:11:73:PRO:HD2	2.15	0.47
8:11:79:LEU:HD23	8:11:82:ALA:HB3	1.96	0.47
11:14:30:THR:HG22	54:01:810:U:O4	2.15	0.47
18:21:58:ALA:HA	18:21:62:ASP:OD1	2.15	0.47
30:33:63:TYR:CD2	54:01:242:G:H5''	2.49	0.47
31:34:1:MET:HE2	31:34:36:ARG:HB2	1.96	0.47
44:N:13:VAL:HA	44:N:59:GLN:HE22	1.80	0.47
44:N:68:ARG:HG2	44:N:68:ARG:HH11	1.79	0.47
49:S:36:ARG:HG2	53:A:1320:C:N4	2.30	0.47
53:A:622:A:H2'	53:A:623:C:H5'	1.96	0.47
53:A:726:C:H2'	53:A:727:G:H8	1.79	0.47
53:A:990:C:H2'	53:A:991:U:O4'	2.15	0.47
53:A:1023:U:H2'	53:A:1024:G:O4'	2.14	0.47
53:A:1391:U:H2'	53:A:1392:G:C8	2.49	0.47
54:01:1196:C:H2'	54:01:1197:G:H8	1.78	0.47
54:01:2697:G:H2'	54:01:2698:U:O4'	2.15	0.47
54:01:2841:C:H2'	54:01:2842:G:H8	1.78	0.47
58:Y:27:G:H2'	58:Y:28:G:O4'	2.14	0.47
58:Y:64:A:H4'	59:Z:379:GLY:HA3	1.97	0.47
1:04:240:GLY:HA3	54:01:2597:G:H5'	1.96	0.47
5:08:85:LYS:C	5:08:86:LEU:HD12	2.39	0.47
11:14:14:LYS:HG2	54:01:662:G:O2'	2.14	0.47
19:22:39:THR:O	19:22:43:ILE:HG13	2.15	0.47
21:24:26:PHE:CZ	21:24:42:LEU:HD11	2.49	0.47
34:D:101:VAL:HG13	34:D:106:PHE:HB2	1.95	0.47
35:E:156:ARG:NH2	35:E:163:ILE:HG22	2.29	0.47
38:H:10:LEU:HD22	38:H:74:ILE:CD1	2.45	0.47
40:J:40:ILE:HG23	40:J:41:PRO:HD2	1.96	0.47
42:L:54:VAL:HG21	42:L:79:ILE:HD11	1.96	0.47
52:03:192:LEU:C	52:03:196:LEU:HD13	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:03:214:ILE:HD12	52:03:214:ILE:O	2.14	0.47
53:A:644:U:H2'	53:A:645:G:H8	1.79	0.47
53:A:1137:C:C5'	53:A:1138:G:H5'	2.41	0.47
53:A:1508:A:H2'	53:A:1509:C:C6	2.50	0.47
54:01:211:C:H5'	54:01:1366:A:O2'	2.15	0.47
54:01:1409:U:H2'	54:01:1410:G:C8	2.50	0.47
54:01:2368:C:H2'	54:01:2369:A:H8	1.80	0.47
54:01:2630:G:H2'	54:01:2631:G:H8	1.79	0.47
54:01:2731:G:H2'	54:01:2732:G:C8	2.49	0.47
58:Y:27:G:O2'	58:Y:28:G:H5'	2.15	0.47
59:Z:134:LEU:HB2	59:Z:171:ARG:HG2	1.97	0.47
7:10:59:LEU:H	7:10:59:LEU:HD12	1.78	0.47
8:11:52:LEU:HB2	8:11:54:ILE:HD11	1.95	0.47
8:11:90:GLY:C	8:11:91:LYS:HD3	2.39	0.47
9:12:52:ASP:O	9:12:54:ILE:HG13	2.14	0.47
16:19:91:ARG:HH11	16:19:91:ARG:HG3	1.79	0.47
17:20:74:ILE:N	17:20:74:ILE:HD12	2.30	0.47
32:B:162:VAL:HB	32:B:184:ALA:HB2	1.97	0.47
33:C:54:ILE:HG22	33:C:67:ILE:HG12	1.97	0.47
35:E:70:MET:O	35:E:71:ILE:HD13	2.15	0.47
38:H:8:ASP:O	38:H:11:THR:HG22	2.15	0.47
41:K:116:PRO:HB3	53:A:676:A:C1'	2.45	0.47
47:Q:11:VAL:HG13	47:Q:20:ILE:HD11	1.97	0.47
52:03:19:LYS:NZ	52:03:21:TYR:HD1	2.11	0.47
52:03:175:ILE:HB	52:03:188:ASN:CB	2.44	0.47
52:03:190:GLU:O	52:03:194:VAL:HG23	2.15	0.47
53:A:31:G:N2	53:A:47:C:H5''	2.29	0.47
53:A:634:C:H2'	53:A:635:A:C8	2.50	0.47
53:A:876:C:H2'	53:A:877:G:H8	1.79	0.47
53:A:1075:U:H2'	53:A:1076:U:C6	2.50	0.47
53:A:1305:G:H22	53:A:1331:G:H2'	1.79	0.47
54:01:885:C:C2'	54:01:886:A:H5'	2.44	0.47
54:01:1499:C:H2'	54:01:1500:G:H8	1.79	0.47
54:01:1858:A:C2	54:01:1885:A:H1'	2.50	0.47
54:01:2243:U:H2'	54:01:2244:U:C6	2.49	0.47
54:01:2464:G:H2'	54:01:2465:C:H6	1.80	0.47
54:01:2591:C:H2'	54:01:2592:G:H8	1.77	0.47
54:01:2809:A:H2'	54:01:2810:A:C8	2.50	0.47
56:X:68:C:C2	56:X:69:C:H1'	2.50	0.47
58:Y:28:G:H2'	58:Y:29:G:C8	2.49	0.47
59:Z:10:PRO:O	59:Z:74:ARG:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Z:173:SER:HB3	59:Z:184:TRP:CD2	2.50	0.47
59:Z:277:LEU:HD12	59:Z:278:LEU:H	1.79	0.47
59:Z:318:ARG:HH21	59:Z:319:HIS:CD2	2.32	0.47
59:Z:366:ILE:HD12	59:Z:367:ALA:H	1.79	0.47
3:06:105:LEU:HA	3:06:108:ILE:HG12	1.97	0.47
3:06:148:ILE:HD13	3:06:187:VAL:CG1	2.44	0.47
8:11:88:GLY:HA3	54:01:1063:G:O2'	2.15	0.47
8:11:90:GLY:C	8:11:92:PRO:HD3	2.40	0.47
8:11:123:ALA:HA	8:11:126:ARG:NH1	2.30	0.47
21:24:29:ILE:HA	21:24:40:ILE:HG12	1.96	0.47
43:M:94:LEU:C	43:M:108:ARG:HG2	2.40	0.47
53:A:56:U:H2'	53:A:57:G:C8	2.49	0.47
53:A:514:C:H2'	53:A:515:G:C8	2.50	0.47
54:01:1579:A:H2'	54:01:1580:A:O4'	2.14	0.47
54:01:1765:U:H2'	54:01:1766:G:H8	1.79	0.47
54:01:1849:G:H2'	54:01:1850:G:H8	1.79	0.47
54:01:2129:C:H2'	54:01:2159:G:H22	1.80	0.47
59:Z:7:ARG:HH12	59:Z:272:GLU:CG	2.27	0.47
3:06:130:LYS:HB2	3:06:133:LEU:HD12	1.96	0.47
4:07:94:ARG:NH2	26:29:1:MET:HB3	2.30	0.47
6:09:26:ALA:O	6:09:31:VAL:HG23	2.14	0.47
9:12:72:LYS:HB3	9:12:89:PHE:HB2	1.97	0.47
20:23:40:LEU:HB3	20:23:59:GLU:OE2	2.14	0.47
32:B:95:TRP:CH2	32:B:171:ALA:HA	2.49	0.47
34:D:31:CYS:HA	53:A:429:U:OP2	2.15	0.47
50:T:30:PHE:HD2	50:T:56:ILE:HG21	1.80	0.47
53:A:1171:A:H2'	53:A:1172:C:C6	2.49	0.47
54:01:856:G:H2'	54:01:857:G:C8	2.50	0.47
54:01:942:G:H2'	54:01:943:A:O4'	2.14	0.47
54:01:2529:G:OP2	54:01:2530:A:H5''	2.15	0.47
59:Z:167:THR:HG22	59:Z:169:ILE:CD1	2.45	0.47
59:Z:174:ALA:HA	59:Z:177:ALA:HB3	1.96	0.47
1:04:135:PRO:HG2	36:F:80:PHE:HD1	1.79	0.47
3:06:47:LYS:HB2	3:06:51:GLU:HB2	1.97	0.47
4:07:47:LYS:NZ	4:07:51:ASN:HD21	2.13	0.47
4:07:127:TYR:HD2	4:07:155:ILE:HD12	1.80	0.47
21:24:16:ALA:HA	21:24:19:ARG:NH2	2.30	0.47
22:25:39:THR:HG21	54:01:2336:A:N6	2.30	0.47
27:30:52:LYS:HE2	27:30:56:LYS:H	1.79	0.47
37:G:104:VAL:O	37:G:108:ARG:HG2	2.15	0.47
37:G:138:GLU:O	37:G:142:ARG:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:14:ARG:HD2	53:A:875:U:O2'	2.15	0.47
38:H:48:PHE:HB3	38:H:60:LEU:HD23	1.98	0.47
38:H:63:LYS:NZ	38:H:63:LYS:HB3	2.30	0.47
49:S:5:LYS:HG3	49:S:6:LYS:N	2.29	0.47
49:S:35:ARG:NH1	49:S:35:ARG:HB3	2.30	0.47
49:S:54:ARG:HG3	49:S:55:GLN:HG2	1.97	0.47
51:U:50:SER:HA	51:U:53:LYS:HD2	1.97	0.47
52:O3:15:VAL:HG11	52:O3:220:ALA:HB1	1.97	0.47
53:A:86:G:H4'	53:A:87:C:C5	2.50	0.47
53:A:477:C:H2'	53:A:478:A:C8	2.50	0.47
53:A:880:C:O2'	53:A:881:G:H5'	2.15	0.47
54:O1:807:U:H2'	54:O1:808:G:H8	1.80	0.47
54:O1:1119:U:H2'	54:O1:1120:G:H8	1.80	0.47
54:O1:2841:C:H2'	54:O1:2842:G:C8	2.49	0.47
54:O1:2859:G:H2'	54:O1:2860:A:C8	2.50	0.47
59:Z:350:VAL:HG13	59:Z:354:ASP:HB2	1.97	0.47
4:O7:25:MET:HE2	4:O7:25:MET:HA	1.97	0.46
7:10:2:ALA:HB1	7:10:6:GLN:HB2	1.97	0.46
32:B:209:VAL:HA	32:B:212:TYR:HD2	1.79	0.46
33:C:102:ILE:HD12	33:C:102:ILE:O	2.14	0.46
35:E:110:MET:HG3	35:E:139:THR:HG21	1.96	0.46
53:A:422:C:H4'	53:A:423:G:H5''	1.97	0.46
53:A:1033:G:C3'	53:A:1034:G:H5''	2.42	0.46
53:A:1476:A:H2'	53:A:1477:U:O4'	2.15	0.46
54:O1:863:A:H2'	54:O1:864:G:C8	2.50	0.46
54:O1:975:A:H1'	54:O1:990:A:C6	2.50	0.46
54:O1:1285:A:H2	54:O1:1328:A:H5''	1.80	0.46
54:O1:1434:A:H2'	54:O1:1435:G:C8	2.49	0.46
54:O1:1744:A:H3'	54:O1:1745:A:H8	1.80	0.46
54:O1:2292:U:H2'	54:O1:2293:G:C8	2.50	0.46
58:Y:76:A:H5'	59:Z:220:ILE:HD11	1.96	0.46
1:O4:216:ARG:HG3	1:O4:216:ARG:NH1	2.31	0.46
1:O4:224:MET:HE2	54:O1:782:A:C6	2.49	0.46
4:O7:39:VAL:HG12	4:O7:84:ILE:O	2.16	0.46
6:O9:83:LYS:HA	6:O9:149:GLU:HB3	1.98	0.46
32:B:46:VAL:HA	32:B:49:PHE:CE1	2.50	0.46
33:C:49:ALA:HB1	33:C:75:VAL:HG22	1.98	0.46
35:E:28:ARG:HH12	53:A:15:G:H4'	1.80	0.46
41:K:84:MET:SD	41:K:110:THR:OG1	2.73	0.46
48:R:41:SER:HB3	48:R:51:GLN:HG2	1.97	0.46
53:A:1502:A:H5'	53:A:1504:G:N7	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:662:G:O2'	54:01:663:G:H5'	2.15	0.46
54:01:736:C:H2'	54:01:737:C:C6	2.50	0.46
54:01:769:U:H2'	54:01:770:G:C8	2.49	0.46
54:01:1170:C:H2'	54:01:1171:G:N7	2.30	0.46
54:01:1388:G:H2'	54:01:1389:G:H8	1.80	0.46
54:01:2055:C:H5'	54:01:2056:G:O5'	2.15	0.46
54:01:2127:G:H2'	54:01:2128:G:O4'	2.15	0.46
54:01:2537:U:H2'	54:01:2538:C:H6	1.80	0.46
59:Z:243:GLU:HA	59:Z:252:LYS:HA	1.97	0.46
59:Z:373:ARG:HA	59:Z:387:VAL:HG23	1.97	0.46
3:06:21:ARG:HG2	3:06:110:SER:OG	2.16	0.46
5:08:41:GLU:HG3	5:08:54:ARG:NH2	2.30	0.46
6:09:31:VAL:N	6:09:32:PRO:HD2	2.30	0.46
37:G:99:ALA:O	37:G:103:ILE:HG13	2.15	0.46
38:H:29:SER:HB2	53:A:589:U:H5''	1.97	0.46
39:I:49:GLN:N	39:I:50:PRO:CD	2.78	0.46
43:M:85:TYR:O	43:M:89:ARG:HG2	2.14	0.46
43:M:88:LEU:HD23	43:M:88:LEU:O	2.16	0.46
45:O:21:THR:HG21	53:A:658:C:H1'	1.97	0.46
45:O:34:GLN:HG2	45:O:58:MET:HE1	1.96	0.46
53:A:1203:C:H2'	53:A:1204:A:H8	1.80	0.46
54:01:57:C:H2'	54:01:58:G:O4'	2.15	0.46
54:01:244:A:H2'	54:01:245:G:O4'	2.15	0.46
54:01:302:C:H2'	54:01:303:G:H8	1.80	0.46
54:01:593:U:H2'	54:01:594:U:C6	2.49	0.46
54:01:796:C:H2'	54:01:797:G:C8	2.50	0.46
54:01:1594:U:H2'	54:01:1595:C:C6	2.50	0.46
54:01:1999:C:H5''	54:01:2723:C:O2'	2.16	0.46
54:01:2123:G:N2	54:01:2175:C:H42	2.13	0.46
59:Z:12:VAL:HG22	59:Z:202:PRO:HD3	1.97	0.46
59:Z:324:LYS:CE	59:Z:342:GLU:HA	2.45	0.46
2:05:8:LYS:HB2	2:05:201:LEU:HD11	1.97	0.46
2:05:159:LYS:HE2	54:01:2512:C:O2'	2.15	0.46
4:07:140:ILE:HD12	4:07:140:ILE:N	2.30	0.46
8:11:59:THR:HB	8:11:67:THR:CG2	2.45	0.46
14:17:74:VAL:O	14:17:78:VAL:HG23	2.15	0.46
32:B:94:ARG:HG2	53:A:1100:C:OP2	2.15	0.46
32:B:118:THR:HA	32:B:121:GLN:NE2	2.25	0.46
34:D:103:ARG:HD2	34:D:167:PRO:HG2	1.96	0.46
34:D:186:GLU:HB3	34:D:189:ASP:OD2	2.15	0.46
35:E:45:VAL:HG11	35:E:116:VAL:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:E:79:THR:OG1	35:E:80:LEU:N	2.48	0.46
38:H:80:PRO:HG2	53:A:878:A:C5'	2.45	0.46
40:J:53:ILE:HG13	44:N:84:ARG:CD	2.45	0.46
53:A:458:U:H2'	53:A:459:A:H8	1.81	0.46
53:A:579:A:H2'	53:A:580:C:C6	2.50	0.46
53:A:742:G:H2'	53:A:743:A:H8	1.80	0.46
53:A:784:A:H4'	54:01:1837:C:OP1	2.16	0.46
54:01:1278:C:H2'	54:01:1279:G:C8	2.49	0.46
54:01:1411:U:H2'	54:01:1412:U:C6	2.50	0.46
54:01:1989:G:H2'	54:01:1990:C:O4'	2.16	0.46
54:01:2001:C:H4'	54:01:2689:U:O2'	2.15	0.46
54:01:2292:U:H2'	54:01:2293:G:H8	1.81	0.46
54:01:2628:C:H3'	54:01:2629:U:H5'	1.97	0.46
56:W:6:G:O2'	56:W:7:G:H5'	2.15	0.46
56:W:48:C:H2'	56:W:59:A:H4'	1.97	0.46
59:Z:131:ILE:HG13	59:Z:199:ILE:HD12	1.98	0.46
2:05:133:THR:HG23	2:05:134:HIS:N	2.31	0.46
4:07:23:SER:HB3	4:07:26:GLN:HG3	1.98	0.46
4:07:127:TYR:CD2	4:07:155:ILE:HD12	2.51	0.46
15:18:80:VAL:HG23	15:18:80:VAL:O	2.15	0.46
42:L:20:VAL:HB	42:L:94:TYR:CE1	2.50	0.46
44:N:20:PHE:O	44:N:21:ALA:CB	2.64	0.46
48:R:33:THR:HG23	48:R:35:SER:H	1.79	0.46
49:S:36:ARG:HG2	53:A:1320:C:H41	1.80	0.46
54:01:862:G:H2'	54:01:863:A:O4'	2.15	0.46
54:01:1765:U:H2'	54:01:1766:G:C8	2.51	0.46
54:01:1893:C:H2'	54:01:1894:C:H5'	1.97	0.46
54:01:2475:C:H2'	54:01:2476:A:H5'	1.97	0.46
55:02:70:C:H2'	55:02:71:C:C6	2.50	0.46
58:Y:7:A:H3'	58:Y:8:U:C5'	2.46	0.46
59:Z:206:ILE:HG22	59:Z:270:ALA:HB3	1.98	0.46
59:Z:332:PHE:O	59:Z:333:ARG:HG2	2.16	0.46
1:04:61:TYR:HE1	54:01:1816:C:H3'	1.80	0.46
2:05:51:THR:HB	2:05:79:LEU:HD23	1.98	0.46
7:10:11:ILE:HD11	7:10:62:ARG:HG2	1.96	0.46
9:12:69:ARG:HA	9:12:89:PHE:HD2	1.80	0.46
11:14:23:ILE:HD12	11:14:23:ILE:N	2.30	0.46
13:16:79:LEU:HD23	13:16:83:LEU:HB2	1.97	0.46
27:30:11:LYS:HA	27:30:14:MET:HE2	1.98	0.46
40:J:30:LYS:HA	40:J:34:ALA:HA	1.98	0.46
44:N:86:ALA:HA	44:N:89:ARG:NH1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:206:C:H2'	53:A:207:C:O4'	2.16	0.46
53:A:418:C:H2'	53:A:419:C:C6	2.51	0.46
53:A:886:G:H2'	53:A:887:G:O4'	2.15	0.46
54:01:1468:U:H2'	54:01:1522:A:N6	2.31	0.46
54:01:2156:G:C2'	54:01:2157:G:H5'	2.45	0.46
55:02:5:U:H2'	55:02:6:G:H8	1.81	0.46
58:Y:15:G:N2	58:Y:21:A:H1'	2.31	0.46
59:Z:305:GLU:CB	59:Z:389:ALA:HB3	2.46	0.46
6:09:132:PHE:HB2	6:09:140:ALA:HB3	1.98	0.46
10:13:2:ILE:HB	10:13:33:ALA:HB3	1.97	0.46
13:16:30:ARG:HH21	13:16:31:HIS:HE1	1.64	0.46
17:20:37:GLU:O	17:20:39:LEU:HD12	2.16	0.46
17:20:54:VAL:HG12	17:20:55:ASP:N	2.31	0.46
19:22:1:MET:HE2	19:22:3:ARG:HB2	1.96	0.46
20:23:48:VAL:C	20:23:50:ALA:H	2.24	0.46
32:B:95:TRP:HZ2	32:B:100:LEU:HG	1.80	0.46
33:C:133:MET:O	33:C:137:VAL:HG23	2.15	0.46
37:G:68:VAL:HG21	37:G:103:ILE:HD11	1.98	0.46
53:A:35:G:H2'	53:A:36:C:C6	2.49	0.46
53:A:358:U:H2'	53:A:359:G:C8	2.51	0.46
53:A:429:U:H4'	53:A:430:A:O5'	2.14	0.46
53:A:536:C:H2'	53:A:537:G:C8	2.51	0.46
53:A:1163:A:H2'	53:A:1164:G:C8	2.50	0.46
54:01:100:U:H5''	54:01:101:A:O5'	2.16	0.46
54:01:575:A:H2'	54:01:576:U:H6	1.79	0.46
54:01:2055:C:H2'	54:01:2504:U:H5'	1.98	0.46
54:01:2273:A:H2'	54:01:2274:A:C8	2.50	0.46
1:04:200:MET:CE	53:A:773:G:H4'	2.45	0.46
2:05:121:THR:HB	2:05:127:PHE:CE2	2.50	0.46
3:06:131:THR:HG23	54:01:321:U:H5''	1.97	0.46
4:07:163:GLU:HA	4:07:166:ARG:NH1	2.31	0.46
8:11:101:SER:HA	8:11:140:GLU:O	2.16	0.46
9:12:110:PRO:O	9:12:115:GLY:HA3	2.16	0.46
11:14:93:ASN:C	11:14:95:LEU:H	2.24	0.46
40:J:9:ARG:HB3	40:J:73:LEU:HD23	1.97	0.46
40:J:65:TYR:HB3	44:N:95:LEU:HD11	1.98	0.46
43:M:7:ASN:ND2	43:M:9:PRO:HD3	2.31	0.46
52:03:10:VAL:O	52:03:14:LYS:HG3	2.16	0.46
52:03:181:ASP:O	52:03:185:LEU:HG	2.16	0.46
53:A:59:A:H5''	53:A:387:U:H5''	1.98	0.46
54:01:49:A:H5'	54:01:51:G:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:163:C:H2'	54:01:164:C:O4'	2.16	0.46
54:01:582:A:H2'	54:01:583:G:H8	1.80	0.46
54:01:996:A:H2'	54:01:997:G:C8	2.51	0.46
54:01:1443:U:H2'	54:01:1444:G:H8	1.78	0.46
58:Y:47:U:H2'	58:Y:50:U:OP1	2.16	0.46
58:Y:49:C:H2'	58:Y:50:U:H6	1.81	0.46
1:04:131:MET:HE2	1:04:187:CYS:HB2	1.97	0.46
1:04:174:ARG:HG2	1:04:174:ARG:HH11	1.80	0.46
1:04:206:LYS:HD3	54:01:729:G:C8	2.51	0.46
11:14:17:LYS:HD3	54:01:663:G:H5'	1.97	0.46
13:16:30:ARG:HE	13:16:31:HIS:CE1	2.33	0.46
16:19:12:ARG:HG2	16:19:12:ARG:HH21	1.81	0.46
20:23:5:ARG:HB2	54:01:85:G:OP1	2.16	0.46
30:33:51:LYS:HG3	30:33:52:GLY:N	2.30	0.46
45:O:54:GLY:O	45:O:58:MET:HG2	2.16	0.46
48:R:41:SER:CB	48:R:51:GLN:HE21	2.29	0.46
50:T:54:GLN:N	50:T:55:PRO:HD2	2.31	0.46
53:A:641:U:H4'	53:A:642:A:C8	2.51	0.46
54:01:172:A:H2'	54:01:173:A:H8	1.80	0.46
54:01:1041:G:H2'	54:01:1042:G:H8	1.81	0.46
54:01:1877:A:H2'	54:01:1878:G:O4'	2.16	0.46
54:01:2717:C:H2'	54:01:2718:G:O4'	2.16	0.46
59:Z:246:GLY:CA	59:Z:290:GLN:HG3	2.38	0.46
5:08:125:PRO:HD2	5:08:129:GLU:O	2.15	0.46
30:33:21:PHE:O	30:33:49:VAL:HG23	2.16	0.46
39:I:61:ASP:C	39:I:62:LEU:HD12	2.41	0.46
41:K:28:ASN:HD21	41:K:56:LYS:HD2	1.81	0.46
44:N:2:LYS:O	44:N:5:MET:N	2.48	0.46
52:03:177:LYS:N	52:03:180:PHE:HD2	2.13	0.46
53:A:757:U:H2'	53:A:758:C:O4'	2.16	0.46
53:A:1328:C:H2'	53:A:1329:A:H8	1.81	0.46
54:01:151:C:H2'	54:01:152:A:H8	1.80	0.46
54:01:543:G:H5'	54:01:543:G:H8	1.80	0.46
54:01:1678:A:H2'	54:01:1679:A:O4'	2.16	0.46
54:01:1917:U:C2'	54:01:1918:A:H5'	2.46	0.46
54:01:2234:G:O2'	54:01:2235:G:H5'	2.16	0.46
54:01:2347:C:C5	54:01:2382:G:H1'	2.51	0.46
1:04:75:ALA:HB2	1:04:95:TYR:CD1	2.50	0.45
3:06:163:ASN:HB2	54:01:322:A:OP2	2.16	0.45
6:09:32:PRO:HA	23:26:38:TRP:CD1	2.51	0.45
7:10:24:SER:O	7:10:116:GLU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:10:78:GLY:N	7:10:79:PRO:CD	2.78	0.45
8:11:29:GLN:NE2	54:01:1096:A:H61	2.07	0.45
11:14:29:LYS:HG2	11:14:30:THR:HG23	1.97	0.45
11:14:36:LYS:HE2	54:01:808:G:OP2	2.17	0.45
12:15:13:HIS:HE1	54:01:2265:U:H4'	1.81	0.45
14:17:108:ASP:O	14:17:112:GLU:HG3	2.16	0.45
18:21:74:ILE:HG23	18:21:74:ILE:O	2.16	0.45
32:B:163:ILE:HG22	32:B:168:GLU:OE1	2.16	0.45
34:D:198:LEU:HA	34:D:201:GLU:OE1	2.15	0.45
37:G:100:MET:O	37:G:104:VAL:HG23	2.17	0.45
46:P:78:VAL:O	46:P:78:VAL:HG22	2.16	0.45
47:Q:60:ILE:CG2	47:Q:72:TRP:HB3	2.46	0.45
52:03:165:ASN:HA	52:03:171:ILE:HA	1.98	0.45
53:A:16:A:O2'	53:A:17:U:H5'	2.16	0.45
53:A:1291:U:H2'	53:A:1292:G:C8	2.51	0.45
53:A:1387:G:H2'	53:A:1388:C:C6	2.50	0.45
53:A:1496:C:H2'	53:A:1497:G:O4'	2.15	0.45
54:01:1366:A:H2'	54:01:1367:A:O4'	2.15	0.45
54:01:1444:G:H2'	54:01:1445:G:H8	1.81	0.45
54:01:2009:A:H2'	54:01:2010:G:H8	1.81	0.45
54:01:2086:U:H2'	54:01:2087:G:C8	2.50	0.45
54:01:2475:C:C2'	54:01:2476:A:H5'	2.46	0.45
54:01:2771:C:H2'	54:01:2772:C:H6	1.79	0.45
59:Z:338:THR:H	59:Z:363:ILE:HD11	1.81	0.45
59:Z:376:ILE:HB	59:Z:384:GLY:HA3	1.97	0.45
1:04:163:ILE:HG23	1:04:171:VAL:CG1	2.47	0.45
2:05:194:PRO:HA	54:01:2680:U:H5'	1.99	0.45
8:11:6:ALA:HB3	8:11:60:VAL:O	2.17	0.45
33:C:6:PRO:HG2	33:C:200:TRP:HE1	1.81	0.45
36:F:50:PRO:HG3	36:F:55:HIS:CE1	2.51	0.45
37:G:75:LYS:HD3	37:G:88:VAL:HG11	1.98	0.45
47:Q:48:GLU:HB2	47:Q:51:GLU:CD	2.42	0.45
49:S:69:LYS:O	49:S:72:GLU:HB2	2.17	0.45
50:T:70:LYS:HA	50:T:73:ARG:NE	2.21	0.45
52:03:23:ILE:HA	52:03:26:ALA:HB3	1.98	0.45
53:A:1219:A:H2'	53:A:1220:G:C8	2.51	0.45
54:01:1196:C:H2'	54:01:1197:G:C8	2.51	0.45
54:01:1532:A:H1'	54:01:1540:G:H22	1.81	0.45
59:Z:321:PRO:HG2	59:Z:349:MET:CE	2.45	0.45
1:04:14:HIS:O	1:04:203:VAL:HG21	2.16	0.45
2:05:25:THR:HG21	2:05:193:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:05:111:GLY:HA3	2:05:201:LEU:HD23	1.97	0.45
7:10:98:GLU:HA	7:10:101:LYS:HD3	1.99	0.45
7:10:107:GLU:HG2	7:10:107:GLU:O	2.17	0.45
15:18:91:VAL:HG21	15:18:96:LEU:HD21	1.96	0.45
32:B:20:ARG:HE	32:B:21:TYR:HD1	1.65	0.45
39:I:80:HIS:CD2	39:I:105:ARG:HA	2.52	0.45
51:U:36:PHE:C	51:U:38:GLU:N	2.74	0.45
53:A:211:G:H2'	53:A:212:G:H5'	1.99	0.45
53:A:220:G:O2'	53:A:221:C:H5'	2.16	0.45
53:A:1323:G:H2'	53:A:1324:A:C8	2.51	0.45
54:01:2639:A:H2'	54:01:2640:G:O4'	2.17	0.45
59:Z:64:THR:HG23	59:Z:90:ASN:HB3	1.99	0.45
59:Z:204:ARG:HH11	59:Z:271:GLY:HA3	1.82	0.45
7:10:48:ALA:HB3	7:10:51:TYR:HE1	1.82	0.45
12:15:35:ALA:HB2	12:15:102:LEU:HD11	1.97	0.45
14:17:81:ARG:O	14:17:85:LYS:HG2	2.16	0.45
19:22:47:VAL:HA	19:22:51:PHE:HD2	1.82	0.45
32:B:162:VAL:O	32:B:184:ALA:HB1	2.15	0.45
35:E:15:ILE:HD12	35:E:15:ILE:N	2.31	0.45
36:F:68:GLN:HE22	53:A:738:C:H5'	1.82	0.45
39:I:70:GLY:HA3	53:A:1371:G:O3'	2.16	0.45
48:R:70:THR:CG2	48:R:71:ASP:H	2.11	0.45
52:03:27:ILE:O	52:03:30:LEU:HG	2.17	0.45
52:03:192:LEU:O	52:03:196:LEU:HD13	2.15	0.45
53:A:306:A:O2'	53:A:307:C:H5'	2.17	0.45
53:A:1346:A:O2'	53:A:1347:G:H4'	2.16	0.45
54:01:248:G:C2	54:01:2431:U:H4'	2.51	0.45
54:01:388:G:N7	54:01:390:U:H2'	2.32	0.45
54:01:2146:C:H4'	54:01:2147:A:C5	2.52	0.45
54:01:2406:A:H5'	54:01:2407:A:OP1	2.16	0.45
4:07:36:ASN:HB3	4:07:152:ASP:OD1	2.15	0.45
8:11:79:LEU:CD1	8:11:137:LEU:HD13	2.45	0.45
23:26:25:LYS:HE2	23:26:25:LYS:HA	1.99	0.45
27:30:28:SER:OG	27:30:39:ARG:HD2	2.17	0.45
34:D:50:TYR:CD2	53:A:508:U:H4'	2.51	0.45
40:J:17:LEU:O	40:J:20:GLN:HG2	2.17	0.45
44:N:20:PHE:C	44:N:22:LYS:H	2.24	0.45
46:P:51:ARG:C	46:P:52:LEU:HD12	2.41	0.45
49:S:18:VAL:O	49:S:22:VAL:HG23	2.17	0.45
53:A:599:C:H2'	53:A:600:A:H8	1.82	0.45
54:01:825:A:H2'	54:01:826:U:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:854:C:H2'	54:01:855:G:H8	1.81	0.45
54:01:878:A:H3'	54:01:879:G:C8	2.47	0.45
54:01:1138:G:H2'	54:01:1139:G:O4'	2.16	0.45
54:01:1181:U:H2'	54:01:1182:G:C8	2.51	0.45
54:01:1258:U:H2'	54:01:1259:G:H8	1.82	0.45
54:01:2096:C:H2'	54:01:2097:A:H8	1.81	0.45
54:01:2786:U:O2'	54:01:2787:C:H5'	2.16	0.45
59:Z:304:PHE:HA	59:Z:392:LEU:HD23	1.98	0.45
59:Z:322:PHE:O	59:Z:349:MET:SD	2.75	0.45
59:Z:335:THR:HG21	59:Z:366:ILE:HG12	1.99	0.45
3:06:68:ALA:HA	54:01:1255:U:C5	2.51	0.45
11:14:18:ARG:HH22	54:01:1249:U:H2'	1.81	0.45
14:17:106:LEU:O	14:17:106:LEU:HD23	2.16	0.45
15:18:29:VAL:HG13	15:18:79:VAL:O	2.16	0.45
16:19:78:PHE:HE1	16:19:109:VAL:HA	1.80	0.45
21:24:65:VAL:O	21:24:65:VAL:HG13	2.17	0.45
42:L:43:LYS:HB3	42:L:44:PRO:HD3	1.99	0.45
52:03:26:ALA:HB1	52:03:222:VAL:HG11	1.98	0.45
53:A:335:C:H2'	53:A:336:A:H8	1.79	0.45
53:A:1175:G:H2'	53:A:1176:A:H8	1.81	0.45
53:A:1434:A:H2'	53:A:1435:G:O4'	2.16	0.45
54:01:708:G:N2	54:01:724:U:H1'	2.31	0.45
54:01:1111:A:O2'	54:01:1112:G:H4'	2.17	0.45
54:01:2029:G:O6	54:01:2032:G:H5''	2.16	0.45
54:01:2110:G:H2'	54:01:2120:G:OP1	2.16	0.45
54:01:2220:U:H2'	54:01:2221:G:H8	1.81	0.45
54:01:2398:U:H2'	54:01:2399:G:C8	2.52	0.45
2:05:142:VAL:HB	2:05:143:PRO:HD2	1.98	0.45
4:07:88:VAL:HA	55:02:42:C:O2	2.17	0.45
7:10:11:ILE:O	7:10:15:VAL:HG23	2.17	0.45
15:18:30:TRP:CD2	15:18:37:LYS:HE3	2.51	0.45
24:27:7:ARG:CD	24:27:7:ARG:H	2.29	0.45
25:28:23:LEU:CD2	25:28:28:LEU:HD12	2.46	0.45
41:K:122:PRO:HG2	51:U:34:ARG:O	2.16	0.45
43:M:1:ALA:O	43:M:8:ILE:HG12	2.17	0.45
54:01:394:C:H2'	54:01:395:U:O4'	2.16	0.45
54:01:577:G:OP1	54:01:2502:G:H2'	2.17	0.45
54:01:766:U:H2'	54:01:767:U:C6	2.52	0.45
54:01:1535:A:H3'	54:01:1536:C:H5'	1.99	0.45
54:01:2154:A:H2'	54:01:2155:U:C6	2.51	0.45
54:01:2423:U:O2'	54:01:2425:A:H2'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2601:C:H2'	54:01:2603:G:C8	2.51	0.45
54:01:2623:G:H2'	54:01:2624:G:C8	2.52	0.45
54:01:2723:C:H2'	54:01:2724:U:O4'	2.17	0.45
58:Y:2:C:H4'	59:Z:87:TYR:HE1	1.81	0.45
59:Z:24:LYS:HG2	59:Z:104:VAL:CG2	2.45	0.45
59:Z:304:PHE:CZ	59:Z:360:VAL:HB	2.52	0.45
8:11:12:VAL:O	8:11:13:ALA:C	2.59	0.45
12:15:41:LEU:HD13	12:15:124:LEU:HD22	1.98	0.45
14:17:43:ASN:ND2	14:17:46:GLU:HG2	2.30	0.45
15:18:87:ARG:HB3	15:18:87:ARG:NH1	2.32	0.45
19:22:50:LEU:HD23	24:27:26:PHE:CE2	2.52	0.45
33:C:13:ILE:HD12	33:C:13:ILE:N	2.31	0.45
34:D:94:GLU:HA	34:D:99:ASN:HD22	1.79	0.45
39:I:105:ARG:HH11	39:I:105:ARG:HG3	1.82	0.45
39:I:129:ARG:HG2	39:I:129:ARG:HH11	1.81	0.45
44:N:58:ARG:NH2	53:A:980:C:H4'	2.31	0.45
49:S:9:PHE:CE2	53:A:1318:A:H4'	2.52	0.45
52:03:27:ILE:HB	52:03:182:ALA:CB	2.45	0.45
53:A:142:G:H2'	53:A:143:A:O4'	2.17	0.45
53:A:1118:U:H2'	53:A:1119:C:H6	1.82	0.45
53:A:1158:C:H2'	53:A:1159:U:H4'	1.98	0.45
53:A:1277:C:H2'	53:A:1278:G:H5''	1.98	0.45
54:01:616:A:H2'	54:01:617:G:O4'	2.17	0.45
54:01:808:G:H2'	54:01:809:G:H8	1.82	0.45
54:01:1482:G:H1'	54:01:1509:A:C2	2.52	0.45
54:01:2391:G:H4'	54:01:2392:A:OP1	2.17	0.45
1:04:270:ARG:HB3	1:04:270:ARG:NH1	2.32	0.45
9:12:27:ARG:HH22	54:01:1142:A:H4'	1.82	0.45
16:19:57:ARG:HG2	16:19:57:ARG:HH11	1.81	0.45
22:25:55:LEU:CD1	22:25:76:ILE:HD12	2.47	0.45
31:34:30:GLU:HG3	31:34:32:LYS:H	1.82	0.45
32:B:42:LEU:HA	32:B:45:THR:OG1	2.15	0.45
34:D:113:ALA:O	34:D:117:VAL:HG23	2.17	0.45
37:G:3:ARG:HD2	37:G:4:ARG:NH1	2.31	0.45
38:H:63:LYS:O	38:H:70:VAL:HG23	2.17	0.45
51:U:19:LYS:C	51:U:21:SER:H	2.25	0.45
54:01:576:U:H2'	54:01:577:G:C8	2.52	0.45
54:01:1363:C:H2'	54:01:1364:G:H8	1.82	0.45
54:01:2236:U:H2'	54:01:2237:G:O4'	2.17	0.45
56:W:51:C:H2'	56:W:52:G:C8	2.52	0.45
61:Y:101:PHE:N	59:Z:274:VAL:HA	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:04:96:LYS:HD2	54:01:1490:A:N6	2.31	0.45
23:26:5:GLN:HG3	23:26:49:ARG:H	1.82	0.45
27:30:54:ILE:HG23	27:30:56:LYS:N	2.31	0.45
32:B:221:ARG:NH1	32:B:224:ARG:HH11	2.14	0.45
35:E:25:LYS:HG2	53:A:923:A:OP1	2.17	0.45
35:E:47:PHE:CE2	35:E:137:ARG:HG2	2.52	0.45
38:H:103:VAL:HA	38:H:124:ILE:HA	1.99	0.45
39:I:86:LEU:O	39:I:94:ARG:HD2	2.16	0.45
41:K:59:PRO:HB3	41:K:91:GLY:HA2	1.97	0.45
53:A:1349:A:H2'	53:A:1350:A:O4'	2.17	0.45
53:A:1464:U:H2'	53:A:1465:A:C8	2.51	0.45
54:01:354:A:H2'	54:01:355:U:O4'	2.17	0.45
54:01:1709:U:H2'	54:01:1710:G:H8	1.81	0.45
54:01:2605:U:H2'	54:01:2606:C:C6	2.51	0.45
59:Z:321:PRO:HB2	59:Z:349:MET:HG3	1.98	0.45
59:Z:372:LEU:HB3	59:Z:388:VAL:CG2	2.47	0.45
1:04:233:GLY:HA3	54:01:2598:A:H5''	1.98	0.44
2:05:146:ILE:HA	2:05:159:LYS:HE3	1.98	0.44
5:08:140:ILE:HD12	5:08:141:GLY:N	2.32	0.44
11:14:51:GLU:HB2	11:14:54:GLN:HB3	1.98	0.44
12:15:12:MET:SD	12:15:72:PRO:HD2	2.57	0.44
13:16:10:LEU:O	13:16:12:ARG:HG3	2.17	0.44
13:16:25:ALA:O	13:16:29:VAL:HG23	2.17	0.44
13:16:113:ILE:HG23	13:16:113:ILE:O	2.16	0.44
23:26:7:THR:OG1	23:26:9:LYS:HG3	2.17	0.44
28:31:46:VAL:HG12	28:31:47:ILE:N	2.32	0.44
38:H:55:LYS:HE3	53:A:653:U:O4'	2.17	0.44
38:H:112:ASP:O	38:H:116:ARG:HG2	2.17	0.44
52:03:54:LYS:HE3	52:03:56:ASP:OD2	2.18	0.44
52:03:69:THR:HG23	52:03:159:GLY:HA2	1.99	0.44
53:A:490:C:H2'	53:A:491:G:H8	1.82	0.44
54:01:116:C:H2'	54:01:117:G:O4'	2.17	0.44
54:01:1053:C:C3'	54:01:1054:A:H5''	2.47	0.44
54:01:1097:U:H2'	54:01:1098:A:O4'	2.17	0.44
54:01:1739:A:H2'	54:01:1740:G:O4'	2.18	0.44
54:01:1827:U:O2'	54:01:1828:G:H5'	2.17	0.44
59:Z:15:GLY:HA2	59:Z:79:VAL:H	1.82	0.44
59:Z:19:HIS:CG	59:Z:112:MET:HG3	2.52	0.44
59:Z:184:TRP:HA	59:Z:187:LYS:CD	2.42	0.44
1:04:61:TYR:CE1	54:01:1816:C:H3'	2.52	0.44
1:04:216:ARG:HG3	1:04:216:ARG:HH11	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:07:130:GLY:HA2	4:07:152:ASP:HA	2.00	0.44
10:13:116:ILE:HD12	10:13:116:ILE:C	2.42	0.44
20:23:45:GLN:HB2	20:23:58:VAL:HG23	1.99	0.44
23:26:14:GLY:O	23:26:25:LYS:HE2	2.17	0.44
32:B:95:TRP:CZ3	32:B:171:ALA:HA	2.53	0.44
37:G:13:PRO:HA	37:G:20:GLU:HG3	1.99	0.44
44:N:80:ARG:O	44:N:83:VAL:HG12	2.17	0.44
49:S:49:ALA:HA	49:S:58:PRO:HA	1.99	0.44
52:03:47:ASN:C	52:03:48:LEU:HD23	2.42	0.44
53:A:79:G:H2'	53:A:80:A:O4'	2.17	0.44
53:A:169:C:H2'	53:A:170:U:C6	2.52	0.44
53:A:434:U:H2'	53:A:435:A:H8	1.81	0.44
53:A:715:A:H2'	53:A:716:A:C8	2.52	0.44
53:A:1463:U:H2'	53:A:1464:U:C6	2.52	0.44
54:01:615:U:H5''	54:01:616:A:OP2	2.16	0.44
54:01:1595:C:H2'	54:01:1596:A:H8	1.82	0.44
54:01:2552:U:C6	54:01:2554:U:H5'	2.52	0.44
56:W:69:C:H2'	56:W:70:G:C8	2.52	0.44
59:Z:139:MET:HA	59:Z:139:MET:CE	2.42	0.44
2:05:62:LYS:HB2	2:05:63:PRO:HD3	1.98	0.44
5:08:10:VAL:HG12	5:08:47:ASN:O	2.18	0.44
6:09:57:LYS:O	6:09:61:VAL:HG13	2.17	0.44
8:11:93:ASN:HD22	54:01:1077:A:H5'	1.82	0.44
41:K:110:THR:HB	48:R:72:ARG:NH1	2.32	0.44
41:K:116:PRO:HB3	53:A:676:A:H1'	1.99	0.44
48:R:40:PRO:HG2	48:R:43:ILE:HG12	1.98	0.44
53:A:1370:G:O2'	53:A:1371:G:H5'	2.17	0.44
54:01:322:A:H5'	54:01:340:A:C1'	2.44	0.44
54:01:610:C:H2'	54:01:611:C:H6	1.81	0.44
54:01:1123:C:H2'	54:01:1124:G:H8	1.81	0.44
58:Y:6:G:C3'	58:Y:7:A:H5''	2.37	0.44
59:Z:91:MET:O	59:Z:95:ALA:N	2.50	0.44
59:Z:204:ARG:HA	59:Z:204:ARG:HE	1.82	0.44
1:04:86:ARG:HG2	1:04:86:ARG:NH1	2.32	0.44
1:04:184:GLU:HG3	1:04:186:ASP:H	1.82	0.44
2:05:37:VAL:HG23	2:05:92:VAL:CG2	2.48	0.44
2:05:101:PHE:O	2:05:104:VAL:HG22	2.18	0.44
18:21:13:SER:O	18:21:17:VAL:HG23	2.17	0.44
21:24:51:GLN:OE1	21:24:86:LEU:HD11	2.18	0.44
21:24:51:GLN:CD	21:24:86:LEU:HD11	2.42	0.44
26:29:33:ASN:HD21	43:M:49:GLU:HG3	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:31:52:LYS:NZ	28:31:52:LYS:HB3	2.33	0.44
37:G:68:VAL:HG23	37:G:99:ALA:HB1	2.00	0.44
53:A:55:A:C5	59:Z:222:GLY:HA3	2.52	0.44
53:A:147:G:H2'	53:A:148:G:C8	2.53	0.44
53:A:345:C:H4'	53:A:346:G:C4	2.52	0.44
54:01:745:G:O2'	54:01:748:G:H1'	2.17	0.44
54:01:1318:U:H2'	54:01:1319:C:C6	2.52	0.44
54:01:1476:U:H1'	54:01:1732:C:C2	2.53	0.44
54:01:2040:G:H2'	54:01:2041:U:O4'	2.17	0.44
1:04:207:ALA:HB1	54:01:1790:C:H4'	2.00	0.44
1:04:255:LYS:HD3	1:04:269:ARG:HH12	1.81	0.44
22:25:70:PRO:HB3	55:02:12:C:N4	2.33	0.44
29:32:26:ASN:CG	54:01:682:G:H5'	2.42	0.44
34:D:71:PHE:HE1	34:D:93:LEU:HD11	1.82	0.44
35:E:60:GLN:O	35:E:64:GLU:HG3	2.18	0.44
36:F:50:PRO:HG3	36:F:55:HIS:NE2	2.32	0.44
45:O:86:LEU:HD12	45:O:86:LEU:O	2.17	0.44
53:A:79:G:O2'	53:A:80:A:H5'	2.17	0.44
53:A:1004:A:H1'	53:A:1026:G:C6	2.53	0.44
54:01:1659:G:H2'	54:01:1660:G:O4'	2.17	0.44
54:01:2096:C:H2'	54:01:2097:A:C8	2.52	0.44
54:01:2756:U:H1'	54:01:2757:A:H5''	1.98	0.44
54:01:2900:A:H2'	54:01:2901:C:O4'	2.17	0.44
59:Z:25:THR:HG22	59:Z:46:PHE:HD1	1.82	0.44
1:04:209:ALA:HA	1:04:212:TRP:CE2	2.52	0.44
2:05:97:SER:O	2:05:100:LEU:HD13	2.18	0.44
3:06:77:ILE:HG13	3:06:78:TRP:CD1	2.53	0.44
10:13:48:PRO:HB3	53:A:1422:G:C5'	2.48	0.44
15:18:13:LYS:NZ	15:18:80:VAL:HG23	2.32	0.44
34:D:58:GLN:HG3	53:A:544:G:OP1	2.18	0.44
38:H:85:TYR:HE1	38:H:123:GLU:HB2	1.82	0.44
42:L:35:ARG:HH12	42:L:37:TYR:HB3	1.82	0.44
45:O:87:ARG:NE	45:O:87:ARG:HA	2.32	0.44
51:U:35:GLU:O	51:U:36:PHE:HB2	2.17	0.44
53:A:458:U:H2'	53:A:459:A:C8	2.53	0.44
53:A:865:A:H2'	53:A:866:C:C6	2.52	0.44
53:A:950:U:H2'	53:A:951:G:C8	2.53	0.44
54:01:96:C:H2'	54:01:97:C:C6	2.52	0.44
54:01:213:A:H2'	54:01:214:G:C8	2.52	0.44
54:01:2019:A:H2	54:01:2035:G:H22	1.65	0.44
54:01:2557:G:H2'	54:01:2558:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2776:A:H4'	54:01:2777:G:H5''	1.99	0.44
59:Z:293:ALA:HB1	59:Z:297:THR:CG2	2.48	0.44
3:06:70:SER:HB2	3:06:78:TRP:HZ2	1.83	0.44
4:07:32:LYS:HD3	4:07:91:ARG:HH22	1.82	0.44
18:21:16:LYS:HE3	54:01:1266:G:N7	2.33	0.44
21:24:3:THR:HG23	21:24:62:THR:O	2.18	0.44
32:B:55:GLU:O	32:B:59:ILE:HG12	2.18	0.44
32:B:60:ALA:HB3	32:B:223:GLY:HA3	1.99	0.44
35:E:22:LYS:HB3	35:E:29:ILE:CG2	2.47	0.44
42:L:115:LYS:O	42:L:116:TYR:HB2	2.17	0.44
51:U:6:ARG:C	51:U:8:ASN:H	2.25	0.44
52:03:65:LEU:HD13	52:03:188:ASN:HB3	1.99	0.44
53:A:211:G:C2'	53:A:212:G:H5'	2.47	0.44
53:A:358:U:H2'	53:A:359:G:H8	1.82	0.44
53:A:1301:U:O2	53:A:1301:U:H2'	2.17	0.44
53:A:1306:A:H62	53:A:1331:G:H1'	1.83	0.44
54:01:326:G:H2'	54:01:327:G:H8	1.82	0.44
54:01:2011:U:H2'	54:01:2012:G:O4'	2.17	0.44
59:Z:265:LEU:HD21	59:Z:268:GLY:HA2	2.00	0.44
59:Z:321:PRO:CG	59:Z:349:MET:HE3	2.48	0.44
1:04:156:SER:HB2	54:01:1818:U:H5'	2.00	0.44
1:04:257:ARG:HG3	54:01:1799:G:OP1	2.17	0.44
2:05:141:ARG:HG2	2:05:141:ARG:HH11	1.82	0.44
3:06:47:LYS:HE3	54:01:451:U:OP1	2.18	0.44
6:09:126:GLY:O	6:09:146:VAL:N	2.50	0.44
11:14:49:GLY:HA3	11:14:58:TYR:HE1	1.83	0.44
12:15:64:TRP:HZ3	12:15:106:ASP:HB3	1.83	0.44
16:19:91:ARG:HG3	16:19:91:ARG:NH1	2.33	0.44
32:B:33:ALA:HB3	32:B:37:VAL:O	2.17	0.44
32:B:80:LYS:HB2	32:B:92:ASN:ND2	2.33	0.44
34:D:61:ARG:NH2	34:D:67:LEU:HA	2.33	0.44
36:F:93:LYS:O	36:F:94:HIS:CB	2.65	0.44
40:J:42:LEU:HA	40:J:43:PRO:HD2	1.80	0.44
44:N:2:LYS:HE2	53:A:983:A:H5'	1.98	0.44
48:R:17:VAL:HG22	48:R:18:GLN:N	2.33	0.44
50:T:67:HIS:ND1	50:T:67:HIS:O	2.50	0.44
52:03:50:ILE:HB	52:03:57:GLN:HB3	2.00	0.44
52:03:65:LEU:HD22	52:03:188:ASN:CA	2.45	0.44
53:A:1472:U:H2'	53:A:1473:G:C8	2.53	0.44
54:01:1316:U:H2'	54:01:1317:G:H8	1.82	0.44
54:01:1469:A:H2'	54:01:1470:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2617:U:H2'	54:01:2618:G:O4'	2.18	0.44
54:01:2743:U:H3'	54:01:2744:G:H5''	1.99	0.44
58:Y:73:A:H2'	58:Y:73:A:N3	2.33	0.44
59:Z:66:HIS:CD2	59:Z:66:HIS:N	2.84	0.44
2:05:42:ASN:HB3	54:01:2784:U:H4'	1.98	0.44
23:26:69:GLU:O	23:26:73:ARG:HG3	2.18	0.44
34:D:33:ILE:HG13	34:D:34:GLU:N	2.32	0.44
37:G:39:GLU:HG2	37:G:43:TYR:CE2	2.53	0.44
38:H:4:ASP:HB2	53:A:877:G:O2'	2.17	0.44
40:J:86:ALA:HA	40:J:90:LEU:HD12	2.00	0.44
44:N:27:LYS:O	44:N:31:SER:HB2	2.18	0.44
46:P:14:ARG:HH11	46:P:14:ARG:HG3	1.82	0.44
48:R:56:ARG:O	48:R:60:ARG:HG3	2.17	0.44
53:A:211:G:H3'	53:A:211:G:N3	2.33	0.44
53:A:264:C:H2'	53:A:265:G:O4'	2.18	0.44
53:A:407:U:H2'	53:A:408:A:H8	1.82	0.44
53:A:707:U:H2'	53:A:708:C:C6	2.53	0.44
53:A:1354:U:H2'	53:A:1355:G:C8	2.52	0.44
54:01:744:U:H2'	54:01:745:G:O4'	2.17	0.44
54:01:2141:G:H2'	54:01:2142:A:C8	2.48	0.44
54:01:2231:U:H2'	54:01:2232:C:H6	1.83	0.44
54:01:2293:G:H2'	54:01:2294:G:C8	2.52	0.44
54:01:2743:U:H2'	54:01:2744:G:H5''	1.99	0.44
54:01:2836:U:H2'	54:01:2837:A:C8	2.53	0.44
59:Z:137:CYS:HB2	59:Z:172:GLY:C	2.43	0.44
4:07:105:ILE:HG13	4:07:106:ALA:N	2.33	0.43
11:14:55:MET:SD	11:14:59:ARG:HD3	2.58	0.43
16:19:48:ASP:O	16:19:52:ARG:N	2.47	0.43
38:H:5:PRO:O	38:H:8:ASP:HB3	2.17	0.43
40:J:34:ALA:O	40:J:35:GLN:HB3	2.18	0.43
47:Q:5:ARG:HD2	53:A:636:U:OP1	2.17	0.43
54:01:68:G:H2'	54:01:69:C:O4'	2.18	0.43
54:01:1295:C:H2'	54:01:1296:G:C8	2.53	0.43
54:01:2144:G:H1'	54:01:2147:A:H61	1.83	0.43
54:01:2329:U:H2'	54:01:2330:G:C8	2.53	0.43
54:01:2869:G:H2'	54:01:2870:C:O4'	2.17	0.43
55:02:91:C:H2'	55:02:92:C:C6	2.52	0.43
59:Z:212:LEU:HD23	59:Z:212:LEU:C	2.43	0.43
1:04:66:PHE:HZ	1:04:86:ARG:HE	1.66	0.43
1:04:213:ARG:HH11	1:04:213:ARG:HG3	1.83	0.43
6:09:94:ILE:HB	6:09:122:LEU:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:11:56:VAL:HG21	8:11:68:PHE:HD2	1.84	0.43
11:14:79:LEU:HD23	11:14:82:LEU:HD22	2.00	0.43
32:B:187:ASP:HB3	32:B:190:SER:OG	2.18	0.43
33:C:143:LEU:HD23	33:C:143:LEU:O	2.18	0.43
37:G:139:ASP:O	37:G:143:MET:HG2	2.18	0.43
40:J:80:THR:HB	40:J:83:THR:OG1	2.19	0.43
45:O:31:LEU:O	45:O:35:ILE:HG13	2.18	0.43
52:03:170:ILE:HG21	54:01:2177:C:H1'	2.00	0.43
53:A:323:U:H2'	53:A:324:G:O4'	2.18	0.43
53:A:392:C:H2'	53:A:393:A:C8	2.51	0.43
53:A:1109:C:H2'	53:A:1110:A:O4'	2.18	0.43
53:A:1492:A:H2'	54:01:1913:A:H2	1.82	0.43
54:01:629:G:H5''	54:01:650:C:O2'	2.18	0.43
54:01:859:G:HO2'	54:01:860:U:H6	1.64	0.43
54:01:898:C:H2'	54:01:899:A:O4'	2.18	0.43
54:01:1001:A:H2'	54:01:1002:G:O4'	2.18	0.43
54:01:1105:U:C2'	54:01:1106:G:H5''	2.47	0.43
54:01:2194:U:H2'	54:01:2195:U:C6	2.53	0.43
59:Z:98:MET:O	59:Z:127:VAL:HG13	2.17	0.43
59:Z:238:VAL:HG23	59:Z:266:ASP:O	2.18	0.43
2:05:3:GLY:O	2:05:4:LEU:HD12	2.18	0.43
2:05:4:LEU:HD23	2:05:32:ASN:ND2	2.27	0.43
3:06:164:LEU:HD12	3:06:164:LEU:H	1.83	0.43
4:07:70:ARG:HD2	54:01:2298:A:OP1	2.18	0.43
12:15:5:LYS:C	12:15:6:ARG:HG3	2.43	0.43
12:15:34:LYS:HD3	21:24:82:TYR:HA	1.99	0.43
15:18:90:ALA:HB2	15:18:112:ARG:HA	2.00	0.43
17:20:13:ARG:HG2	17:20:13:ARG:HH11	1.84	0.43
17:20:59:ILE:HG23	17:20:101:ILE:HD13	1.99	0.43
18:21:57:ASN:ND2	18:21:61:ASN:HD22	2.16	0.43
26:29:42:PRO:O	26:29:46:GLY:HA3	2.17	0.43
33:C:22:PHE:CE2	40:J:11:LYS:HG3	2.53	0.43
35:E:113:VAL:HG13	35:E:114:LEU:CD1	2.47	0.43
36:F:75:GLU:O	36:F:79:ARG:HD2	2.18	0.43
40:J:102:LEU:N	40:J:102:LEU:HD12	2.33	0.43
42:L:53:ARG:HA	42:L:63:THR:HA	2.00	0.43
48:R:44:THR:O	48:R:46:THR:N	2.44	0.43
52:03:31:LYS:HD2	52:03:182:ALA:N	2.34	0.43
53:A:77:A:H2'	53:A:78:A:C8	2.54	0.43
54:01:1113:U:H2'	54:01:1114:C:C6	2.53	0.43
54:01:2052:A:H2'	54:01:2053:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2208:C:H2'	54:01:2209:G:H8	1.80	0.43
54:01:2352:A:H2'	54:01:2353:G:O4'	2.18	0.43
58:Y:72:C:H2'	58:Y:73:A:O4'	2.18	0.43
59:Z:324:LYS:HE3	59:Z:342:GLU:C	2.44	0.43
1:04:86:ARG:HG2	1:04:86:ARG:HH11	1.82	0.43
4:07:154:THR:HG21	54:01:2314:A:O4'	2.18	0.43
10:13:66:LYS:NZ	10:13:66:LYS:HB3	2.33	0.43
30:33:31:ILE:O	30:33:31:ILE:HG22	2.19	0.43
33:C:70:ALA:HB2	33:C:114:LEU:HD13	2.00	0.43
39:I:14:SER:HB2	39:I:69:GLY:HA3	2.01	0.43
40:J:59:LYS:HD3	53:A:973:G:OP1	2.18	0.43
45:O:30:LEU:HD21	53:A:658:C:OP1	2.18	0.43
53:A:955:U:H3	53:A:1225:A:H61	1.66	0.43
53:A:1203:C:H2'	53:A:1204:A:C8	2.54	0.43
53:A:1306:A:H2'	53:A:1307:U:O4'	2.18	0.43
54:01:69:C:O2'	54:01:70:G:H5'	2.18	0.43
54:01:365:U:H2'	54:01:366:C:C6	2.53	0.43
54:01:1045:C:H5'	54:01:1046:A:H5'	1.98	0.43
54:01:1061:U:H4'	54:01:1070:A:N3	2.33	0.43
54:01:1186:G:H2'	54:01:1187:G:O4'	2.18	0.43
54:01:1565:C:O2'	54:01:1566:A:H2'	2.18	0.43
54:01:1764:C:H2'	54:01:1765:U:C6	2.54	0.43
54:01:2376:A:H2'	54:01:2377:A:O4'	2.18	0.43
54:01:2555:U:H2'	54:01:2556:C:H5'	2.01	0.43
54:01:2846:G:H2'	54:01:2847:U:O4'	2.18	0.43
59:Z:32:THR:HB	59:Z:42:ALA:HB3	2.00	0.43
59:Z:297:THR:CG2	59:Z:298:ILE:HD12	2.46	0.43
3:06:199:MET:HE2	3:06:200:LEU:CD1	2.48	0.43
4:07:32:LYS:HD3	4:07:91:ARG:NH2	2.33	0.43
6:09:9:VAL:C	6:09:11:ASN:H	2.26	0.43
19:22:7:LEU:HD22	19:22:46:ALA:HA	2.01	0.43
21:24:26:PHE:HE2	21:24:89:ILE:HG13	1.83	0.43
23:26:71:ARG:HD2	23:26:77:TYR:OH	2.17	0.43
26:29:13:THR:HA	26:29:23:LYS:HA	1.99	0.43
32:B:221:ARG:HH11	32:B:221:ARG:HG2	1.83	0.43
35:E:158:LYS:HZ1	38:H:63:LYS:CE	2.31	0.43
44:N:4:SER:O	44:N:8:ARG:N	2.51	0.43
49:S:62:THR:HG22	49:S:63:ASP:N	2.33	0.43
51:U:13:VAL:HG13	51:U:15:LEU:HG	1.99	0.43
53:A:1094:G:H2'	53:A:1094:G:N3	2.34	0.43
54:01:1222:U:H2'	54:01:1223:G:H8	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:1326:U:H2'	54:01:1327:A:C8	2.53	0.43
54:01:1595:C:H2'	54:01:1596:A:C8	2.53	0.43
54:01:2478:A:C2	54:01:2529:G:H2'	2.53	0.43
59:Z:137:CYS:HB2	59:Z:172:GLY:O	2.19	0.43
1:04:43:ASN:HD21	54:01:1806:C:H1'	1.84	0.43
3:06:159:LEU:O	54:01:321:U:H4'	2.19	0.43
27:30:49:ARG:HG2	54:01:2884:U:H6	1.83	0.43
32:B:46:VAL:HA	32:B:49:PHE:CZ	2.54	0.43
32:B:96:LEU:HD22	53:A:1103:C:H5'	1.99	0.43
33:C:10:ARG:HA	33:C:13:ILE:HD13	2.01	0.43
34:D:59:LYS:HE3	34:D:194:ILE:HG22	2.00	0.43
35:E:89:THR:O	35:E:89:THR:HG22	2.18	0.43
35:E:121:ASN:C	35:E:122:VAL:HG22	2.44	0.43
53:A:32:A:H2'	53:A:33:A:C8	2.53	0.43
53:A:203:G:H1'	53:A:465:A:H61	1.84	0.43
53:A:666:G:H5'	53:A:726:C:H1'	2.01	0.43
53:A:691:G:H2'	53:A:692:U:C6	2.54	0.43
54:01:741:U:H2'	54:01:742:A:H8	1.82	0.43
54:01:1177:G:H2'	54:01:1178:C:O4'	2.18	0.43
54:01:1310:G:H3'	54:01:1311:G:C8	2.53	0.43
54:01:2139:U:H2'	54:01:2140:G:C8	2.54	0.43
54:01:2396:G:H2'	54:01:2397:G:H8	1.83	0.43
54:01:2634:A:H2'	54:01:2635:A:C8	2.54	0.43
59:Z:123:ARG:HB2	59:Z:162:PHE:CZ	2.53	0.43
59:Z:241:GLU:OE2	59:Z:252:LYS:HD3	2.19	0.43
59:Z:269:ARG:CD	59:Z:272:GLU:HG2	2.48	0.43
3:06:18:THR:HG22	3:06:19:PHE:HD1	1.84	0.43
3:06:163:ASN:ND2	54:01:323:C:H5''	2.34	0.43
5:08:41:GLU:HB2	5:08:54:ARG:HE	1.84	0.43
6:09:73:ASN:HB3	6:09:108:VAL:HG23	2.01	0.43
11:14:96:LYS:HB2	11:14:96:LYS:NZ	2.33	0.43
12:15:40:ARG:HH11	12:15:93:VAL:HG11	1.84	0.43
13:16:3:HIS:CD2	54:01:2820:A:H4'	2.53	0.43
13:16:47:VAL:O	13:16:50:PRO:HD2	2.19	0.43
16:19:41:ALA:HB1	54:01:534:U:H5'	2.00	0.43
24:27:43:LEU:HD23	24:27:43:LEU:O	2.19	0.43
27:30:33:SER:HB3	27:30:35:GLU:HG3	2.00	0.43
32:B:67:LEU:HD12	32:B:153:MET:HE1	1.99	0.43
41:K:22:ILE:HG23	41:K:31:VAL:HG22	2.00	0.43
52:03:27:ILE:CB	52:03:182:ALA:HB1	2.47	0.43
52:03:63:THR:O	52:03:160:GLN:NE2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:269:C:H2'	53:A:270:A:C8	2.54	0.43
54:01:146:A:H2'	54:01:147:C:C6	2.53	0.43
54:01:494:G:H2'	54:01:495:G:H8	1.84	0.43
59:Z:70:ASP:N	59:Z:70:ASP:OD1	2.52	0.43
8:11:78:LEU:O	8:11:78:LEU:HD23	2.18	0.43
8:11:127:SER:HA	54:01:1080:A:H1'	2.01	0.43
12:15:12:MET:HG2	12:15:72:PRO:HG2	2.01	0.43
32:B:103:TRP:CH2	32:B:107:ARG:HD3	2.54	0.43
34:D:23:GLY:HA3	53:A:409:U:OP1	2.18	0.43
34:D:186:GLU:HG3	34:D:188:SER:H	1.82	0.43
35:E:160:VAL:HG13	35:E:161:GLU:N	2.33	0.43
40:J:41:PRO:HG3	53:A:1150:A:N3	2.34	0.43
41:K:91:GLY:C	41:K:93:GLU:H	2.26	0.43
47:Q:22:VAL:HG21	47:Q:60:ILE:HD11	2.01	0.43
53:A:505:G:OP2	53:A:535:A:H5'	2.18	0.43
53:A:772:U:H2'	53:A:773:G:C8	2.53	0.43
53:A:945:G:H2'	53:A:945:G:N3	2.33	0.43
54:01:1286:A:H1'	54:01:1288:G:OP2	2.18	0.43
54:01:1695:G:H2'	54:01:1696:G:O4'	2.19	0.43
54:01:1911:U:H2'	54:01:1918:A:N1	2.34	0.43
54:01:2014:A:H2'	54:01:2015:A:C8	2.54	0.43
59:Z:12:VAL:HB	59:Z:76:TYR:HE1	1.81	0.43
59:Z:269:ARG:NE	59:Z:272:GLU:HG2	2.33	0.43
59:Z:333:ARG:HH12	59:Z:372:LEU:HD13	1.83	0.43
59:Z:335:THR:HG22	59:Z:337:VAL:HG22	2.00	0.43
1:04:211:ARG:HH11	1:04:211:ARG:HG3	1.84	0.43
4:07:132:ARG:CZ	54:01:2305:U:H4'	2.49	0.43
8:11:11:GLN:HG2	8:11:54:ILE:O	2.18	0.43
11:14:29:LYS:C	11:14:30:THR:HG23	2.44	0.43
12:15:4:PRO:HG3	12:15:68:PHE:HE2	1.83	0.43
12:15:71:LYS:HB3	12:15:93:VAL:O	2.18	0.43
13:16:83:LEU:HD22	13:16:86:ARG:HH22	1.83	0.43
14:17:110:ALA:HB1	14:17:115:LEU:HD23	2.01	0.43
32:B:26:MET:CE	32:B:192:PRO:HD3	2.49	0.43
33:C:39:ARG:HA	33:C:54:ILE:HD11	2.01	0.43
33:C:91:ALA:HA	33:C:94:ALA:HB3	2.01	0.43
35:E:133:ILE:HD12	35:E:133:ILE:N	2.33	0.43
40:J:28:THR:O	40:J:28:THR:HG22	2.19	0.43
43:M:16:ILE:HD12	43:M:16:ILE:H	1.84	0.43
44:N:12:ARG:HH21	44:N:58:ARG:HH21	1.67	0.43
47:Q:16:MET:O	47:Q:19:SER:OG	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:923:A:H2'	53:A:924:C:O4'	2.18	0.43
53:A:1286:U:C2'	53:A:1287:A:H5'	2.49	0.43
54:01:197:A:H4'	54:01:2069:G:OP2	2.18	0.43
54:01:507:A:C5'	54:01:508:A:H5''	2.33	0.43
54:01:657:U:H2'	54:01:658:U:C6	2.53	0.43
54:01:814:C:H1'	54:01:1225:G:N2	2.34	0.43
54:01:950:G:H2'	54:01:951:C:O4'	2.19	0.43
54:01:1396:U:H5''	54:01:1397:U:OP2	2.19	0.43
54:01:2364:C:H2'	54:01:2365:G:O4'	2.17	0.43
54:01:2861:U:H2'	54:01:2862:G:C8	2.53	0.43
55:02:118:C:H2'	55:02:119:A:C8	2.54	0.43
59:Z:236:ILE:HD12	59:Z:268:GLY:O	2.19	0.43
2:05:5:VAL:HG21	2:05:80:TRP:CE3	2.53	0.43
3:06:118:LEU:HD11	3:06:188:MET:SD	2.59	0.43
5:08:3:VAL:CG2	54:01:2751:G:H4'	2.49	0.43
5:08:26:LYS:HB2	5:08:31:GLU:HG3	2.01	0.43
7:10:60:LEU:HD12	7:10:60:LEU:N	2.33	0.43
7:10:97:LYS:O	7:10:100:ALA:HB3	2.19	0.43
7:10:118:ILE:CG2	7:10:119:PRO:HD3	2.41	0.43
13:16:78:LYS:HG2	13:16:83:LEU:HG	2.01	0.43
27:30:11:LYS:HD2	27:30:14:MET:HE3	2.01	0.43
32:B:153:MET:HG2	32:B:155:GLY:H	1.83	0.43
34:D:57:LYS:HD2	34:D:203:TYR:OH	2.19	0.43
35:E:133:ILE:O	35:E:137:ARG:HG3	2.19	0.43
38:H:86:LYS:HD2	38:H:90:GLU:CG	2.49	0.43
41:K:22:ILE:HG12	41:K:31:VAL:HG13	1.99	0.43
41:K:28:ASN:ND2	41:K:56:LYS:HD2	2.33	0.43
43:M:14:ALA:HA	43:M:44:ILE:HD11	2.00	0.43
50:T:82:ILE:HD12	50:T:83:ASN:N	2.33	0.43
51:U:16:ARG:NE	51:U:19:LYS:HE2	2.34	0.43
53:A:36:C:H2'	53:A:37:U:O4'	2.17	0.43
53:A:90:C:H2'	53:A:91:U:C6	2.54	0.43
54:01:581:C:H2'	54:01:582:A:H8	1.84	0.43
54:01:755:U:H2'	54:01:756:A:C8	2.54	0.43
54:01:1287:A:O2'	54:01:1288:G:H5'	2.18	0.43
54:01:1563:U:H2'	54:01:1564:C:C6	2.54	0.43
54:01:1827:U:H2'	54:01:1828:G:O4'	2.19	0.43
54:01:2298:A:H2'	54:01:2299:U:O4'	2.18	0.43
54:01:2423:U:H5'	54:01:2424:C:C5'	2.49	0.43
54:01:2589:A:H2'	54:01:2590:A:C8	2.53	0.43
54:01:2714:G:H2'	54:01:2715:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Y:16:U:H1'	58:Y:60:U:O2'	2.19	0.43
58:Y:54:U:H5'	59:Z:319:HIS:HE1	1.84	0.43
59:Z:219:SER:HB2	59:Z:283:ARG:CD	2.49	0.43
2:05:11:MET:HE3	2:05:25:THR:OG1	2.19	0.42
4:07:7:TYR:O	4:07:12:VAL:HG23	2.19	0.42
4:07:153:ILE:HD12	4:07:153:ILE:N	2.34	0.42
4:07:163:GLU:HA	4:07:166:ARG:HH12	1.84	0.42
7:10:27:VAL:HG11	7:10:54:VAL:HG23	2.01	0.42
9:12:35:ARG:HB2	9:12:54:ILE:HD11	2.01	0.42
13:16:1:MET:C	13:16:2:ARG:HG3	2.44	0.42
16:19:71:ASN:OD1	16:19:109:VAL:HG21	2.19	0.42
19:22:74:ILE:HG13	19:22:74:ILE:O	2.19	0.42
32:B:56:LEU:HD23	32:B:59:ILE:HD11	2.01	0.42
34:D:131:ILE:HG12	53:A:620:C:C2	2.54	0.42
42:L:27:PRO:HG3	53:A:553:A:H1'	2.00	0.42
42:L:49:ARG:HH22	53:A:522:C:N4	2.17	0.42
43:M:85:TYR:CE2	53:A:1321:U:H5''	2.54	0.42
51:U:7:GLU:HG3	51:U:11:PHE:HB3	2.01	0.42
52:03:11:ILE:CG2	52:03:220:ALA:HB2	2.49	0.42
53:A:91:U:H2'	53:A:92:U:O4'	2.18	0.42
53:A:730:G:N2	53:A:765:G:H5''	2.33	0.42
53:A:900:A:H2'	53:A:901:A:C8	2.54	0.42
53:A:1399:C:H1'	53:A:1400:C:OP2	2.19	0.42
53:A:1469:C:H2'	53:A:1470:U:O4'	2.19	0.42
53:A:1486:G:H2'	53:A:1487:G:O4'	2.19	0.42
54:01:1213:A:H61	54:01:1236:G:H1'	1.83	0.42
54:01:1441:G:H2'	54:01:1442:U:C6	2.54	0.42
54:01:2027:G:H2'	54:01:2028:U:C6	2.54	0.42
54:01:2293:G:H2'	54:01:2294:G:H8	1.83	0.42
54:01:2690:U:O2'	54:01:2872:A:H1'	2.19	0.42
61:Y:101:PHE:N	59:Z:261:PHE:H	2.17	0.42
59:Z:25:THR:HG22	59:Z:46:PHE:CD1	2.54	0.42
59:Z:247:ILE:HG23	59:Z:364:HIS:CB	2.49	0.42
1:04:123:ILE:O	1:04:123:ILE:HG22	2.19	0.42
3:06:105:LEU:CD2	3:06:108:ILE:HD11	2.45	0.42
5:08:132:LEU:HD12	5:08:132:LEU:O	2.19	0.42
8:11:7:TYR:HA	8:11:58:ILE:O	2.19	0.42
16:19:56:PHE:CZ	54:01:536:G:H4'	2.54	0.42
16:19:90:ASP:OD2	16:19:92:LYS:HB3	2.20	0.42
47:Q:29:LYS:HB2	47:Q:36:PHE:CE1	2.53	0.42
53:A:303:A:H2'	53:A:304:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:991:U:C5	53:A:1212:U:H1'	2.54	0.42
54:01:499:U:H2'	54:01:500:G:O4'	2.19	0.42
54:01:1083:U:H2'	54:01:1085:A:OP2	2.19	0.42
54:01:1444:G:H2'	54:01:1445:G:C8	2.53	0.42
59:Z:52:ALA:HB3	59:Z:55:GLU:HB2	2.00	0.42
59:Z:304:PHE:O	59:Z:359:VAL:HG22	2.19	0.42
1:04:1:ALA:N	1:04:19:VAL:HB	2.34	0.42
1:04:243:PRO:C	1:04:251:THR:HG22	2.44	0.42
7:10:3:LEU:HD12	7:10:5:LEU:H	1.85	0.42
7:10:72:LEU:HD12	7:10:72:LEU:H	1.85	0.42
21:24:21:ARG:HA	21:24:25:LYS:O	2.19	0.42
31:34:30:GLU:OE2	31:34:31:PRO:HD2	2.18	0.42
35:E:96:GLN:HG3	35:E:97:PRO:HD2	2.00	0.42
37:G:17:PHE:CZ	37:G:22:LEU:HD21	2.54	0.42
41:K:123:PRO:O	51:U:34:ARG:N	2.52	0.42
42:L:68:GLY:HA3	42:L:98:ARG:NH1	2.34	0.42
50:T:67:HIS:O	50:T:68:LYS:HG2	2.19	0.42
52:03:38:PHE:CD1	54:01:2127:G:H4'	2.53	0.42
53:A:607:A:H2'	53:A:608:A:H8	1.84	0.42
53:A:1325:C:O2'	53:A:1326:U:H5'	2.19	0.42
53:A:1481:U:H2'	53:A:1482:G:C8	2.54	0.42
54:01:151:C:H2'	54:01:152:A:C8	2.54	0.42
54:01:226:A:H2'	54:01:227:A:O4'	2.18	0.42
54:01:947:A:H2'	54:01:948:C:C6	2.54	0.42
54:01:1015:U:H2'	54:01:1016:G:C8	2.55	0.42
54:01:1547:C:H2'	54:01:1548:A:C8	2.55	0.42
54:01:1704:C:H2'	54:01:1705:A:C8	2.54	0.42
54:01:1747:U:H2'	54:01:1748:C:C6	2.54	0.42
54:01:1928:A:H2'	54:01:1929:G:O4'	2.19	0.42
54:01:2126:A:N1	54:01:2163:A:H1'	2.34	0.42
54:01:2322:A:H2'	54:01:2323:G:O4'	2.20	0.42
54:01:2789:C:H2'	54:01:2893:A:N7	2.35	0.42
59:Z:28:THR:HA	59:Z:31:ILE:HD12	2.00	0.42
59:Z:310:ILE:HG13	59:Z:350:VAL:HG11	2.01	0.42
59:Z:324:LYS:HE3	59:Z:342:GLU:CA	2.49	0.42
1:04:163:ILE:HG23	1:04:171:VAL:HG13	2.02	0.42
2:05:164:GLN:HE22	54:01:2822:G:H5''	1.84	0.42
3:06:33:VAL:HG12	3:06:94:GLN:HE22	1.84	0.42
6:09:5:LEU:CD2	6:09:13:GLY:HA2	2.50	0.42
6:09:78:VAL:HG11	6:09:102:ALA:HB1	2.02	0.42
7:10:58:THR:HA	7:10:63:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:26:GLY:HA3	54:01:1140:C:H5'	2.00	0.42
14:17:107:ALA:HB1	14:17:111:ARG:HH22	1.84	0.42
18:21:88:ARG:HG3	18:21:88:ARG:HH21	1.83	0.42
27:30:3:GLN:HA	54:01:2615:U:C2	2.54	0.42
32:B:19:THR:OG1	32:B:20:ARG:N	2.52	0.42
38:H:52:GLY:HA3	38:H:56:PRO:HA	2.00	0.42
38:H:87:ARG:O	38:H:91:LEU:HG	2.19	0.42
43:M:72:ILE:O	43:M:76:ILE:HG13	2.20	0.42
52:03:163:TYR:CD2	52:03:171:ILE:HD11	2.54	0.42
53:A:1098:C:H2'	53:A:1099:G:O4'	2.19	0.42
54:01:1060:U:H5'	54:01:1062:G:C5'	2.49	0.42
54:01:1891:G:H2'	54:01:1892:C:C6	2.54	0.42
54:01:2039:U:H2'	54:01:2040:G:C8	2.55	0.42
54:01:2395:C:H2'	54:01:2396:G:O4'	2.19	0.42
56:X:17:C:H5'	56:X:61:C:OP1	2.19	0.42
58:Y:26:A:H2'	58:Y:27:G:O4'	2.19	0.42
3:06:163:ASN:HD21	54:01:323:C:H5''	1.84	0.42
4:07:30:VAL:HG13	4:07:30:VAL:O	2.20	0.42
8:11:21:PRO:HB2	8:11:22:PRO:HD3	2.00	0.42
25:28:50:VAL:HB	25:28:53:MET:CG	2.49	0.42
30:33:60:CYS:SG	30:33:61:LEU:N	2.92	0.42
32:B:125:PHE:CE1	32:B:127:LYS:HE2	2.55	0.42
34:D:172:VAL:HG22	34:D:174:ALA:N	2.30	0.42
37:G:58:LEU:O	37:G:62:GLU:N	2.49	0.42
38:H:116:ARG:HG3	38:H:116:ARG:NH1	2.35	0.42
49:S:13:HIS:HE1	49:S:34:SER:HB2	1.84	0.42
53:A:459:A:H2'	53:A:460:A:C8	2.54	0.42
53:A:664:G:N2	53:A:741:G:H1	2.14	0.42
53:A:882:C:O2'	53:A:883:C:H5'	2.19	0.42
54:01:519:U:H2'	54:01:520:G:H8	1.85	0.42
54:01:598:U:H2'	54:01:599:A:C8	2.54	0.42
54:01:851:C:O2'	54:01:852:U:H5'	2.19	0.42
54:01:1092:C:H2'	54:01:1093:G:O4'	2.18	0.42
54:01:2155:U:H2'	54:01:2156:G:O4'	2.20	0.42
54:01:2190:G:H2'	54:01:2191:A:C8	2.54	0.42
54:01:2411:A:H2'	54:01:2412:A:C8	2.53	0.42
54:01:2740:A:H2'	54:01:2741:A:C8	2.55	0.42
56:X:4:G:H2'	56:X:5:G:O4'	2.20	0.42
59:Z:350:VAL:CG1	59:Z:354:ASP:HB2	2.49	0.42
4:07:52:ALA:HA	4:07:149:ARG:NE	2.35	0.42
5:08:126:THR:HG22	5:08:127:GLN:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:09:33:GLN:HB2	6:09:35:LYS:HG2	2.02	0.42
6:09:84:ALA:CB	6:09:90:LEU:HD12	2.48	0.42
7:10:67:THR:N	7:10:68:PRO:CD	2.83	0.42
26:29:43:PHE:HB2	26:29:47:LYS:HE3	2.01	0.42
27:30:37:HIS:HB3	27:30:43:THR:HG22	2.02	0.42
30:33:61:LEU:HD13	30:33:64:ALA:HB3	2.02	0.42
32:B:96:LEU:HD13	53:A:1103:C:H4'	2.01	0.42
37:G:11:ILE:HG13	37:G:20:GLU:OE2	2.20	0.42
37:G:71:THR:O	37:G:90:VAL:HG12	2.20	0.42
39:I:89:TYR:HB3	39:I:93:LEU:CD1	2.46	0.42
40:J:66:GLU:HG2	44:N:98:ALA:HB2	2.00	0.42
42:L:98:ARG:NH1	42:L:106:VAL:HG22	2.34	0.42
43:M:48:SER:O	43:M:52:ILE:HG13	2.20	0.42
50:T:8:LYS:HA	50:T:11:ILE:HG12	2.01	0.42
53:A:634:C:H2'	53:A:635:A:H8	1.85	0.42
53:A:783:C:O2'	53:A:784:A:H5'	2.20	0.42
53:A:1366:C:H2'	53:A:1367:C:C6	2.55	0.42
54:01:1106:G:H2'	54:01:1107:G:O4'	2.19	0.42
54:01:2881:U:H2'	54:01:2882:A:H8	1.84	0.42
59:Z:7:ARG:NH2	59:Z:269:ARG:HG2	2.33	0.42
59:Z:321:PRO:HB3	59:Z:351:MET:HA	2.02	0.42
7:10:94:ARG:O	7:10:98:GLU:HG2	2.19	0.42
8:11:56:VAL:HG22	8:11:57:VAL:N	2.35	0.42
9:12:14:ASP:CG	9:12:15:TRP:N	2.76	0.42
9:12:47:HIS:ND1	9:12:48:VAL:HG23	2.34	0.42
9:12:136:GLN:HE21	54:01:2899:A:C5'	2.33	0.42
17:20:20:VAL:O	17:20:96:VAL:HG22	2.20	0.42
18:21:24:ILE:HG13	18:21:24:ILE:O	2.20	0.42
34:D:96:ARG:HG2	34:D:96:ARG:HH11	1.84	0.42
36:F:8:PHE:CZ	36:F:60:VAL:HG11	2.54	0.42
37:G:14:ASP:HB3	37:G:17:PHE:O	2.20	0.42
50:T:20:ASN:OD1	50:T:65:LEU:HD13	2.20	0.42
53:A:22:G:H5'	53:A:561:U:O2	2.19	0.42
53:A:188:C:H2'	53:A:189:A:O4'	2.20	0.42
53:A:518:C:H4'	53:A:519:C:H5''	2.01	0.42
53:A:621:A:H2'	53:A:622:A:C8	2.55	0.42
53:A:1516:G:H2'	53:A:1518:A:OP2	2.19	0.42
54:01:128:C:H2'	54:01:129:C:C6	2.55	0.42
54:01:130:C:H2'	54:01:131:A:O4'	2.19	0.42
54:01:275:C:H2'	54:01:276:U:C4'	2.47	0.42
54:01:519:U:H2'	54:01:520:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:567:U:H2'	54:01:568:U:O4'	2.19	0.42
54:01:853:C:H2'	54:01:854:C:C6	2.54	0.42
54:01:1070:A:O2'	54:01:1071:G:P	2.78	0.42
54:01:1077:A:C2'	54:01:1078:U:H5'	2.47	0.42
54:01:1144:A:H2'	54:01:1145:C:C6	2.55	0.42
54:01:1525:A:H2'	54:01:1526:C:O4'	2.18	0.42
54:01:2632:A:H2'	54:01:2633:G:C8	2.53	0.42
55:02:106:G:H2'	55:02:107:G:O4'	2.20	0.42
59:Z:144:GLU:HG2	59:Z:147:GLU:OE1	2.20	0.42
59:Z:327:ARG:CD	59:Z:340:THR:HA	2.50	0.42
9:12:27:ARG:HD2	9:12:27:ARG:N	2.34	0.42
18:21:14:ALA:HB2	18:21:101:SER:HB3	2.01	0.42
19:22:61:LEU:HD11	19:22:82:LYS:HD3	2.02	0.42
42:L:58:ASN:OD1	42:L:60:PHE:HD2	2.03	0.42
43:M:76:ILE:O	43:M:80:MET:HG3	2.20	0.42
48:R:11:ARG:NH1	48:R:15:GLU:HB2	2.35	0.42
50:T:4:LYS:HZ1	53:A:61:G:P	2.43	0.42
54:01:796:C:H2'	54:01:797:G:H8	1.83	0.42
54:01:864:G:O2'	54:01:865:C:H5'	2.19	0.42
54:01:1023:U:O2'	54:01:1122:G:H5'	2.19	0.42
54:01:1483:G:H4'	54:01:1510:G:H21	1.85	0.42
1:04:244:VAL:HG12	1:04:250:GLN:HA	2.02	0.42
14:17:26:LEU:HD23	14:17:92:PHE:HD1	1.85	0.42
16:19:49:ARG:HH11	16:19:49:ARG:CB	2.32	0.42
17:20:14:VAL:HG21	17:20:98:ILE:CG1	2.50	0.42
17:20:88:GLY:H	54:01:1225:G:H5'	1.85	0.42
28:31:5:ARG:HG2	28:31:23:THR:HB	2.02	0.42
32:B:104:LYS:NZ	53:A:1073:U:H4'	2.35	0.42
32:B:163:ILE:O	32:B:185:ILE:HG23	2.19	0.42
32:B:202:ASN:ND2	32:B:204:ASP:OD1	2.53	0.42
35:E:10:LEU:HD12	35:E:11:GLN:N	2.35	0.42
35:E:15:ILE:HD11	35:E:37:VAL:HG23	2.02	0.42
38:H:31:LEU:O	38:H:35:ILE:HG13	2.20	0.42
50:T:79:THR:HG22	50:T:83:ASN:HD22	1.83	0.42
53:A:184:G:H2'	53:A:185:U:C6	2.54	0.42
53:A:1208:C:H2'	53:A:1209:C:C6	2.55	0.42
53:A:1230:C:H5'	56:W:30:G:H5'	2.02	0.42
53:A:1417:G:N2	53:A:1482:G:H2'	2.35	0.42
53:A:1470:U:O2'	53:A:1471:U:H5'	2.19	0.42
53:A:1526:G:H2'	53:A:1527:U:C6	2.55	0.42
54:01:155:A:H2'	54:01:156:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:302:C:H2'	54:01:303:G:C8	2.55	0.42
54:01:333:G:H2'	54:01:333:G:N3	2.35	0.42
54:01:386:G:H3'	54:01:387:U:C5'	2.49	0.42
54:01:445:C:O2'	54:01:446:G:H5'	2.20	0.42
54:01:863:A:H4'	55:02:100:G:N2	2.34	0.42
54:01:1471:G:H2'	54:01:1472:C:C6	2.55	0.42
54:01:2215:C:H2'	54:01:2216:G:H8	1.85	0.42
54:01:2464:G:H2'	54:01:2465:C:C6	2.54	0.42
59:Z:13:ASN:O	59:Z:98:MET:HA	2.20	0.42
59:Z:44:ARG:HD2	59:Z:48:GLN:OE1	2.20	0.42
59:Z:69:TYR:CE1	59:Z:78:HIS:HB2	2.54	0.42
59:Z:170:VAL:CG1	59:Z:194:PHE:HE2	2.32	0.42
59:Z:246:GLY:H	59:Z:250:THR:CG2	2.33	0.42
1:04:62:ARG:HD2	1:04:83:ASP:CG	2.45	0.42
4:07:58:ALA:HB1	4:07:139:GLU:HB3	2.02	0.42
5:08:87:GLN:NE2	5:08:162:ARG:HD2	2.29	0.42
8:11:40:ALA:HA	8:11:43:ALA:HB3	2.02	0.42
9:12:73:VAL:CG1	9:12:86:GLN:HB2	2.50	0.42
11:14:110:VAL:HG21	11:14:127:VAL:HG22	2.02	0.42
14:17:105:ALA:HA	14:17:108:ASP:OD2	2.19	0.42
19:22:50:LEU:HD12	19:22:50:LEU:N	2.35	0.42
20:23:42:LYS:CE	54:01:499:U:H5''	2.44	0.42
28:31:37:LYS:HB2	28:31:48:TYR:CE2	2.55	0.42
29:32:1:MET:HE1	29:32:3:ARG:NH1	2.35	0.42
38:H:94:VAL:HB	38:H:99:GLY:C	2.45	0.42
40:J:15:HIS:HB3	40:J:70:HIS:CD2	2.55	0.42
44:N:2:LYS:HD2	53:A:1049:U:O2'	2.19	0.42
46:P:79:ASN:HB2	46:P:82:ALA:HB3	2.01	0.42
49:S:52:ASN:CG	49:S:53:GLY:N	2.78	0.42
53:A:363:A:H2'	53:A:364:A:O4'	2.19	0.42
54:01:326:G:H2'	54:01:327:G:C8	2.55	0.42
54:01:492:A:H2'	54:01:493:G:O4'	2.20	0.42
54:01:828:U:H4'	54:01:831:G:N1	2.35	0.42
54:01:1123:C:H2'	54:01:1124:G:C8	2.55	0.42
54:01:1923:U:H2'	54:01:1924:C:H6	1.85	0.42
54:01:2277:G:C3'	54:01:2278:A:H5''	2.49	0.42
54:01:2790:U:H5''	54:01:2791:G:OP1	2.20	0.42
1:04:252:LYS:HD3	54:01:1901:A:H4'	2.02	0.41
4:07:35:LEU:HD21	4:07:98:PHE:CZ	2.55	0.41
4:07:151:LEU:HA	54:01:2305:U:C4	2.55	0.41
8:11:25:PRO:HB2	58:Y:56:C:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:12:113:PRO:HB2	54:01:557:C:H5''	2.02	0.41
13:16:2:ARG:CB	13:16:5:LYS:HD2	2.49	0.41
22:25:36:GLN:CD	22:25:39:THR:HA	2.45	0.41
23:26:15:ASN:HD22	54:01:381:G:H5''	1.85	0.41
24:27:42:LEU:O	24:27:46:VAL:HG23	2.20	0.41
31:34:36:ARG:HD3	54:01:2742:G:OP1	2.19	0.41
32:B:51:GLU:O	32:B:54:ALA:HB3	2.20	0.41
35:E:81:GLN:HG2	35:E:146:MET:HE3	2.02	0.41
38:H:84:ILE:CG2	38:H:86:LYS:HE3	2.50	0.41
49:S:35:ARG:HB3	49:S:35:ARG:HH11	1.85	0.41
53:A:769:G:O2'	53:A:770:C:H5'	2.20	0.41
53:A:1173:U:H2'	53:A:1174:G:H8	1.85	0.41
53:A:1256:A:H1'	53:A:1258:G:N9	2.34	0.41
54:01:225:C:H2'	54:01:226:A:O4'	2.20	0.41
54:01:540:C:H2'	54:01:541:A:C8	2.55	0.41
54:01:948:C:H2'	54:01:949:G:H8	1.84	0.41
54:01:1314:C:H42	54:01:1338:G:H1	1.68	0.41
54:01:1701:A:H2'	54:01:1702:G:H5'	2.02	0.41
54:01:2038:G:H2'	54:01:2039:U:O4'	2.19	0.41
54:01:2215:C:H2'	54:01:2216:G:C8	2.54	0.41
54:01:2791:G:H2'	54:01:2792:A:O4'	2.20	0.41
59:Z:91:MET:SD	59:Z:91:MET:C	3.03	0.41
59:Z:305:GLU:N	59:Z:392:LEU:HD23	2.35	0.41
1:04:257:ARG:HH21	1:04:266:ILE:CD1	2.23	0.41
4:07:41:GLU:O	4:07:48:LEU:HD23	2.20	0.41
8:11:83:ALA:HA	8:11:100:ILE:HD11	2.02	0.41
11:14:69:ARG:HH11	11:14:69:ARG:HG3	1.85	0.41
22:25:17:LEU:HD11	22:25:37:ARG:NH2	2.35	0.41
26:29:46:GLY:HA2	26:29:49:ARG:NH2	2.35	0.41
28:31:16:THR:HG21	28:31:39:ASP:OD2	2.21	0.41
36:F:12:PRO:HD2	36:F:54:LEU:CD2	2.32	0.41
39:I:46:VAL:HG21	39:I:75:ALA:HB1	2.01	0.41
39:I:54:VAL:HG23	39:I:54:VAL:O	2.20	0.41
47:Q:16:MET:HG3	47:Q:19:SER:OG	2.20	0.41
53:A:179:A:H2'	53:A:180:U:O4'	2.20	0.41
53:A:690:G:H2'	53:A:691:G:O4'	2.20	0.41
54:01:967:U:H2'	54:01:968:C:C6	2.55	0.41
54:01:1182:G:H2'	54:01:1183:U:O4'	2.20	0.41
54:01:1368:G:H2'	54:01:1369:G:H8	1.85	0.41
54:01:2150:C:H2'	54:01:2151:U:O4'	2.20	0.41
54:01:2197:U:H1'	54:01:2198:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:02:60:C:H2'	55:02:61:G:H8	1.85	0.41
59:Z:198:TYR:O	59:Z:200:PRO:HD3	2.20	0.41
2:05:98:VAL:HG22	2:05:180:VAL:HG13	2.03	0.41
2:05:129:THR:HG23	2:05:140:HIS:O	2.20	0.41
3:06:1:MET:HE3	3:06:20:GLY:HA3	2.00	0.41
6:09:57:LYS:O	6:09:61:VAL:HG22	2.20	0.41
8:11:55:PRO:CG	8:11:71:LYS:HE2	2.50	0.41
15:18:29:VAL:CG1	15:18:79:VAL:HG22	2.51	0.41
21:24:80:HIS:ND1	21:24:81:PRO:CD	2.81	0.41
35:E:155:LYS:HB2	35:E:155:LYS:NZ	2.35	0.41
40:J:53:ILE:HG13	44:N:84:ARG:NE	2.35	0.41
52:03:211:LYS:HG2	54:01:2177:C:H4'	2.02	0.41
53:A:46:G:OP1	53:A:307:C:H4'	2.20	0.41
53:A:756:C:H2'	53:A:757:U:O4'	2.21	0.41
54:01:214:G:H2'	54:01:215:G:C8	2.55	0.41
54:01:705:A:C2	54:01:727:A:H1'	2.56	0.41
54:01:736:C:H2'	54:01:737:C:H6	1.86	0.41
54:01:2266:A:H4'	54:01:2267:A:N3	2.35	0.41
54:01:2347:C:H5	54:01:2382:G:H1'	1.83	0.41
56:X:38:A:H2'	56:X:39:C:O4'	2.20	0.41
6:09:74:ALA:C	6:09:76:GLU:HG3	2.46	0.41
10:13:70:ARG:HG2	10:13:70:ARG:HH11	1.85	0.41
21:24:48:MET:HE3	21:24:51:GLN:HE21	1.85	0.41
26:29:45:THR:O	26:29:49:ARG:HG2	2.20	0.41
33:C:173:PRO:HB2	33:C:176:THR:OG1	2.20	0.41
34:D:7:LYS:HE2	53:A:408:A:OP2	2.21	0.41
36:F:36:ILE:HD11	36:F:62:MET:HB3	2.02	0.41
43:M:26:LYS:O	43:M:29:SER:HB3	2.20	0.41
47:Q:7:LEU:HD23	47:Q:24:ILE:HD13	2.01	0.41
47:Q:17:GLU:OE2	53:A:255:G:H1'	2.20	0.41
49:S:57:VAL:HA	49:S:58:PRO:HD3	1.91	0.41
52:03:53:ARG:CB	56:X:62:C:H4'	2.50	0.41
53:A:628:G:H2'	53:A:629:A:C8	2.54	0.41
53:A:985:C:H2'	53:A:986:U:C6	2.55	0.41
53:A:1052:U:H2'	53:A:1200:C:N4	2.35	0.41
53:A:1405:G:O2'	53:A:1406:U:H5'	2.20	0.41
54:01:168:G:H2'	54:01:169:G:C8	2.56	0.41
54:01:357:C:H2'	54:01:358:U:C6	2.55	0.41
54:01:634:C:H2'	54:01:635:C:H6	1.85	0.41
54:01:1106:G:H5'	54:01:1106:G:H8	1.85	0.41
54:01:1336:A:H2'	54:01:1337:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:2590:A:H2'	54:01:2591:C:H6	1.84	0.41
56:W:47:U:H3'	56:W:48:C:C5'	2.50	0.41
59:Z:133:PHE:CD1	59:Z:170:VAL:HG23	2.53	0.41
59:Z:299:LYS:HD3	59:Z:299:LYS:C	2.45	0.41
5:08:93:TYR:CD1	5:08:106:LEU:HA	2.56	0.41
7:10:48:ALA:HB3	7:10:51:TYR:OH	2.20	0.41
8:11:7:TYR:HB3	8:11:59:THR:HG23	2.03	0.41
17:20:14:VAL:HG11	17:20:98:ILE:HG13	2.02	0.41
19:22:7:LEU:HD22	19:22:46:ALA:CA	2.50	0.41
25:28:46:MET:O	25:28:49:ALA:HB3	2.21	0.41
26:29:58:ASP:OD1	26:29:58:ASP:N	2.53	0.41
32:B:16:GLY:HA3	32:B:39:ILE:HA	2.02	0.41
33:C:146:LYS:N	33:C:146:LYS:HD2	2.36	0.41
33:C:147:GLY:HA3	33:C:171:ARG:O	2.20	0.41
37:G:42:VAL:O	37:G:46:LEU:HD13	2.21	0.41
39:I:30:ASN:O	39:I:31:GLN:HB2	2.20	0.41
51:U:11:PHE:O	51:U:13:VAL:N	2.54	0.41
52:03:31:LYS:HA	52:03:34:ALA:CB	2.41	0.41
53:A:170:U:O2'	53:A:171:A:H5'	2.21	0.41
54:01:570:G:O2'	54:01:571:U:H5'	2.20	0.41
54:01:1282:U:H2'	54:01:1283:G:O4'	2.21	0.41
54:01:1858:A:H1'	54:01:1885:A:C2	2.55	0.41
54:01:2448:A:H3'	54:01:2449:U:H2'	2.01	0.41
54:01:2713:U:H3'	54:01:2714:G:H5''	2.03	0.41
54:01:2888:C:H2'	54:01:2889:C:C6	2.55	0.41
55:02:100:G:H2'	55:02:101:A:O4'	2.20	0.41
56:X:27:U:H2'	56:X:28:C:C6	2.56	0.41
57:V:8:A:H2'	57:V:9:G:C8	2.56	0.41
58:Y:4:C:H2'	58:Y:5:G:H8	1.85	0.41
59:Z:22:HIS:HB3	59:Z:104:VAL:HG12	2.02	0.41
59:Z:91:MET:HE1	59:Z:121:LEU:HD12	2.02	0.41
59:Z:115:THR:O	59:Z:119:ILE:HG13	2.19	0.41
59:Z:121:LEU:O	59:Z:125:VAL:N	2.54	0.41
59:Z:145:LEU:O	59:Z:149:VAL:HG23	2.21	0.41
59:Z:227:VAL:CG1	59:Z:276:VAL:HB	2.50	0.41
2:05:207:VAL:HG21	54:01:2771:C:H5''	2.02	0.41
4:07:70:ARG:HG2	4:07:70:ARG:NH2	2.36	0.41
6:09:111:ALA:HB3	6:09:114:GLU:OE1	2.21	0.41
7:10:118:ILE:HD12	7:10:118:ILE:HA	1.86	0.41
8:11:52:LEU:HA	8:11:53:PRO:HD3	1.90	0.41
9:12:2:LYS:HB3	54:01:995:C:H42	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:C:196:GLY:HA3	53:A:1057:G:O3'	2.20	0.41
34:D:165:GLU:O	34:D:166:LYS:HB2	2.21	0.41
40:J:32:THR:OG1	40:J:82:LYS:HB3	2.21	0.41
40:J:53:ILE:HG12	53:A:1060:U:H5'	2.02	0.41
53:A:778:G:H2'	53:A:779:C:O4'	2.20	0.41
53:A:1436:U:H2'	53:A:1437:A:C8	2.54	0.41
54:01:287:G:H2'	54:01:288:U:C6	2.56	0.41
54:01:922:C:H2'	54:01:923:G:H8	1.86	0.41
54:01:962:G:O2'	54:01:963:U:H5'	2.20	0.41
54:01:1039:A:H2	54:01:1116:G:H22	1.68	0.41
54:01:1283:G:H1'	54:01:1329:U:O2	2.21	0.41
54:01:1842:G:H2'	54:01:1843:C:C6	2.56	0.41
54:01:2163:A:N3	54:01:2164:C:H5'	2.36	0.41
2:05:177:VAL:HG22	2:05:178:VAL:N	2.36	0.41
4:07:3:LEU:HA	4:07:6:TYR:HB3	2.03	0.41
4:07:94:ARG:HG2	26:29:9:TYR:CE2	2.56	0.41
12:15:5:LYS:HD2	12:15:6:ARG:CG	2.50	0.41
17:20:27:ILE:HG13	17:20:33:VAL:HG11	2.02	0.41
20:23:9:GLU:OE2	20:23:21:ARG:HB3	2.20	0.41
33:C:112:ALA:HB2	33:C:182:ASP:HB3	2.03	0.41
37:G:145:GLU:HA	37:G:148:LYS:HB2	2.02	0.41
38:H:10:LEU:HD22	38:H:74:ILE:HD11	2.02	0.41
40:J:81:GLU:O	40:J:84:VAL:HG12	2.21	0.41
47:Q:46:HIS:HA	47:Q:70:LYS:HE3	2.03	0.41
52:03:164:ARG:HD2	52:03:165:ASN:O	2.20	0.41
53:A:39:G:O2'	53:A:40:C:H5'	2.20	0.41
54:01:566:U:H2'	54:01:567:U:O4'	2.21	0.41
54:01:633:A:H2'	54:01:634:C:H5'	2.03	0.41
54:01:799:G:H5'	54:01:800:A:H2'	2.01	0.41
54:01:2143:C:H2'	54:01:2144:G:C8	2.56	0.41
54:01:2286:G:H4'	54:01:2287:A:O5'	2.21	0.41
58:Y:65:G:H2'	58:Y:66:U:C6	2.55	0.41
59:Z:112:MET:HB2	59:Z:115:THR:OG1	2.21	0.41
59:Z:328:PRO:CD	59:Z:341:ILE:HD11	2.51	0.41
1:04:143:VAL:HB	1:04:153:LEU:HB2	2.02	0.41
1:04:154:ALA:HB2	1:04:161:VAL:HG23	2.01	0.41
6:09:87:GLU:HG2	36:F:21:MET:HE2	2.03	0.41
20:23:6:ARG:HB2	54:01:85:G:P	2.60	0.41
20:23:82:VAL:HG12	20:23:83:GLY:N	2.35	0.41
33:C:150:VAL:HG12	33:C:199:VAL:HG23	2.03	0.41
35:E:86:GLY:N	35:E:93:VAL:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:F:64:VAL:CG2	36:F:65:GLU:H	2.30	0.41
36:F:97:THR:O	36:F:98:GLU:HB2	2.20	0.41
41:K:70:ALA:O	41:K:74:LYS:HG3	2.20	0.41
41:K:115:ILE:HD12	51:U:23:GLU:OE1	2.20	0.41
42:L:29:LYS:CG	42:L:56:LEU:HD22	2.51	0.41
43:M:100:ARG:HH11	43:M:100:ARG:HG3	1.86	0.41
44:N:41:TRP:CZ2	49:S:10:ILE:HD11	2.56	0.41
47:Q:13:SER:H	47:Q:21:VAL:CG1	2.34	0.41
52:O3:189:LEU:C	52:O3:189:LEU:HD13	2.46	0.41
53:A:246:A:N3	53:A:247:G:H1'	2.35	0.41
53:A:272:C:H2'	53:A:273:U:C6	2.56	0.41
54:O1:8:C:H2'	54:O1:9:G:O4'	2.21	0.41
54:O1:438:G:H2'	54:O1:439:A:C8	2.56	0.41
54:O1:783:A:H2'	54:O1:784:G:H5'	2.03	0.41
54:O1:2128:G:H2'	54:O1:2129:C:O4'	2.20	0.41
54:O1:2249:U:H3'	54:O1:2250:G:C5'	2.50	0.41
54:O1:2267:A:C5'	54:O1:2268:A:H5'	2.48	0.41
54:O1:2389:G:H5''	54:O1:2390:U:O4'	2.21	0.41
59:Z:227:VAL:HG11	59:Z:292:LEU:HD11	2.02	0.41
59:Z:305:GLU:C	59:Z:389:ALA:HB3	2.46	0.41
3:O6:88:ARG:O	3:O6:90:GLN:HG2	2.20	0.41
4:O7:24:VAL:HG12	55:O2:55:U:H4'	2.03	0.41
6:O9:94:ILE:N	6:O9:94:ILE:HD12	2.36	0.41
7:10:91:ALA:O	7:10:92:ALA:HB3	2.21	0.41
8:11:9:LYS:HG2	8:11:57:VAL:HG22	2.03	0.41
12:15:86:LYS:HG3	54:O1:956:G:OP1	2.21	0.41
13:16:71:ARG:CZ	54:O1:2708:G:H1'	2.51	0.41
14:17:30:ARG:HA	14:17:35:ILE:HG13	2.02	0.41
19:22:54:GLU:HB3	19:22:88:LYS:HE3	2.02	0.41
20:23:45:GLN:HE22	20:23:54:PRO:HD2	1.86	0.41
23:26:31:ASN:CG	54:O1:2230:G:H1'	2.46	0.41
29:32:6:GLN:HA	29:32:7:PRO:HD2	1.93	0.41
29:32:34:ARG:NH2	29:32:39:ARG:HD2	2.31	0.41
32:B:191:ASP:OD1	32:B:193:ASP:HB2	2.21	0.41
32:B:206:ILE:HA	32:B:209:VAL:HG22	2.02	0.41
33:C:5:HIS:CG	44:N:88:MET:HB3	2.56	0.41
37:G:22:LEU:C	37:G:22:LEU:HD12	2.45	0.41
38:H:94:VAL:HG21	38:H:100:ILE:O	2.21	0.41
39:I:40:ARG:C	39:I:44:ARG:HH21	2.29	0.41
40:J:15:HIS:O	40:J:18:ILE:HG22	2.21	0.41
41:K:127:ARG:HH22	53:A:1522:U:H5''	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:M:56:ARG:HA	43:M:59:VAL:HG22	2.02	0.41
45:O:52:ARG:HH11	45:O:52:ARG:HG2	1.85	0.41
47:Q:65:PRO:O	53:A:264:C:O2'	2.38	0.41
48:R:41:SER:HB2	48:R:51:GLN:HE21	1.86	0.41
52:O3:33:LEU:HD22	52:O3:220:ALA:CB	2.50	0.41
52:O3:41:SER:O	52:O3:217:THR:HG23	2.21	0.41
53:A:163:C:H2'	53:A:164:G:O4'	2.21	0.41
53:A:599:C:H2'	53:A:600:A:C8	2.56	0.41
53:A:666:G:H2'	53:A:667:G:C8	2.52	0.41
53:A:704:A:H2'	53:A:705:G:O4'	2.21	0.41
53:A:1030:U:H2'	53:A:1031:C:H5'	2.03	0.41
53:A:1128:C:O2'	53:A:1129:C:H5'	2.21	0.41
53:A:1137:C:H5'	53:A:1138:G:C5'	2.45	0.41
53:A:1368:A:O2'	53:A:1369:C:H5'	2.20	0.41
53:A:1509:C:O2'	53:A:1510:C:H5'	2.20	0.41
54:O1:195:A:H2'	54:O1:198:C:N4	2.36	0.41
54:O1:974:G:H1'	54:O1:975:A:C8	2.56	0.41
54:O1:1363:C:H2'	54:O1:1364:G:C8	2.56	0.41
54:O1:1475:G:O2'	54:O1:1476:U:P	2.78	0.41
54:O1:2066:C:O2'	54:O1:2067:G:H5'	2.21	0.41
54:O1:2181:U:H2'	54:O1:2182:U:O4'	2.21	0.41
54:O1:2220:U:H2'	54:O1:2221:G:C8	2.56	0.41
54:O1:2692:G:O2'	54:O1:2693:G:H5'	2.21	0.41
54:O1:2876:G:H2'	54:O1:2877:G:O4'	2.20	0.41
56:X:71:C:H2'	56:X:72:A:C8	2.56	0.41
59:Z:129:TYR:HB3	59:Z:199:ILE:CG1	2.51	0.41
59:Z:134:LEU:HB3	59:Z:146:LEU:HD12	2.03	0.41
59:Z:137:CYS:HB3	59:Z:184:TRP:CH2	2.56	0.41
1:O4:96:LYS:HD2	54:O1:1490:A:H62	1.86	0.41
1:O4:231:HIS:HA	1:O4:241:LYS:HD2	2.03	0.41
3:O6:47:LYS:O	3:O6:83:VAL:HB	2.20	0.41
4:O7:82:TYR:CD1	4:O7:83:PRO:HD2	2.56	0.41
7:10:33:VAL:HA	54:O1:1055:G:H4'	2.02	0.41
10:13:93:GLN:HA	10:13:94:PRO:HD2	1.93	0.41
11:14:42:SER:HB2	54:O1:672:C:H5	1.86	0.41
14:17:33:ARG:HG2	14:17:34:HIS:CD2	2.56	0.41
16:19:5:ARG:HH21	16:19:5:ARG:CG	2.34	0.41
20:23:97:SER:O	20:23:98:ASN:CB	2.68	0.41
32:B:34:ARG:HG2	32:B:34:ARG:HH11	1.85	0.41
32:B:76:SER:HA	32:B:79:VAL:CG2	2.51	0.41
35:E:28:ARG:NH1	53:A:15:G:H4'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:F:38:ARG:NH1	36:F:98:GLU:H	2.19	0.41
51:U:64:ALA:C	51:U:66:ARG:H	2.29	0.41
52:03:38:PHE:HB2	52:03:39:VAL:H	1.75	0.41
52:03:67:HIS:CD2	52:03:188:ASN:HD21	2.39	0.41
52:03:170:ILE:N	52:03:170:ILE:HD12	2.36	0.41
52:03:207:VAL:O	52:03:210:LYS:HG3	2.21	0.41
53:A:483:C:H2'	53:A:484:G:C8	2.56	0.41
53:A:608:A:H2'	53:A:609:A:O4'	2.21	0.41
53:A:1324:A:H2'	53:A:1325:C:O4'	2.21	0.41
53:A:1424:U:H2'	53:A:1425:U:O4'	2.21	0.41
54:01:1499:C:H2'	54:01:1500:G:C8	2.55	0.41
54:01:1853:A:H2'	54:01:1854:A:C8	2.56	0.41
54:01:1917:U:O2'	54:01:1918:A:H5'	2.21	0.41
55:02:49:C:H2'	55:02:50:A:C8	2.56	0.41
59:Z:103:LEU:HB3	59:Z:132:VAL:HG22	2.03	0.41
59:Z:225:THR:O	59:Z:225:THR:HG22	2.19	0.41
3:06:21:ARG:HH21	3:06:106:LYS:HE2	1.86	0.40
6:09:99:ILE:HD12	6:09:117:LEU:HD21	2.02	0.40
7:10:98:GLU:O	7:10:102:ALA:N	2.53	0.40
8:11:134:SER:HB2	8:11:135:MET:HE2	2.02	0.40
13:16:68:ALA:HA	54:01:2707:U:O2'	2.20	0.40
15:18:102:ARG:NH1	15:18:102:ARG:HG3	2.36	0.40
22:25:14:ALA:HB1	54:01:2271:G:OP1	2.21	0.40
33:C:123:LEU:HD13	33:C:195:ILE:HG21	2.02	0.40
34:D:144:ILE:HB	34:D:149:LYS:HZ1	1.85	0.40
36:F:42:TRP:HE3	36:F:45:ARG:NH2	2.19	0.40
36:F:88:MET:HB3	48:R:63:TYR:HE2	1.85	0.40
38:H:80:PRO:HG2	53:A:878:A:H5'	2.02	0.40
43:M:84:CYS:HB2	49:S:72:GLU:OE1	2.21	0.40
48:R:25:ILE:HA	48:R:28:LEU:HB3	2.03	0.40
51:U:34:ARG:HD3	51:U:34:ARG:HA	1.94	0.40
52:03:27:ILE:HA	52:03:30:LEU:HG	2.03	0.40
53:A:321:A:O2'	53:A:322:C:H5'	2.21	0.40
53:A:641:U:H4'	53:A:642:A:H8	1.85	0.40
53:A:744:C:H2'	53:A:745:G:H8	1.86	0.40
53:A:1026:G:H2'	53:A:1027:C:C6	2.55	0.40
53:A:1413:A:H2	53:A:1487:G:H22	1.69	0.40
54:01:186:G:H2'	54:01:187:G:H8	1.85	0.40
54:01:548:G:H2'	54:01:549:G:O4'	2.21	0.40
54:01:553:G:H2'	54:01:554:U:O4'	2.20	0.40
54:01:634:C:H6	54:01:634:C:O5'	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:01:772:C:O2'	54:01:773:U:H5'	2.20	0.40
54:01:808:G:H2'	54:01:809:G:C8	2.56	0.40
54:01:1554:U:O2'	54:01:1555:G:H5''	2.21	0.40
54:01:2214:C:H2'	54:01:2215:C:H5'	2.03	0.40
55:02:60:C:H2'	55:02:61:G:C8	2.56	0.40
55:02:65:U:H3'	55:02:108:A:H61	1.86	0.40
55:02:119:A:H2'	55:02:120:A:O4'	2.22	0.40
59:Z:18:GLY:O	59:Z:118:HIS:CD2	2.74	0.40
59:Z:214:ILE:HD12	59:Z:290:GLN:CB	2.37	0.40
59:Z:304:PHE:O	59:Z:359:VAL:HG13	2.21	0.40
59:Z:321:PRO:CB	59:Z:349:MET:HE3	2.51	0.40
7:10:93:ALA:O	7:10:129:LEU:HD13	2.20	0.40
9:12:136:GLN:HE21	54:01:2899:A:H5''	1.85	0.40
11:14:110:VAL:CG2	11:14:127:VAL:HG22	2.51	0.40
13:16:12:ARG:HD3	13:16:16:HIS:ND1	2.36	0.40
15:18:26:GLU:HA	15:18:43:GLU:HA	2.03	0.40
18:21:81:SER:O	18:21:83:LYS:HD2	2.21	0.40
23:26:2:ARG:HD2	23:26:29:LEU:HD22	2.02	0.40
23:26:6:VAL:HG23	23:26:50:VAL:HG12	2.03	0.40
27:30:13:GLY:HA3	54:01:16:C:H5''	2.04	0.40
34:D:131:ILE:HG23	53:A:403:C:H5'	2.03	0.40
34:D:183:ARG:HG2	34:D:183:ARG:HH11	1.85	0.40
37:G:12:LEU:CD1	37:G:13:PRO:HD2	2.44	0.40
43:M:7:ASN:HD22	43:M:9:PRO:HD3	1.85	0.40
49:S:77:ARG:HH11	53:A:1222:G:H5''	1.85	0.40
52:03:19:LYS:HZ3	52:03:21:TYR:HD1	1.68	0.40
52:03:60:ARG:HG3	52:03:164:ARG:HB2	2.03	0.40
53:A:349:A:H2'	53:A:350:G:O4'	2.22	0.40
53:A:476:U:H2'	53:A:477:C:C6	2.57	0.40
53:A:986:U:H2'	53:A:987:G:O4'	2.20	0.40
54:01:1148:U:H2'	54:01:1149:G:O4'	2.22	0.40
54:01:1179:G:C4	54:01:1180:U:H1'	2.56	0.40
54:01:1300:G:H4'	54:01:1301:A:H5''	2.04	0.40
54:01:1336:A:H2'	54:01:1337:G:C8	2.56	0.40
54:01:1637:A:H5'	54:01:1760:C:O2'	2.21	0.40
59:Z:206:ILE:HG21	59:Z:269:ARG:HB2	2.03	0.40
59:Z:225:THR:HG22	59:Z:278:LEU:HB2	2.02	0.40
59:Z:259:GLU:HG3	59:Z:263:LYS:O	2.21	0.40
59:Z:303:LYS:CG	59:Z:361:THR:HG22	2.33	0.40
1:04:245:THR:C	1:04:247:TRP:H	2.29	0.40
7:10:51:TYR:OH	7:10:89:PRO:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:11:24:GLY:HA3	8:11:25:PRO:HD3	1.93	0.40
11:14:109:LYS:HE2	54:01:636:G:N7	2.35	0.40
12:15:73:ILE:HD13	12:15:73:ILE:HA	1.94	0.40
15:18:105:LYS:HG3	53:A:1432:G:H5''	2.02	0.40
19:22:15:HIS:HE1	19:22:17:SER:HB3	1.86	0.40
35:E:114:LEU:O	35:E:119:VAL:HG22	2.21	0.40
36:F:14:GLN:HB3	36:F:17:GLN:CD	2.46	0.40
37:G:3:ARG:HH11	37:G:4:ARG:NH1	2.18	0.40
37:G:55:LYS:HB2	37:G:60:ALA:HB2	2.01	0.40
39:I:121:ARG:HH11	53:A:1345:U:H5''	1.86	0.40
52:03:33:LEU:HD22	52:03:220:ALA:HB3	2.03	0.40
52:03:166:ASP:OD2	52:03:170:ILE:HB	2.21	0.40
53:A:5:U:H4'	53:A:6:G:C5	2.57	0.40
53:A:746:A:H2'	53:A:747:A:C8	2.57	0.40
53:A:1090:U:O2'	53:A:1091:U:H5'	2.22	0.40
54:01:542:C:H2'	54:01:543:G:H5'	2.02	0.40
54:01:839:U:H2'	54:01:840:C:H6	1.80	0.40
54:01:1060:U:C5'	54:01:1062:G:H5'	2.51	0.40
54:01:1190:G:H2'	54:01:1191:G:H8	1.86	0.40
54:01:1360:G:H2'	54:01:1361:G:H5'	2.04	0.40
54:01:1548:A:H2'	54:01:1549:A:H8	1.86	0.40
54:01:1981:A:H5''	54:01:1982:U:OP2	2.21	0.40
54:01:2290:G:H2'	54:01:2291:U:O4'	2.20	0.40
55:02:80:U:H2'	55:02:81:G:H8	1.85	0.40
56:X:21:A:N6	56:X:47:U:H5''	2.36	0.40
59:Z:148:LEU:HD12	59:Z:149:VAL:N	2.36	0.40
3:06:29:HIS:HA	3:06:32:VAL:HG12	2.03	0.40
4:07:94:ARG:HH22	26:29:1:MET:HB3	1.86	0.40
8:11:55:PRO:HG2	8:11:71:LYS:HE2	2.03	0.40
12:15:41:LEU:HB2	12:15:46:ILE:HD11	2.04	0.40
14:17:49:VAL:HG21	14:17:82:ALA:HA	2.03	0.40
17:20:93:PHE:HE2	17:20:95:ASP:OD2	2.05	0.40
20:23:45:GLN:NE2	20:23:55:GLY:H	2.18	0.40
21:24:56:PHE:CE1	21:24:61:LEU:HD21	2.56	0.40
27:30:9:ARG:HB2	54:01:17:G:OP1	2.22	0.40
32:B:89:PHE:CE1	32:B:152:ASP:HB2	2.52	0.40
33:C:68:HIS:HA	33:C:103:ALA:O	2.21	0.40
33:C:149:LYS:HG2	33:C:200:TRP:HB2	2.04	0.40
41:K:87:GLY:N	41:K:113:THR:HG22	2.35	0.40
46:P:6:LEU:HD13	46:P:17:TYR:CG	2.56	0.40
46:P:20:VAL:CG2	46:P:21:VAL:N	2.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Q:65:PRO:HG3	53:A:234:C:O2'	2.21	0.40
50:T:8:LYS:O	50:T:12:GLN:N	2.50	0.40
52:03:33:LEU:HD13	52:03:220:ALA:HB3	2.03	0.40
53:A:460:A:H2'	53:A:461:A:C8	2.56	0.40
53:A:505:G:H2'	53:A:506:G:C8	2.57	0.40
53:A:751:U:H2'	53:A:752:G:O4'	2.21	0.40
54:01:20:C:H2'	54:01:21:A:C8	2.57	0.40
54:01:878:A:H5'	54:01:879:G:OP2	2.21	0.40
54:01:948:C:OP1	54:01:962:G:OP1	2.39	0.40
54:01:1420:A:H5'	54:01:1421:G:OP2	2.21	0.40
54:01:1486:U:H2'	54:01:1487:U:C6	2.56	0.40
54:01:2024:G:H2'	54:01:2025:C:O4'	2.21	0.40
54:01:2263:C:H2'	54:01:2264:C:O4'	2.21	0.40
58:Y:26:A:H3'	58:Y:27:G:C8	2.56	0.40
59:Z:261:PHE:O	59:Z:262:ARG:HG2	2.21	0.40
1:04:135:PRO:HG2	36:F:80:PHE:CD1	2.55	0.40
4:07:92:GLY:O	4:07:95:MET:HG3	2.21	0.40
17:20:53:PHE:O	17:20:54:VAL:C	2.64	0.40
21:24:20:LEU:HD11	21:24:41:GLU:CG	2.50	0.40
22:25:30:GLY:N	22:25:57:ALA:O	2.49	0.40
39:I:38:PHE:O	39:I:41:GLU:HB2	2.22	0.40
46:P:40:ASN:ND2	46:P:43:ALA:HB2	2.36	0.40
47:Q:47:ASP:HB2	47:Q:74:LEU:HD22	2.04	0.40
47:Q:59:GLU:HB3	47:Q:75:VAL:HB	2.02	0.40
51:U:28:LEU:HD23	51:U:28:LEU:O	2.21	0.40
53:A:119:A:H4'	53:A:120:A:C8	2.56	0.40
53:A:357:G:O2'	53:A:358:U:H5'	2.22	0.40
53:A:687:A:N3	53:A:688:G:H1'	2.36	0.40
53:A:1251:A:H2'	53:A:1252:A:O4'	2.21	0.40
53:A:1254:A:H2'	53:A:1255:G:C8	2.56	0.40
54:01:20:C:H2'	54:01:21:A:H8	1.86	0.40
54:01:222:A:N6	54:01:232:G:H1'	2.36	0.40
54:01:809:G:O2'	54:01:810:U:H5'	2.21	0.40
54:01:1045:C:H5'	54:01:1046:A:C5'	2.51	0.40
54:01:1307:A:H2'	54:01:1308:A:H5'	2.04	0.40
54:01:2078:C:O2'	54:01:2079:U:H5'	2.21	0.40
54:01:2146:C:H4'	54:01:2147:A:C4	2.56	0.40
54:01:2619:C:O2'	54:01:2620:C:H5'	2.21	0.40
54:01:2685:G:H2'	54:01:2686:G:H8	1.86	0.40
54:01:2752:C:H2'	54:01:2753:A:O4'	2.22	0.40
56:X:59:A:C2'	56:X:60:U:H5'	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Y:68:C:H2'	58:Y:69:G:C8	2.56	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	04	269/271 (99%)	233 (87%)	33 (12%)	3 (1%)	11	43
2	05	207/209 (99%)	184 (89%)	23 (11%)	0	100	100
3	06	199/201 (99%)	175 (88%)	22 (11%)	2 (1%)	12	45
4	07	175/177 (99%)	154 (88%)	20 (11%)	1 (1%)	21	54
5	08	174/176 (99%)	155 (89%)	13 (8%)	6 (3%)	3	23
6	09	147/149 (99%)	117 (80%)	26 (18%)	4 (3%)	4	27
7	10	129/131 (98%)	97 (75%)	22 (17%)	10 (8%)	1	8
8	11	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	2	22
9	12	140/142 (99%)	132 (94%)	7 (5%)	1 (1%)	18	51
10	13	120/122 (98%)	101 (84%)	17 (14%)	2 (2%)	7	35
11	14	141/143 (99%)	112 (79%)	23 (16%)	6 (4%)	2	18
12	15	134/136 (98%)	115 (86%)	18 (13%)	1 (1%)	18	51
13	16	118/120 (98%)	102 (86%)	14 (12%)	2 (2%)	7	35
14	17	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
15	18	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
16	19	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
17	20	101/103 (98%)	83 (82%)	16 (16%)	2 (2%)	6	32
18	21	108/110 (98%)	95 (88%)	11 (10%)	2 (2%)	6	33
19	22	91/93 (98%)	78 (86%)	13 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	23	100/102 (98%)	83 (83%)	14 (14%)	3 (3%)	3	25
21	24	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
22	25	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	26	75/77 (97%)	66 (88%)	9 (12%)	0	100	100
24	27	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	36
25	28	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	29	64/66 (97%)	51 (80%)	13 (20%)	0	100	100
27	30	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
28	31	48/50 (96%)	45 (94%)	2 (4%)	1 (2%)	5	31
29	32	44/46 (96%)	37 (84%)	7 (16%)	0	100	100
30	33	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	7	36
31	34	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	4	26
32	B	216/218 (99%)	180 (83%)	30 (14%)	6 (3%)	4	26
33	C	204/206 (99%)	187 (92%)	16 (8%)	1 (0%)	24	57
34	D	203/205 (99%)	167 (82%)	31 (15%)	5 (2%)	4	28
35	E	155/157 (99%)	133 (86%)	15 (10%)	7 (4%)	2	17
36	F	98/100 (98%)	75 (76%)	18 (18%)	5 (5%)	1	15
37	G	149/151 (99%)	129 (87%)	18 (12%)	2 (1%)	9	39
38	H	127/129 (98%)	120 (94%)	6 (5%)	1 (1%)	16	49
39	I	125/127 (98%)	98 (78%)	22 (18%)	5 (4%)	2	20
40	J	96/98 (98%)	78 (81%)	10 (10%)	8 (8%)	0	8
41	K	114/116 (98%)	92 (81%)	19 (17%)	3 (3%)	4	27
42	L	121/123 (98%)	95 (78%)	18 (15%)	8 (7%)	1	12
43	M	112/114 (98%)	95 (85%)	14 (12%)	3 (3%)	4	27
44	N	98/100 (98%)	86 (88%)	11 (11%)	1 (1%)	12	45
45	O	86/88 (98%)	74 (86%)	11 (13%)	1 (1%)	10	41
46	P	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	28
47	Q	78/80 (98%)	61 (78%)	11 (14%)	6 (8%)	1	9
48	R	63/65 (97%)	50 (79%)	7 (11%)	6 (10%)	0	6
49	S	77/79 (98%)	66 (86%)	9 (12%)	2 (3%)	4	27
50	T	83/85 (98%)	75 (90%)	7 (8%)	1 (1%)	10	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	U	63/65 (97%)	41 (65%)	15 (24%)	7 (11%)	0	4
52	03	130/234 (56%)	107 (82%)	22 (17%)	1 (1%)	16	49
59	Z	390/392 (100%)	329 (84%)	55 (14%)	6 (2%)	8	37
All	All	6366/6574 (97%)	5449 (86%)	776 (12%)	141 (2%)	7	30

All (141) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	06	83	VAL
5	08	46	ASP
5	08	47	ASN
5	08	119	GLY
6	09	9	VAL
7	10	58	THR
7	10	80	THR
7	10	108	VAL
7	10	118	ILE
8	11	90	GLY
10	13	35	VAL
17	20	54	VAL
20	23	98	ASN
24	27	24	GLU
32	B	17	HIS
32	B	19	THR
32	B	73	ARG
36	F	54	LEU
36	F	99	ALA
39	I	57	VAL
39	I	90	ASP
39	I	91	GLU
40	J	34	ALA
40	J	58	ASN
42	L	102	ASP
45	O	46	LYS
48	R	71	ASP
51	U	24	LYS
51	U	34	ARG
59	Z	198	TYR
1	04	232	GLY
3	06	11	ALA
4	07	149	ARG

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Mol	Chain	Res	Type
5	08	45	ALA
6	09	10	ALA
6	09	15	LEU
7	10	114	GLU
8	11	13	ALA
11	14	31	GLY
11	14	36	LYS
11	14	65	GLY
18	21	63	GLY
18	21	64	ALA
20	23	6	ARG
30	33	31	ILE
32	B	87	ASP
34	D	23	GLY
34	D	169	TRP
35	E	23	THR
35	E	89	THR
35	E	99	SER
35	E	122	VAL
36	F	53	LYS
36	F	94	HIS
37	G	18	GLY
37	G	20	GLU
38	H	47	ASP
39	I	125	GLN
40	J	35	GLN
40	J	38	GLY
40	J	92	LEU
41	K	125	LYS
42	L	77	SER
42	L	101	LEU
44	N	3	GLN
46	P	79	ASN
47	Q	17	GLU
47	Q	49	ASN
48	R	45	GLY
48	R	46	THR
50	T	68	LYS
51	U	14	ALA
51	U	64	ALA
6	09	41	LYS
7	10	81	LEU

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Mol	Chain	Res	Type
11	14	29	LYS
11	14	86	GLU
31	34	36	ARG
34	D	152	SER
35	E	90	GLY
40	J	89	ARG
42	L	2	THR
42	L	23	LEU
46	P	44	SER
47	Q	50	ASN
48	R	10	CYS
49	S	4	LEU
51	U	9	GLU
51	U	12	ASP
59	Z	3	GLU
59	Z	367	ALA
7	10	119	PRO
7	10	123	ILE
10	13	93	GLN
12	15	70	ASP
13	16	117	ASP
20	23	51	LEU
35	E	121	ASN
39	I	102	PHE
41	K	13	LYS
42	L	24	GLU
42	L	33	CYS
43	M	4	ALA
59	Z	51	ASN
5	08	117	PRO
5	08	175	LYS
7	10	48	ALA
7	10	68	PRO
17	20	29	THR
28	31	40	PRO
32	B	18	GLN
34	D	47	LEU
34	D	167	PRO
41	K	92	ARG
42	L	27	PRO
47	Q	80	LYS
51	U	66	ARG

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Mol	Chain	Res	Type
52	03	52	ALA
59	Z	295	PRO
1	04	233	GLY
8	11	11	GLN
11	14	88	GLY
32	B	88	GLN
33	C	46	LEU
35	E	98	ALA
36	F	56	LYS
40	J	42	LEU
43	M	65	GLU
47	Q	70	LYS
48	R	11	ARG
8	11	19	PRO
40	J	33	GLY
43	M	6	ILE
1	04	7	PRO
9	12	81	ILE
13	16	105	GLY
49	S	53	GLY
59	Z	122	GLY
8	11	4	VAL
47	Q	31	PRO
48	R	20	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	04	216/216 (100%)	212 (98%)	4 (2%)	50	67
2	05	164/164 (100%)	164 (100%)	0	100	100
3	06	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	07	148/148 (100%)	148 (100%)	0	100	100
5	08	137/137 (100%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	09	114/114 (100%)	114 (100%)	0	100	100
7	10	100/100 (100%)	99 (99%)	1 (1%)	68	75
8	11	109/109 (100%)	107 (98%)	2 (2%)	51	68
9	12	116/116 (100%)	114 (98%)	2 (2%)	53	69
10	13	103/103 (100%)	101 (98%)	2 (2%)	50	67
11	14	102/102 (100%)	99 (97%)	3 (3%)	37	60
12	15	109/109 (100%)	107 (98%)	2 (2%)	51	68
13	16	100/100 (100%)	99 (99%)	1 (1%)	68	75
14	17	86/86 (100%)	86 (100%)	0	100	100
15	18	99/99 (100%)	99 (100%)	0	100	100
16	19	89/89 (100%)	89 (100%)	0	100	100
17	20	84/84 (100%)	84 (100%)	0	100	100
18	21	93/93 (100%)	92 (99%)	1 (1%)	65	74
19	22	80/80 (100%)	79 (99%)	1 (1%)	61	72
20	23	83/83 (100%)	83 (100%)	0	100	100
21	24	78/78 (100%)	78 (100%)	0	100	100
22	25	57/57 (100%)	57 (100%)	0	100	100
23	26	67/67 (100%)	67 (100%)	0	100	100
24	27	55/55 (100%)	54 (98%)	1 (2%)	51	68
25	28	48/48 (100%)	48 (100%)	0	100	100
26	29	59/59 (100%)	59 (100%)	0	100	100
27	30	47/47 (100%)	47 (100%)	0	100	100
28	31	45/45 (100%)	45 (100%)	0	100	100
29	32	38/38 (100%)	38 (100%)	0	100	100
30	33	51/51 (100%)	51 (100%)	0	100	100
31	34	34/34 (100%)	33 (97%)	1 (3%)	37	60
32	B	180/180 (100%)	178 (99%)	2 (1%)	65	74
33	C	170/170 (100%)	167 (98%)	3 (2%)	51	68
34	D	172/172 (100%)	172 (100%)	0	100	100
35	E	119/119 (100%)	119 (100%)	0	100	100
36	F	87/87 (100%)	85 (98%)	2 (2%)	44	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	G	124/124 (100%)	124 (100%)	0	100	100
38	H	104/104 (100%)	104 (100%)	0	100	100
39	I	105/105 (100%)	105 (100%)	0	100	100
40	J	86/86 (100%)	84 (98%)	2 (2%)	44	64
41	K	89/89 (100%)	87 (98%)	2 (2%)	45	65
42	L	103/103 (100%)	102 (99%)	1 (1%)	68	75
43	M	92/92 (100%)	89 (97%)	3 (3%)	33	58
44	N	83/83 (100%)	83 (100%)	0	100	100
45	O	76/76 (100%)	76 (100%)	0	100	100
46	P	65/65 (100%)	64 (98%)	1 (2%)	57	70
47	Q	74/74 (100%)	74 (100%)	0	100	100
48	R	56/56 (100%)	55 (98%)	1 (2%)	51	68
49	S	70/70 (100%)	69 (99%)	1 (1%)	59	71
50	T	65/65 (100%)	65 (100%)	0	100	100
51	U	55/55 (100%)	51 (93%)	4 (7%)	13	40
52	03	110/181 (61%)	104 (94%)	6 (6%)	19	47
59	Z	324/325 (100%)	315 (97%)	9 (3%)	38	60
All	All	5285/5357 (99%)	5226 (99%)	59 (1%)	63	74

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	04	132	ARG
1	04	239	PHE
1	04	252	LYS
1	04	261	ARG
3	06	83	VAL
7	10	50	VAL
8	11	112	LYS
8	11	131	THR
9	12	57	LEU
9	12	81	ILE
10	13	61	VAL
10	13	104	THR
11	14	27	LEU
11	14	96	LYS

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Mol	Chain	Res	Type
11	14	110	VAL
12	15	5	LYS
12	15	6	ARG
13	16	13	ASN
18	21	3	THR
19	22	32	LEU
24	27	7	ARG
31	34	15	LYS
32	B	35	ASN
32	B	114	LYS
33	C	78	LYS
33	C	156	LEU
33	C	163	ARG
36	F	12	PRO
36	F	94	HIS
40	J	10	LEU
40	J	30	LYS
41	K	12	ARG
41	K	30	ILE
42	L	28	GLN
43	M	3	ILE
43	M	6	ILE
43	M	99	GLN
46	P	19	VAL
48	R	70	THR
49	S	10	ILE
51	U	10	PRO
51	U	28	LEU
51	U	38	GLU
51	U	67	THR
52	03	4	LEU
52	03	10	VAL
52	03	25	GLU
52	03	33	LEU
52	03	41	SER
52	03	55	SER
59	Z	68	GLU
59	Z	91	MET
59	Z	98	MET
59	Z	225	THR
59	Z	236	ILE
59	Z	237	LYS

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Mol	Chain	Res	Type
59	Z	356	ILE
59	Z	358	MET
59	Z	391	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (128) such sidechains are listed below:

Mol	Chain	Res	Type
1	04	24	HIS
1	04	36	ASN
1	04	85	ASN
1	04	89	ASN
1	04	127	ASN
1	04	133	ASN
1	04	152	GLN
2	05	32	ASN
2	05	49	GLN
3	06	90	GLN
3	06	94	GLN
3	06	156	ASN
3	06	163	ASN
4	07	26	GLN
4	07	51	ASN
4	07	80	GLN
5	08	87	GLN
5	08	114	HIS
5	08	138	GLN
6	09	11	ASN
6	09	33	GLN
6	09	66	ASN
6	09	119	ASN
6	09	133	GLN
7	10	6	GLN
7	10	88	HIS
7	10	103	ASN
8	11	5	GLN
8	11	29	GLN
8	11	30	GLN
8	11	42	ASN
8	11	93	ASN
9	12	135	GLN
9	12	136	GLN
11	14	38	GLN

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Mol	Chain	Res	Type
12	15	3	GLN
12	15	13	HIS
12	15	22	GLN
13	16	3	HIS
13	16	23	ASN
13	16	31	HIS
13	16	81	ASN
15	18	6	GLN
15	18	11	GLN
15	18	65	ASN
16	19	36	GLN
16	19	43	GLN
17	20	6	GLN
17	20	18	GLN
17	20	82	HIS
17	20	87	GLN
18	21	57	ASN
19	22	59	ASN
20	23	45	GLN
20	23	53	GLN
20	23	68	ASN
20	23	73	ASN
21	24	49	ASN
22	25	8	ASN
22	25	42	HIS
23	26	16	ASN
24	27	27	ASN
24	27	39	GLN
24	27	41	HIS
27	30	4	GLN
27	30	5	ASN
28	31	18	HIS
28	31	25	ASN
29	32	16	HIS
29	32	26	ASN
32	B	23	ASN
32	B	35	ASN
32	B	121	GLN
32	B	177	ASN
33	C	31	ASN
33	C	40	GLN
33	C	139	ASN

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Mol	Chain	Res	Type
34	D	88	ASN
34	D	99	ASN
34	D	125	ASN
34	D	139	ASN
35	E	147	ASN
36	F	17	GLN
36	F	37	HIS
36	F	58	HIS
36	F	68	GLN
36	F	81	ASN
37	G	121	ASN
37	G	129	ASN
37	G	147	ASN
38	H	17	GLN
38	H	66	GLN
39	I	30	ASN
39	I	31	GLN
39	I	36	GLN
39	I	80	HIS
39	I	125	GLN
40	J	20	GLN
40	J	58	ASN
40	J	64	GLN
41	K	28	ASN
41	K	80	ASN
42	L	4	ASN
42	L	111	GLN
43	M	7	ASN
43	M	13	HIS
44	N	42	ASN
44	N	59	GLN
44	N	65	GLN
45	O	36	ASN
45	O	45	HIS
46	P	26	ASN
46	P	63	GLN
48	R	51	GLN
49	S	13	HIS
50	T	60	GLN
52	03	20	GLN
52	03	57	GLN
52	03	67	HIS

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Mol	Chain	Res	Type
52	03	160	GLN
52	03	203	GLN
59	Z	22	HIS
59	Z	63	ASN
59	Z	66	HIS
59	Z	90	ASN
59	Z	97	GLN
59	Z	329	GLN
59	Z	355	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	A	1538/1539 (99%)	162 (10%)	9 (0%)
54	01	2902/2903 (99%)	358 (12%)	16 (0%)
55	02	119/120 (99%)	11 (9%)	2 (1%)
56	W	76/77 (98%)	7 (9%)	0
56	X	76/77 (98%)	13 (17%)	0
57	V	17/18 (94%)	2 (11%)	0
58	Y	75/76 (98%)	14 (18%)	0
All	All	4803/4810 (99%)	567 (11%)	27 (0%)

All (567) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	A	6	G
53	A	9	G
53	A	22	G
53	A	31	G
53	A	32	A
53	A	39	G
53	A	47	C
53	A	51	A
53	A	71	A
53	A	82	G
53	A	87	C
53	A	121	U
53	A	130	A
53	A	173	U
53	A	183	C
53	A	184	G

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Mol	Chain	Res	Type
53	A	197	A
53	A	209	U
53	A	210	C
53	A	226	G
53	A	247	G
53	A	251	G
53	A	266	G
53	A	267	C
53	A	279	A
53	A	281	G
53	A	289	G
53	A	306	A
53	A	328	C
53	A	345	C
53	A	346	G
53	A	351	G
53	A	352	C
53	A	363	A
53	A	367	U
53	A	372	C
53	A	411	A
53	A	412	A
53	A	413	G
53	A	422	C
53	A	429	U
53	A	430	A
53	A	439	U
53	A	467	U
53	A	484	G
53	A	485	U
53	A	486	U
53	A	496	A
53	A	497	G
53	A	509	A
53	A	510	A
53	A	527	G
53	A	531	U
53	A	532	A
53	A	533	A
53	A	547	A
53	A	559	A
53	A	561	U

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Mol	Chain	Res	Type
53	A	572	A
53	A	573	A
53	A	575	G
53	A	576	C
53	A	577	G
53	A	607	A
53	A	633	G
53	A	642	A
53	A	665	A
53	A	703	G
53	A	713	G
53	A	724	G
53	A	731	G
53	A	755	G
53	A	777	A
53	A	815	A
53	A	817	C
53	A	818	G
53	A	819	A
53	A	821	G
53	A	832	G
53	A	842	U
53	A	843	U
53	A	844	G
53	A	846	G
53	A	873	A
53	A	890	G
53	A	902	G
53	A	926	G
53	A	934	C
53	A	960	U
53	A	961	U
53	A	966	G
53	A	969	A
53	A	975	A
53	A	976	G
53	A	977	A
53	A	992	U
53	A	993	G
53	A	994	A
53	A	1004	A
53	A	1020	G

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Mol	Chain	Res	Type
53	A	1028	C
53	A	1031	C
53	A	1033	G
53	A	1034	G
53	A	1053	G
53	A	1054	C
53	A	1085	U
53	A	1094	G
53	A	1101	A
53	A	1129	C
53	A	1130	A
53	A	1137	C
53	A	1138	G
53	A	1139	G
53	A	1159	U
53	A	1160	G
53	A	1168	U
53	A	1182	G
53	A	1184	G
53	A	1190	G
53	A	1191	A
53	A	1196	A
53	A	1198	G
53	A	1201	A
53	A	1202	U
53	A	1207	G
53	A	1213	A
53	A	1225	A
53	A	1238	A
53	A	1241	G
53	A	1256	A
53	A	1257	A
53	A	1258	G
53	A	1260	G
53	A	1275	A
53	A	1278	G
53	A	1280	A
53	A	1282	C
53	A	1286	U
53	A	1287	A
53	A	1290	G
53	A	1300	G

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Mol	Chain	Res	Type
53	A	1317	C
53	A	1323	G
53	A	1346	A
53	A	1347	G
53	A	1363	A
53	A	1381	U
53	A	1395	C
53	A	1400	C
53	A	1446	A
53	A	1448	C
53	A	1452	C
53	A	1475	G
53	A	1492	A
53	A	1503	A
53	A	1506	U
53	A	1517	G
53	A	1529	G
53	A	1530	G
53	A	1534	A
53	A	1540	U
54	01	10	A
54	01	12	U
54	01	34	U
54	01	35	G
54	01	46	G
54	01	50	U
54	01	51	G
54	01	63	A
54	01	71	A
54	01	74	A
54	01	75	G
54	01	102	U
54	01	118	A
54	01	120	U
54	01	138	U
54	01	139	U
54	01	140	C
54	01	141	G
54	01	142	A
54	01	158	U
54	01	162	U
54	01	163	C

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Mol	Chain	Res	Type
54	01	181	A
54	01	196	A
54	01	216	A
54	01	221	A
54	01	222	A
54	01	228	C
54	01	229	C
54	01	242	G
54	01	248	G
54	01	249	C
54	01	255	A
54	01	266	G
54	01	276	U
54	01	281	C
54	01	294	A
54	01	301	G
54	01	311	A
54	01	312	G
54	01	322	A
54	01	323	C
54	01	329	G
54	01	330	A
54	01	353	C
54	01	361	G
54	01	371	A
54	01	372	G
54	01	373	U
54	01	386	G
54	01	387	U
54	01	404	A
54	01	406	G
54	01	411	G
54	01	422	A
54	01	424	G
54	01	451	U
54	01	455	C
54	01	457	A
54	01	481	G
54	01	491	G
54	01	504	A
54	01	505	A
54	01	506	G

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Mol	Chain	Res	Type
54	01	508	A
54	01	529	A
54	01	531	C
54	01	532	A
54	01	542	C
54	01	543	G
54	01	545	U
54	01	547	A
54	01	563	A
54	01	572	A
54	01	573	U
54	01	575	A
54	01	588	U
54	01	603	A
54	01	616	A
54	01	627	A
54	01	637	A
54	01	646	U
54	01	654	A
54	01	669	G
54	01	677	A
54	01	686	U
54	01	687	C
54	01	695	G
54	01	730	A
54	01	747	C
54	01	748	G
54	01	752	A
54	01	776	G
54	01	782	A
54	01	784	G
54	01	785	G
54	01	805	G
54	01	812	C
54	01	819	A
54	01	827	U
54	01	828	U
54	01	830	G
54	01	845	A
54	01	846	U
54	01	847	U
54	01	858	G

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Mol	Chain	Res	Type
54	01	859	G
54	01	860	U
54	01	878	A
54	01	886	A
54	01	888	C
54	01	889	C
54	01	896	A
54	01	907	G
54	01	910	A
54	01	915	C
54	01	932	U
54	01	941	A
54	01	946	C
54	01	961	C
54	01	974	G
54	01	983	A
54	01	990	A
54	01	995	C
54	01	996	A
54	01	1012	U
54	01	1013	C
54	01	1021	A
54	01	1022	G
54	01	1026	G
54	01	1033	U
54	01	1045	C
54	01	1046	A
54	01	1054	A
54	01	1057	A
54	01	1060	U
54	01	1062	G
54	01	1065	U
54	01	1066	U
54	01	1068	G
54	01	1071	G
54	01	1079	C
54	01	1084	A
54	01	1088	A
54	01	1090	A
54	01	1103	A
54	01	1104	C
54	01	1106	G

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Mol	Chain	Res	Type
54	01	1111	A
54	01	1112	G
54	01	1131	G
54	01	1132	U
54	01	1135	C
54	01	1143	A
54	01	1157	G
54	01	1174	U
54	01	1176	U
54	01	1177	G
54	01	1179	G
54	01	1180	U
54	01	1206	G
54	01	1212	G
54	01	1238	G
54	01	1248	G
54	01	1250	G
54	01	1251	C
54	01	1253	A
54	01	1256	G
54	01	1271	G
54	01	1272	A
54	01	1301	A
54	01	1321	A
54	01	1329	U
54	01	1330	C
54	01	1332	G
54	01	1345	C
54	01	1365	A
54	01	1378	A
54	01	1379	U
54	01	1383	A
54	01	1395	A
54	01	1416	G
54	01	1419	A
54	01	1420	A
54	01	1428	C
54	01	1454	C
54	01	1461	C
54	01	1476	U
54	01	1482	G
54	01	1490	A

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Mol	Chain	Res	Type
54	01	1491	G
54	01	1498	C
54	01	1515	A
54	01	1524	G
54	01	1533	C
54	01	1535	A
54	01	1536	C
54	01	1555	G
54	01	1560	G
54	01	1569	A
54	01	1581	G
54	01	1608	A
54	01	1611	C
54	01	1616	A
54	01	1634	A
54	01	1646	C
54	01	1647	U
54	01	1648	U
54	01	1674	G
54	01	1715	G
54	01	1729	U
54	01	1730	C
54	01	1738	G
54	01	1758	U
54	01	1764	C
54	01	1773	A
54	01	1780	A
54	01	1800	C
54	01	1801	A
54	01	1808	A
54	01	1816	C
54	01	1829	A
54	01	1847	A
54	01	1871	A
54	01	1901	A
54	01	1906	G
54	01	1913	A
54	01	1929	G
54	01	1930	G
54	01	1931	U
54	01	1937	A
54	01	1944	U

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Mol	Chain	Res	Type
54	01	1955	U
54	01	1967	C
54	01	1970	A
54	01	1971	U
54	01	1972	G
54	01	1991	U
54	01	1992	G
54	01	1993	U
54	01	1997	C
54	01	2022	U
54	01	2023	C
54	01	2030	A
54	01	2031	A
54	01	2036	C
54	01	2043	C
54	01	2049	G
54	01	2055	C
54	01	2056	G
54	01	2060	A
54	01	2061	G
54	01	2062	A
54	01	2069	G
54	01	2072	C
54	01	2095	A
54	01	2096	C
54	01	2108	A
54	01	2111	U
54	01	2112	G
54	01	2115	G
54	01	2118	U
54	01	2119	A
54	01	2124	G
54	01	2125	G
54	01	2127	G
54	01	2131	U
54	01	2132	U
54	01	2133	G
54	01	2145	C
54	01	2147	A
54	01	2162	G
54	01	2164	C
54	01	2172	U

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Mol	Chain	Res	Type
54	01	2173	A
54	01	2189	U
54	01	2198	A
54	01	2203	U
54	01	2204	G
54	01	2211	A
54	01	2213	U
54	01	2225	A
54	01	2238	G
54	01	2239	G
54	01	2250	G
54	01	2259	U
54	01	2278	A
54	01	2283	C
54	01	2287	A
54	01	2297	A
54	01	2305	U
54	01	2309	A
54	01	2325	G
54	01	2327	A
54	01	2334	U
54	01	2350	C
54	01	2382	G
54	01	2383	G
54	01	2385	C
54	01	2392	A
54	01	2402	U
54	01	2406	A
54	01	2407	A
54	01	2423	U
54	01	2424	C
54	01	2429	G
54	01	2430	A
54	01	2435	A
54	01	2441	U
54	01	2448	A
54	01	2476	A
54	01	2498	C
54	01	2502	G
54	01	2503	A
54	01	2504	U
54	01	2505	G

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Mol	Chain	Res	Type
54	01	2518	A
54	01	2529	G
54	01	2547	A
54	01	2554	U
54	01	2567	G
54	01	2572	A
54	01	2602	A
54	01	2609	U
54	01	2613	U
54	01	2629	U
54	01	2646	C
54	01	2655	G
54	01	2682	A
54	01	2685	G
54	01	2689	U
54	01	2690	U
54	01	2714	G
54	01	2733	A
54	01	2744	G
54	01	2748	A
54	01	2757	A
54	01	2764	A
54	01	2765	A
54	01	2771	C
54	01	2778	A
54	01	2779	U
54	01	2791	G
54	01	2794	C
54	01	2797	U
54	01	2798	U
54	01	2799	A
54	01	2800	A
54	01	2809	A
54	01	2818	U
54	01	2820	A
54	01	2821	A
54	01	2833	U
54	01	2848	G
54	01	2867	G
54	01	2868	A
54	01	2880	C
54	01	2884	U

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Mol	Chain	Res	Type
55	02	4	C
55	02	12	C
55	02	13	G
55	02	24	G
55	02	35	C
55	02	44	G
55	02	67	G
55	02	89	U
55	02	108	A
55	02	109	A
55	02	116	G
56	X	8	U
56	X	9	G
56	X	10	G
56	X	14	A
56	X	19	G
56	X	20	U
56	X	21	A
56	X	22	G
56	X	30	G
56	X	34	C
56	X	61	C
56	X	64	G
56	X	70	G
57	V	12	A
57	V	19	U
56	W	9	G
56	W	19	G
56	W	20	U
56	W	47	U
56	W	48	C
56	W	61	C
56	W	76	A
58	Y	7	A
58	Y	8	U
58	Y	9	A
58	Y	10	G
58	Y	18	G
58	Y	21	A
58	Y	26	A
58	Y	44	G
58	Y	45	U

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Mol	Chain	Res	Type
58	Y	46	G
58	Y	48	C
58	Y	55	U
58	Y	61	C
58	Y	63	G

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	246	A
53	A	280	C
53	A	429	U
53	A	438	U
53	A	495	A
53	A	960	U
53	A	1129	C
53	A	1190	G
53	A	1399	C
54	01	265	A
54	01	372	G
54	01	421	C
54	01	490	C
54	01	859	G
54	01	1020	A
54	01	1070	A
54	01	1111	A
54	01	1130	U
54	01	1475	G
54	01	1930	G
54	01	2286	G
54	01	2296	U
54	01	2326	C
54	01	2391	G
54	01	2756	U
55	02	66	A
55	02	88	C

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

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](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
62	GCP	Z	401	-	32,34,34	2.09	12 (37%)	49,54,54	2.50	14 (28%)
61	PHE	Y	101	58	10,11,12	1.13	0	8,13,15	0.30	0
60	FME	W	101	-	8,9,10	0.77	0	8,9,11	1.26	1 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	GCP	Z	401	-	-	9/19/38/38	0/3/3/3
61	PHE	Y	101	58	-	1/5/6/8	0/1/1/1
60	FME	W	101	-	-	3/7/9/11	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	Z	401	GCP	PA-O3A	-5.25	1.53	1.59
62	Z	401	GCP	C1'-N9	4.34	1.59	1.47
62	Z	401	GCP	PB-O3A	-4.01	1.53	1.58
62	Z	401	GCP	C2-N2	3.06	1.41	1.34
62	Z	401	GCP	C2'-C3'	2.96	1.61	1.53
62	Z	401	GCP	O4'-C1'	2.70	1.48	1.42
62	Z	401	GCP	C5'-C4'	2.55	1.59	1.51
62	Z	401	GCP	C8-N9	2.43	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	Z	401	GCP	C4-N9	2.25	1.43	1.38
62	Z	401	GCP	C3'-C4'	2.20	1.58	1.53
62	Z	401	GCP	O4'-C4'	2.03	1.49	1.45
62	Z	401	GCP	C2'-C1'	2.00	1.59	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	Z	401	GCP	C1'-N9-C4	7.76	149.41	126.49
62	Z	401	GCP	C1'-N9-C8	-7.61	105.11	126.73
62	Z	401	GCP	O1G-PG-C3B	-7.27	95.52	111.37
62	Z	401	GCP	O5'-PA-O1A	-4.06	92.84	108.94
62	Z	401	GCP	O2B-PB-O1B	3.85	122.48	109.95
62	Z	401	GCP	O2A-PA-O3A	-3.50	97.80	107.27
62	Z	401	GCP	C2'-C1'-N9	3.45	122.86	113.25
62	Z	401	GCP	O4'-C1'-C2'	-3.22	99.72	106.62
62	Z	401	GCP	O3G-PG-O1G	3.07	120.34	112.39
62	Z	401	GCP	O3'-C3'-C4'	-2.96	102.59	111.08
62	Z	401	GCP	O2G-PG-C3B	2.89	113.42	106.40
62	Z	401	GCP	PB-O3A-PA	2.79	141.47	132.37
60	W	101	FME	O-C-CA	-2.46	118.45	124.77
62	Z	401	GCP	O4'-C4'-C5'	2.42	117.09	109.33
62	Z	401	GCP	O2A-PA-O1A	2.29	123.09	112.44

There are no chirality outliers.

All (13) torsion outliers are listed below:

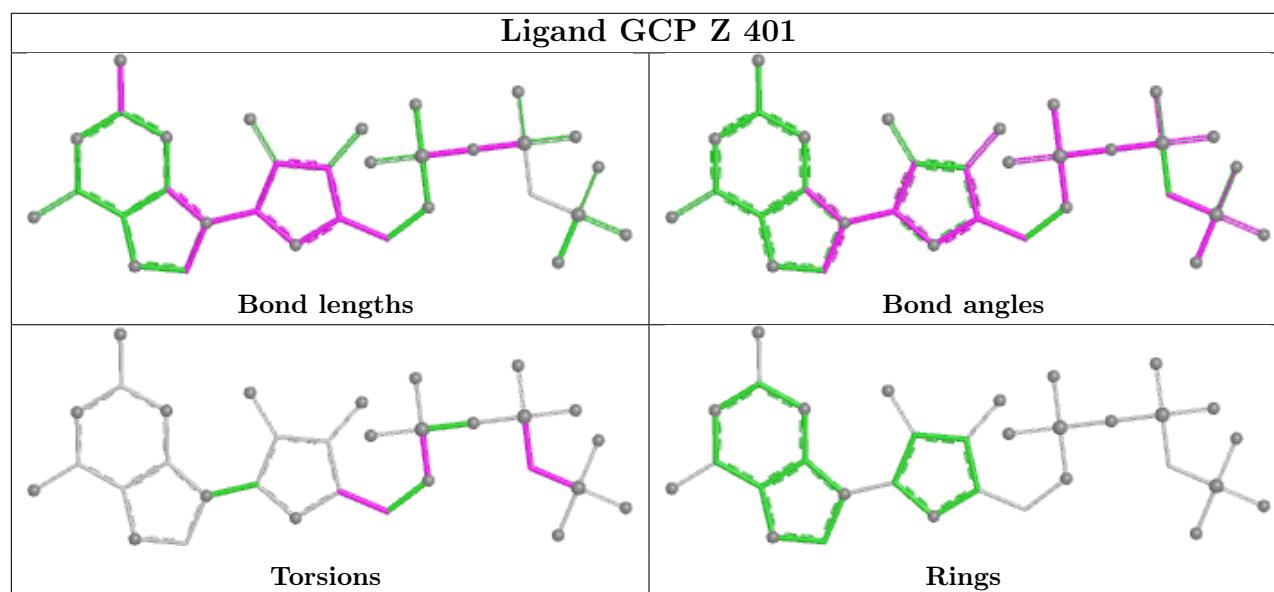
Mol	Chain	Res	Type	Atoms
60	W	101	FME	O1-CN-N-CA
60	W	101	FME	O-C-CA-CB
61	Y	101	PHE	O-C-CA-CB
62	Z	401	GCP	PB-C3B-PG-O1G
62	Z	401	GCP	PB-C3B-PG-O2G
62	Z	401	GCP	PG-C3B-PB-O1B
62	Z	401	GCP	C5'-O5'-PA-O3A
62	Z	401	GCP	C5'-O5'-PA-O2A
60	W	101	FME	C-CA-CB-CG
62	Z	401	GCP	O4'-C4'-C5'-O5'
62	Z	401	GCP	PB-C3B-PG-O3G
62	Z	401	GCP	C5'-O5'-PA-O1A
62	Z	401	GCP	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	Y	101	PHE	3	0
60	W	101	FME	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

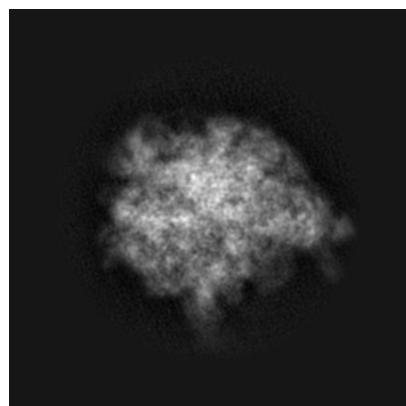
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8616. These allow visual inspection of the internal detail of the map and identification of artifacts.

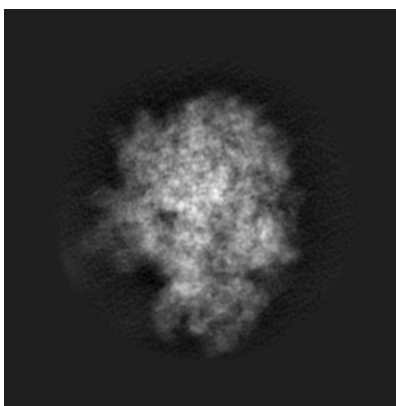
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

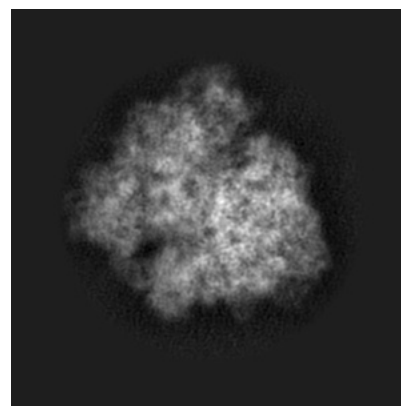
6.1.1 Primary map



X

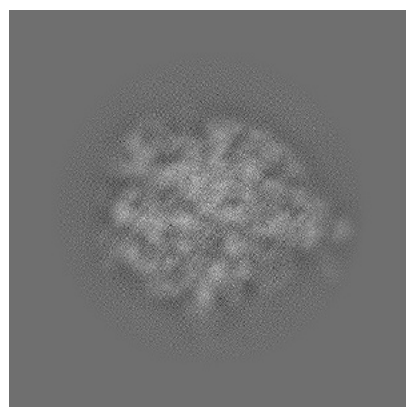


Y

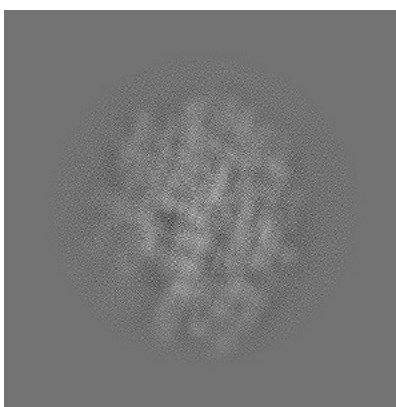


Z

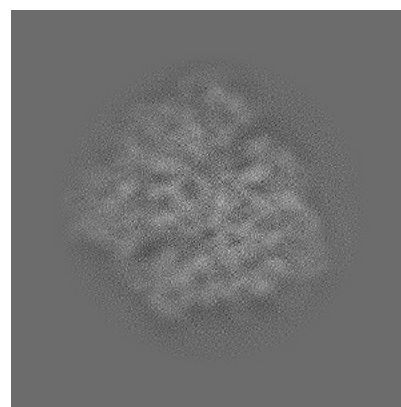
6.1.2 Raw map



X



Y

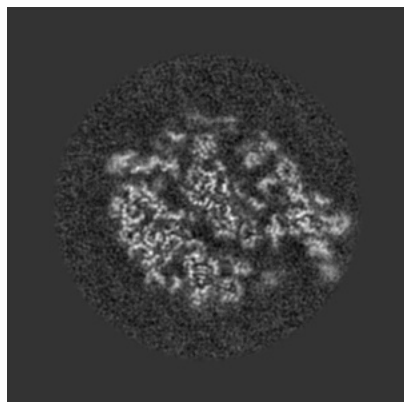


Z

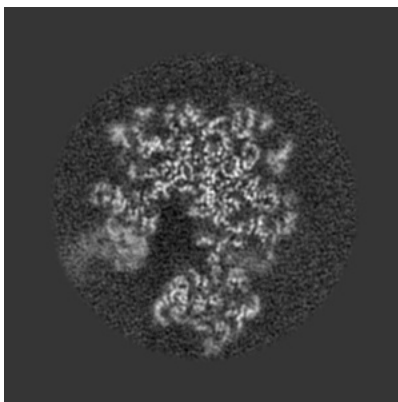
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

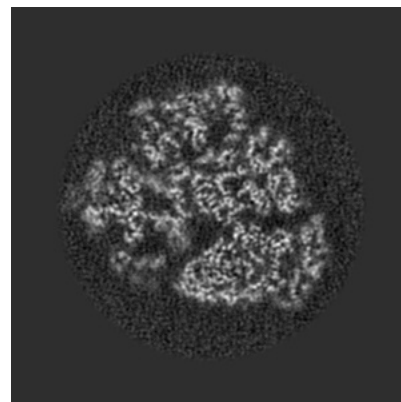
6.2.1 Primary map



X Index: 240

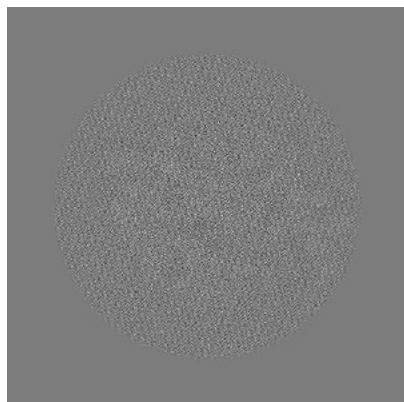


Y Index: 240

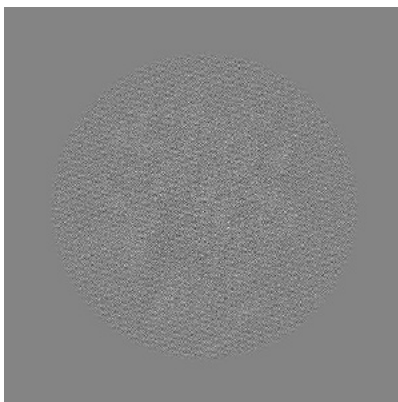


Z Index: 240

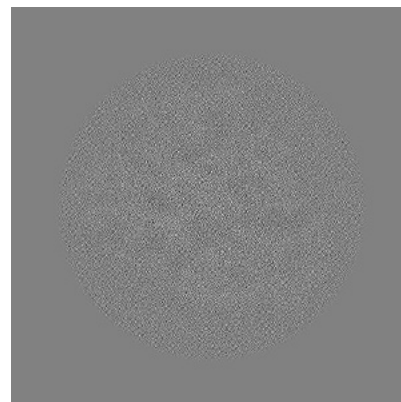
6.2.2 Raw map



X Index: 240



Y Index: 240

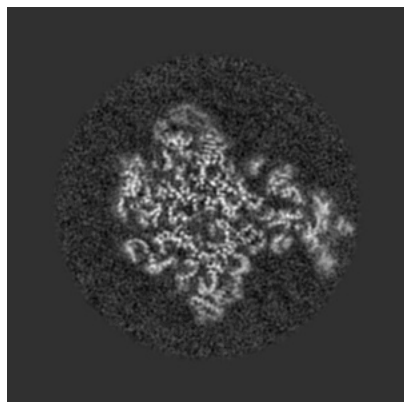


Z Index: 240

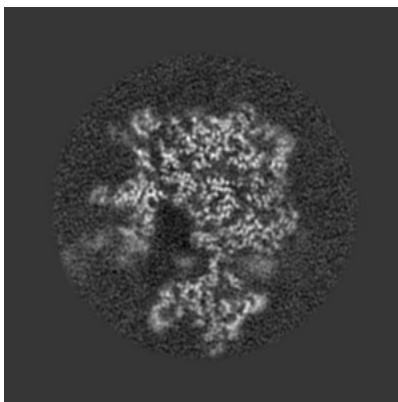
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

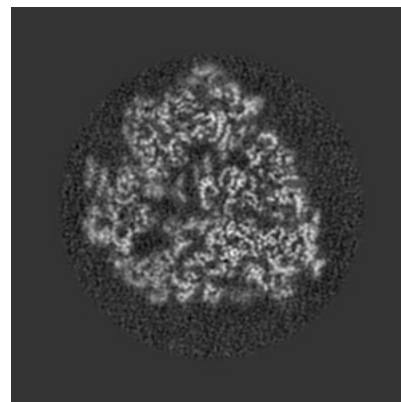
6.3.1 Primary map



X Index: 251

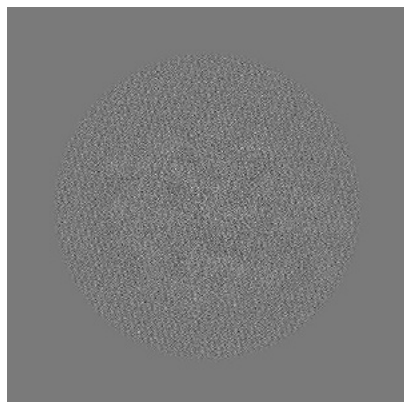


Y Index: 248

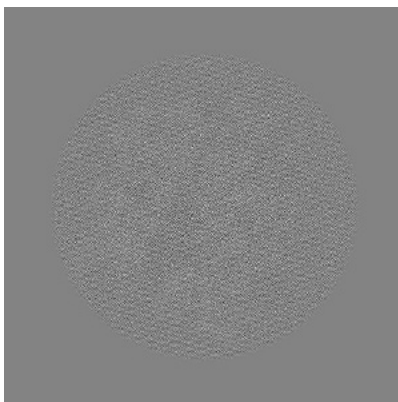


Z Index: 228

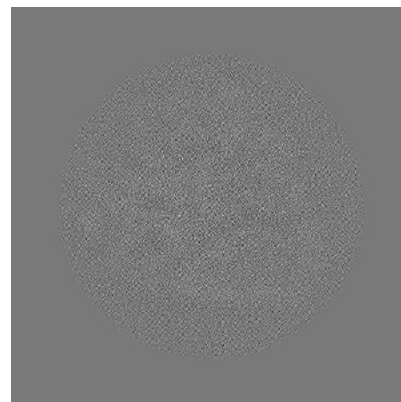
6.3.2 Raw map



X Index: 235



Y Index: 234

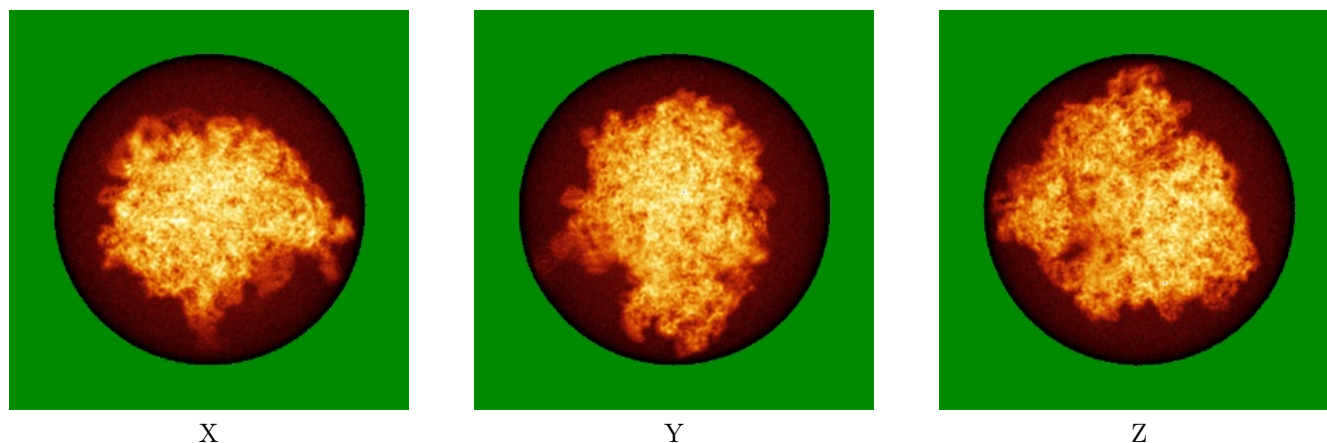


Z Index: 235

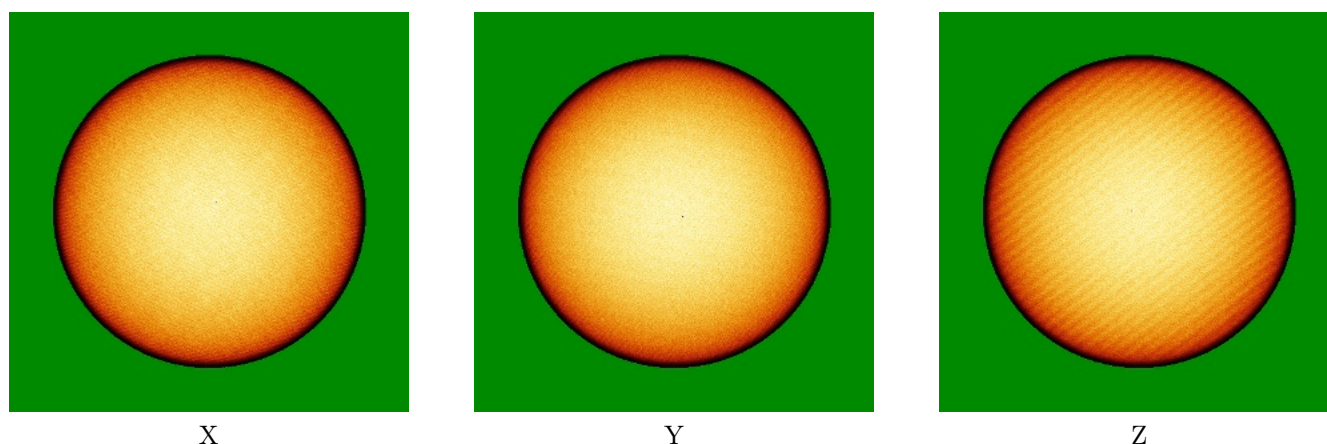
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

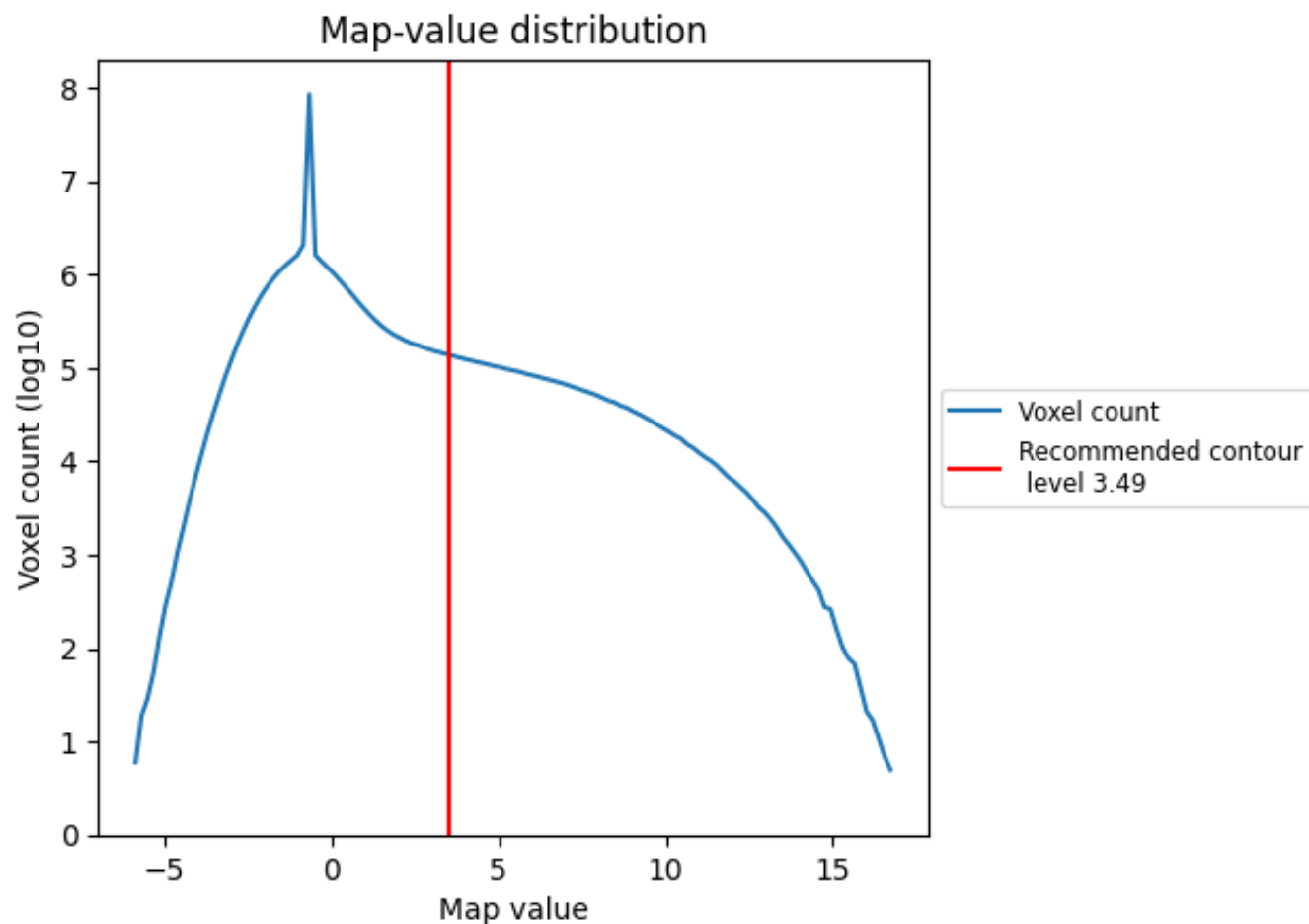
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

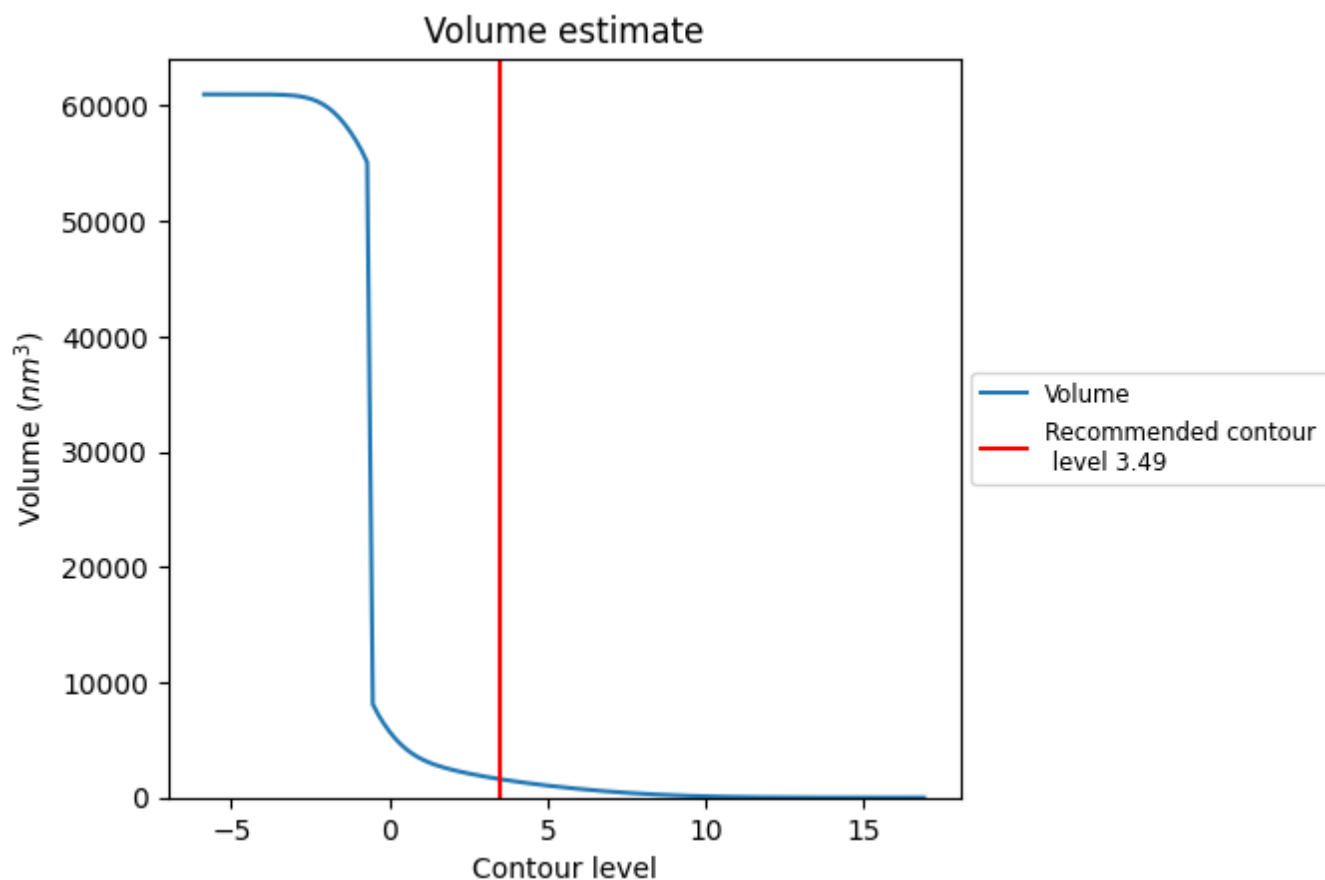
This section contains the results of statistical analysis of the map.

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.

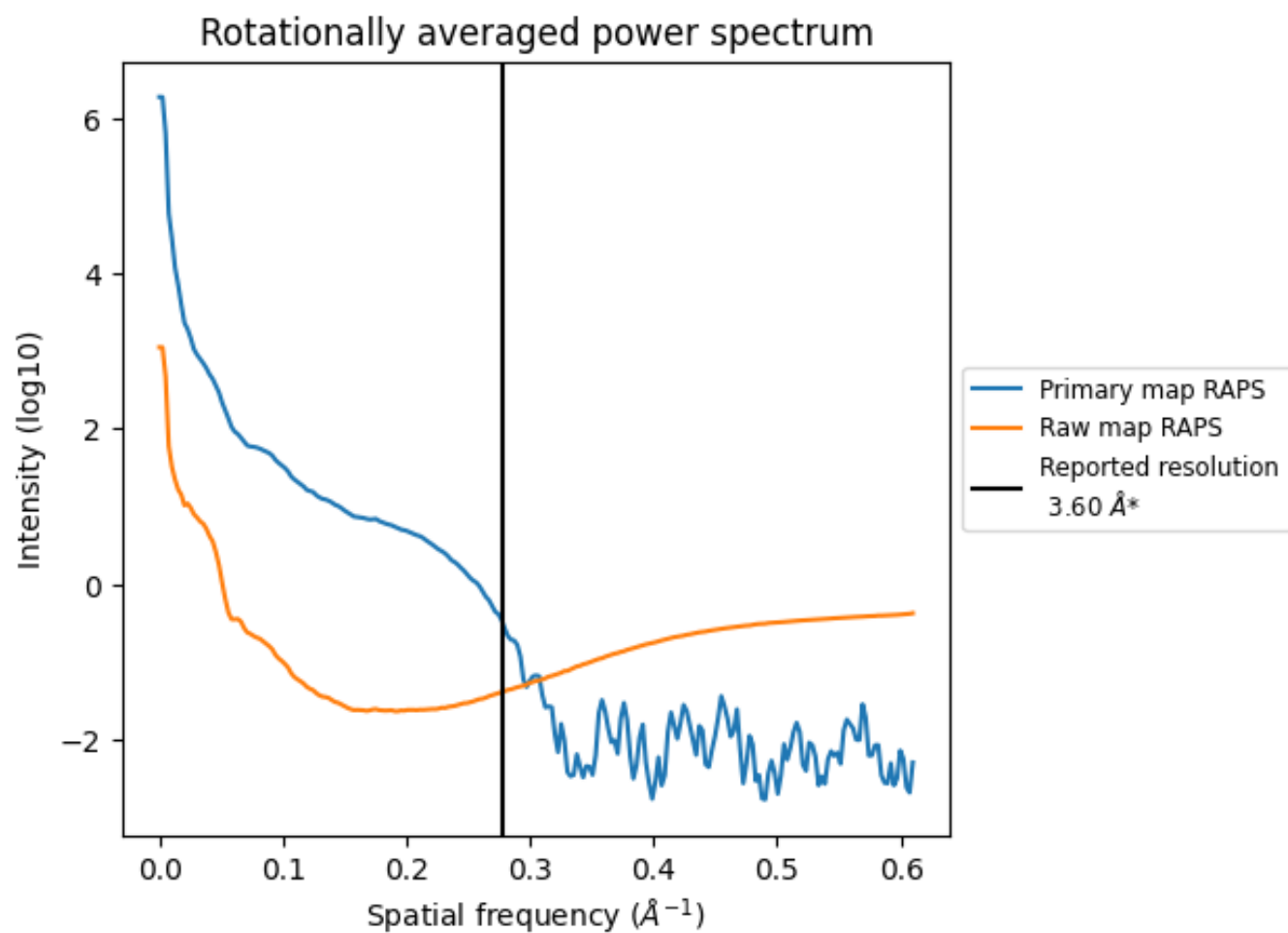
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1602 nm³; this corresponds to an approximate mass of 1447 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 ⓘ

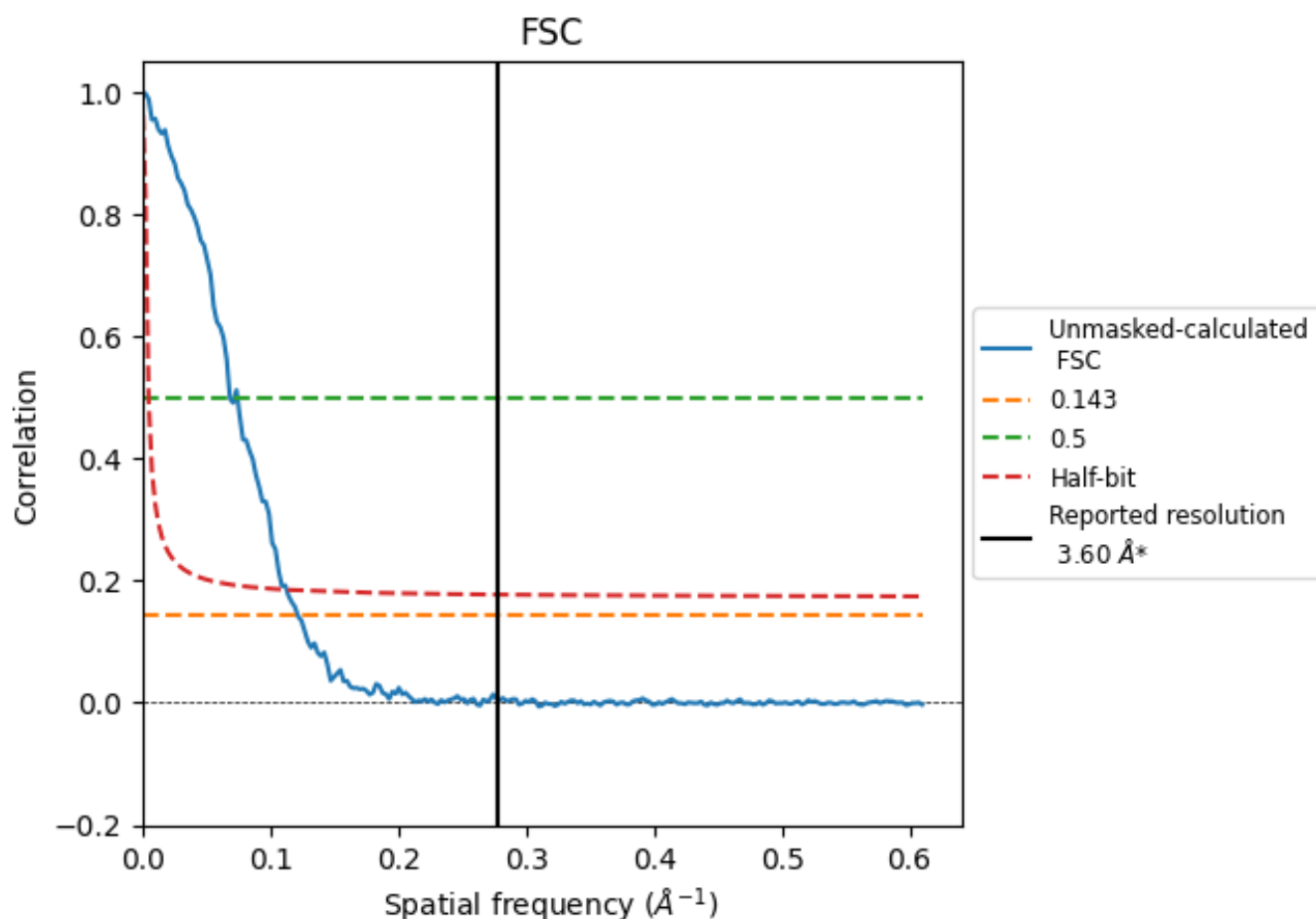


*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

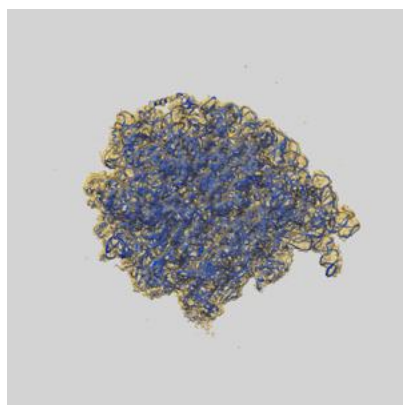
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.22	14.60	8.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.22 differs from the reported value 3.6 by more than 10 %

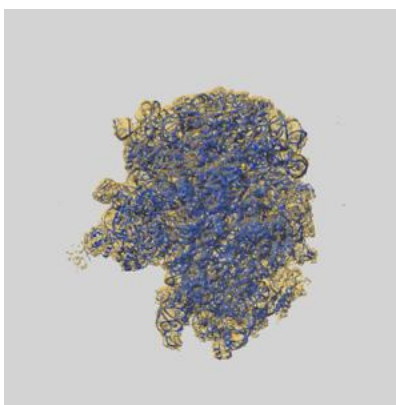
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8616 and PDB model 5UYL. Per-residue inclusion information can be found in section 3 on page 17.

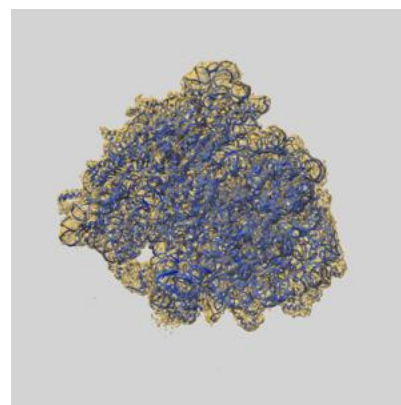
9.1 Map-model overlay [i](#)



X



Y



Z

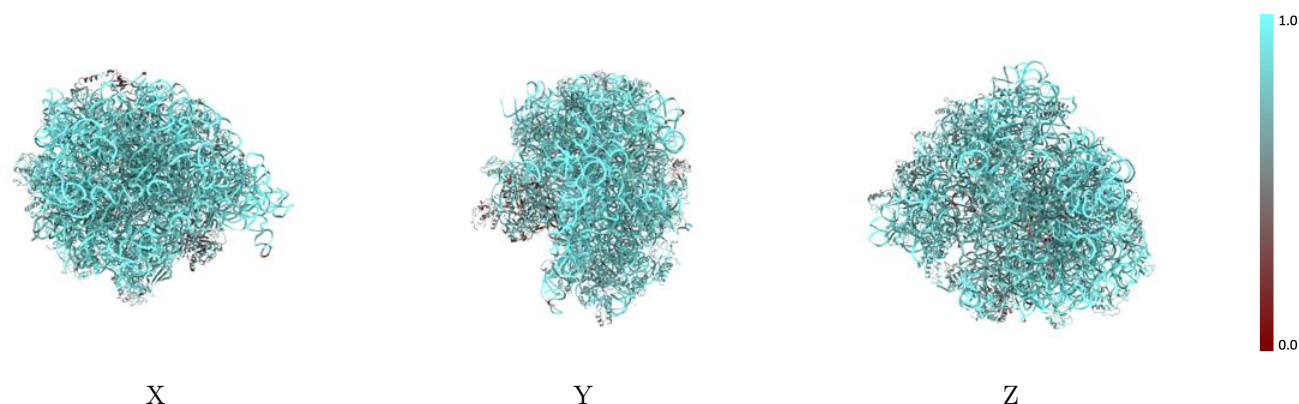
The images above show the 3D surface view of the map at the recommended contour level 3.49 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



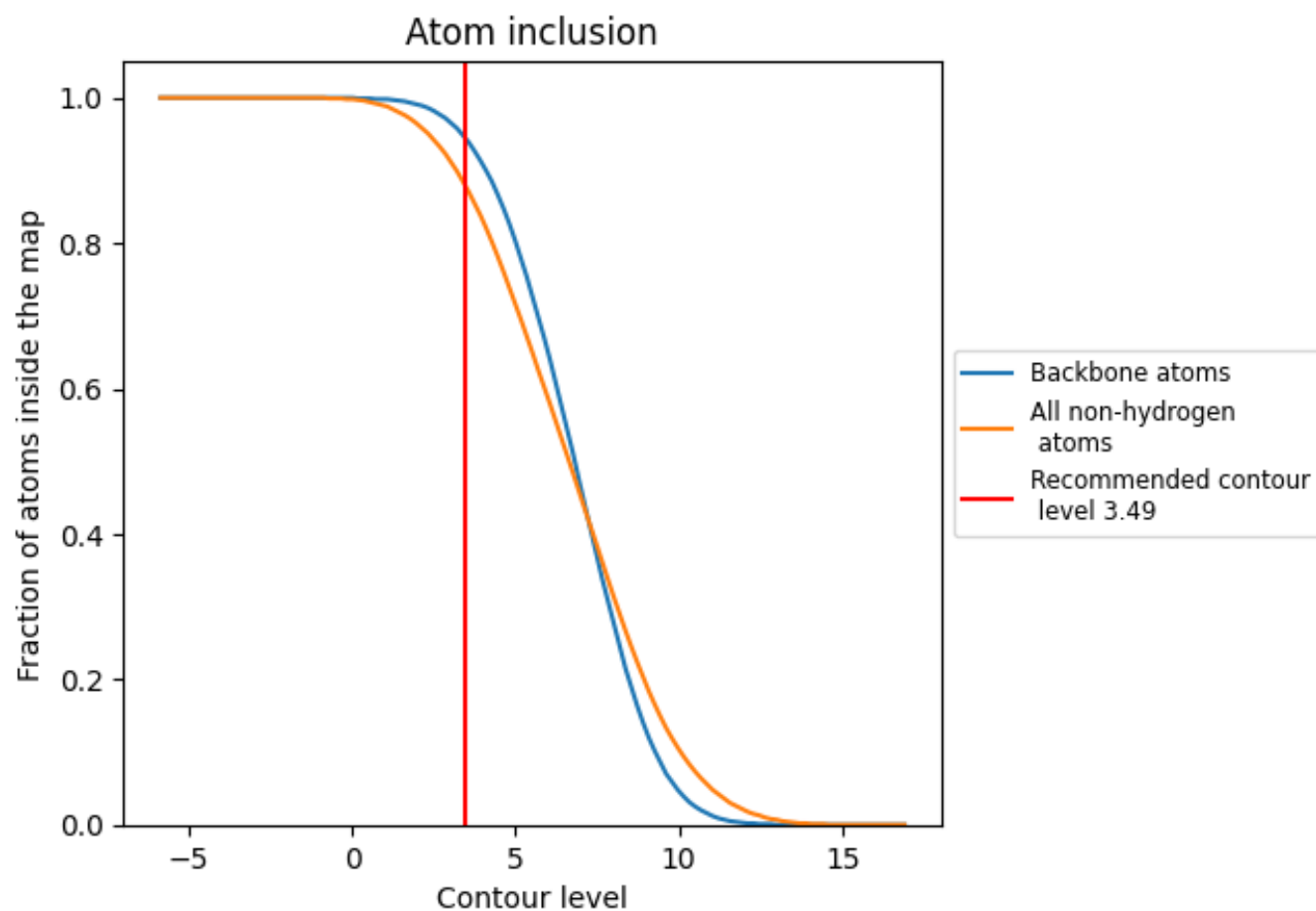
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.49).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 88% 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 (3.49) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.3810
01	 0.9530	 0.4000
02	 0.9570	 0.3730
03	 0.5970	 0.2350
04	 0.8040	 0.4330
05	 0.7940	 0.4310
06	 0.7790	 0.3860
07	 0.7820	 0.3530
08	 0.7750	 0.3720
09	 0.5360	 0.3080
10	 0.4460	 0.2140
11	 0.5150	 0.2080
12	 0.7810	 0.3960
13	 0.7100	 0.4240
14	 0.7940	 0.3990
15	 0.7350	 0.4180
16	 0.8340	 0.4040
17	 0.8230	 0.3770
18	 0.7610	 0.4100
19	 0.8220	 0.4130
20	 0.7800	 0.4140
21	 0.7360	 0.3880
22	 0.7590	 0.3830
23	 0.7790	 0.3690
24	 0.7670	 0.3860
25	 0.7980	 0.4290
26	 0.7870	 0.4160
27	 0.7340	 0.3290
28	 0.8050	 0.3940
29	 0.7480	 0.3170
30	 0.7690	 0.4020
31	 0.6820	 0.3880
32	 0.7940	 0.4060
33	 0.8000	 0.4280
34	 0.7770	 0.4210



Continued on next page...

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Chain	Atom inclusion	Q-score
A	 0.9540	 0.3910
B	 0.7390	 0.3350
C	 0.7380	 0.3780
D	 0.7550	 0.3570
E	 0.7880	 0.3850
F	 0.7920	 0.3690
G	 0.7590	 0.3510
H	 0.7870	 0.3940
I	 0.7910	 0.3560
J	 0.6640	 0.3400
K	 0.7580	 0.3800
L	 0.7490	 0.4060
M	 0.7770	 0.3540
N	 0.7510	 0.3510
O	 0.7910	 0.3580
P	 0.8330	 0.3880
Q	 0.7870	 0.3860
R	 0.8040	 0.3760
S	 0.7910	 0.3700
T	 0.7780	 0.3470
U	 0.6310	 0.2810
V	 0.6570	 0.2880
W	 0.8770	 0.3650
X	 0.7320	 0.2090
Y	 0.7600	 0.2310
Z	 0.5560	 0.2740