



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 09:04 AM UTC

PDB ID : 8S8K / pdb_00008s8k
EMDB ID : EMD-19808
Title : Structure of a yeast 48S-AUC preinitiation complex in swivelled conformation
(model py48S-AUC-swiv-eIF1)
Authors : Villamayor-Belinchon, L.; Sharma, P.; Llacer, J.L.; Hussain, T.
Deposited on : 2024-03-06
Resolution : 4.00 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

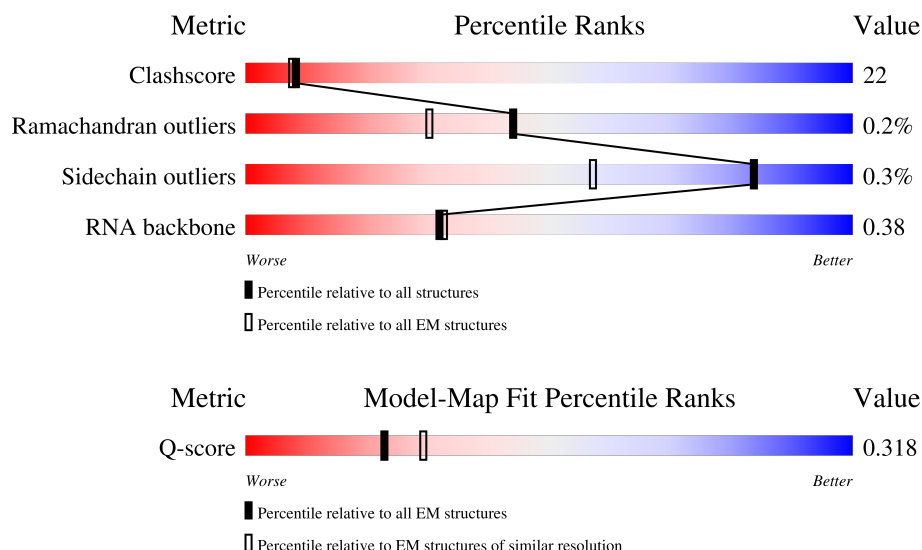
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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.



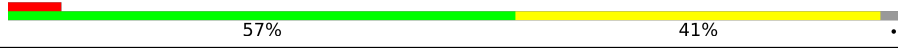
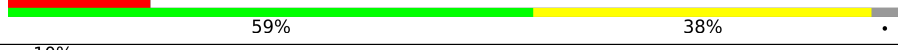
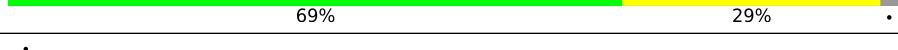
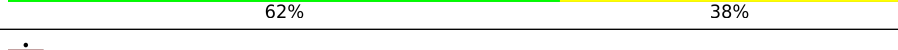
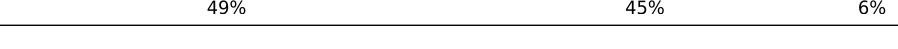
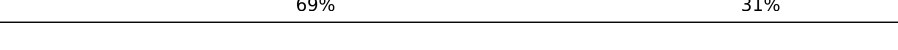
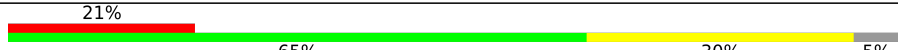
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	2	1798	
2	A	254	
3	B	255	

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Mol	Chain	Length	Quality of chain
4	C	259	
5	E	261	
6	G	236	
7	H	190	
8	I	201	
9	J	188	
10	L	156	
11	N	151	
12	O	137	
13	V	87	
14	W	130	
15	X	145	
16	Y	135	
17	a	103	
18	b	82	
19	e	63	
20	h	25	
21	D	237	
22	F	227	
23	K	106	
24	M	134	
25	P	142	
26	Q	143	
27	R	136	
28	S	146	

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Mol	Chain	Length	Quality of chain
29	T	144	
30	U	117	
31	Z	108	
32	c	67	
33	d	56	
34	f	150	
35	i	153	
36	m	108	
37	3	49	
38	1	75	
39	j	304	
40	k	527	
41	l	270	
42	n	812	
43	g	326	

2 Entry composition [i](#)

There are 47 unique types of molecules in this entry. The entry contains 87738 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 RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1798	Total	C	N	O	P	0	0
			38190	17073	6722	12597	1798		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	219	Total	C	N	O	S	0	0
			1702	1085	299	316	2		

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	229	Total	C	N	O	S	0	0
			1809	1143	331	332	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	220	Total	C	N	O	S	0	0
			1648	1053	291	300	4		

- Molecule 5 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 6 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	230	Total	C	N	O	S	0	0
			1832	1146	352	330	4		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	184	Total	C	N	O	0	0
			1483	950	270	263		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	188	Total	C	N	O	S	0	0
			1489	923	300	265	1		

- Molecule 9 is a protein called KLLA0E23673p.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 10 is a protein called KLLA0A10483p.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	153	Total	C	N	O	S	0	0
			1235	791	235	206	3		

- Molecule 11 is a protein called KLLA0F18040p.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	151	Total	C	N	O	S	0	0
			1195	761	224	207	3		

- Molecule 12 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	129	Total	C	N	O	S	0	0
			955	585	191	176	3		

- Molecule 13 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 15 is a protein called KLLA0B11231p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	X	144	Total	C	N	O	S	0	0
			1119	708	218	191	2		

- Molecule 16 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Y	134	Total	C	N	O	S	0	0
			1061	665	207	189			

- Molecule 17 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	102	Total	C	N	O	S	0	0
			797	492	168	132	5		

- Molecule 18 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	81	Total	C	N	O	S	0	0
			609	379	112	113	5		

- Molecule 19 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	e	60	Total	C	N	O	S	0	0
			472	295	96	80	1		

- Molecule 20 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	h	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 21 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D	227	Total	C	N	O	S	0	0
			1774	1126	320	323	5		

- Molecule 22 is a protein called KLLA0D10659p.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 23 is a protein called KLLA0B08173p.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 24 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	M	117	Total	C	N	O		0	0
			867	544	152	171			

- Molecule 25 is a protein called KLLA0F07843p.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	117	Total	C	N	O	S	0	0
			923	592	165	161	5		

- Molecule 26 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	141	Total	C	N	O		0	0
			1105	709	204	192			

- Molecule 27 is a protein called KLLA0B01474p.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	130	Total	C	N	O	S	0	0
			1033	643	194	193	3		

- Molecule 28 is a protein called KLLA0B01562p.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	145	Total	C	N	O	S	0	0
			1189	739	239	209	2		

- Molecule 29 is a protein called KLLA0A07194p.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	143	Total	C	N	O		0	0
			1110	693	210	207			

- Molecule 30 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	78	Total	C	N	O	S	0	0
			594	376	111	106	1		

- Molecule 32 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	64	Total	C	N	O	S	0	0
			499	308	99	91	1		

- Molecule 33 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	55	Total	C	N	O	S	0	0
			461	289	93	78	1		

- Molecule 34 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	74	Total	C	N	O	S	0	0
			584	374	111	95	4		

- Molecule 35 is a protein called Eukaryotic translation initiation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	96	Total	C	N	O	S	0	0
			769	477	143	144	5		

- Molecule 36 is a protein called Eukaryotic translation initiation factor eIF-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	86	Total	C	N	O	S	0	0
			695	439	128	124	4		

- Molecule 37 is a RNA chain called mRNA (5'-R(P*AP*AP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
37	3	6	Total	C	N	O	P	6	0
			256	116	50	78	12		

- Molecule 38 is a RNA chain called Met-tRNAi.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	1	75	Total	C	N	O	P	0	0
			1639	734	298	531	76		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	267	Total	C	N	O	S	0	0
			2139	1366	355	407	11		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	470	Total	C	N	O	S	0	0
			3596	2279	633	666	18		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 2 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	134	Total	C	N	O	S	0	0
			1083	689	194	193	7		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	n	93	Total	C	N	O	0	0
			464	278	93	93		

- Molecule 43 is a protein called KLLA0E12277p.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	320	Total	C	N	O	S	0	0
			2469	1561	432	471	5		

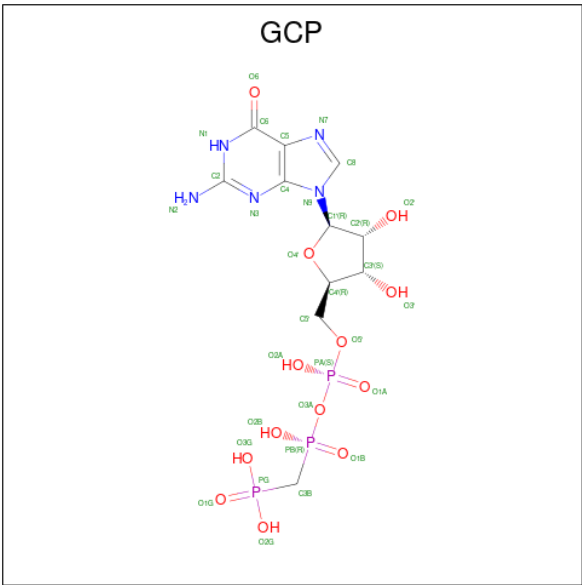
- Molecule 44 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
44	2	94	Total	Mg	0
			94	94	
44	X	1	Total	Mg	0
			1	1	
44	k	1	Total	Mg	0
			1	1	

- Molecule 45 is ZINC ION (CCD ID: ZN) (formula: Zn).

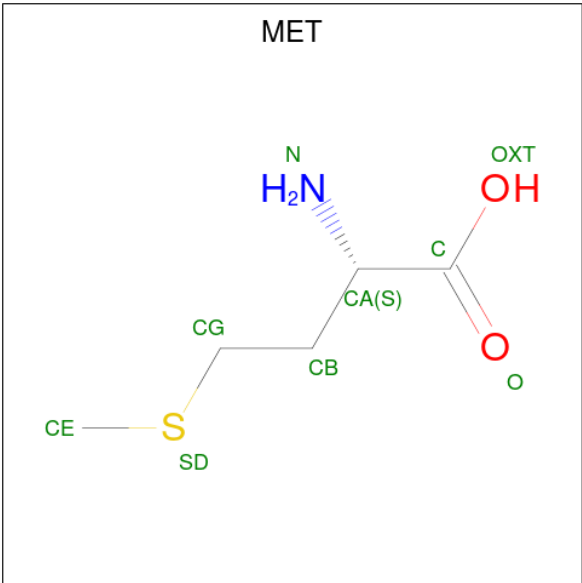
Mol	Chain	Residues	Atoms		AltConf
45	a	1	Total	Zn	0
			1	1	
45	b	1	Total	Zn	0
			1	1	
45	f	1	Total	Zn	0
			1	1	
45	l	1	Total	Zn	0
			1	1	

- Molecule 46 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 47 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S) (labeled as "Ligand of Interest" by depositor).

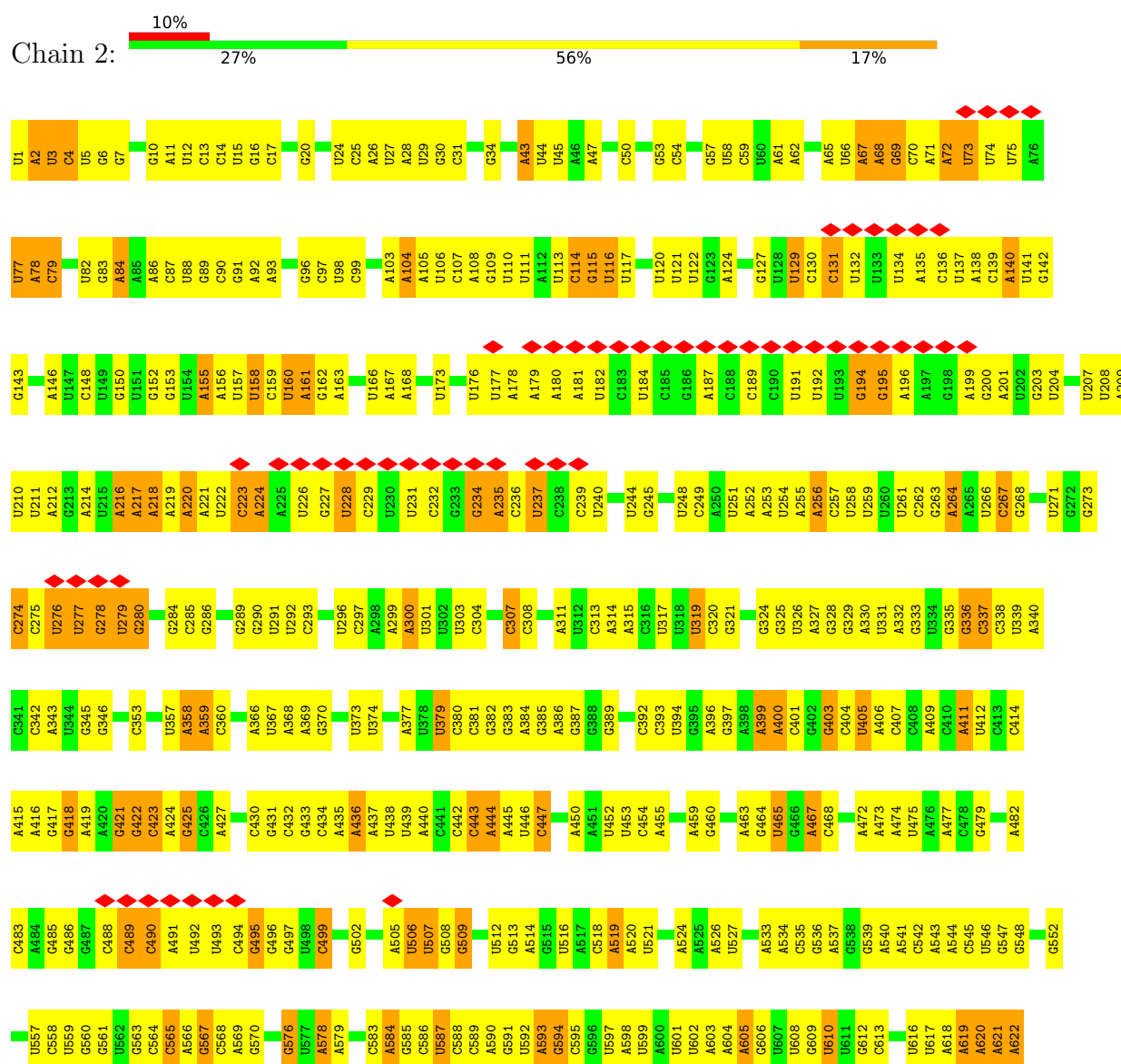


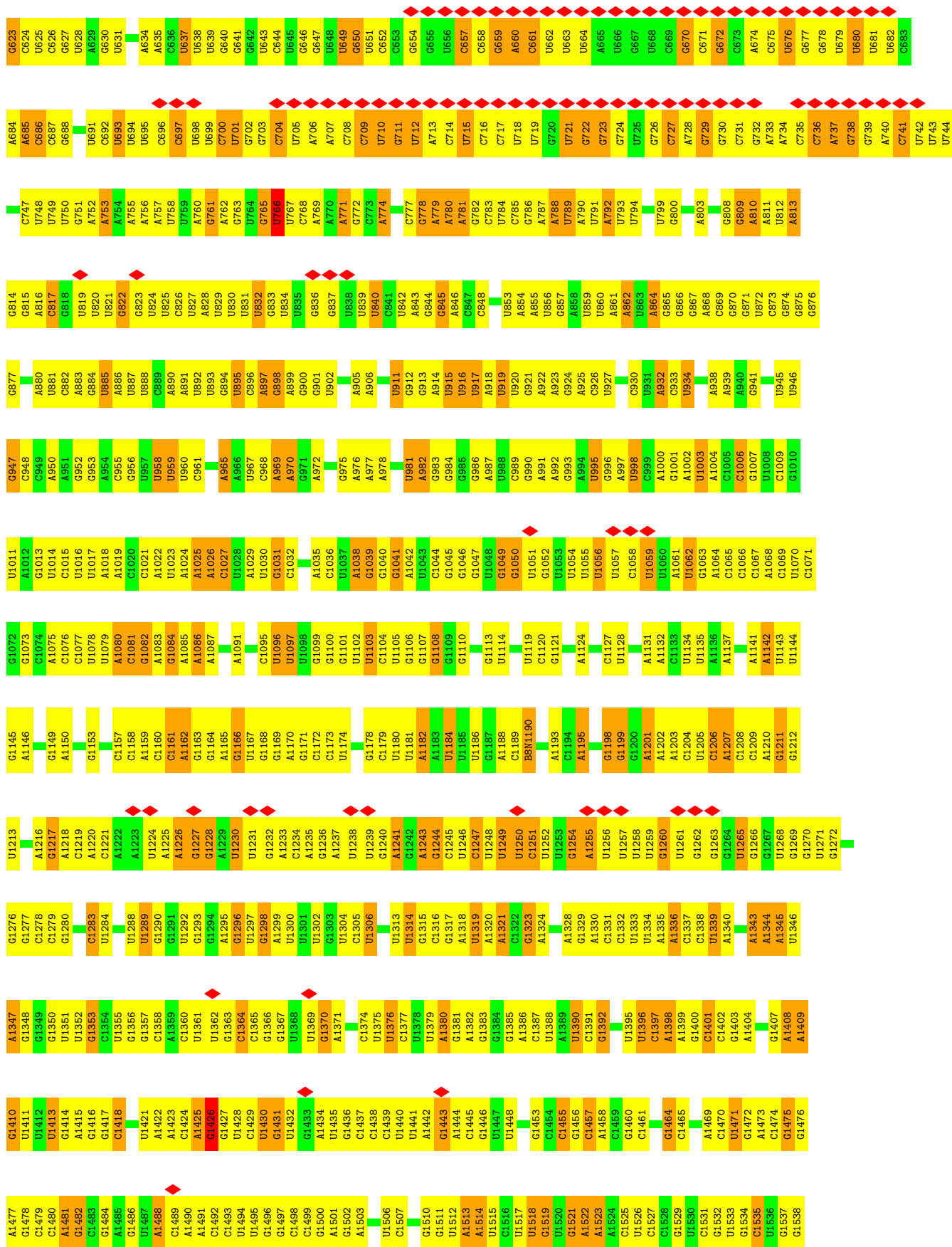
Mol	Chain	Residues	Atoms					AltConf
47	k	1	Total	C	N	O	S	0
			8	5	1	1	1	

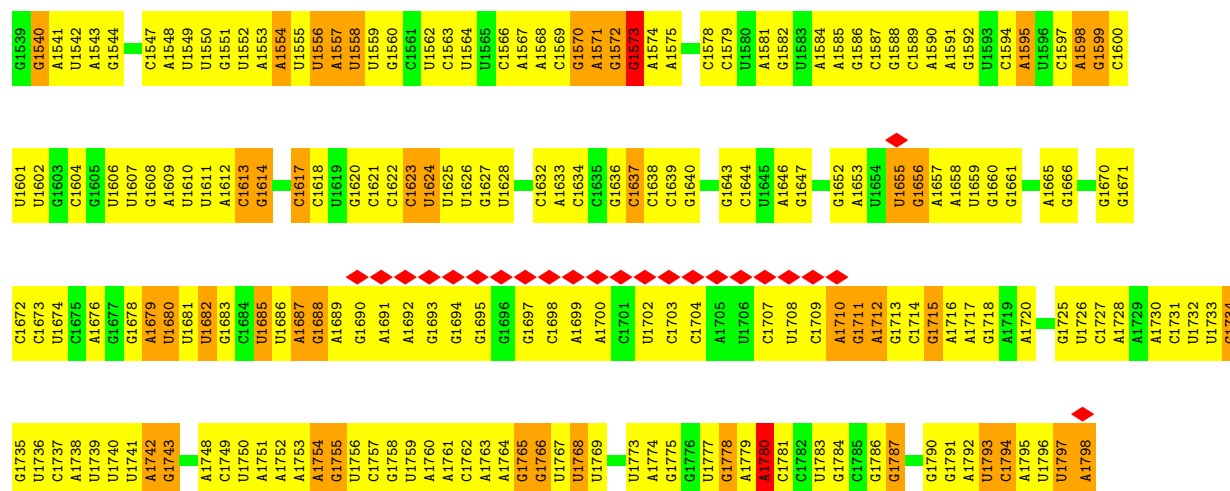
3 Residue-property plots

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.

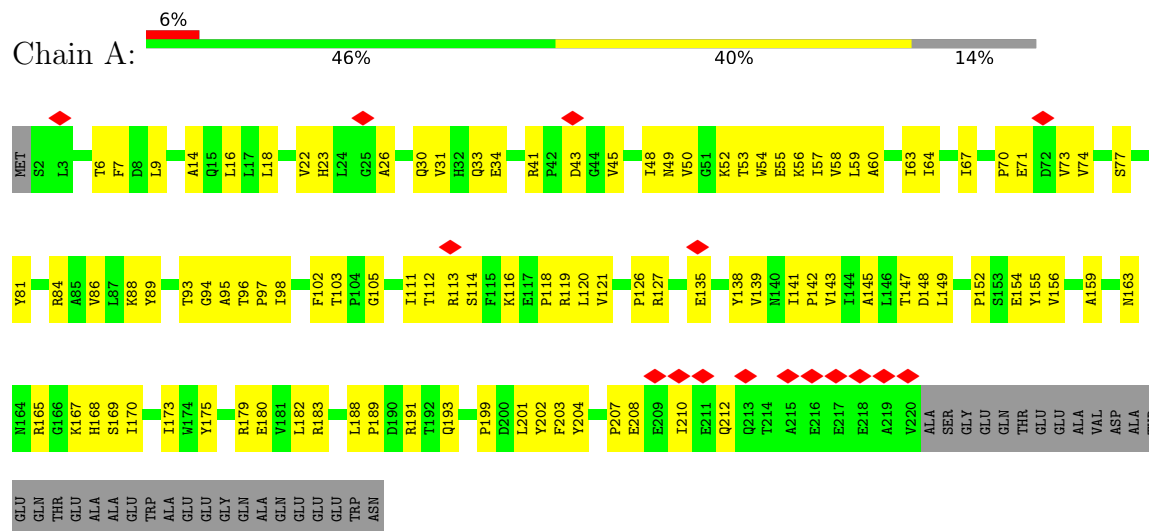
• Molecule 1: 18S ribosomal RNA



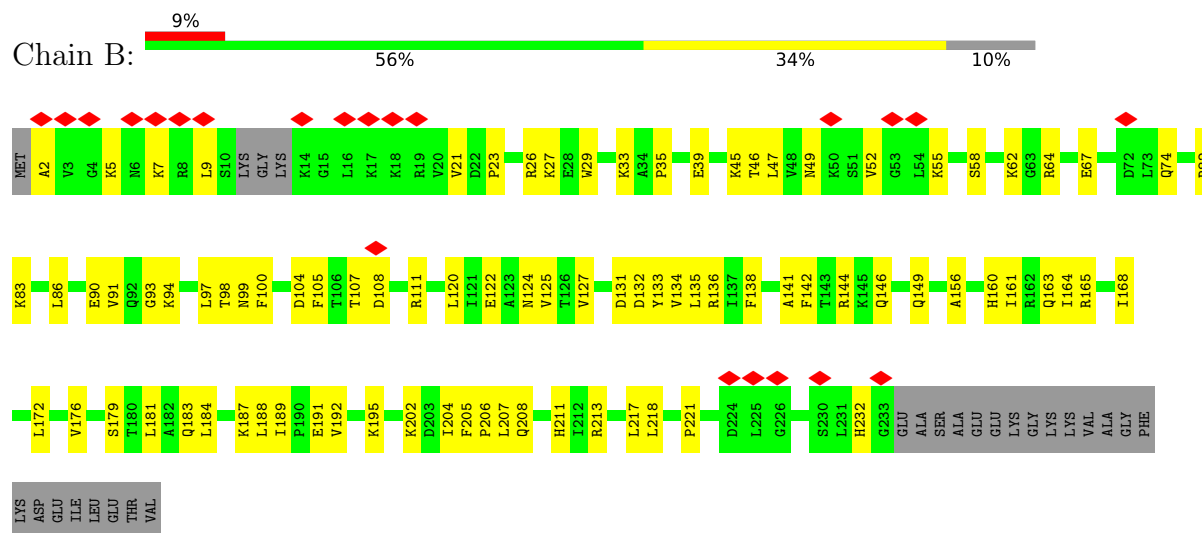




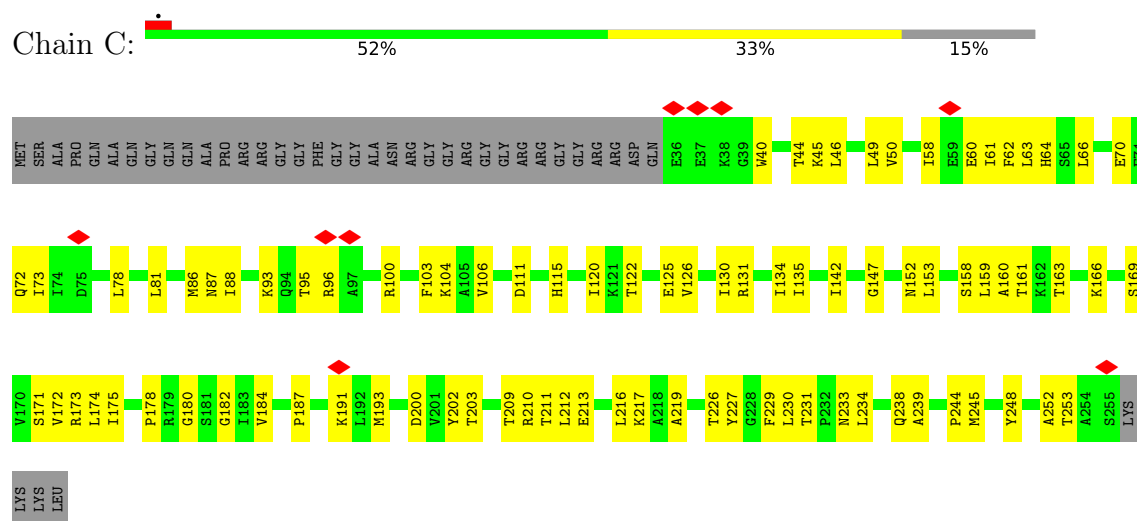
• Molecule 2: Small ribosomal subunit protein uS2



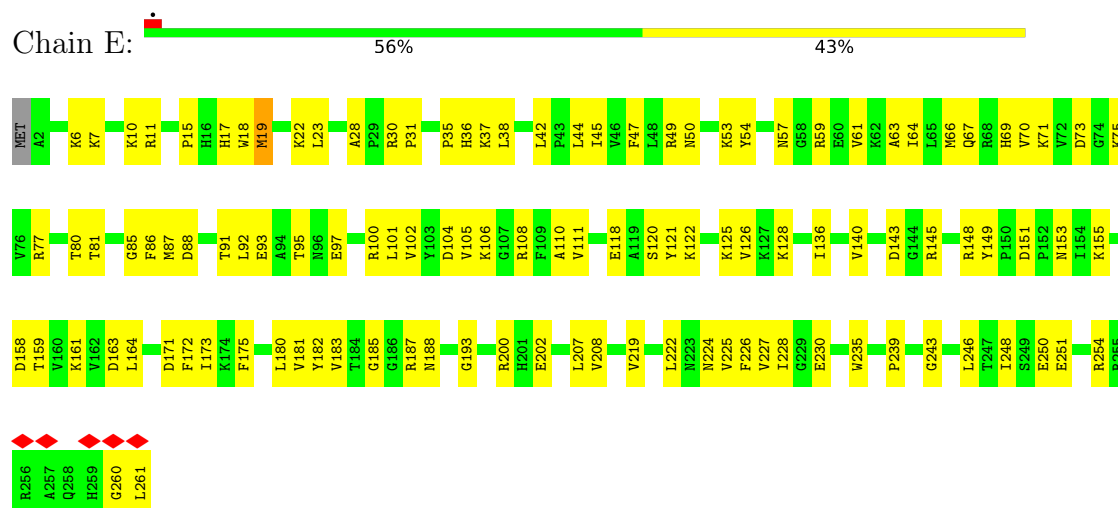
• Molecule 3: Small ribosomal subunit protein eS1



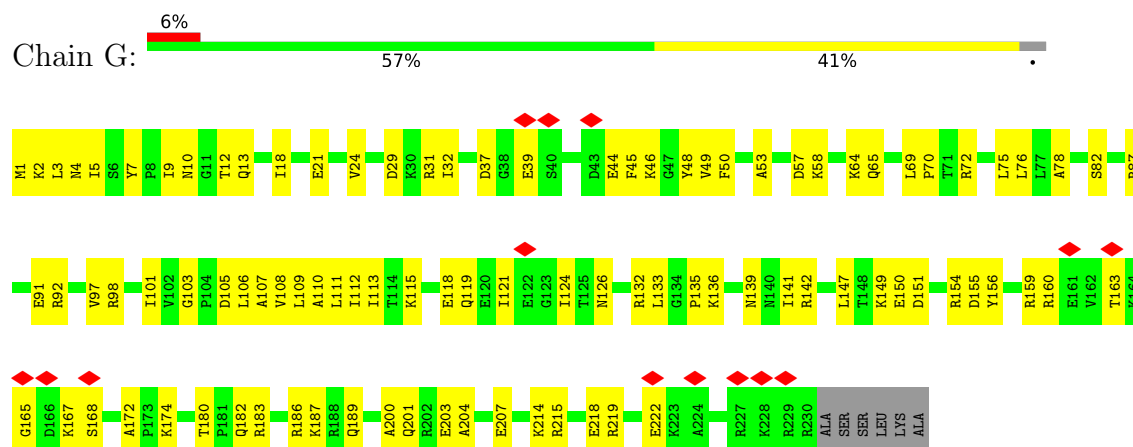
• Molecule 4: Small ribosomal subunit protein uS5



• Molecule 5: 40S ribosomal protein S4

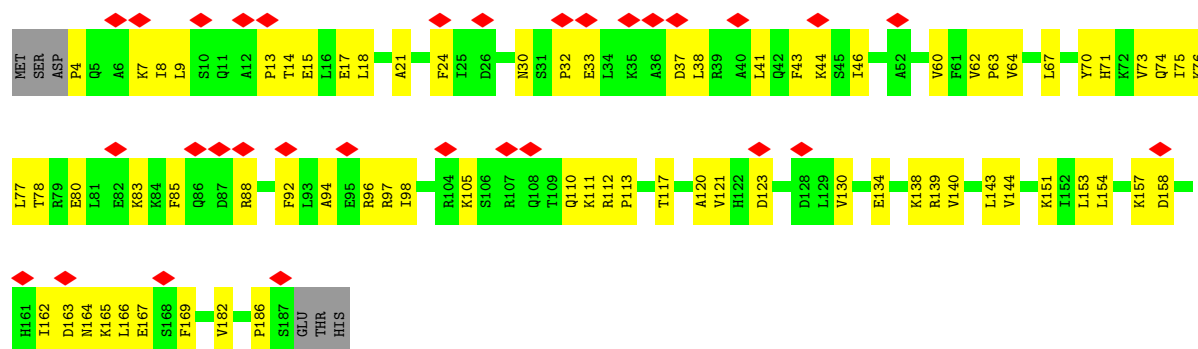


• Molecule 6: Small ribosomal subunit protein eS6

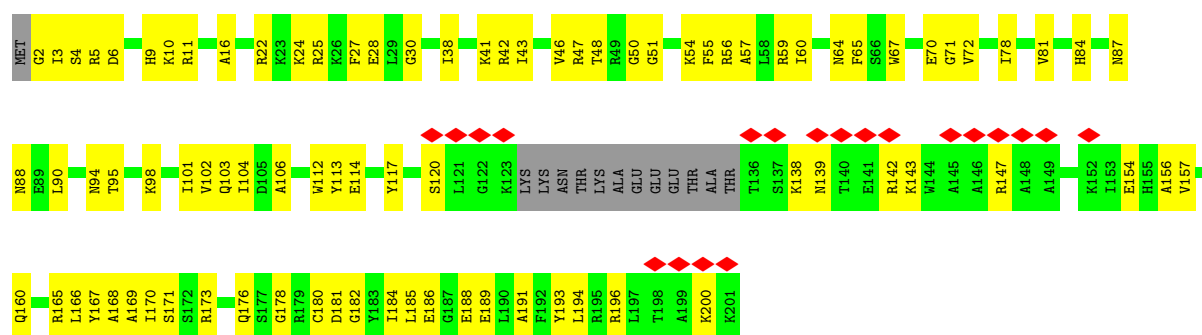


• Molecule 7: 40S ribosomal protein S7

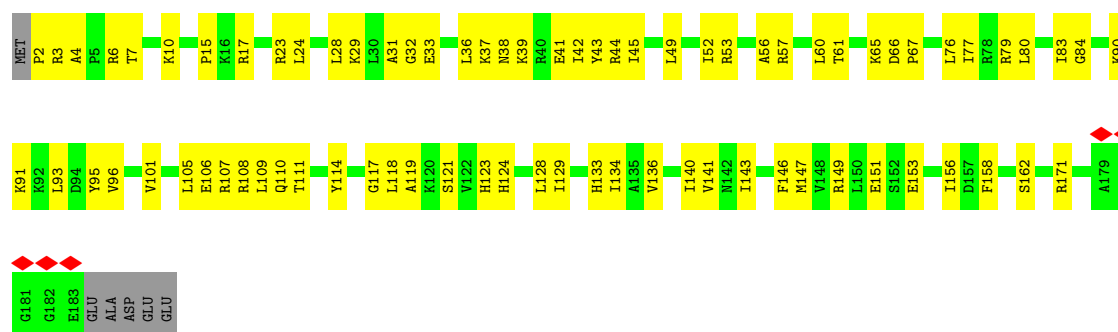




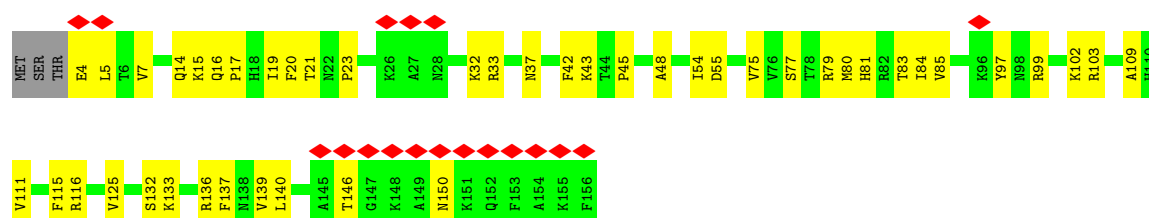
• Molecule 8: 40S ribosomal protein S8



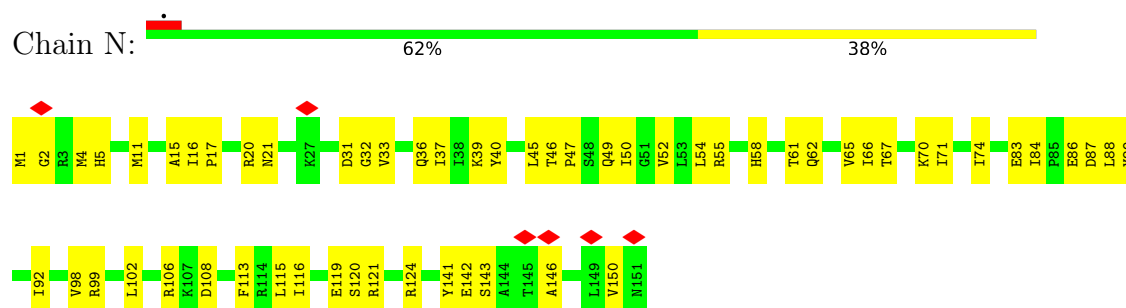
• Molecule 9: KLLA0E23673p



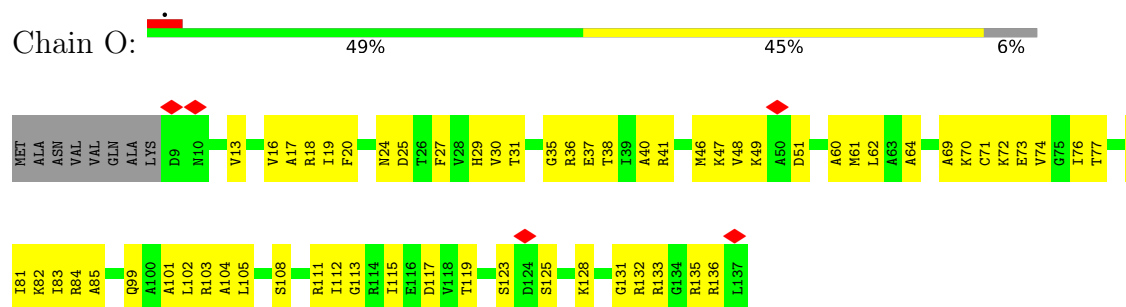
• Molecule 10: KLLA0A10483p



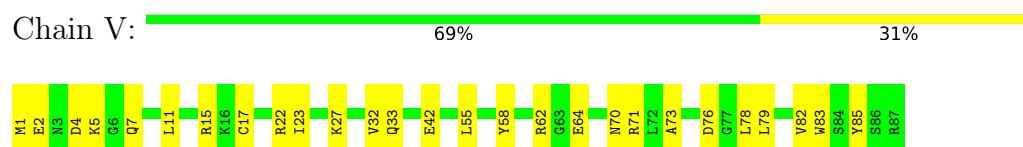
- Molecule 11: KLLA0F18040p



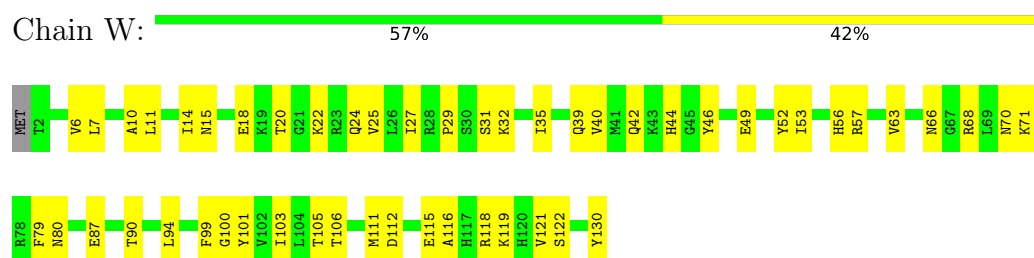
- Molecule 12: Small ribosomal subunit protein uS11



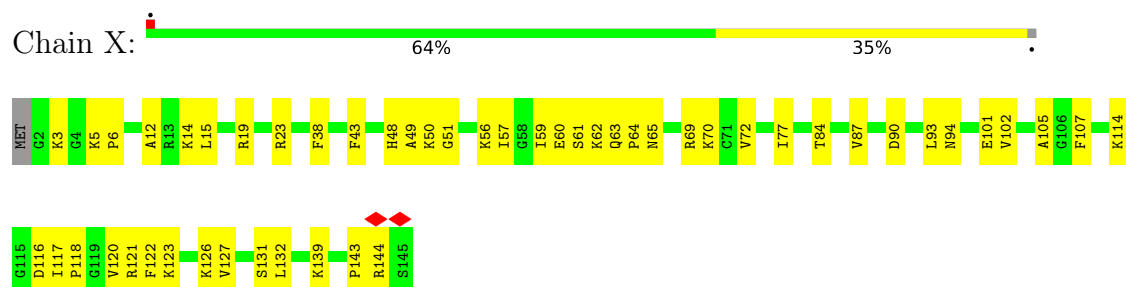
- Molecule 13: 40S ribosomal protein S21



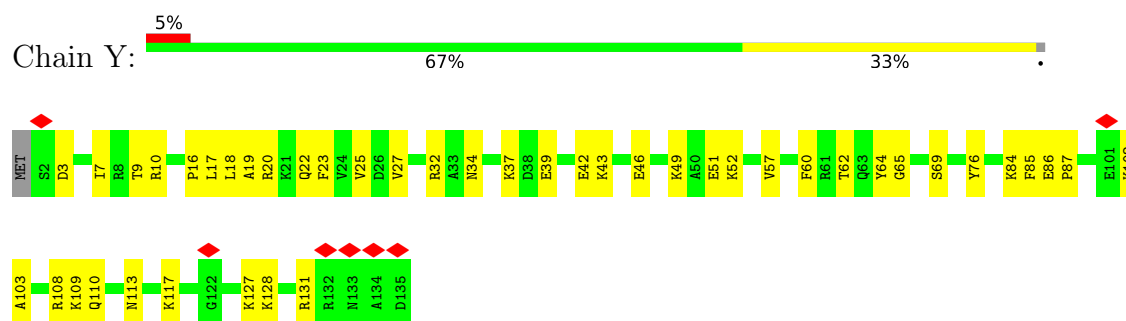
- Molecule 14: Small ribosomal subunit protein uS8



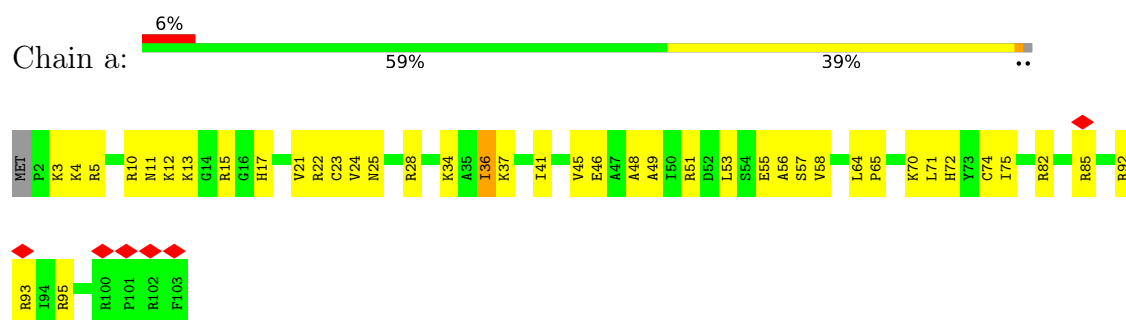
- Molecule 15: KLLA0B11231p



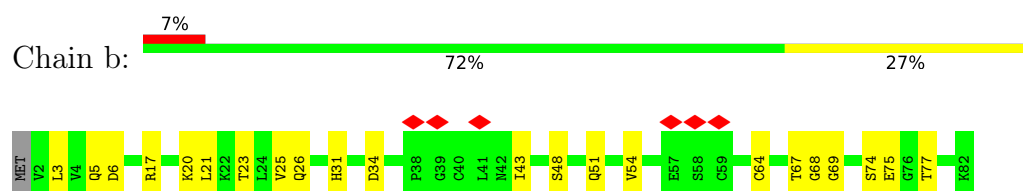
- Molecule 16: 40S ribosomal protein S24



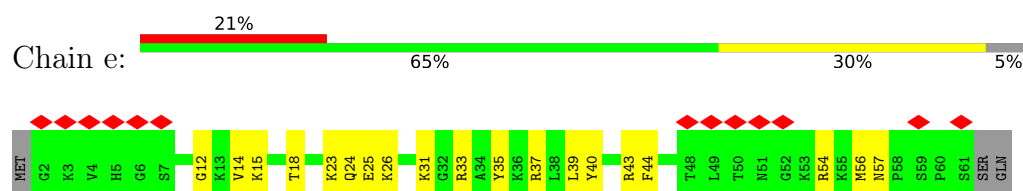
- Molecule 17: 40S ribosomal protein S26



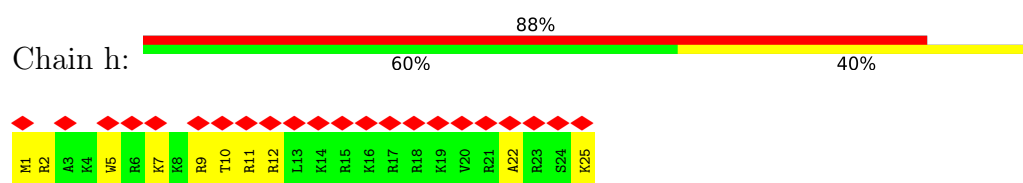
- Molecule 18: 40S ribosomal protein S27



- Molecule 19: 40S ribosomal protein S30

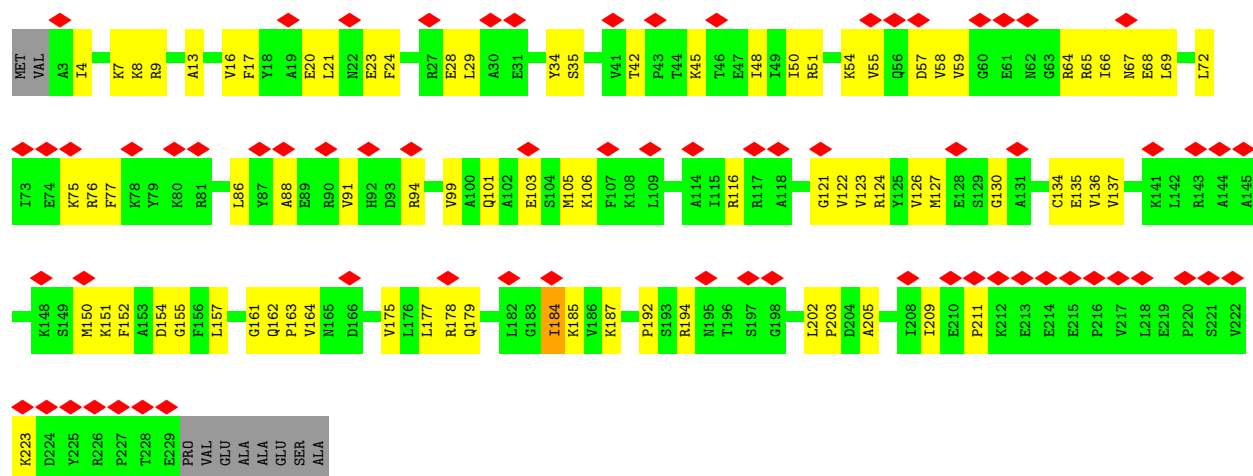


- Molecule 20: 60S ribosomal protein L41-A

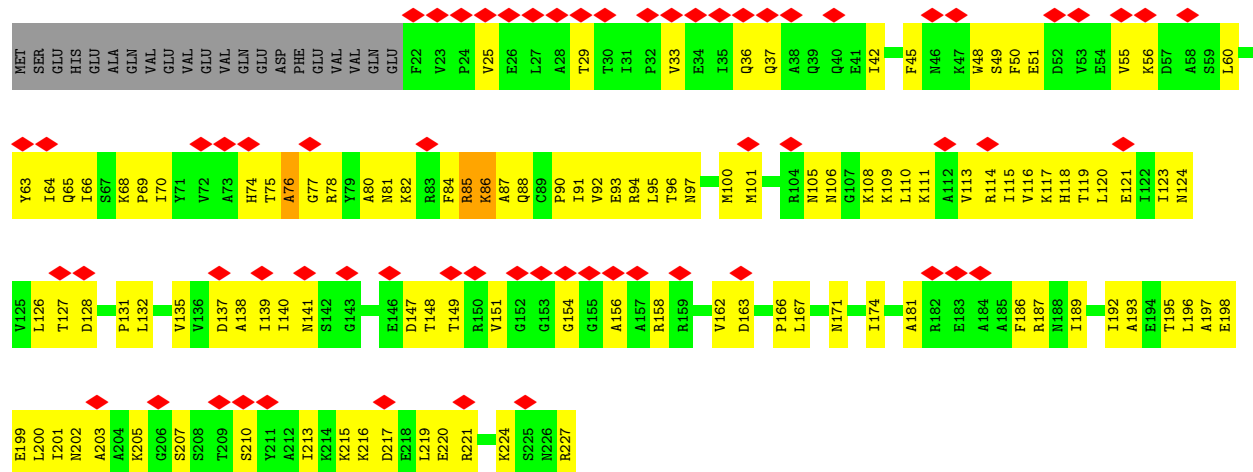
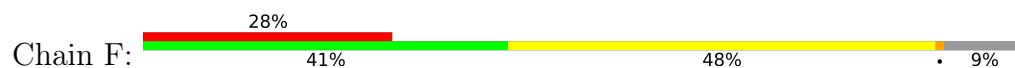


- Molecule 21: 40S ribosomal protein S3

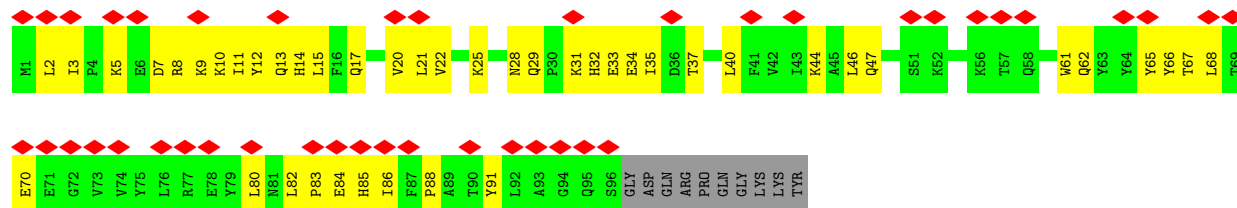
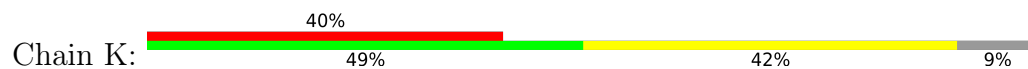




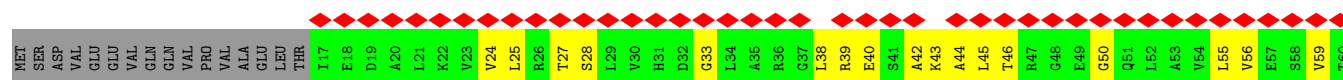
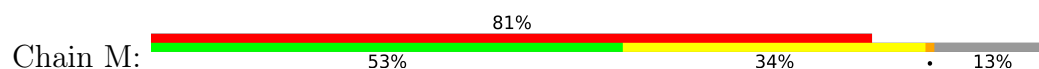
• Molecule 22: KLLA0D10659p

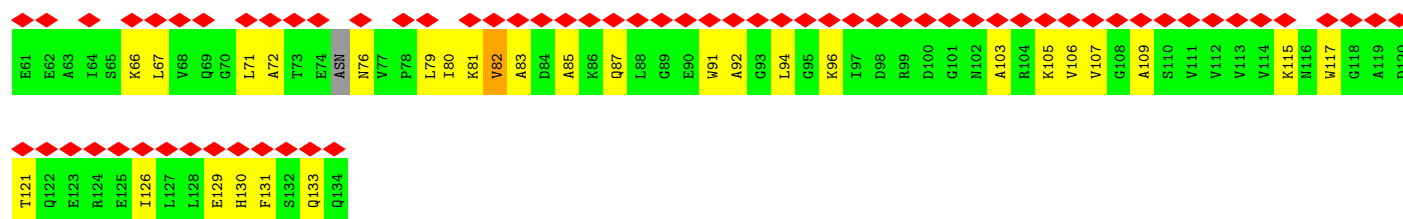


• Molecule 23: KLLA0B08173p

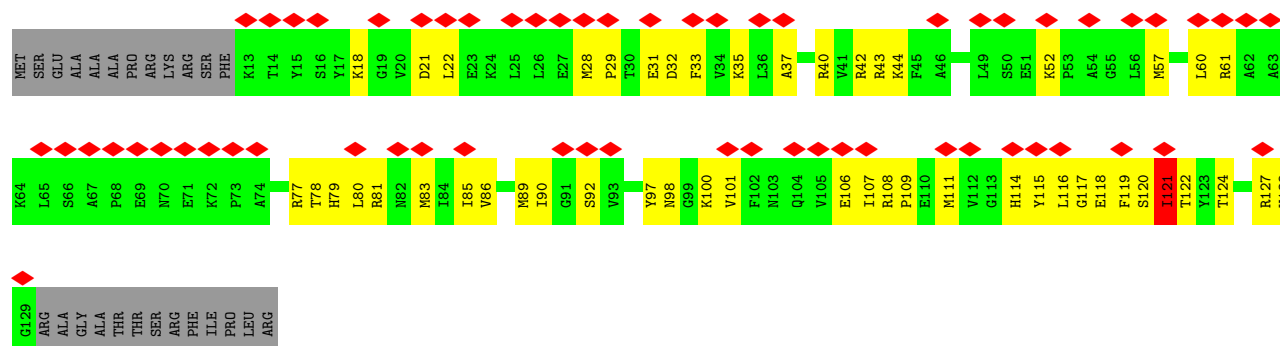
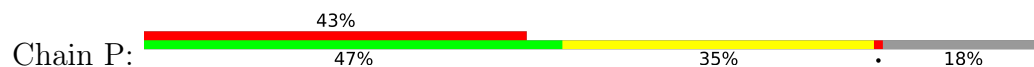


• Molecule 24: 40S ribosomal protein S12

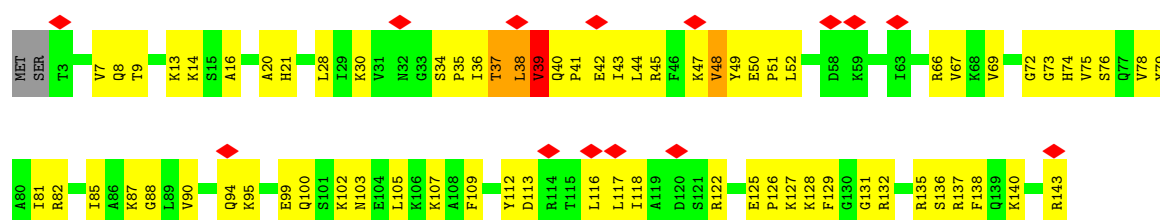




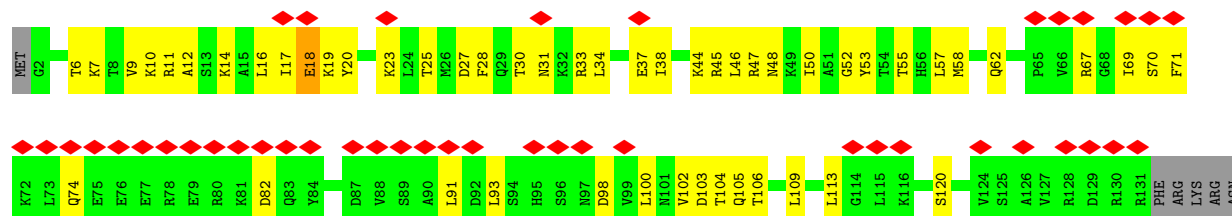
• Molecule 25: KLLA0F07843p



• Molecule 26: Small ribosomal subunit protein uS9

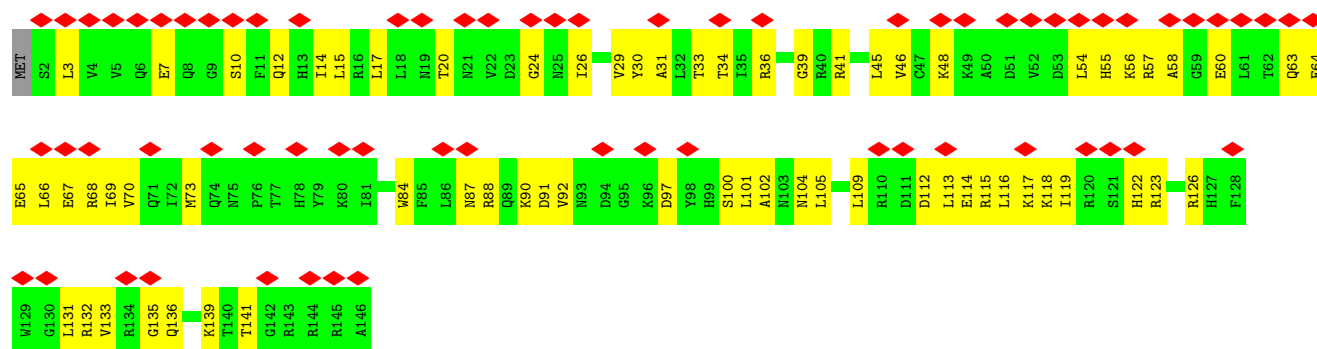


• Molecule 27: KLLA0B01474p



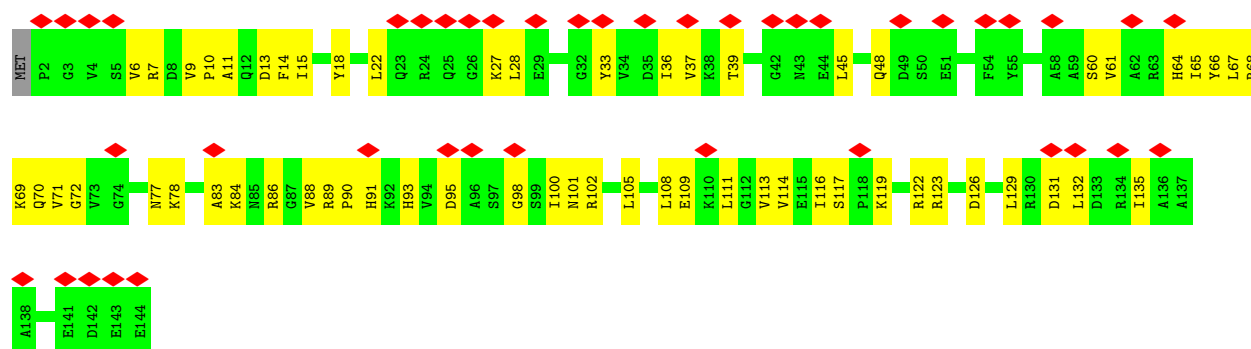
• Molecule 28: KLLA0B01562p





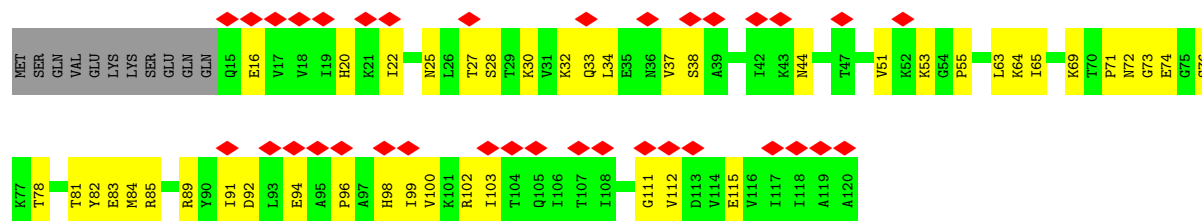
• Molecule 29: KLLA0A07194p

Chain T: 29% 58% 42%



• Molecule 30: Small ribosomal subunit protein uS10

Chain U: 30% 53% 38% 9%

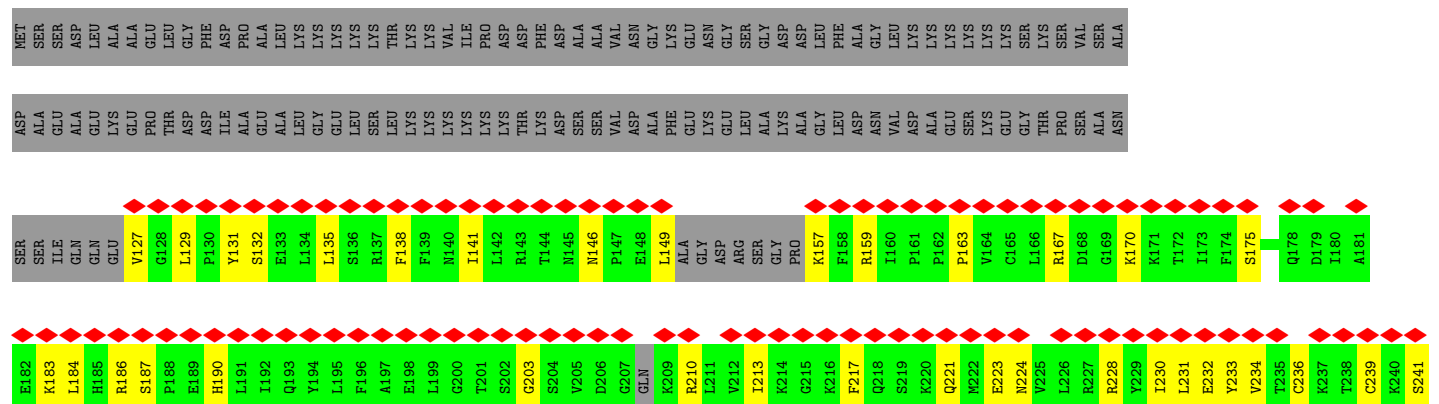


• Molecule 31: 40S ribosomal protein S25

Chain Z: 65% 49% 23% 28%



• Molecule 32: Small ribosomal subunit protein eS28







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66217	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.547	Depositor
Minimum map value	-0.320	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	402.0, 402.0, 402.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MA6, RIA, 1MG, B8N, 5MC, M2G, T6A, GCP, 1MA, MG, 7MG, 2MG, H2U, PSU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	2	0.23	0/42410	0.33	0/66079
2	A	0.31	0/1742	0.50	0/2383
3	B	0.24	0/1833	0.46	0/2467
4	C	0.29	0/1678	0.46	0/2277
5	E	0.30	0/2122	0.50	1/2861 (0.0%)
6	G	0.21	0/1855	0.44	0/2479
7	H	0.24	0/1507	0.44	0/2028
8	I	0.27	0/1515	0.44	0/2029
9	J	0.27	0/1495	0.48	0/2001
10	L	0.27	0/1263	0.43	0/1700
11	N	0.24	0/1218	0.39	0/1638
12	O	0.32	0/966	0.47	0/1297
13	V	0.25	0/696	0.40	0/938
14	W	0.32	0/1039	0.49	0/1399
15	X	0.26	0/1137	0.44	0/1516
16	Y	0.22	0/1075	0.41	0/1433
17	a	0.72	2/810 (0.2%)	0.55	1/1087 (0.1%)
18	b	0.21	0/619	0.40	0/837
19	e	0.24	0/480	0.40	0/640
20	h	0.17	0/234	0.34	0/300
21	D	0.19	0/1800	0.41	0/2421
22	F	0.20	0/1628	0.45	0/2198
23	K	0.15	0/831	0.41	0/1123
24	M	0.18	0/873	0.49	0/1180
25	P	0.23	0/942	0.45	0/1269
26	Q	0.25	0/1125	0.50	0/1510
27	R	0.25	0/1044	0.51	1/1402 (0.1%)
28	S	0.21	0/1208	0.39	0/1624
29	T	0.24	0/1129	0.43	0/1520
30	U	0.20	0/857	0.45	0/1158
31	Z	0.13	0/603	0.36	0/814
32	c	0.20	0/501	0.61	1/673 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.22	0/473	0.52	0/629
34	f	0.18	0/597	0.52	1/795 (0.1%)
35	i	0.25	0/778	0.57	0/1038
36	m	0.32	0/703	0.52	0/938
37	3	0.07	0/286	0.17	0/440
38	l	0.18	0/1529	0.36	0/2376
39	j	0.18	0/2171	0.48	1/2924 (0.0%)
40	k	0.16	0/3657	0.38	0/4946
41	l	0.12	0/1099	0.33	0/1469
42	n	0.10	0/461	0.25	0/640
43	g	0.22	0/2523	0.49	1/3434 (0.0%)
All	All	0.24	2/92512 (0.0%)	0.40	7/133910 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	a	25	ASN	C-N	17.08	1.57	1.33
17	a	74	CYS	C-N	-8.72	1.22	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	j	223	VAL	N-CA-C	-6.10	107.55	113.53
17	a	74	CYS	O-C-N	-5.97	115.37	122.65
5	E	19	MET	CB-CG-SD	-5.73	95.52	112.70
27	R	18	GLU	CA-CB-CG	-5.67	102.75	114.10
34	f	133	HIS	CB-CA-C	-5.27	110.48	116.54
32	c	19	THR	N-CA-C	5.10	115.03	108.34
43	g	135	TRP	CA-CB-CG	5.05	123.20	113.60

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	2	38190	0	19213	1136	0
2	A	1702	0	1695	109	0
3	B	1809	0	1872	81	0
4	C	1648	0	1727	93	0
5	E	2078	0	2157	95	0
6	G	1832	0	1919	102	0
7	H	1483	0	1579	75	0
8	I	1489	0	1504	83	0
9	J	1471	0	1554	76	0
10	L	1235	0	1299	43	0
11	N	1195	0	1263	64	0
12	O	955	0	987	82	0
13	V	687	0	682	35	0
14	W	1021	0	1056	61	0
15	X	1119	0	1198	57	0
16	Y	1061	0	1111	46	0
17	a	797	0	835	60	0
18	b	609	0	629	25	0
19	e	472	0	508	27	0
20	h	233	0	284	10	0
21	D	1774	0	1855	100	0
22	F	1609	0	1679	128	0
23	K	809	0	810	62	0
24	M	867	0	884	39	0
25	P	923	0	960	62	0
26	Q	1105	0	1170	124	0
27	R	1033	0	1082	64	0
28	S	1189	0	1211	90	0
29	T	1110	0	1124	65	0
30	U	845	0	913	60	0
31	Z	594	0	590	19	0
32	c	499	0	536	46	0
33	d	461	0	448	48	0
34	f	584	0	602	104	0
35	i	769	0	765	54	0
36	m	695	0	729	45	0
37	3	256	0	132	4	0
38	1	1639	0	852	35	0
39	j	2139	0	2205	92	0
40	k	3596	0	3713	136	0
41	l	1083	0	1120	40	0
42	n	464	0	207	1	0
43	g	2469	0	2403	168	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	2	94	0	0	0	0
44	X	1	0	0	0	0
44	k	1	0	0	0	0
45	a	1	0	0	0	0
45	b	1	0	0	0	0
45	f	1	0	0	0	0
45	l	1	0	0	0	0
46	k	32	0	14	2	0
47	k	8	0	8	0	0
All	All	87738	0	69084	3375	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 22.

All (3375) 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)
34:f:116:LYS:HG3	34:f:129:PHE:CE1	1.53	1.41
21:D:75:LYS:HZ2	23:K:22:VAL:CB	1.35	1.39
34:f:116:LYS:CG	34:f:129:PHE:HE1	1.40	1.33
21:D:75:LYS:NZ	23:K:22:VAL:HB	1.44	1.31
34:f:116:LYS:CG	34:f:129:PHE:CE1	2.11	1.30
21:D:150:MET:HE2	21:D:152:PHE:CZ	1.65	1.29
34:f:142:CYS:HB3	34:f:145:THR:CG2	1.60	1.28
34:f:120:GLU:OE2	34:f:126:PRO:HA	1.40	1.20
6:G:39:GLU:CG	6:G:46:LYS:HZ3	1.55	1.20
1:2:1581:A:C5	22:F:80:ALA:HB1	1.77	1.18
21:D:75:LYS:HZ2	23:K:22:VAL:CA	1.57	1.16
22:F:85:ARG:HD3	22:F:88:GLN:HB2	1.29	1.15
25:P:57:MET:CE	25:P:61:ARG:HG3	1.76	1.14
1:2:1581:A:C2	22:F:80:ALA:HB3	1.80	1.14
5:E:95:THR:O	5:E:97:GLU:HG2	1.49	1.12
2:A:167:LYS:HE2	2:A:204:TYR:HB3	1.29	1.12
28:S:12:GLN:NE2	28:S:15:LEU:HD23	1.65	1.12
39:j:7:ARG:HD2	39:j:40:ASP:OD1	1.47	1.11
34:f:124:CYS:SG	34:f:141:LYS:HB2	1.91	1.10
24:M:67:LEU:HD13	34:f:108:VAL:HG13	1.33	1.10
1:2:1755:G:H4'	35:i:41:MET:HE1	1.28	1.09
28:S:46:VAL:HG11	28:S:73:MET:HE3	1.26	1.08
12:O:99:GLN:HE22	17:a:45:VAL:HA	1.07	1.07
32:c:25:VAL:CG1	32:c:43:ASN:HB2	1.84	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:39:VAL:HG22	26:Q:45:ARG:NE	1.68	1.07
26:Q:49:TYR:HD1	26:Q:52:LEU:HD21	1.09	1.07
25:P:57:MET:HE3	25:P:61:ARG:HG3	1.31	1.07
26:Q:35:PRO:HD2	26:Q:38:LEU:HD22	1.32	1.07
26:Q:99:GLU:OE1	43:g:58:PRO:CG	2.02	1.07
21:D:105:MET:HE1	21:D:136:VAL:HG21	1.31	1.06
7:H:9:LEU:HD21	7:H:43:PHE:HB2	1.34	1.06
8:I:189:GLU:OE2	8:I:193:TYR:HE2	1.37	1.06
25:P:52:LYS:HE3	25:P:80:LEU:HD21	1.35	1.06
8:I:189:GLU:OE2	8:I:193:TYR:CE2	2.09	1.05
22:F:84:PHE:CE2	32:c:49:ARG:NH1	2.23	1.05
28:S:12:GLN:OE1	28:S:15:LEU:HD21	1.55	1.05
32:c:25:VAL:HG11	32:c:43:ASN:HB2	1.34	1.05
26:Q:99:GLU:CD	26:Q:103:ASN:HD21	1.64	1.05
26:Q:105:LEU:HG	26:Q:109:PHE:HE2	1.15	1.05
6:G:39:GLU:HG3	6:G:46:LYS:NZ	1.72	1.04
2:A:167:LYS:HZ1	2:A:203:PHE:HB3	1.22	1.04
34:f:142:CYS:HB3	34:f:145:THR:HG22	1.33	1.03
26:Q:49:TYR:CD1	26:Q:52:LEU:HD21	1.93	1.02
25:P:111:MET:SD	25:P:119:PHE:HE2	1.82	1.02
6:G:39:GLU:HG3	6:G:46:LYS:HZ3	0.89	1.01
1:2:1581:A:C6	22:F:80:ALA:CB	2.44	1.00
4:C:93:LYS:HB3	4:C:100:ARG:HG2	1.39	1.00
26:Q:39:VAL:HG22	26:Q:45:ARG:HE	0.86	1.00
34:f:106:TYR:CE1	34:f:129:PHE:HZ	1.78	1.00
34:f:116:LYS:HG2	34:f:129:PHE:CE1	1.96	1.00
34:f:142:CYS:HB3	34:f:145:THR:HG23	1.42	1.00
34:f:124:CYS:SG	34:f:141:LYS:CB	2.50	1.00
1:2:1581:A:C2	22:F:80:ALA:CB	2.45	1.00
32:c:18:ARG:HG2	32:c:26:THR:HG22	1.41	1.00
17:a:24:VAL:HG11	17:a:71:LEU:HD22	1.40	0.99
16:Y:76:TYR:CE1	16:Y:86:GLU:OE2	2.14	0.99
1:2:1479:C:H5'	26:Q:40:GLN:OE1	1.59	0.99
23:K:3:ILE:HG23	23:K:8:ARG:HH21	1.26	0.99
4:C:93:LYS:HD3	4:C:100:ARG:HD2	1.41	0.99
14:W:112:ASP:OD1	14:W:115:GLU:HG3	1.59	0.99
40:k:201:MET:HA	40:k:204:MET:HE3	1.44	0.99
25:P:86:VAL:HG12	25:P:89:MET:HE3	1.40	0.99
35:i:87:ASP:C	35:i:88:GLN:OE1	2.06	0.98
43:g:110:ASP:OD1	43:g:128:ARG:HD2	1.61	0.98
21:D:8:LYS:HD3	33:d:34:TYR:HE1	1.29	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:84:PHE:CZ	32:c:49:ARG:NH1	2.33	0.97
34:f:130:LEU:HD11	34:f:139:CYS:HB2	1.42	0.97
26:Q:37:THR:CA	26:Q:49:TYR:OH	2.13	0.96
21:D:75:LYS:HZ2	23:K:22:VAL:HB	0.91	0.96
30:U:34:LEU:HB3	30:U:89:ARG:HH12	1.31	0.96
28:S:126:ARG:NH2	28:S:135:GLY:H	1.64	0.95
1:2:1069:C:H4'	18:b:17:ARG:HD2	1.47	0.95
21:D:105:MET:HG2	21:D:122:VAL:HG21	1.48	0.95
16:Y:76:TYR:HE1	16:Y:86:GLU:OE2	1.46	0.95
12:O:99:GLN:NE2	17:a:46:GLU:OE1	2.00	0.94
39:j:12:LYS:HA	39:j:40:ASP:OD2	1.67	0.94
28:S:56:LYS:HD2	28:S:60:GLU:OE1	1.67	0.94
1:2:975:G:H1	1:2:1022:A:HO2'	1.07	0.94
1:2:1581:A:C5	22:F:80:ALA:CB	2.51	0.93
24:M:82:VAL:HG12	24:M:83:ALA:H	1.30	0.93
26:Q:105:LEU:HG	26:Q:109:PHE:CE2	2.02	0.93
15:X:62:LYS:HE3	15:X:118:PRO:HB3	1.48	0.93
21:D:150:MET:HE2	21:D:152:PHE:CE1	2.02	0.93
21:D:150:MET:CE	21:D:152:PHE:CZ	2.52	0.93
32:c:42:ARG:NH1	32:c:43:ASN:OD1	2.01	0.93
34:f:116:LYS:CG	34:f:129:PHE:CD1	2.51	0.93
1:2:1581:A:N3	22:F:80:ALA:HB3	1.84	0.92
34:f:116:LYS:HG3	34:f:129:PHE:CD1	2.04	0.92
34:f:116:LYS:HG3	34:f:129:PHE:HE1	0.95	0.92
21:D:75:LYS:NZ	23:K:22:VAL:CB	2.14	0.92
27:R:33:ARG:HG3	43:g:128:ARG:NH1	1.84	0.92
28:S:126:ARG:HH22	28:S:135:GLY:N	1.68	0.92
34:f:130:LEU:CD1	34:f:139:CYS:HB2	1.99	0.92
6:G:50:PHE:HB3	6:G:111:LEU:HD12	1.52	0.91
21:D:75:LYS:NZ	23:K:22:VAL:CA	2.31	0.91
23:K:3:ILE:HG21	23:K:8:ARG:HE	1.35	0.91
25:P:111:MET:SD	25:P:119:PHE:CE2	2.63	0.91
9:J:136:VAL:HG22	9:J:156:ILE:HD13	1.51	0.91
4:C:93:LYS:HB3	4:C:100:ARG:CG	2.00	0.91
21:D:184:ILE:HD12	21:D:185:LYS:N	1.86	0.91
26:Q:39:VAL:CG2	26:Q:45:ARG:HE	1.81	0.91
28:S:116:LEU:HD21	28:S:123:ARG:HG2	1.51	0.91
21:D:8:LYS:CD	33:d:34:TYR:HE1	1.81	0.90
1:2:1164:G:H4'	22:F:101:MET:CE	2.00	0.90
13:V:76:ASP:OD2	13:V:78:LEU:CD2	2.19	0.90
28:S:126:ARG:HH22	28:S:135:GLY:H	0.90	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1581:A:C4	22:F:80:ALA:CB	2.54	0.90
21:D:8:LYS:HD3	33:d:34:TYR:CE1	2.06	0.90
26:Q:37:THR:HA	26:Q:49:TYR:HH	1.34	0.89
27:R:7:LYS:HE2	27:R:11:ARG:HH11	1.37	0.89
1:2:1581:A:C6	22:F:80:ALA:HB1	2.08	0.89
12:O:99:GLN:HE22	17:a:45:VAL:CA	1.85	0.89
29:T:9:VAL:HG22	29:T:10:PRO:HD2	1.53	0.89
35:i:30:GLU:HG3	35:i:33:GLN:NE2	1.87	0.89
39:j:54:ARG:O	39:j:55:ARG:O	1.91	0.89
27:R:70:SER:HA	27:R:74:GLN:NE2	1.88	0.89
21:D:123:VAL:HG12	21:D:127:MET:HE1	1.54	0.89
26:Q:37:THR:HA	26:Q:49:TYR:OH	1.69	0.89
28:S:12:GLN:CD	28:S:15:LEU:CD2	2.46	0.89
1:2:1161:C:H2'	1:2:1162:A:H8	1.37	0.89
13:V:76:ASP:OD2	13:V:78:LEU:HD23	1.73	0.88
1:2:1581:A:C4	22:F:80:ALA:HB1	2.08	0.88
1:2:1586:G:H1	1:2:1606:U:H3	1.18	0.88
1:2:536:G:H3'	9:J:171:ARG:HH22	1.38	0.88
28:S:46:VAL:HG21	28:S:73:MET:HE1	1.55	0.88
1:2:1753:A:OP2	15:X:63:GLN:NE2	2.08	0.87
7:H:32:PRO:HG2	7:H:33:GLU:OE2	1.74	0.87
29:T:37:VAL:HG12	29:T:39:THR:H	1.39	0.87
1:2:588:C:O3'	19:e:56:MET:HE1	1.75	0.87
7:H:9:LEU:CD2	7:H:43:PHE:HB2	2.04	0.87
2:A:119:ARG:NH1	4:C:245:MET:SD	2.48	0.86
34:f:106:TYR:HE1	34:f:129:PHE:HZ	1.17	0.86
43:g:258:TRP:HB3	43:g:269:ILE:HD11	1.57	0.86
21:D:150:MET:HE2	21:D:152:PHE:HZ	1.12	0.86
27:R:53:TYR:O	27:R:57:LEU:HD13	1.75	0.86
32:c:19:THR:HG21	32:c:27:GLN:NE2	1.89	0.86
25:P:57:MET:CE	25:P:61:ARG:CG	2.53	0.86
34:f:142:CYS:CB	34:f:145:THR:CG2	2.52	0.86
12:O:99:GLN:NE2	17:a:45:VAL:HA	1.90	0.86
26:Q:99:GLU:OE1	43:g:58:PRO:HG2	1.74	0.86
40:k:182:ARG:HH21	40:k:184:LYS:HA	1.41	0.85
23:K:80:LEU:HD22	23:K:82:LEU:HB2	1.58	0.85
34:f:119:LYS:HG3	34:f:120:GLU:H	1.41	0.85
1:2:917:U:H2'	1:2:918:A:C8	2.12	0.85
32:c:18:ARG:HG2	32:c:26:THR:CG2	2.05	0.85
34:f:106:TYR:CE1	34:f:129:PHE:CZ	2.64	0.85
43:g:20:TRP:HE1	43:g:313:THR:HB	1.40	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:136:VAL:HG22	9:J:156:ILE:CD1	2.06	0.85
35:i:88:GLN:OE1	35:i:88:GLN:N	2.08	0.85
18:b:54:VAL:HG12	18:b:64:CYS:SG	2.15	0.85
43:g:112:LEU:HD21	43:g:128:ARG:HE	1.40	0.84
1:2:13:C:H1'	1:2:1298:G:H21	1.42	0.84
22:F:154:GLY:O	37:3:26[B]:A:N6	2.09	0.84
28:S:12:GLN:CD	28:S:15:LEU:HD23	2.01	0.84
2:A:148:ASP:OD1	2:A:149:LEU:N	2.10	0.84
1:2:960:U:H5''	11:N:71:ILE:HD13	1.58	0.84
15:X:57:ILE:HD12	15:X:59:ILE:HD11	1.59	0.84
40:k:120:ILE:HA	40:k:291:ILE:HD11	1.57	0.84
1:2:787:A:OP2	5:E:108:ARG:NH2	2.11	0.84
43:g:90:LEU:HB2	43:g:104:PHE:HB2	1.58	0.84
1:2:1161:C:H2'	1:2:1162:A:C8	2.11	0.84
1:2:1164:G:H4'	22:F:101:MET:SD	2.18	0.83
29:T:88:VAL:HG13	29:T:89:ARG:HE	1.41	0.83
39:j:7:ARG:HB3	39:j:40:ASP:OD1	1.77	0.83
26:Q:37:THR:CA	26:Q:49:TYR:HH	1.89	0.83
28:S:12:GLN:OE1	28:S:15:LEU:CD2	2.26	0.83
1:2:1581:A:N1	22:F:80:ALA:CB	2.41	0.83
27:R:10:LYS:HD3	27:R:53:TYR:CE2	2.13	0.83
1:2:917:U:H2'	1:2:918:A:H8	1.41	0.82
1:2:1408:A:H5''	26:Q:118:ILE:HD11	1.60	0.82
1:2:1266:G:H1	1:2:1440:U:H3	1.26	0.82
29:T:9:VAL:CG2	29:T:10:PRO:HD2	2.08	0.82
6:G:39:GLU:O	6:G:46:LYS:NZ	2.13	0.82
1:2:631:U:OP2	10:L:102:LYS:NZ	2.13	0.82
1:2:917:U:H4'	12:O:18:ARG:HD3	1.62	0.82
26:Q:35:PRO:HD2	26:Q:38:LEU:CD2	2.09	0.82
30:U:82:TYR:HB3	33:d:52:PHE:HB3	1.59	0.82
28:S:46:VAL:HG11	28:S:73:MET:CE	2.10	0.82
27:R:53:TYR:O	27:R:57:LEU:CD1	2.28	0.82
34:f:133:HIS:CG	34:f:134:GLY:H	1.98	0.82
40:k:351:ASP:HB2	40:k:377:ILE:HD12	1.62	0.82
21:D:150:MET:CE	21:D:152:PHE:HZ	1.88	0.82
26:Q:36:ILE:C	26:Q:49:TYR:HH	1.87	0.81
1:2:1543:A:H5'	28:S:133:VAL:HB	1.62	0.81
23:K:3:ILE:CG2	23:K:8:ARG:HH21	1.93	0.81
33:d:22:ARG:NH2	33:d:36:LEU:HA	1.95	0.81
34:f:130:LEU:HD23	34:f:137:PHE:HB3	1.63	0.81
39:j:19:ILE:HG13	39:j:72:VAL:HG23	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1392:G:OP1	43:g:292:GLN:NE2	2.13	0.81
1:2:28:A:N1	1:2:597:U:C4	2.49	0.81
22:F:85:ARG:HD3	22:F:88:GLN:CB	2.10	0.81
1:2:1232:G:OP2	34:f:92:ARG:NH2	2.13	0.80
24:M:82:VAL:HG12	24:M:83:ALA:N	1.92	0.80
26:Q:37:THR:N	26:Q:49:TYR:OH	2.14	0.80
23:K:3:ILE:HG23	23:K:8:ARG:NH2	1.95	0.80
26:Q:105:LEU:O	26:Q:109:PHE:CD2	2.35	0.80
36:m:58:LEU:O	36:m:62:PHE:HD2	1.64	0.80
1:2:587:U:OP1	19:e:26:LYS:NZ	2.15	0.80
2:A:167:LYS:HE2	2:A:204:TYR:CB	2.09	0.80
1:2:608:U:O2'	15:X:23:ARG:NH1	2.15	0.80
8:I:104:ILE:HB	8:I:166:LEU:HB2	1.63	0.80
26:Q:105:LEU:O	26:Q:109:PHE:HD2	1.65	0.80
1:2:1653:A:N6	1:2:1743:G:O2'	2.15	0.80
4:C:93:LYS:HB3	4:C:100:ARG:CD	2.12	0.80
40:k:148:TYR:HB3	40:k:183:TYR:HB3	1.63	0.79
43:g:20:TRP:NE1	43:g:313:THR:HB	1.97	0.79
34:f:119:LYS:HG3	34:f:120:GLU:N	1.98	0.79
39:j:208:ALA:HA	39:j:211:MET:HE2	1.65	0.79
43:g:7:MET:HE3	43:g:8:LEU:H	1.47	0.79
1:2:1003:U:O4	36:m:59:LYS:NZ	2.14	0.79
34:f:133:HIS:CD2	34:f:134:GLY:H	2.00	0.79
1:2:983:G:H1	1:2:1016:U:H5	1.30	0.79
23:K:9:LYS:O	23:K:9:LYS:HD2	1.82	0.79
1:2:658:C:H2'	1:2:659:G:H8	1.46	0.78
7:H:15:GLU:HA	7:H:18:LEU:HD12	1.64	0.78
11:N:15:ALA:HB1	18:b:26:GLN:NE2	1.97	0.78
1:2:613:C:OP1	15:X:3:LYS:NZ	2.17	0.78
1:2:899:A:H3'	1:2:900:G:H21	1.49	0.78
43:g:151:TRP:HB2	43:g:179:MET:HE2	1.66	0.77
6:G:132:ARG:NE	6:G:133:LEU:HD22	2.00	0.77
35:i:30:GLU:HG3	35:i:33:GLN:HE21	1.45	0.77
7:H:166:LEU:O	7:H:169:PHE:HB2	1.83	0.77
26:Q:37:THR:HG23	26:Q:49:TYR:OH	1.83	0.77
6:G:12:THR:HB	6:G:124:ILE:HG13	1.67	0.77
38:1:20:A:N6	38:1:57:G:N3	2.32	0.77
27:R:17:ILE:HD13	27:R:58:MET:HE1	1.65	0.77
43:g:20:TRP:CD1	43:g:313:THR:HA	2.19	0.77
43:g:186:TRP:HZ3	43:g:195:ILE:HD12	1.49	0.77
1:2:1277:G:H1	1:2:1428:U:H3	1.31	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1345:A:OP2	1:2:1347:A:N6	2.17	0.77
7:H:67:LEU:HD22	7:H:94:ALA:HB2	1.67	0.77
12:O:112:ILE:O	17:a:57:SER:HA	1.85	0.77
15:X:143:PRO:O	15:X:144:ARG:HD3	1.85	0.77
1:2:1481:A:OP2	1:2:1519:G:N2	2.13	0.76
21:D:105:MET:CG	21:D:122:VAL:HG21	2.14	0.76
43:g:134:VAL:HB	43:g:143:TYR:HB2	1.66	0.76
12:O:47:LYS:HB3	12:O:62:LEU:HD23	1.68	0.76
30:U:51:VAL:HG13	30:U:94:GLU:HB2	1.66	0.76
26:Q:45:ARG:HG3	26:Q:49:TYR:CE2	2.20	0.76
28:S:12:GLN:HE22	28:S:15:LEU:HD23	1.46	0.76
25:P:57:MET:HE2	25:P:61:ARG:HG3	1.66	0.76
1:2:1283:C:N4	1:2:1421:U:O4	2.19	0.76
25:P:32:ASP:HA	25:P:35:LYS:HD2	1.68	0.76
1:2:1356:G:O2'	29:T:126:ASP:OD1	2.04	0.76
5:E:246:LEU:HD21	5:E:254:ARG:HH11	1.50	0.76
26:Q:99:GLU:OE2	26:Q:103:ASN:ND2	2.18	0.76
30:U:38:SER:HB3	30:U:89:ARG:HH21	1.51	0.76
39:j:7:ARG:CD	39:j:40:ASP:OD1	2.32	0.76
14:W:6:VAL:HG23	14:W:29:PRO:HG2	1.67	0.75
40:k:238:ILE:HG23	40:k:514:TRP:HB3	1.68	0.75
9:J:153:GLU:OE2	9:J:153:GLU:N	2.17	0.75
26:Q:99:GLU:OE1	43:g:58:PRO:CB	2.34	0.75
41:l:244:THR:HA	41:l:259:CYS:HA	1.68	0.75
1:2:617:U:O4	1:2:1085:A:N6	2.19	0.75
11:N:55:ARG:NH2	18:b:51:GLN:OE1	2.20	0.75
21:D:105:MET:HE1	21:D:136:VAL:CG2	2.13	0.75
1:2:628:U:OP2	1:2:968:C:N4	2.19	0.75
1:2:952:G:H2'	1:2:953:G:H8	1.52	0.75
1:2:1581:A:C6	22:F:80:ALA:HB2	2.20	0.75
25:P:57:MET:HE2	25:P:61:ARG:CG	2.15	0.75
25:P:98:ASN:ND2	25:P:121:ILE:O	2.20	0.75
30:U:99:ILE:HA	30:U:102:ARG:NE	2.02	0.75
26:Q:82:ARG:NH1	26:Q:113:ASP:OD2	2.20	0.74
26:Q:105:LEU:CG	26:Q:109:PHE:HE2	1.99	0.74
1:2:1481:A:H2'	1:2:1482:G:C8	2.22	0.74
1:2:1581:A:N1	22:F:80:ALA:HB2	2.02	0.74
34:f:116:LYS:NZ	34:f:120:GLU:HB2	2.01	0.74
41:l:186:ARG:NH2	41:l:244:THR:O	2.21	0.74
1:2:1464:G:O2'	1:2:1600:C:OP1	2.05	0.74
33:d:22:ARG:HH21	33:d:36:LEU:HA	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:146:GLN:HB2	3:B:149:GLN:HG3	1.67	0.74
14:W:24:GLN:N	14:W:24:GLN:OE1	2.20	0.74
1:2:869:C:O2	18:b:51:GLN:NE2	2.19	0.74
1:2:1046:G:H1	1:2:1070:U:H3	1.34	0.74
9:J:41:GLU:OE1	9:J:44:ARG:NH2	2.21	0.74
1:2:1416:G:H4'	26:Q:128:LYS:HZ3	1.52	0.74
26:Q:81:ILE:O	26:Q:85:ILE:HD12	1.87	0.74
43:g:14:LEU:HB2	43:g:317:ILE:HB	1.69	0.74
2:A:167:LYS:NZ	2:A:203:PHE:HB3	2.02	0.74
1:2:4:C:H5'	4:C:209:THR:HG21	1.69	0.74
25:P:52:LYS:HB3	25:P:80:LEU:HD21	1.70	0.74
34:f:120:GLU:OE2	34:f:126:PRO:CA	2.30	0.74
26:Q:40:GLN:O	26:Q:42:GLU:CD	2.31	0.74
43:g:238:PHE:CE2	43:g:239:MET:HE1	2.23	0.74
1:2:521:U:H5''	16:Y:37:LYS:HG3	1.68	0.74
26:Q:37:THR:CG2	26:Q:49:TYR:OH	2.36	0.74
4:C:161:THR:HG21	4:C:229:PHE:HD2	1.52	0.73
25:P:79:HIS:HA	25:P:97:TYR:HB2	1.71	0.73
25:P:31:GLU:HG2	25:P:35:LYS:HE2	1.68	0.73
40:k:231:GLU:HA	40:k:441:LEU:HD12	1.71	0.73
6:G:39:GLU:HA	6:G:46:LYS:HE2	1.67	0.73
40:k:457:GLU:N	40:k:457:GLU:OE2	2.22	0.73
1:2:1581:A:C4	22:F:80:ALA:HB3	2.20	0.73
3:B:108:ASP:OD2	17:a:65:PRO:HB2	1.89	0.73
6:G:132:ARG:HE	6:G:133:LEU:HD22	1.50	0.73
1:2:1170:A:H2'	1:2:1171:G:C8	2.24	0.73
26:Q:99:GLU:CD	26:Q:103:ASN:ND2	2.44	0.73
41:l:184:LEU:HD23	41:l:234:VAL:HG21	1.71	0.73
41:l:163:PRO:HG2	41:l:223:GLU:HG2	1.71	0.73
43:g:115:ALA:HB3	43:g:124:ILE:HB	1.68	0.73
1:2:1085:A:H5'	4:C:169:SER:HB3	1.70	0.72
25:P:52:LYS:HE3	25:P:80:LEU:CD2	2.17	0.72
7:H:144:VAL:HA	14:W:42:GLN:HE21	1.52	0.72
8:I:188:GLU:OE1	8:I:188:GLU:N	2.22	0.72
15:X:62:LYS:HZ1	15:X:118:PRO:CA	2.02	0.72
38:l:9:IMG:H4'	38:l:45:U:H2'	1.71	0.72
1:2:317:U:H4'	8:I:11:ARG:HH21	1.54	0.72
28:S:12:GLN:CD	28:S:15:LEU:HD21	2.12	0.72
2:A:167:LYS:CE	2:A:204:TYR:HB3	2.13	0.72
26:Q:45:ARG:HG3	26:Q:49:TYR:HE2	1.55	0.72
1:2:711:G:H1	1:2:727:C:H42	1.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:870:G:H2'	1:2:871:G:C8	2.24	0.72
15:X:60:GLU:OE1	15:X:60:GLU:N	2.21	0.72
26:Q:45:ARG:O	26:Q:49:TYR:HD2	1.72	0.72
1:2:824:U:H2'	1:2:825:U:H6	1.55	0.72
4:C:125:GLU:OE1	4:C:125:GLU:N	2.22	0.72
34:f:106:TYR:HE1	34:f:129:PHE:CZ	2.05	0.72
16:Y:86:GLU:OE1	16:Y:86:GLU:HA	1.90	0.72
29:T:117:SER:HA	29:T:123:ARG:HE	1.55	0.72
40:k:313:PRO:HA	40:k:345:GLY:HA3	1.70	0.72
23:K:9:LYS:HD2	23:K:9:LYS:C	2.15	0.71
1:2:1525:C:OP1	22:F:108:LYS:NZ	2.24	0.71
34:f:119:LYS:HG2	34:f:137:PHE:CE2	2.25	0.71
12:O:133:ARG:HA	17:a:28:ARG:HE	1.54	0.71
28:S:122:HIS:HE1	28:S:126:ARG:NH1	1.88	0.71
35:i:99:GLU:HA	35:i:102:THR:HG22	1.71	0.71
40:k:192:VAL:HB	40:k:211:MET:HE1	1.71	0.71
1:2:7:G:N7	4:C:210:ARG:NH2	2.37	0.71
1:2:1783:U:P	12:O:133:ARG:HH22	2.14	0.71
11:N:47:PRO:HD2	11:N:86:GLU:HG2	1.73	0.71
21:D:24:PHE:HE2	23:K:65:TYR:CE2	2.07	0.71
28:S:126:ARG:NE	28:S:132:ARG:O	2.22	0.71
1:2:760:A:N1	1:2:789:U:C4	2.59	0.71
34:f:116:LYS:CE	34:f:120:GLU:HB2	2.21	0.71
38:1:74:C:H4'	38:1:75:C:H5'	1.71	0.71
8:I:67:TRP:O	8:I:71:GLY:N	2.23	0.71
18:b:75:GLU:OE1	18:b:75:GLU:N	2.24	0.71
9:J:66:ASP:OD1	9:J:67:PRO:HD2	1.91	0.71
32:c:66:LEU:CD2	32:c:67:ARG:HG2	2.20	0.71
3:B:2:ALA:N	12:O:48:VAL:O	2.24	0.71
10:L:99:ARG:HB2	15:X:12:ALA:HB2	1.73	0.71
12:O:128:LYS:HB3	17:a:22:ARG:HD3	1.72	0.71
1:2:751:G:H2'	1:2:752:A:H8	1.56	0.70
7:H:9:LEU:HD13	7:H:17:GLU:OE1	1.91	0.70
1:2:28:A:N1	1:2:597:U:O4	2.24	0.70
1:2:790:A:H2'	1:2:791:U:C6	2.26	0.70
10:L:132:SER:O	10:L:136:ARG:NH1	2.23	0.70
26:Q:37:THR:N	26:Q:49:TYR:HH	1.89	0.70
7:H:140:VAL:HB	14:W:52:TYR:HB3	1.72	0.70
8:I:101:ILE:HD12	8:I:185:LEU:HD11	1.73	0.70
21:D:211:PRO:HD3	27:R:19:LYS:NZ	2.05	0.70
1:2:148:C:H1'	6:G:132:ARG:HH12	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1610:U:H1'	22:F:101:MET:HE3	1.72	0.70
13:V:42:GLU:OE1	13:V:42:GLU:N	2.20	0.70
34:f:139:CYS:SG	34:f:140:GLY:N	2.64	0.70
1:2:1443:G:N2	34:f:87:THR:O	2.24	0.70
3:B:97:LEU:HG	3:B:232:HIS:ND1	2.06	0.70
21:D:29:LEU:HB2	21:D:34:TYR:HB2	1.71	0.70
29:T:27:LYS:HB3	29:T:111:LEU:HD11	1.74	0.70
1:2:1279:C:H5'	33:d:44:ARG:HH12	1.56	0.70
26:Q:40:GLN:N	26:Q:41:PRO:HD2	2.06	0.70
43:g:238:PHE:CD2	43:g:239:MET:HE1	2.27	0.70
1:2:475:U:O4	9:J:37:LYS:NZ	2.24	0.70
2:A:53:THR:O	2:A:57:ILE:HD12	1.92	0.70
9:J:93:LEU:HD12	9:J:96:VAL:HG11	1.73	0.70
25:P:52:LYS:CE	25:P:80:LEU:HD11	2.22	0.70
40:k:182:ARG:NH2	40:k:184:LYS:HA	2.07	0.70
41:l:203:GLY:HA3	41:l:213:ILE:HG22	1.74	0.70
41:l:236:CYS:SG	41:l:266:ARG:NH2	2.64	0.70
1:2:142:G:H2'	1:2:143:G:C8	2.27	0.70
34:f:119:LYS:CB	34:f:137:PHE:CE2	2.75	0.70
2:A:54:TRP:HA	2:A:57:ILE:HD13	1.74	0.70
22:F:151:VAL:HG13	32:c:67:ARG:HD2	1.74	0.70
5:E:59:ARG:HH22	16:Y:87:PRO:HG3	1.57	0.69
34:f:116:LYS:HG2	34:f:129:PHE:CD1	2.23	0.69
34:f:119:LYS:HB2	34:f:137:PHE:CE2	2.27	0.69
34:f:120:GLU:CD	34:f:126:PRO:HA	2.17	0.69
3:B:35:PRO:HA	3:B:232:HIS:CD2	2.27	0.69
1:2:1562:U:H2'	1:2:1563:C:C6	2.27	0.69
11:N:36:GLN:OE1	11:N:39:LYS:HD3	1.91	0.69
1:2:1279:C:H4'	30:U:69:LYS:HB3	1.75	0.69
34:f:116:LYS:HE2	34:f:120:GLU:HB2	1.73	0.69
1:2:1777:U:O4	20:h:12:ARG:NH1	2.26	0.69
3:B:141:ALA:HB1	3:B:207:LEU:HD11	1.74	0.69
6:G:46:LYS:HB2	6:G:118:GLU:OE2	1.92	0.69
32:c:18:ARG:NH1	32:c:26:THR:HG21	2.06	0.69
4:C:213:GLU:OE2	4:C:217:LYS:HD2	1.93	0.69
5:E:126:VAL:HG21	5:E:155:LYS:O	1.92	0.69
1:2:824:U:H2'	1:2:825:U:C6	2.28	0.69
4:C:78:LEU:O	4:C:81:LEU:HD23	1.92	0.69
15:X:62:LYS:HZ1	15:X:118:PRO:HA	1.56	0.69
18:b:67:THR:HG22	18:b:68:GLY:H	1.57	0.69
25:P:127:ARG:NH1	25:P:128:HIS:O	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:d:43:PHE:HZ	33:d:52:PHE:CD2	2.11	0.69
34:f:116:LYS:HZ3	34:f:120:GLU:HB2	1.56	0.69
43:g:21:VAL:HG11	43:g:317:ILE:HD11	1.75	0.69
10:L:54:ILE:HG23	10:L:55:ASP:H	1.58	0.69
12:O:31:THR:OG1	12:O:37:GLU:O	2.10	0.69
43:g:19:GLY:HA3	43:g:39:ARG:HB2	1.74	0.69
1:2:331:U:O2	8:I:5:ARG:NH1	2.26	0.69
1:2:1416:G:H4'	26:Q:128:LYS:NZ	2.08	0.69
2:A:112:THR:HG22	2:A:114:SER:H	1.55	0.69
16:Y:76:TYR:CZ	16:Y:86:GLU:OE2	2.46	0.69
35:i:87:ASP:CB	35:i:88:GLN:OE1	2.41	0.69
1:2:299:A:H2'	1:2:300:A:C8	2.28	0.68
1:2:1162:A:N3	1:2:1611:U:O2'	2.25	0.68
7:H:9:LEU:CD2	7:H:43:PHE:O	2.41	0.68
28:S:48:LYS:HE3	28:S:54:LEU:HD11	1.75	0.68
34:f:119:LYS:CG	34:f:120:GLU:H	2.05	0.68
40:k:352:GLU:OE2	40:k:376:ASN:ND2	2.27	0.68
1:2:1537:G:H1	28:S:26:ILE:HD11	1.58	0.68
6:G:167:LYS:NZ	6:G:168:SER:O	2.26	0.68
11:N:20:ARG:HH21	14:W:56:HIS:HB3	1.58	0.68
24:M:129:GLU:HA	24:M:133:GLN:HB2	1.74	0.68
27:R:33:ARG:HG3	43:g:128:ARG:HH12	1.58	0.68
27:R:47:ARG:NH1	27:R:48:ASN:OD1	2.19	0.68
1:2:15:U:O2'	1:2:619:A:N6	2.26	0.68
3:B:67:GLU:OE2	3:B:83:LYS:HG3	1.93	0.68
8:I:154:GLU:OE2	8:I:157:VAL:HG23	1.93	0.68
40:k:499:ILE:HD11	40:k:517:ILE:HG13	1.74	0.68
1:2:945:U:H5''	3:B:165:ARG:HH12	1.58	0.68
1:2:990:G:H1'	1:2:1013:G:H22	1.56	0.68
1:2:1794:C:O2'	17:a:95:ARG:NH1	2.26	0.68
39:j:74:LEU:HD11	39:j:86:SER:HB2	1.76	0.68
1:2:697:C:H3'	7:H:105:LYS:HZ3	1.58	0.68
1:2:780:A:O5'	1:2:781:A:N6	2.27	0.68
1:2:1164:G:H4'	22:F:101:MET:HE1	1.76	0.68
22:F:85:ARG:CD	22:F:88:GLN:HB2	2.18	0.68
39:j:54:ARG:C	39:j:55:ARG:O	2.36	0.68
39:j:134:LEU:HD23	39:j:144:ALA:HB1	1.74	0.68
39:j:149:ILE:HD11	39:j:177:LEU:HB3	1.76	0.68
1:2:923:A:H2'	1:2:924:G:C8	2.29	0.68
1:2:1780:MA6:OP1	20:h:9:ARG:NH2	2.27	0.68
1:2:1266:G:HO2'	1:2:1446:G:HO2'	1.42	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Y:76:TYR:OH	16:Y:86:GLU:OE2	2.12	0.68
40:k:113:LYS:NZ	40:k:194:CYS:O	2.22	0.68
1:2:107:C:H2'	1:2:108:A:H8	1.58	0.68
7:H:162:ILE:HG21	7:H:169:PHE:HZ	1.58	0.68
22:F:50:PHE:CD2	22:F:69:PRO:HA	2.29	0.68
31:Z:88:ILE:HG23	31:Z:89:ILE:HG12	1.74	0.68
40:k:201:MET:O	40:k:204:MET:HG2	1.93	0.68
43:g:154:LYS:HG3	43:g:208:VAL:HG23	1.76	0.68
1:2:1542:U:OP1	28:S:136:GLN:NE2	2.26	0.68
21:D:94:ARG:O	21:D:101:GLN:NE2	2.27	0.68
23:K:8:ARG:HG2	23:K:12:TYR:CZ	2.29	0.68
32:c:25:VAL:HG12	32:c:43:ASN:HB2	1.73	0.68
36:m:84:GLN:OE1	36:m:84:GLN:N	2.27	0.68
39:j:222:LEU:HB2	40:k:330:ILE:HD11	1.75	0.68
1:2:29:U:H2'	1:2:30:G:H8	1.60	0.67
1:2:1021:C:O2'	1:2:1124:A:N1	2.27	0.67
12:O:85:ALA:H	12:O:119:THR:HG22	1.60	0.67
13:V:7:GLN:OE1	13:V:7:GLN:N	2.27	0.67
21:D:157:LEU:HD13	21:D:187:LYS:HD2	1.75	0.67
23:K:8:ARG:HG2	23:K:12:TYR:CE2	2.28	0.67
34:f:133:HIS:CG	34:f:134:GLY:N	2.61	0.67
1:2:707:A:H61	1:2:730:G:H1	1.41	0.67
1:2:867:G:H1	1:2:959:U:H3	1.40	0.67
1:2:952:G:H2'	1:2:953:G:C8	2.29	0.67
1:2:1143:U:H2'	1:2:1144:U:C6	2.30	0.67
16:Y:127:LYS:HZ1	16:Y:131:ARG:HB3	1.59	0.67
35:i:99:GLU:O	35:i:103:LEU:HD23	1.95	0.67
39:j:236:ASP:O	39:j:238:GLN:OE1	2.11	0.67
1:2:1617:C:H2'	1:2:1618:C:H6	1.58	0.67
15:X:62:LYS:CE	15:X:118:PRO:HB3	2.22	0.67
34:f:142:CYS:CB	34:f:145:THR:HG22	2.16	0.67
43:g:208:VAL:HG11	43:g:249:ALA:HA	1.75	0.67
1:2:67:A:O2'	1:2:69:G:OP1	2.12	0.67
1:2:916:U:O2	12:O:41:ARG:NH1	2.28	0.67
8:I:106:ALA:HB2	8:I:166:LEU:HG	1.77	0.67
12:O:16:VAL:HG12	12:O:80:HIS:HB2	1.75	0.67
29:T:7:ARG:HH21	29:T:67:LEU:HA	1.57	0.67
30:U:65:ILE:HG21	33:d:43:PHE:HE2	1.58	0.67
1:2:1367:G:H5''	29:T:69:LYS:HD3	1.76	0.67
1:2:686:C:O3'	14:W:118:ARG:NH1	2.25	0.67
1:2:1601:U:OP2	26:Q:132:ARG:NH1	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:39:GLU:CG	6:G:46:LYS:NZ	2.43	0.67
1:2:657:C:O2	1:2:674:A:N6	2.25	0.67
2:A:84:ARG:NH2	27:R:82:ASP:OD1	2.27	0.67
3:B:133:TYR:HE2	3:B:181:LEU:HD13	1.60	0.67
8:I:138:LYS:NZ	8:I:142:ARG:NH2	2.42	0.67
43:g:184:ARG:HD3	43:g:186:TRP:CH2	2.30	0.67
1:2:405:U:H2'	1:2:406:A:H8	1.60	0.67
1:2:1084:G:OP2	4:C:166:LYS:NZ	2.27	0.67
1:2:1759:U:H4'	1:2:1780:MA6:H2	1.77	0.67
4:C:50:VAL:HG11	4:C:73:ILE:HG12	1.76	0.67
22:F:114:ARG:HD3	26:Q:43:ILE:HD11	1.77	0.67
28:S:12:GLN:NE2	28:S:14:ILE:O	2.28	0.67
1:2:379:U:H5'	1:2:380:C:H5	1.60	0.67
1:2:1044:C:H2'	1:2:1045:G:H8	1.60	0.67
5:E:93:GLU:N	5:E:93:GLU:OE1	2.24	0.67
1:2:925:A:H2'	1:2:926:C:C6	2.30	0.67
29:T:9:VAL:HG22	29:T:10:PRO:CD	2.25	0.67
1:2:162:G:OP2	1:2:162:G:N2	2.22	0.66
1:2:1338:C:O2'	1:2:1340:A:N7	2.27	0.66
15:X:50:LYS:NZ	15:X:101:GLU:OE1	2.24	0.66
40:k:140:LEU:HD12	40:k:192:VAL:HG13	1.76	0.66
1:2:1598:A:H2'	1:2:1599:G:H5''	1.76	0.66
6:G:32:ILE:HG23	6:G:53:ALA:HA	1.75	0.66
12:O:64:ALA:HB1	12:O:105:LEU:HD22	1.76	0.66
29:T:105:LEU:HA	29:T:108:LEU:HD12	1.77	0.66
34:f:130:LEU:CD2	34:f:137:PHE:HB3	2.24	0.66
21:D:75:LYS:NZ	23:K:22:VAL:HA	2.10	0.66
22:F:189:ILE:CD1	31:Z:66:VAL:HG21	2.25	0.66
1:2:296:U:H5''	5:E:37:LYS:HD2	1.77	0.66
1:2:319:U:O2'	42:n:189:LYS:O	2.13	0.66
12:O:60:ALA:HB1	12:O:101:ALA:HB2	1.76	0.66
1:2:1:U:OP2	9:J:53:ARG:NH2	2.28	0.66
7:H:110:GLN:HG2	7:H:111:LYS:H	1.60	0.66
21:D:124:ARG:HA	21:D:127:MET:HE2	1.76	0.66
26:Q:45:ARG:O	26:Q:48:VAL:CG1	2.44	0.66
34:f:130:LEU:HD11	34:f:139:CYS:CB	2.22	0.66
34:f:136:ARG:HG3	34:f:136:ARG:O	1.96	0.66
4:C:40:TRP:NE1	4:C:70:GLU:OE2	2.28	0.66
13:V:76:ASP:OD2	13:V:78:LEU:HD21	1.96	0.66
22:F:213:ILE:HD12	22:F:216:LYS:HE3	1.76	0.66
41:l:259:CYS:HB2	41:l:266:ARG:HH12	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:g:307:THR:HG22	43:g:321:GLN:HG3	1.77	0.66
1:2:1235:A:H1'	34:f:136:ARG:NH1	2.09	0.66
43:g:17:HIS:NE2	43:g:46:TRP:HZ2	1.93	0.66
1:2:1334:U:O2'	33:d:56:ARG:NH1	2.29	0.66
2:A:71:GLU:OE1	2:A:71:GLU:N	2.22	0.66
5:E:86:PHE:CE1	5:E:87:MET:HG3	2.30	0.66
30:U:30:LYS:NZ	30:U:111:GLY:HA3	2.10	0.66
1:2:1562:U:H2'	1:2:1563:C:H6	1.61	0.66
1:2:1581:A:OP1	26:Q:135:ARG:NH1	2.26	0.66
24:M:56:VAL:HG21	24:M:85:ALA:HB2	1.77	0.66
30:U:98:HIS:HB2	30:U:102:ARG:HH21	1.61	0.66
43:g:14:LEU:HD21	43:g:56:GLY:H	1.61	0.66
1:2:207:U:H2'	1:2:208:U:C6	2.31	0.66
1:2:883:A:H2'	1:2:884:G:C8	2.31	0.66
26:Q:69:VAL:HG11	26:Q:81:ILE:HD11	1.76	0.66
29:T:66:TYR:HE1	29:T:129:LEU:HG	1.59	0.66
40:k:426:ILE:HD11	40:k:490:PRO:HB2	1.77	0.66
43:g:174:PHE:CE2	43:g:186:TRP:HD1	2.12	0.66
1:2:1333:U:H4'	30:U:85:ARG:NH2	2.11	0.65
1:2:1571:A:H4'	1:2:1572:G:O5'	1.96	0.65
40:k:144:ASN:HB3	40:k:188:HIS:HE2	1.59	0.65
1:2:1482:G:H21	1:2:1604:C:H1'	1.59	0.65
2:A:74:VAL:HG21	2:A:118:PRO:HG3	1.77	0.65
2:A:183:ARG:HD3	2:A:191:ARG:HG2	1.78	0.65
3:B:108:ASP:OD2	17:a:65:PRO:CB	2.44	0.65
43:g:20:TRP:CD1	43:g:313:THR:CA	2.79	0.65
8:I:67:TRP:CE2	8:I:70:GLU:OE1	2.49	0.65
43:g:70:GLN:OE1	43:g:112:LEU:HA	1.96	0.65
1:2:1007:G:OP1	12:O:135:ARG:NH2	2.29	0.65
1:2:1159:A:H2'	1:2:1160:C:C6	2.32	0.65
1:2:1582:G:C8	26:Q:122:ARG:HB3	2.32	0.65
4:C:46:LEU:HD13	4:C:66:LEU:HD21	1.77	0.65
21:D:209:ILE:O	27:R:20:TYR:OH	2.12	0.65
43:g:109:GLY:O	43:g:127:SER:OG	2.14	0.65
1:2:544:A:H2'	19:e:31:LYS:HD3	1.78	0.65
25:P:37:ALA:O	25:P:42:ARG:NH1	2.30	0.65
35:i:58:MET:HE2	35:i:88:GLN:HE21	1.62	0.65
1:2:65:A:O5'	6:G:136:LYS:NZ	2.28	0.65
2:A:60:ALA:O	2:A:64:ILE:HD12	1.96	0.65
3:B:108:ASP:CG	17:a:65:PRO:HB2	2.22	0.65
3:B:131:ASP:OD1	3:B:132:ASP:N	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:T:70:GLN:HE22	29:T:119:LYS:HD2	1.62	0.65
31:Z:95:HIS:HB3	31:Z:98:GLN:HE21	1.61	0.65
43:g:44:ILE:HB	43:g:46:TRP:CZ2	2.32	0.65
1:2:867:G:H2'	1:2:868:A:H8	1.62	0.65
14:W:24:GLN:NE2	18:b:5:GLN:H	1.94	0.65
26:Q:36:ILE:C	26:Q:49:TYR:OH	2.39	0.65
28:S:41:ARG:NH2	29:T:36:ILE:O	2.30	0.65
5:E:31:PRO:HG2	5:E:38:LEU:HB2	1.77	0.65
23:K:70:GLU:OE1	23:K:91:TYR:OH	2.15	0.65
36:m:59:LYS:HE2	36:m:66:GLY:H	1.61	0.65
40:k:238:ILE:HG22	40:k:239:MET:HE2	1.77	0.65
1:2:1235:A:N3	34:f:136:ARG:NH2	2.45	0.65
4:C:180:GLY:N	4:C:200:ASP:OD2	2.30	0.65
17:a:51:ARG:HH12	17:a:55:GLU:HB3	1.62	0.65
24:M:66:LYS:HG2	34:f:108:VAL:HG21	1.78	0.65
32:c:25:VAL:HG11	32:c:43:ASN:CB	2.19	0.65
40:k:247:LEU:HD23	40:k:283:ILE:HD13	1.78	0.65
1:2:1589:C:H2'	1:2:1590:A:H8	1.61	0.65
2:A:167:LYS:HZ1	2:A:203:PHE:CB	2.04	0.65
39:j:25:GLN:HG3	39:j:26:GLN:HG2	1.79	0.65
5:E:23:LEU:HD12	9:J:3:ARG:HH22	1.62	0.64
7:H:38:LEU:HD11	7:H:73:VAL:HG11	1.79	0.64
22:F:189:ILE:HD13	31:Z:66:VAL:HG21	1.79	0.64
26:Q:99:GLU:OE1	43:g:58:PRO:HG3	1.94	0.64
43:g:36:SER:OG	43:g:46:TRP:CZ2	2.51	0.64
1:2:291:U:H2'	1:2:292:U:C6	2.32	0.64
9:J:84:GLY:HA3	9:J:107:ARG:HH21	1.61	0.64
21:D:75:LYS:CE	23:K:22:VAL:HB	2.25	0.64
21:D:75:LYS:HZ1	23:K:22:VAL:HB	1.54	0.64
35:i:27:ILE:O	35:i:95:TYR:OH	2.14	0.64
39:j:247:ALA:O	39:j:251:ILE:HD12	1.97	0.64
43:g:171:ARG:NH1	43:g:189:ASN:OD1	2.30	0.64
1:2:353:C:H5''	8:I:16:ALA:HB2	1.79	0.64
1:2:563:G:N2	1:2:576:G:OP1	2.30	0.64
1:2:709:C:H41	1:2:730:G:H21	1.44	0.64
1:2:1186:U:O4	1:2:1199:G:N2	2.29	0.64
1:2:1670:G:H2'	1:2:1671:G:H8	1.62	0.64
3:B:192:VAL:HA	3:B:195:LYS:HE2	1.78	0.64
7:H:71:HIS:HA	7:H:74:GLN:HG2	1.78	0.64
16:Y:76:TYR:OH	16:Y:86:GLU:CD	2.40	0.64
30:U:98:HIS:HB2	30:U:102:ARG:NH2	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:f:116:LYS:HZ3	34:f:120:GLU:N	1.95	0.64
43:g:11:ARG:HB3	43:g:55:PHE:CZ	2.33	0.64
1:2:405:U:H2'	1:2:406:A:C8	2.33	0.64
1:2:1531:C:OP2	31:Z:77:ARG:NH1	2.31	0.64
11:N:16:ILE:O	14:W:57:ARG:NH2	2.29	0.64
11:N:142:GLU:OE1	11:N:142:GLU:N	2.31	0.64
13:V:62:ARG:NH1	14:W:20:THR:O	2.30	0.64
40:k:320:SER:HB2	40:k:407:CYS:HA	1.77	0.64
1:2:403:G:O2'	6:G:91:GLU:OE2	2.15	0.64
1:2:1219:C:H2'	1:2:1220:A:H8	1.62	0.64
4:C:147:GLY:N	4:C:158:SER:O	2.31	0.64
22:F:85:ARG:NE	22:F:88:GLN:HG3	2.13	0.64
26:Q:99:GLU:OE1	43:g:58:PRO:HB2	1.97	0.64
1:2:585:G:P	19:e:23:LYS:HZ3	2.20	0.64
26:Q:47:LYS:HG2	26:Q:79:TYR:HE1	1.62	0.64
29:T:116:ILE:HA	29:T:122:ARG:HG3	1.80	0.64
7:H:75:ILE:HG13	7:H:76:LYS:H	1.63	0.64
1:2:77:U:O2	6:G:159:ARG:NH2	2.31	0.64
1:2:129:U:O4'	1:2:263:G:N1	2.31	0.64
1:2:477:A:H2	1:2:509:G:H22	1.46	0.64
1:2:1621:C:H2'	1:2:1622:C:H6	1.63	0.64
1:2:563:G:N1	1:2:579:A:OP2	2.31	0.64
1:2:758:U:OP1	5:E:22:LYS:NZ	2.31	0.64
1:2:1001:G:H4'	36:m:67:ASN:OD1	1.98	0.64
1:2:1783:U:H2'	1:2:1784:G:H8	1.62	0.64
22:F:49:SER:OG	22:F:51:GLU:OE1	2.16	0.64
26:Q:50:GLU:N	26:Q:51:PRO:HD2	2.12	0.64
28:S:36:ARG:HB3	28:S:102:ALA:HA	1.79	0.64
34:f:143:HIS:CE1	34:f:144:SER:OG	2.51	0.64
1:2:646:G:H2'	1:2:647:G:H8	1.63	0.63
1:2:862:A:H4'	14:W:57:ARG:HB3	1.80	0.63
21:D:178:ARG:NH1	21:D:178:ARG:O	2.31	0.63
40:k:205:LEU:HD12	40:k:465:ASN:HD22	1.63	0.63
1:2:68:A:OP1	6:G:160:ARG:NH2	2.31	0.63
1:2:333:G:O6	8:I:5:ARG:NH2	2.30	0.63
1:2:1474:C:H2'	1:2:1475:G:H8	1.64	0.63
7:H:9:LEU:HD22	7:H:43:PHE:O	1.97	0.63
1:2:399:A:H4'	1:2:400:A:H5''	1.81	0.63
1:2:738:G:H2'	1:2:739:G:C8	2.33	0.63
5:E:246:LEU:HD21	5:E:254:ARG:NH1	2.13	0.63
1:2:1482:G:N2	1:2:1604:C:O2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:124:ASN:HD21	3:B:136:ARG:HD3	1.64	0.63
28:S:24:GLY:HA2	28:S:58:ALA:HB3	1.80	0.63
28:S:46:VAL:HG21	28:S:73:MET:CE	2.25	0.63
40:k:440:LEU:O	40:k:450:GLN:NE2	2.30	0.63
41:l:132:SER:HA	41:l:135:LEU:HD12	1.80	0.63
1:2:234:G:H2'	1:2:235:A:C8	2.33	0.63
4:C:233:ASN:HB2	13:V:1:MET:HG2	1.81	0.63
41:l:157:LYS:NZ	41:l:183:LYS:O	2.32	0.63
43:g:312:TYR:HE2	43:g:318:ARG:HB2	1.62	0.63
1:2:1212:G:H1	1:2:1448:U:H3	1.47	0.63
1:2:1640:G:H5'	20:h:1:MET:HG3	1.81	0.63
1:2:1779:A:H2'	1:2:1780:MA6:H8	1.81	0.63
22:F:147:ASP:OD1	22:F:148:THR:N	2.29	0.63
29:T:10:PRO:HG2	29:T:13:ASP:OD2	1.99	0.63
39:j:174:SER:O	39:j:178:THR:OG1	2.13	0.63
2:A:41:ARG:HG2	2:A:43:ASP:H	1.64	0.63
9:J:39:LYS:HG2	9:J:42:ILE:HD12	1.81	0.63
1:2:637:U:O2'	7:H:112:ARG:NH2	2.32	0.63
22:F:85:ARG:C	22:F:87:ALA:H	2.06	0.63
23:K:88:PRO:HD2	23:K:91:TYR:HD2	1.62	0.63
26:Q:45:ARG:CG	26:Q:49:TYR:HE2	2.12	0.63
30:U:98:HIS:C	30:U:102:ARG:HH21	2.07	0.63
1:2:1299:A:OP1	4:C:104:LYS:NZ	2.31	0.62
29:T:83:ALA:HB1	29:T:91:HIS:HB3	1.80	0.62
43:g:110:ASP:OD1	43:g:128:ARG:CD	2.42	0.62
1:2:990:G:N2	1:2:1013:G:O6	2.33	0.62
1:2:1754:A:OP1	35:i:66:ARG:NH2	2.32	0.62
17:a:4:LYS:HG3	17:a:5:ARG:NE	2.15	0.62
32:c:66:LEU:HD23	32:c:67:ARG:N	2.14	0.62
3:B:46:THR:OG1	3:B:64:ARG:NH2	2.31	0.62
8:I:104:ILE:O	8:I:165:ARG:HA	1.99	0.62
24:M:105:LYS:HD2	24:M:106:VAL:HG22	1.82	0.62
1:2:443:C:OP1	16:Y:102:LYS:NZ	2.33	0.62
1:2:1069:C:H4'	18:b:17:ARG:CD	2.25	0.62
1:2:1279:C:OP1	33:d:44:ARG:NH2	2.32	0.62
6:G:57:ASP:OD1	6:G:58:LYS:N	2.33	0.62
10:L:116:ARG:NH1	10:L:116:ARG:HA	2.14	0.62
21:D:184:ILE:HD12	21:D:184:ILE:C	2.25	0.62
24:M:28:SER:O	24:M:33:GLY:N	2.29	0.62
28:S:56:LYS:NZ	28:S:60:GLU:CD	2.58	0.62
1:2:536:G:H3'	9:J:171:ARG:NH2	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:894:G:H21	12:O:41:ARG:NH2	1.97	0.62
1:2:1765:G:H4'	1:2:1766:G:O5'	1.98	0.62
9:J:17:ARG:O	9:J:23:ARG:NH2	2.33	0.62
32:c:21:SER:CB	32:c:67:ARG:NH1	2.62	0.62
1:2:1131:A:H2'	1:2:1132:A:H8	1.64	0.62
3:B:105:PHE:HE1	3:B:213:ARG:HA	1.64	0.62
10:L:16:GLN:HB2	10:L:19:ILE:HD13	1.80	0.62
26:Q:36:ILE:HG12	26:Q:49:TYR:CZ	2.35	0.62
28:S:63:GLN:O	28:S:66:LEU:N	2.32	0.62
28:S:122:HIS:CE1	28:S:126:ARG:HH11	2.17	0.62
43:g:36:SER:HG	43:g:46:TRP:NE1	1.96	0.62
43:g:151:TRP:HB2	43:g:179:MET:CE	2.29	0.62
1:2:716:C:N4	1:2:722:G:O6	2.33	0.62
1:2:1332:C:H1'	21:D:162:GLN:NE2	2.15	0.62
7:H:8:ILE:HD11	7:H:21:ALA:HB1	1.81	0.62
43:g:86:TRP:HA	43:g:110:ASP:HB2	1.81	0.62
1:2:29:U:H2'	1:2:30:G:C8	2.34	0.62
1:2:328:G:H2'	1:2:329:G:H8	1.65	0.62
1:2:1365:C:O2'	29:T:7:ARG:NH1	2.33	0.62
13:V:70:ASN:HD21	13:V:82:VAL:HG12	1.64	0.62
15:X:121:ARG:O	15:X:122:PHE:CD1	2.53	0.62
16:Y:39:GLU:OE1	16:Y:39:GLU:HA	1.99	0.62
1:2:587:U:O2	19:e:57:ASN:ND2	2.31	0.62
1:2:688:G:OP2	14:W:119:LYS:NZ	2.30	0.62
1:2:771:A:O2'	9:J:6:ARG:NH2	2.31	0.62
1:2:917:U:H4'	12:O:18:ARG:CD	2.29	0.62
1:2:1357:G:H2'	1:2:1358:C:C6	2.35	0.62
7:H:123:ASP:OD1	7:H:138:LYS:NZ	2.32	0.62
9:J:151:GLU:N	9:J:151:GLU:OE2	2.32	0.62
26:Q:41:PRO:HB2	26:Q:44:LEU:HB2	1.82	0.62
28:S:56:LYS:CD	28:S:60:GLU:OE1	2.44	0.62
34:f:133:HIS:NE2	34:f:136:ARG:NH2	2.48	0.62
43:g:15:GLU:HG3	43:g:316:VAL:HG11	1.81	0.62
1:2:965:A:OP2	11:N:124:ARG:NH1	2.32	0.61
1:2:1591:A:H2'	1:2:1592:G:H8	1.65	0.61
6:G:70:PRO:O	6:G:98:ARG:NH2	2.33	0.61
12:O:61:MET:HG3	12:O:104:ALA:HB2	1.80	0.61
30:U:34:LEU:HB3	30:U:89:ARG:NH1	2.10	0.61
34:f:130:LEU:HD23	34:f:137:PHE:CB	2.30	0.61
1:2:129:U:H5'	1:2:263:G:H22	1.64	0.61
1:2:512:U:H2'	1:2:513:G:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:589:C:H2'	1:2:590:A:H8	1.64	0.61
1:2:893:U:H2'	1:2:894:G:C8	2.34	0.61
6:G:58:LYS:HA	6:G:107:ALA:HB2	1.81	0.61
23:K:15:LEU:HD21	23:K:68:LEU:HD21	1.82	0.61
1:2:590:A:H2'	1:2:591:G:C8	2.35	0.61
1:2:890:A:H2'	1:2:891:A:H8	1.65	0.61
39:j:91:SER:HB3	39:j:94:ASP:HB2	1.82	0.61
43:g:17:HIS:HE2	43:g:46:TRP:HZ2	1.48	0.61
1:2:367:U:O4	1:2:368:A:N6	2.34	0.61
5:E:11:ARG:HA	5:E:28:ALA:HB2	1.83	0.61
28:S:55:HIS:O	28:S:57:ARG:NH1	2.33	0.61
28:S:122:HIS:HE1	28:S:126:ARG:HH11	1.47	0.61
30:U:64:LYS:HB3	30:U:83:GLU:HG2	1.81	0.61
1:2:758:U:H5''	9:J:7:THR:HG21	1.82	0.61
1:2:1252:U:H5'	34:f:140:GLY:HA3	1.81	0.61
34:f:119:LYS:CG	34:f:120:GLU:N	2.64	0.61
39:j:46:ILE:HG13	39:j:85:LEU:HB2	1.83	0.61
1:2:406:A:H2'	1:2:407:C:C6	2.35	0.61
1:2:1532:G:O6	31:Z:77:ARG:NH2	2.34	0.61
4:C:161:THR:HG21	4:C:229:PHE:CD2	2.35	0.61
27:R:18:GLU:CD	27:R:70:SER:H	2.09	0.61
4:C:193:MET:HA	4:C:193:MET:HE3	1.83	0.61
21:D:69:LEU:HD13	21:D:72:LEU:HD12	1.81	0.61
29:T:9:VAL:CG2	29:T:10:PRO:CD	2.78	0.61
43:g:210:GLN:HE22	43:g:252:PHE:HB2	1.66	0.61
1:2:883:A:H2'	1:2:884:G:H8	1.66	0.61
12:O:102:LEU:HD23	17:a:53:LEU:HD21	1.83	0.61
39:j:21:MET:HE2	39:j:68:ASN:HB3	1.82	0.61
40:k:429:ASP:OD2	40:k:484:ARG:NH2	2.34	0.61
1:2:735:C:O2'	1:2:736:C:O5'	2.15	0.61
1:2:1164:G:H2'	1:2:1165:A:C8	2.36	0.61
15:X:143:PRO:C	15:X:144:ARG:HD3	2.26	0.61
36:m:59:LYS:HE2	36:m:66:GLY:N	2.16	0.61
40:k:200:LEU:O	40:k:204:MET:HE3	2.01	0.61
43:g:210:GLN:NE2	43:g:211:PRO:O	2.33	0.61
1:2:97:C:H2'	1:2:98:U:C6	2.36	0.60
1:2:1333:U:H4'	30:U:85:ARG:HH22	1.65	0.60
2:A:7:PHE:HA	2:A:191:ARG:NH2	2.15	0.60
2:A:167:LYS:HE3	2:A:204:TYR:O	2.01	0.60
40:k:166:SER:OG	40:k:384:GLN:NE2	2.34	0.60
1:2:331:U:OP1	8:I:56:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1252:U:C5'	34:f:140:GLY:HA3	2.30	0.60
1:2:1319:U:H2'	1:2:1321:A:H5'	1.83	0.60
1:2:1599:G:O4'	29:T:89:ARG:NH1	2.34	0.60
24:M:55:LEU:HD22	24:M:79:LEU:HD22	1.82	0.60
29:T:88:VAL:HG22	29:T:89:ARG:HH21	1.67	0.60
30:U:22:ILE:HG21	30:U:100:VAL:HG11	1.82	0.60
1:2:327:A:H2'	1:2:328:G:H8	1.66	0.60
1:2:1551:G:N7	25:P:43:ARG:NH2	2.49	0.60
2:A:88:LYS:HD2	2:A:201:LEU:HD23	1.84	0.60
8:I:87:ASN:OD1	8:I:88:ASN:N	2.35	0.60
14:W:111:MET:HE2	14:W:116:ALA:N	2.16	0.60
27:R:37:GLU:HG3	27:R:38:ILE:HG23	1.83	0.60
28:S:17:LEU:HD11	28:S:66:LEU:HD12	1.83	0.60
1:2:236:C:H5''	1:2:237:U:H5'	1.84	0.60
1:2:761:G:N2	1:2:762:A:N7	2.50	0.60
3:B:136:ARG:HH12	3:B:218:LEU:HD21	1.67	0.60
11:N:31:ASP:OD1	11:N:32:GLY:N	2.35	0.60
24:M:82:VAL:CG1	24:M:83:ALA:N	2.64	0.60
26:Q:40:GLN:H	26:Q:41:PRO:HD2	1.65	0.60
28:S:56:LYS:NZ	28:S:60:GLU:OE1	2.35	0.60
41:l:236:CYS:CB	41:l:239:CYS:SG	2.89	0.60
1:2:1500:G:N2	1:2:1503:A:OP2	2.23	0.60
3:B:132:ASP:HB3	3:B:221:PRO:HG3	1.82	0.60
6:G:147:LEU:HD13	6:G:156:TYR:CE2	2.35	0.60
29:T:13:ASP:OD1	29:T:14:PHE:N	2.34	0.60
32:c:66:LEU:HD23	32:c:67:ARG:H	1.66	0.60
40:k:201:MET:CA	40:k:204:MET:HE3	2.27	0.60
1:2:12:U:H2'	1:2:13:C:H6	1.66	0.60
1:2:142:G:OP2	6:G:139:ASN:ND2	2.34	0.60
5:E:92:LEU:HD22	16:Y:17:LEU:HD21	1.84	0.60
13:V:64:GLU:HA	13:V:64:GLU:OE2	2.02	0.60
43:g:30:GLN:HE22	43:g:78:GLY:HA3	1.66	0.60
1:2:1554:A:H5''	25:P:40:ARG:HH21	1.67	0.60
3:B:35:PRO:HA	3:B:232:HIS:HD2	1.67	0.60
11:N:5:HIS:HE2	11:N:121:ARG:HG3	1.67	0.60
21:D:130:GLY:O	21:D:194:ARG:NH2	2.34	0.60
34:f:124:CYS:SG	34:f:141:LYS:HB3	2.41	0.60
36:m:72:PRO:O	36:m:73:GLU:HG3	2.01	0.60
43:g:85:SER:OG	43:g:87:ASP:OD1	2.19	0.60
43:g:210:GLN:OE1	43:g:252:PHE:N	2.33	0.60
1:2:803:A:N3	14:W:105:THR:OG1	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:93:THR:HG23	2:A:95:ALA:H	1.67	0.60
8:I:81:VAL:HG12	8:I:94:ASN:HA	1.82	0.60
17:a:51:ARG:NH1	17:a:55:GLU:HB3	2.16	0.60
30:U:34:LEU:O	30:U:89:ARG:NH2	2.35	0.60
43:g:20:TRP:HD1	43:g:313:THR:O	1.85	0.60
2:A:154:GLU:OE1	2:A:154:GLU:N	2.35	0.60
4:C:45:LYS:NZ	4:C:253:THR:OG1	2.34	0.60
5:E:6:LYS:O	5:E:30:ARG:NH1	2.35	0.60
6:G:132:ARG:HE	6:G:133:LEU:CD2	2.15	0.60
7:H:162:ILE:HG23	7:H:165:LYS:HD2	1.84	0.60
10:L:83:THR:OG1	10:L:109:ALA:O	2.18	0.60
12:O:117:ASP:OD1	12:O:119:THR:HG23	2.02	0.60
21:D:42:THR:OG1	21:D:45:LYS:O	2.16	0.60
39:j:36:LEU:HD13	39:j:39:TYR:HD2	1.67	0.60
43:g:13:THR:HG22	43:g:318:ARG:HG2	1.83	0.60
1:2:646:G:H2'	1:2:647:G:C8	2.36	0.60
11:N:5:HIS:HD2	11:N:121:ARG:HE	1.49	0.60
19:e:35:TYR:HE1	19:e:39:LEU:HD11	1.66	0.60
19:e:54:ARG:HG2	19:e:56:MET:HG2	1.84	0.60
32:c:62:GLU:C	32:c:62:GLU:OE1	2.45	0.60
1:2:894:G:H2'	1:2:895:U:C6	2.37	0.59
2:A:118:PRO:O	2:A:141:ILE:HD12	2.02	0.59
9:J:156:ILE:HG23	9:J:156:ILE:O	2.01	0.59
27:R:104:THR:OG1	27:R:105:GLN:NE2	2.35	0.59
43:g:285:PHE:HB3	43:g:288:TYR:CE2	2.36	0.59
25:P:106:GLU:OE2	25:P:108:ARG:NE	2.34	0.59
34:f:119:LYS:HG2	34:f:137:PHE:CD2	2.37	0.59
36:m:84:GLN:O	36:m:84:GLN:HG2	2.02	0.59
38:1:32:C:N4	38:1:33:U:O4	2.36	0.59
43:g:11:ARG:HB3	43:g:55:PHE:CE1	2.36	0.59
12:O:81:ILE:HB	12:O:115:ILE:HA	1.84	0.59
1:2:392:C:OP2	8:I:2:GLY:N	2.35	0.59
1:2:1432:U:H4'	33:d:24:SER:HB2	1.85	0.59
1:2:1553:A:OP1	25:P:44:LYS:NZ	2.34	0.59
12:O:103:ARG:NH2	17:a:48:ALA:O	2.35	0.59
17:a:51:ARG:HG2	32:c:60:GLU:OE2	2.02	0.59
24:M:24:VAL:HA	24:M:27:THR:HG22	1.84	0.59
1:2:627:G:OP1	11:N:124:ARG:NE	2.35	0.59
1:2:925:A:H2	12:O:125:SER:HB3	1.68	0.59
1:2:1637:5MC:H2'	1:2:1638:C:O4'	2.02	0.59
12:O:29:HIS:HD2	12:O:41:ARG:HA	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Y:127:LYS:NZ	16:Y:131:ARG:HB3	2.16	0.59
3:B:136:ARG:NH1	3:B:218:LEU:HD21	2.17	0.59
12:O:131:GLY:O	17:a:22:ARG:NH2	2.36	0.59
25:P:114:HIS:HB3	25:P:118:GLU:OE1	2.02	0.59
25:P:118:GLU:HG3	25:P:119:PHE:CD1	2.37	0.59
33:d:3:HIS:HB3	33:d:6:VAL:HG12	1.84	0.59
1:2:129:U:OP1	1:2:131:C:N4	2.25	0.59
1:2:700:C:H2'	1:2:701:U:C6	2.37	0.59
1:2:981:U:O4	1:2:982:A:N6	2.36	0.59
6:G:139:ASN:OD1	6:G:149:LYS:NZ	2.33	0.59
25:P:107:ILE:HA	25:P:111:MET:HG3	1.84	0.59
34:f:123:ASN:CB	34:f:146:PHE:HE2	2.15	0.59
38:1:12:G:H2'	38:1:13:C:C6	2.37	0.59
1:2:339:U:H2'	1:2:340:A:H8	1.68	0.59
1:2:622:A:N6	1:2:969:A:OP1	2.36	0.59
1:2:1472:G:H2'	1:2:1473:A:C8	2.37	0.59
1:2:1786:G:H5''	12:O:132:ARG:HH21	1.67	0.59
2:A:49:ASN:HD21	2:A:52:LYS:HD2	1.68	0.59
25:P:85:ILE:HD13	25:P:111:MET:HB3	1.83	0.59
27:R:7:LYS:HE2	27:R:11:ARG:NH1	2.14	0.59
28:S:90:LYS:N	28:S:97:ASP:OD1	2.31	0.59
29:T:27:LYS:C	29:T:28:LEU:HD12	2.27	0.59
31:Z:50:ILE:HD11	31:Z:71:LEU:HD21	1.85	0.59
34:f:119:LYS:CG	34:f:137:PHE:CE2	2.85	0.59
43:g:93:TRP:HD1	43:g:100:SER:HA	1.68	0.59
1:2:855:A:N7	7:H:97:ARG:N	2.48	0.59
8:I:22:ARG:HD2	8:I:25:ARG:HH11	1.68	0.59
1:2:559:U:H2'	1:2:560:G:H8	1.68	0.59
1:2:917:U:C5'	12:O:18:ARG:HD3	2.33	0.59
1:2:1564:U:H5''	28:S:39:GLY:N	2.18	0.59
9:J:31:ALA:HA	9:J:36:LEU:HD12	1.85	0.59
18:b:34:ASP:HB3	18:b:43:ILE:HD11	1.85	0.59
21:D:75:LYS:HZ2	23:K:22:VAL:N	1.99	0.59
23:K:7:ASP:OD1	23:K:10:LYS:NZ	2.26	0.59
30:U:44:ASN:HB3	30:U:103:ILE:HD12	1.85	0.59
38:1:39:C:O2'	39:j:57:ARG:NH2	2.36	0.59
39:j:16:ILE:HD11	39:j:74:LEU:O	2.03	0.59
39:j:241:ILE:HG22	39:j:268:PRO:HB2	1.84	0.59
1:2:649:U:O4	1:2:685:A:N6	2.36	0.58
1:2:1333:U:O3'	30:U:85:ARG:NH1	2.36	0.58
4:C:229:PHE:HE1	14:W:70:ASN:ND2	2.00	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:R:34:LEU:O	27:R:38:ILE:HG12	2.03	0.58
1:2:3:U:O2'	9:J:17:ARG:NH2	2.36	0.58
1:2:1114:U:H5''	20:h:10:THR:HG21	1.84	0.58
5:E:118:GLU:OE2	5:E:118:GLU:N	2.36	0.58
5:E:181:VAL:HG21	5:E:225:VAL:HG13	1.85	0.58
5:E:207:LEU:HD12	5:E:219:VAL:HG22	1.84	0.58
8:I:138:LYS:HZ2	8:I:142:ARG:NH2	1.99	0.58
13:V:70:ASN:HD21	13:V:82:VAL:CG1	2.16	0.58
17:a:4:LYS:HE3	17:a:92:ARG:CZ	2.32	0.58
28:S:126:ARG:HH21	28:S:133:VAL:C	2.11	0.58
32:c:19:THR:HG21	32:c:27:GLN:HE21	1.66	0.58
1:2:152:G:H2'	1:2:153:G:C8	2.38	0.58
1:2:1381:G:H2'	1:2:1382:A:C8	2.38	0.58
1:2:1472:G:H2'	1:2:1473:A:H8	1.67	0.58
1:2:1477:A:H5''	29:T:60:SER:HB3	1.86	0.58
10:L:14:GLN:HB3	10:L:54:ILE:HG21	1.86	0.58
12:O:111:ARG:HB3	17:a:58:VAL:HG13	1.84	0.58
16:Y:127:LYS:NZ	16:Y:127:LYS:O	2.32	0.58
43:g:14:LEU:HD21	43:g:56:GLY:N	2.18	0.58
43:g:117:ASP:OD2	43:g:121:SER:OG	2.21	0.58
43:g:246:GLU:HB3	43:g:264:ALA:HB2	1.84	0.58
1:2:12:U:H2'	1:2:13:C:C6	2.38	0.58
1:2:857:G:H4'	7:H:113:PRO:HG3	1.84	0.58
1:2:1252:U:H4'	34:f:140:GLY:HA3	1.84	0.58
1:2:1774:A:H2'	1:2:1775:G:C8	2.38	0.58
3:B:47:LEU:HB3	12:O:37:GLU:OE2	2.03	0.58
5:E:125:LYS:HB2	5:E:226:PHE:CE1	2.39	0.58
12:O:99:GLN:NE2	17:a:46:GLU:H	2.02	0.58
15:X:61:SER:OG	15:X:65:ASN:O	2.21	0.58
34:f:116:LYS:CB	34:f:129:PHE:HE1	2.11	0.58
1:2:520:A:N3	16:Y:34:ASN:ND2	2.52	0.58
1:2:1357:G:H2'	1:2:1358:C:H6	1.67	0.58
1:2:1626:U:H2'	1:2:1627:G:H8	1.69	0.58
23:K:8:ARG:HA	23:K:11:ILE:HG12	1.84	0.58
23:K:10:LYS:HA	23:K:13:GLN:HG3	1.85	0.58
1:2:268:G:OP2	6:G:186:ARG:NH2	2.35	0.58
1:2:1017:U:O4	1:2:1018:A:N6	2.36	0.58
1:2:1670:G:H2'	1:2:1671:G:C8	2.37	0.58
3:B:164:ILE:O	3:B:168:ILE:HG12	2.03	0.58
21:D:69:LEU:O	21:D:72:LEU:HB2	2.02	0.58
33:d:46:LYS:O	33:d:50:ILE:HD12	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:f:139:CYS:SG	34:f:141:LYS:N	2.76	0.58
40:k:377:ILE:HA	40:k:400:THR:HG22	1.85	0.58
41:l:187:SER:OG	41:l:190:HIS:ND1	2.32	0.58
1:2:216:A:H2'	1:2:217:A:C8	2.39	0.58
1:2:255:A:H2'	1:2:256:A:C8	2.38	0.58
5:E:125:LYS:HB2	5:E:226:PHE:CD1	2.38	0.58
8:I:185:LEU:HD22	8:I:189:GLU:HG3	1.85	0.58
9:J:93:LEU:O	9:J:96:VAL:HG12	2.03	0.58
26:Q:82:ARG:HD3	26:Q:116:LEU:HD23	1.86	0.58
40:k:110:ALA:H	46:k:601:GCP:H3B1	1.68	0.58
1:2:945:U:H5''	3:B:165:ARG:HH22	1.69	0.58
10:L:37:ASN:OD1	10:L:37:ASN:O	2.22	0.58
14:W:44:HIS:CD2	14:W:101:TYR:HE2	2.22	0.58
39:j:49:SER:O	39:j:88:ARG:NE	2.36	0.58
1:2:325:G:H2'	1:2:326:U:C6	2.39	0.58
1:2:627:G:N1	1:2:969:A:OP2	2.22	0.58
1:2:1198:G:H22	33:d:31:ILE:HD13	1.69	0.58
1:2:1240:G:H4'	25:P:78:THR:HA	1.85	0.58
5:E:67:GLN:HB2	5:E:69:HIS:CD2	2.39	0.58
8:I:70:GLU:OE1	8:I:70:GLU:N	2.37	0.58
26:Q:30:LYS:HB2	26:Q:66:ARG:HD3	1.85	0.58
26:Q:45:ARG:O	26:Q:48:VAL:HG12	2.04	0.58
36:m:78:ILE:HG13	36:m:78:ILE:O	2.04	0.58
1:2:1266:G:N2	1:2:1440:U:O2	2.32	0.58
1:2:1551:G:N2	1:2:1554:A:OP2	2.36	0.58
2:A:96:THR:HG21	2:A:116:LYS:HE2	1.86	0.58
5:E:85:GLY:N	5:E:88:ASP:OD2	2.35	0.58
5:E:185:GLY:C	5:E:224:ASN:HD22	2.12	0.58
9:J:128:LEU:HD22	9:J:133:HIS:CE1	2.39	0.58
11:N:86:GLU:H	11:N:86:GLU:CD	2.12	0.58
43:g:213:PRO:HD3	43:g:252:PHE:HB3	1.86	0.58
4:C:142:ILE:HD11	13:V:27:LYS:HG3	1.86	0.57
5:E:75:LYS:HB3	5:E:77:ARG:HH12	1.67	0.57
31:Z:43:ASP:H	31:Z:46:LYS:HD2	1.68	0.57
32:c:66:LEU:HD22	32:c:67:ARG:HG2	1.85	0.57
40:k:220:GLY:H	40:k:250:LYS:HB2	1.67	0.57
1:2:1581:A:O2'	22:F:81:ASN:HB2	2.04	0.57
1:2:1749:C:H2'	1:2:1750:U:C6	2.39	0.57
2:A:182:LEU:HB3	2:A:188:LEU:HD23	1.86	0.57
7:H:15:GLU:HA	7:H:18:LEU:CD1	2.30	0.57
7:H:157:LYS:HD3	7:H:158:ASP:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:45:PRO:HG3	10:L:115:PHE:CE1	2.40	0.57
16:Y:42:GLU:OE1	16:Y:43:LYS:HG2	2.04	0.57
22:F:42:ILE:HB	22:F:69:PRO:HB2	1.86	0.57
31:Z:65:LEU:HD11	31:Z:80:LEU:HD13	1.86	0.57
34:f:133:HIS:CD2	34:f:136:ARG:NH2	2.72	0.57
1:2:110:U:OP1	1:2:753:A:O2'	2.20	0.57
3:B:104:ASP:OD1	3:B:105:PHE:N	2.37	0.57
5:E:88:ASP:OD1	5:E:122:LYS:NZ	2.28	0.57
24:M:94:LEU:HD11	24:M:109:ALA:HB2	1.86	0.57
28:S:101:LEU:H	28:S:104:ASN:HB2	1.69	0.57
33:d:21:CYS:HB3	33:d:25:GLY:H	1.69	0.57
39:j:244:LEU:HD12	39:j:268:PRO:HB3	1.85	0.57
40:k:106:ILE:HG13	40:k:216:LEU:HA	1.86	0.57
43:g:20:TRP:NE1	43:g:313:THR:CB	2.67	0.57
1:2:1198:G:H2'	1:2:1198:G:N3	2.18	0.57
1:2:1426:2MG:N2	30:U:74:GLU:OE1	2.33	0.57
4:C:93:LYS:HD3	4:C:100:ARG:CD	2.25	0.57
28:S:30:TYR:O	28:S:33:THR:OG1	2.14	0.57
32:c:21:SER:HB3	32:c:67:ARG:CZ	2.34	0.57
38:1:11:C:H2'	38:1:12:G:C8	2.39	0.57
40:k:192:VAL:CG1	40:k:211:MET:HE1	2.34	0.57
1:2:1145:G:H2'	1:2:1146:A:C8	2.40	0.57
4:C:153:LEU:HD23	13:V:4:ASP:OD2	2.04	0.57
5:E:126:VAL:HG22	5:E:158:ASP:O	2.04	0.57
13:V:73:ALA:HB1	13:V:79:LEU:HD23	1.85	0.57
40:k:201:MET:HA	40:k:204:MET:CE	2.29	0.57
4:C:115:HIS:CE1	13:V:11:LEU:HD11	2.40	0.57
22:F:85:ARG:HG3	22:F:85:ARG:O	2.05	0.57
29:T:68:ARG:HG2	29:T:69:LYS:H	1.69	0.57
1:2:437:A:H1'	1:2:464:G:H22	1.69	0.57
1:2:959:U:H5'	11:N:55:ARG:HH11	1.69	0.57
5:E:15:PRO:HG2	5:E:18:TRP:CD1	2.40	0.57
5:E:47:PHE:CE2	5:E:101:LEU:HD21	2.40	0.57
8:I:67:TRP:CD1	8:I:184:ILE:HD11	2.39	0.57
27:R:103:ASP:OD1	27:R:104:THR:N	2.33	0.57
32:c:18:ARG:CG	32:c:26:THR:HG22	2.24	0.57
39:j:216:MET:HG2	39:j:239:LYS:HD2	1.87	0.57
1:2:327:A:H2'	1:2:328:G:C8	2.39	0.57
1:2:885:U:H2'	1:2:886:A:C8	2.40	0.57
1:2:1613:C:OP2	32:c:47:PRO:HB3	2.05	0.57
3:B:133:TYR:CE2	3:B:181:LEU:HD13	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:78:LEU:HB2	4:C:81:LEU:HD21	1.86	0.57
16:Y:51:GLU:OE1	16:Y:51:GLU:N	2.27	0.57
29:T:64:HIS:CE1	29:T:68:ARG:HE	2.21	0.57
39:j:222:LEU:HD21	40:k:324:ASN:HB3	1.87	0.57
2:A:74:VAL:HG23	2:A:118:PRO:HB3	1.86	0.57
3:B:107:THR:O	3:B:111:ARG:HG2	2.04	0.57
25:P:60:LEU:HD11	25:P:92:SER:HB2	1.86	0.57
26:Q:45:ARG:O	26:Q:48:VAL:HG13	2.04	0.57
27:R:23:LYS:O	27:R:34:LEU:HD13	2.05	0.57
32:c:66:LEU:HD23	32:c:67:ARG:HG2	1.85	0.57
36:m:85:ARG:HH12	36:m:107:GLY:HA2	1.69	0.57
1:2:627:G:OP1	11:N:120:SER:OG	2.23	0.57
1:2:739:G:H2'	1:2:740:A:C8	2.40	0.57
1:2:1225:A:O2'	1:2:1255:A:N1	2.37	0.57
5:E:64:ILE:HD12	16:Y:17:LEU:HB3	1.87	0.57
9:J:140:ILE:HG23	16:Y:64:TYR:CD2	2.40	0.57
14:W:35:ILE:O	14:W:39:GLN:HG3	2.05	0.57
15:X:70:LYS:HB3	15:X:93:LEU:HD12	1.87	0.57
1:2:90:C:H2'	1:2:91:G:C8	2.40	0.56
1:2:1063:G:O2'	3:B:204:ILE:O	2.23	0.56
1:2:1513:A:O2'	1:2:1515:U:OP2	2.22	0.56
40:k:146:LYS:HE3	40:k:166:SER:HA	1.87	0.56
1:2:383:G:H2'	1:2:384:A:C8	2.40	0.56
4:C:126:VAL:O	4:C:130:ILE:HD12	2.04	0.56
5:E:47:PHE:HE2	5:E:101:LEU:HD21	1.69	0.56
16:Y:46:GLU:O	16:Y:49:LYS:NZ	2.38	0.56
26:Q:20:ALA:HA	26:Q:66:ARG:O	2.04	0.56
27:R:25:THR:HG1	27:R:30:THR:HG1	1.53	0.56
1:2:65:A:H2	1:2:84:A:H62	1.54	0.56
1:2:566:A:H1'	19:e:14:VAL:HG23	1.86	0.56
1:2:590:A:H5''	9:J:24:LEU:HD11	1.88	0.56
1:2:658:C:H2'	1:2:659:G:C8	2.34	0.56
1:2:799:U:H2'	1:2:800:G:H8	1.70	0.56
1:2:947:G:H2'	1:2:948:C:H6	1.70	0.56
1:2:1502:G:H2'	1:2:1503:A:C8	2.41	0.56
2:A:48:ILE:HG12	2:A:149:LEU:HD11	1.86	0.56
2:A:88:LYS:HE2	2:A:202:TYR:CE1	2.39	0.56
10:L:97:TYR:CE2	15:X:15:LEU:HB3	2.41	0.56
10:L:116:ARG:HA	10:L:116:ARG:CZ	2.35	0.56
22:F:65:GLN:CD	22:F:66:ILE:H	2.13	0.56
31:Z:80:LEU:HD12	31:Z:83:LEU:HD12	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:d:21:CYS:HA	33:d:30:LEU:HD11	1.88	0.56
1:2:97:C:H2'	1:2:98:U:H6	1.69	0.56
1:2:1581:A:H62	1:2:1610:U:H5	1.53	0.56
14:W:111:MET:HE3	14:W:115:GLU:HB2	1.86	0.56
25:P:115:TYR:O	25:P:118:GLU:HG2	2.05	0.56
36:m:58:LEU:O	36:m:62:PHE:CD2	2.52	0.56
40:k:143:ALA:HB3	40:k:191:PHE:HB2	1.88	0.56
43:g:36:SER:OG	43:g:46:TRP:HZ2	1.89	0.56
43:g:43:LEU:HG	43:g:93:TRP:HZ3	1.69	0.56
1:2:692:C:H2'	1:2:693:U:C6	2.40	0.56
1:2:1335:A:H2'	1:2:1336:A:O4'	2.06	0.56
1:2:1657:A:H2'	1:2:1658:A:H8	1.70	0.56
2:A:33:GLN:HA	2:A:33:GLN:OE1	2.04	0.56
5:E:45:ILE:HA	5:E:61:VAL:HG11	1.86	0.56
9:J:76:LEU:O	9:J:80:LEU:HD23	2.05	0.56
1:2:1170:A:H2'	1:2:1171:G:H8	1.68	0.56
6:G:4:ASN:OD1	6:G:110:ALA:HA	2.06	0.56
7:H:144:VAL:HA	14:W:42:GLN:NE2	2.20	0.56
22:F:70:ILE:HA	26:Q:112:TYR:OH	2.06	0.56
43:g:230:TRP:HD1	43:g:237:ALA:HA	1.69	0.56
9:J:129:ILE:HA	9:J:134:ILE:HG21	1.87	0.56
21:D:24:PHE:CE1	21:D:28:GLU:HG3	2.40	0.56
21:D:116:ARG:HD2	21:D:152:PHE:CZ	2.40	0.56
22:F:75:THR:C	22:F:77:GLY:H	2.13	0.56
40:k:97:ARG:HH22	40:k:385:ASN:HD22	1.53	0.56
1:2:1778:G:OP2	36:m:56:LYS:NZ	2.30	0.56
1:2:1795:A:H5'	17:a:95:ARG:NH1	2.21	0.56
9:J:133:HIS:HD2	9:J:158:PHE:CD1	2.23	0.56
16:Y:23:PHE:CE2	16:Y:25:VAL:HG22	2.41	0.56
22:F:126:LEU:O	22:F:127:THR:OG1	2.22	0.56
35:i:62:ARG:HG3	35:i:90:ASP:HB2	1.87	0.56
43:g:34:LEU:HB3	43:g:46:TRP:HD1	1.71	0.56
43:g:301:TRP:CZ3	43:g:308:LEU:HB2	2.41	0.56
1:2:624:C:H2'	1:2:625:U:C6	2.41	0.56
1:2:630:G:N2	1:2:1103:U:OP1	2.39	0.56
1:2:1044:C:H2'	1:2:1045:G:C8	2.39	0.56
1:2:1479:C:C5'	26:Q:40:GLN:OE1	2.46	0.56
1:2:1480:C:H2'	1:2:1481:A:H5''	1.88	0.56
1:2:1582:G:C8	26:Q:122:ARG:HD2	2.41	0.56
11:N:99:ARG:HH12	11:N:143:SER:HA	1.70	0.56
23:K:82:LEU:HD21	23:K:86:ILE:HB	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:45:ARG:CD	26:Q:49:TYR:HE2	2.19	0.56
1:2:274:C:O2'	1:2:276:U:O4	2.17	0.56
1:2:339:U:H2'	1:2:340:A:C8	2.41	0.56
1:2:680:U:O2'	1:2:682:U:OP1	2.14	0.56
7:H:98:ILE:HD11	7:H:121:VAL:HG21	1.88	0.56
16:Y:42:GLU:HB3	16:Y:52:LYS:HD2	1.88	0.56
22:F:97:ASN:HA	22:F:100:MET:CE	2.36	0.56
32:c:21:SER:HB3	32:c:67:ARG:NH1	2.20	0.56
40:k:145:ALA:HB3	40:k:191:PHE:HE2	1.71	0.56
1:2:28:A:C6	1:2:597:U:O4	2.59	0.55
1:2:921:G:H2'	1:2:922:A:H8	1.71	0.55
1:2:1626:U:H2'	1:2:1627:G:C8	2.41	0.55
2:A:55:GLU:HA	2:A:55:GLU:OE2	2.06	0.55
35:i:30:GLU:O	35:i:30:GLU:CD	2.49	0.55
1:2:1035:A:H2'	1:2:1036:C:C6	2.42	0.55
1:2:1496:G:H5''	29:T:72:GLY:HA3	1.88	0.55
5:E:250:GLU:O	5:E:254:ARG:HG2	2.06	0.55
6:G:78:ALA:HB2	6:G:92:ARG:HG3	1.88	0.55
11:N:98:VAL:HG12	11:N:115:LEU:HD12	1.88	0.55
1:2:843:A:H2'	1:2:844:G:C8	2.40	0.55
1:2:1386:A:H5''	27:R:48:ASN:ND2	2.21	0.55
1:2:1424:C:H3'	1:2:1425:A:H4'	1.87	0.55
21:D:202:LEU:HB2	21:D:205:ALA:HB2	1.87	0.55
22:F:55:VAL:HG23	22:F:140:ILE:HD11	1.87	0.55
22:F:86:LYS:O	22:F:94:ARG:NH1	2.39	0.55
32:c:9:LEU:HD11	32:c:53:ILE:HG22	1.87	0.55
32:c:29:ARG:NE	32:c:41:VAL:HG22	2.21	0.55
1:2:853:U:O4	1:2:854:A:N6	2.39	0.55
1:2:917:U:OP1	12:O:84:ARG:NH1	2.39	0.55
7:H:33:GLU:CD	7:H:33:GLU:H	2.14	0.55
8:I:67:TRP:CG	8:I:184:ILE:HD11	2.42	0.55
28:S:84:TRP:HZ2	29:T:33:TYR:OH	1.89	0.55
28:S:122:HIS:CE1	28:S:126:ARG:NH1	2.71	0.55
29:T:15:ILE:HD12	29:T:60:SER:HA	1.87	0.55
5:E:69:HIS:ND1	5:E:93:GLU:OE2	2.38	0.55
7:H:75:ILE:HG13	7:H:76:LYS:N	2.22	0.55
15:X:43:PHE:HE1	15:X:49:ALA:HB3	1.71	0.55
34:f:119:LYS:HG2	34:f:137:PHE:HE2	1.71	0.55
43:g:17:HIS:NE2	43:g:46:TRP:CZ2	2.73	0.55
1:2:1080:A:O2'	1:2:1081:C:H2'	2.06	0.55
1:2:1586:G:O6	1:2:1606:U:O4	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:16:LEU:HD21	2:A:199:PRO:HG3	1.87	0.55
2:A:55:GLU:HB3	13:V:79:LEU:HD12	1.87	0.55
2:A:81:TYR:HB3	2:A:170:ILE:HD11	1.88	0.55
3:B:160:HIS:HA	3:B:163:GLN:OE1	2.06	0.55
22:F:166:PRO:HD3	32:c:54:LEU:HD13	1.88	0.55
22:F:202:ASN:HA	22:F:205:LYS:HZ3	1.71	0.55
36:m:38:THR:C	36:m:39:LEU:HD12	2.31	0.55
41:l:157:LYS:HD2	41:l:159:ARG:HB2	1.88	0.55
1:2:1564:U:H5''	28:S:39:GLY:H	1.71	0.55
4:C:58:ILE:HD13	4:C:78:LEU:HD11	1.89	0.55
7:H:46:ILE:HG12	7:H:60:VAL:HG23	1.88	0.55
9:J:84:GLY:HA3	9:J:107:ARG:NH2	2.21	0.55
12:O:20:PHE:HB3	12:O:27:PHE:HB2	1.89	0.55
13:V:58:TYR:CZ	13:V:62:ARG:HD2	2.40	0.55
22:F:119:THR:HG21	22:F:196:LEU:HD22	1.89	0.55
26:Q:131:GLY:HA2	26:Q:138:PHE:CD1	2.41	0.55
1:2:107:C:H2'	1:2:108:A:C8	2.41	0.55
1:2:565:C:P	35:i:62:ARG:HH21	2.30	0.55
1:2:865:G:OP1	11:N:2:GLY:N	2.39	0.55
1:2:1198:G:H1	33:d:31:ILE:HD11	1.71	0.55
2:A:121:VAL:CG1	2:A:143:VAL:HG12	2.37	0.55
3:B:122:GLU:OE2	3:B:213:ARG:NH2	2.40	0.55
5:E:23:LEU:HA	9:J:3:ARG:HH12	1.72	0.55
6:G:29:ASP:OD1	6:G:29:ASP:O	2.25	0.55
15:X:6:PRO:HG3	15:X:14:LYS:HD2	1.89	0.55
30:U:98:HIS:ND1	30:U:102:ARG:NH2	2.55	0.55
40:k:192:VAL:CB	40:k:211:MET:HE1	2.36	0.55
1:2:521:U:O2'	16:Y:60:PHE:O	2.23	0.55
3:B:144:ARG:HB2	3:B:208:GLN:HB2	1.87	0.55
7:H:163:ASP:OD1	7:H:164:ASN:N	2.40	0.55
11:N:4:MET:HG3	11:N:5:HIS:CD2	2.42	0.55
21:D:223:LYS:HB3	43:g:198:ASP:HB2	1.88	0.55
39:j:22:VAL:O	39:j:68:ASN:HA	2.07	0.55
39:j:112:LEU:HB3	39:j:123:LEU:HD11	1.89	0.55
43:g:36:SER:OG	43:g:46:TRP:NE1	2.40	0.55
1:2:1097:U:H1'	14:W:71:LYS:HD3	1.87	0.55
1:2:1302:U:O2'	1:2:1321:A:OP2	2.25	0.55
7:H:30:ASN:HB3	7:H:33:GLU:OE1	2.07	0.55
19:e:54:ARG:HD3	19:e:56:MET:HG2	1.88	0.55
21:D:75:LYS:NZ	23:K:22:VAL:N	2.55	0.55
22:F:162:VAL:HA	32:c:42:ARG:HH22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:c:49:ARG:HG3	32:c:50:GLU:OE2	2.07	0.55
40:k:506:GLU:O	40:k:508:HIS:N	2.40	0.55
1:2:445:A:OP1	5:E:57:ASN:ND2	2.41	0.54
1:2:760:A:N1	1:2:789:U:O4	2.39	0.54
2:A:96:THR:HG21	2:A:116:LYS:CE	2.37	0.54
12:O:103:ARG:HH21	17:a:49:ALA:HB2	1.72	0.54
26:Q:9:THR:HG21	26:Q:88:GLY:HA2	1.88	0.54
27:R:53:TYR:O	27:R:57:LEU:HD12	2.05	0.54
29:T:89:ARG:HA	29:T:89:ARG:NE	2.22	0.54
1:2:31:C:O2'	1:2:546:U:OP1	2.25	0.54
1:2:58:U:O2'	1:2:450:A:N3	2.40	0.54
1:2:899:A:H5'	12:O:25:ASP:OD2	2.07	0.54
1:2:1168:G:N2	1:2:1573:7MG:H81	2.22	0.54
1:2:1778:G:O4'	36:m:59:LYS:HB3	2.07	0.54
3:B:138:PHE:HB2	3:B:213:ARG:HG3	1.89	0.54
6:G:2:LYS:HB3	6:G:108:VAL:HG22	1.89	0.54
7:H:154:LEU:O	7:H:186:PRO:HD2	2.08	0.54
15:X:121:ARG:O	15:X:122:PHE:HD1	1.89	0.54
18:b:67:THR:HG22	18:b:68:GLY:N	2.23	0.54
6:G:3:LEU:HD22	6:G:111:LEU:HD21	1.90	0.54
7:H:151:LYS:HG3	7:H:182:VAL:HG13	1.90	0.54
10:L:42:PHE:CG	10:L:140:LEU:HD23	2.42	0.54
23:K:13:GLN:O	23:K:17:GLN:HG3	2.08	0.54
40:k:356:ARG:HH22	40:k:423:LEU:HD23	1.72	0.54
43:g:312:TYR:HB2	43:g:315:ASN:OD1	2.07	0.54
1:2:768:C:C2	9:J:143:ILE:HD13	2.42	0.54
1:2:1318:A:OP2	27:R:67:ARG:NH2	2.39	0.54
1:2:1330:A:H61	21:D:161:GLY:HA3	1.71	0.54
3:B:135:LEU:HD13	3:B:217:LEU:HA	1.90	0.54
7:H:32:PRO:HG2	7:H:33:GLU:CD	2.32	0.54
13:V:2:GLU:HA	13:V:2:GLU:OE2	2.07	0.54
27:R:18:GLU:OE2	27:R:70:SER:N	2.40	0.54
27:R:70:SER:HA	27:R:74:GLN:HE21	1.68	0.54
28:S:45:LEU:HD11	29:T:36:ILE:HG13	1.88	0.54
29:T:11:ALA:O	29:T:15:ILE:HG12	2.07	0.54
30:U:65:ILE:HG12	33:d:52:PHE:HE2	1.72	0.54
33:d:31:ILE:O	33:d:37:ASN:N	2.37	0.54
1:2:324:G:H4'	10:L:83:THR:HG21	1.90	0.54
1:2:1685:U:N3	1:2:1712:A:N1	2.54	0.54
5:E:230:GLU:HA	5:E:230:GLU:OE1	2.08	0.54
28:S:109:LEU:O	28:S:113:LEU:HD23	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:S:112:ASP:HA	28:S:115:ARG:HE	1.73	0.54
34:f:130:LEU:CG	34:f:137:PHE:HB3	2.37	0.54
40:k:92:ALA:HA	40:k:95:ILE:HG22	1.90	0.54
41:l:232:GLU:HG3	41:l:233:TYR:HD1	1.71	0.54
1:2:1589:C:H2'	1:2:1590:A:C8	2.41	0.54
2:A:77:SER:HB2	2:A:86:VAL:HG21	1.88	0.54
5:E:64:ILE:HD11	16:Y:18:LEU:HG	1.89	0.54
7:H:41:LEU:HG	7:H:70:TYR:CE1	2.43	0.54
9:J:109:LEU:HB2	9:J:146:PHE:HB3	1.88	0.54
28:S:46:VAL:CG1	28:S:73:MET:HE3	2.19	0.54
28:S:70:VAL:HA	28:S:73:MET:HB2	1.90	0.54
35:i:38:ILE:HG12	35:i:47:VAL:HG11	1.88	0.54
35:i:99:GLU:OE1	35:i:99:GLU:N	2.30	0.54
1:2:331:U:H1'	8:I:5:ARG:NH1	2.23	0.54
1:2:585:G:H2'	1:2:586:C:C6	2.43	0.54
1:2:588:C:H4'	19:e:56:MET:CE	2.38	0.54
1:2:1661:G:H1	1:2:1736:U:H3	1.56	0.54
9:J:124:HIS:O	9:J:128:LEU:HG	2.07	0.54
23:K:82:LEU:HD23	23:K:83:PRO:O	2.07	0.54
25:P:52:LYS:HE3	25:P:80:LEU:HD11	1.89	0.54
27:R:46:LEU:O	27:R:50:ILE:HG12	2.08	0.54
27:R:109:LEU:O	27:R:113:LEU:HD23	2.07	0.54
30:U:16:GLU:HB2	30:U:98:HIS:HD2	1.72	0.54
36:m:48:GLU:HB2	36:m:96:LEU:HD21	1.90	0.54
39:j:189:GLU:OE1	39:j:226:PRO:HB2	2.08	0.54
40:k:356:ARG:HG3	40:k:424:PRO:HB2	1.90	0.54
43:g:39:ARG:HA	43:g:68:ILE:HG23	1.90	0.54
1:2:61:A:N6	1:2:62:A:N1	2.55	0.54
1:2:1623:C:H2'	1:2:1624:U:H6	1.72	0.54
21:D:20:GLU:HB2	23:K:61:TRP:CZ3	2.43	0.54
23:K:9:LYS:NZ	23:K:13:GLN:HG2	2.23	0.54
24:M:94:LEU:HB2	24:M:107:VAL:HG11	1.90	0.54
30:U:99:ILE:HA	30:U:102:ARG:HE	1.71	0.54
35:i:35:TYR:HE1	35:i:95:TYR:CE2	2.26	0.54
1:2:108:A:H2'	1:2:109:G:C8	2.43	0.54
1:2:224:A:N6	1:2:836:G:O6	2.41	0.54
1:2:1797:U:H4'	1:2:1798:A:OP2	2.07	0.54
2:A:88:LYS:HZ2	2:A:201:LEU:C	2.15	0.54
2:A:116:LYS:C	2:A:118:PRO:HD3	2.32	0.54
5:E:171:ASP:OD1	5:E:172:PHE:N	2.35	0.54
15:X:50:LYS:HD2	15:X:77:ILE:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:126:LYS:HA	15:X:131:SER:HA	1.89	0.54
31:Z:62:VAL:HG13	31:Z:76:ALA:HB3	1.89	0.54
33:d:16:LYS:HE2	33:d:16:LYS:HA	1.89	0.54
34:f:143:HIS:CE1	34:f:144:SER:HG	2.26	0.54
43:g:115:ALA:N	43:g:124:ILE:O	2.34	0.54
1:2:336:G:O3'	8:I:10:LYS:NZ	2.41	0.54
1:2:1038:A:O2'	1:2:1039:G:O5'	2.23	0.54
1:2:1486:G:H3'	1:2:1513:A:H61	1.73	0.54
1:2:1592:G:OP2	1:2:1594:C:N4	2.41	0.54
19:e:54:ARG:CG	19:e:56:MET:HG2	2.38	0.54
21:D:69:LEU:HA	21:D:72:LEU:HD12	1.90	0.54
28:S:56:LYS:HZ2	28:S:60:GLU:CD	2.16	0.54
29:T:61:VAL:O	29:T:65:ILE:HG23	2.07	0.54
30:U:30:LYS:HZ1	30:U:111:GLY:HA3	1.73	0.54
35:i:57:ARG:NH1	35:i:86:ASP:O	2.40	0.54
40:k:356:ARG:HE	40:k:424:PRO:HD2	1.72	0.54
1:2:3:U:O2	9:J:17:ARG:NH2	2.41	0.53
1:2:788:A:C2	1:2:789:U:H1'	2.43	0.53
1:2:1624:U:H2'	1:2:1625:U:H6	1.71	0.53
3:B:144:ARG:HB2	3:B:208:GLN:CB	2.38	0.53
6:G:5:ILE:HD11	6:G:113:ILE:HB	1.90	0.53
26:Q:45:ARG:O	26:Q:49:TYR:CD2	2.59	0.53
1:2:959:U:H5'	11:N:55:ARG:HD3	1.89	0.53
6:G:39:GLU:HA	6:G:46:LYS:CE	2.38	0.53
28:S:114:GLU:HA	28:S:117:LYS:NZ	2.23	0.53
30:U:65:ILE:HG21	33:d:43:PHE:CE2	2.42	0.53
34:f:130:LEU:CD1	34:f:139:CYS:CB	2.81	0.53
1:2:1482:G:N3	1:2:1604:C:O2'	2.36	0.53
1:2:1774:A:H2'	1:2:1775:G:H8	1.73	0.53
4:C:64:HIS:CE1	4:C:244:PRO:HD3	2.44	0.53
7:H:43:PHE:HD2	7:H:60:VAL:HG21	1.73	0.53
23:K:40:LEU:HB3	23:K:44:LYS:NZ	2.23	0.53
36:m:38:THR:OG1	36:m:83:ASP:HB2	2.08	0.53
36:m:92:MET:SD	36:m:97:GLY:HA3	2.48	0.53
43:g:94:ASN:HB3	43:g:97:THR:HB	1.89	0.53
1:2:508:G:H2'	1:2:509:G:C8	2.43	0.53
1:2:899:A:H1'	1:2:914:A:H2	1.73	0.53
1:2:1254:G:O6	24:M:39:ARG:NH1	2.27	0.53
12:O:133:ARG:HA	17:a:28:ARG:NE	2.22	0.53
22:F:224:LYS:HG2	22:F:227:ARG:HH21	1.72	0.53
24:M:117:TRP:HE1	24:M:121:THR:HB	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:113:ASP:O	26:Q:116:LEU:HG	2.08	0.53
27:R:25:THR:OG1	27:R:30:THR:OG1	2.26	0.53
34:f:133:HIS:CD2	34:f:136:ARG:CZ	2.91	0.53
34:f:142:CYS:CB	34:f:145:THR:HG23	2.29	0.53
40:k:439:ARG:HA	40:k:452:LYS:HA	1.89	0.53
1:2:296:U:H2'	1:2:297:C:C6	2.43	0.53
1:2:751:G:H2'	1:2:752:A:C8	2.39	0.53
1:2:810:A:C8	7:H:111:LYS:HB3	2.43	0.53
1:2:917:U:C4'	12:O:18:ARG:HD3	2.36	0.53
1:2:922:A:H2'	1:2:923:A:C8	2.43	0.53
1:2:983:G:H2'	1:2:984:G:H8	1.72	0.53
1:2:1356:G:H2'	1:2:1357:G:C8	2.44	0.53
2:A:180:GLU:HA	2:A:180:GLU:OE1	2.09	0.53
2:A:203:PHE:HZ	27:R:91:LEU:HD11	1.73	0.53
7:H:166:LEU:HD12	7:H:167:GLU:N	2.23	0.53
12:O:112:ILE:N	17:a:56:ALA:O	2.41	0.53
15:X:3:LYS:O	15:X:5:LYS:N	2.36	0.53
40:k:263:GLN:HE21	41:l:131:TYR:HE2	1.52	0.53
43:g:44:ILE:HB	43:g:46:TRP:CH2	2.44	0.53
43:g:218:ALA:HB2	43:g:232:LEU:HD11	1.89	0.53
1:2:20:G:H5'	1:2:570:G:C8	2.44	0.53
1:2:1328:A:H2'	1:2:1329:G:O4'	2.08	0.53
9:J:114:TYR:HA	9:J:119:ALA:HB3	1.91	0.53
13:V:1:MET:HA	13:V:1:MET:HE2	1.90	0.53
28:S:12:GLN:NE2	28:S:15:LEU:CD2	2.52	0.53
32:c:10:ALA:HB2	32:c:32:PHE:HD1	1.72	0.53
38:1:33:U:H1'	38:1:35:A:N7	2.24	0.53
41:l:259:CYS:SG	41:l:260:LYS:N	2.82	0.53
1:2:548:G:H1	1:2:588:C:H5	1.57	0.53
1:2:1168:G:H2'	1:2:1573:7MG:HM72	1.89	0.53
7:H:4:PRO:HA	7:H:7:LYS:HE3	1.91	0.53
12:O:83:ILE:HD11	12:O:102:LEU:HD12	1.90	0.53
34:f:117:LEU:O	34:f:118:ARG:HB2	2.08	0.53
1:2:610:U:O5'	15:X:5:LYS:NZ	2.36	0.53
1:2:749:U:H2'	1:2:750:U:C6	2.43	0.53
1:2:900:G:C6	1:2:901:G:C6	2.97	0.53
1:2:1497:G:H1	1:2:1506:U:H3	1.55	0.53
1:2:1793:U:C6	17:a:75:ILE:HD11	2.44	0.53
4:C:95:THR:HG22	4:C:96:ARG:H	1.74	0.53
13:V:85:TYR:CE2	18:b:6:ASP:HB2	2.44	0.53
22:F:135:VAL:HG22	22:F:200:LEU:HD13	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:S:7:GLU:HB2	28:S:10:SER:HB3	1.91	0.53
29:T:68:ARG:HD2	29:T:71:VAL:HG22	1.90	0.53
34:f:130:LEU:HD12	34:f:139:CYS:HA	1.90	0.53
1:2:1035:A:H2'	1:2:1036:C:H6	1.74	0.53
7:H:9:LEU:HD23	7:H:43:PHE:O	2.09	0.53
21:D:75:LYS:CD	23:K:22:VAL:HB	2.39	0.53
30:U:28:SER:HB2	30:U:112:VAL:HA	1.89	0.53
1:2:585:G:H2'	1:2:586:C:H6	1.73	0.53
1:2:772:G:H21	1:2:774:A:H1'	1.74	0.53
1:2:897:A:H4'	12:O:46:MET:HE2	1.91	0.53
1:2:958:U:H6	11:N:61:THR:HB	1.73	0.53
1:2:1252:U:C4'	34:f:140:GLY:HA3	2.39	0.53
1:2:1500:G:N7	29:T:102:ARG:NH2	2.57	0.53
1:2:1535:C:OP2	1:2:1570:2MG:N2	2.42	0.53
1:2:1737:C:H2'	1:2:1738:A:H8	1.74	0.53
1:2:1768:U:H2'	1:2:1769:U:C6	2.45	0.53
3:B:133:TYR:CE1	3:B:221:PRO:HD2	2.44	0.53
4:C:152:ASN:ND2	13:V:2:GLU:O	2.42	0.53
5:E:181:VAL:HG12	5:E:193:GLY:O	2.09	0.53
21:D:24:PHE:CE2	23:K:65:TYR:CE2	2.94	0.53
38:1:16:H2U:H4'	38:1:16:H2U:OP1	2.07	0.53
1:2:565:C:H5'	35:i:62:ARG:NH2	2.24	0.52
1:2:1584:A:H2'	1:2:1585:A:O4'	2.09	0.52
21:D:137:VAL:HG22	21:D:151:LYS:HG3	1.90	0.52
22:F:50:PHE:CD1	22:F:132:LEU:HD21	2.44	0.52
22:F:56:LYS:NZ	22:F:141:ASN:OD1	2.41	0.52
22:F:85:ARG:CD	22:F:88:GLN:HG3	2.38	0.52
24:M:67:LEU:HA	34:f:108:VAL:CG1	2.39	0.52
34:f:119:LYS:CG	34:f:137:PHE:HE2	2.21	0.52
41:l:221:GLN:HA	41:l:224:ASN:ND2	2.23	0.52
43:g:308:LEU:O	43:g:319:VAL:HG23	2.08	0.52
1:2:163:A:N3	6:G:13:GLN:NE2	2.58	0.52
1:2:799:U:H2'	1:2:800:G:C8	2.44	0.52
1:2:1779:A:H2'	1:2:1780:MA6:C8	2.40	0.52
5:E:71:LYS:HB3	5:E:91:THR:OG1	2.09	0.52
11:N:5:HIS:CD2	11:N:121:ARG:HE	2.26	0.52
15:X:57:ILE:HD12	15:X:59:ILE:CD1	2.34	0.52
22:F:220:GLU:HB3	22:F:224:LYS:NZ	2.25	0.52
23:K:11:ILE:HG22	23:K:35:ILE:HD11	1.91	0.52
26:Q:37:THR:HG23	26:Q:49:TYR:CZ	2.43	0.52
29:T:109:GLU:HG3	29:T:114:VAL:HG12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:U:84:MET:HE1	33:d:52:PHE:CE1	2.44	0.52
39:j:195:TYR:HD1	40:k:374:PHE:H	1.57	0.52
43:g:117:ASP:OD1	43:g:118:ALA:N	2.42	0.52
1:2:1070:U:H2'	1:2:1071:C:C6	2.44	0.52
1:2:1235:A:C4	34:f:136:ARG:NH2	2.77	0.52
3:B:105:PHE:CE1	3:B:213:ARG:HA	2.45	0.52
3:B:133:TYR:CD1	3:B:221:PRO:HD2	2.44	0.52
11:N:142:GLU:HG2	11:N:143:SER:H	1.74	0.52
17:a:10:ARG:HD3	17:a:12:LYS:HD2	1.91	0.52
21:D:50:ILE:HD12	21:D:86:LEU:HD21	1.91	0.52
29:T:14:PHE:HZ	29:T:132:LEU:HG	1.75	0.52
1:2:697:C:OP2	7:H:105:LYS:NZ	2.23	0.52
1:2:871:G:H2'	1:2:872:U:O4'	2.09	0.52
1:2:1002:A:O2'	1:2:1004:A:N7	2.37	0.52
1:2:1624:U:H2'	1:2:1625:U:C6	2.44	0.52
6:G:98:ARG:NH1	6:G:105:ASP:OD2	2.42	0.52
7:H:166:LEU:HA	7:H:169:PHE:CD2	2.44	0.52
17:a:82:ARG:HH22	17:a:85:ARG:NH1	2.06	0.52
27:R:12:ALA:O	27:R:16:LEU:HD23	2.09	0.52
1:2:88:U:H2'	1:2:89:G:H8	1.74	0.52
1:2:328:G:H2'	1:2:329:G:C8	2.45	0.52
1:2:1164:G:H2'	1:2:1165:A:H8	1.73	0.52
1:2:1381:G:H2'	1:2:1382:A:H8	1.74	0.52
1:2:1591:A:H2'	1:2:1592:G:C8	2.44	0.52
6:G:135:PRO:HG2	6:G:141:ILE:HG12	1.91	0.52
17:a:21:VAL:HG21	17:a:72:HIS:ND1	2.23	0.52
26:Q:73:GLY:N	26:Q:76:SER:OG	2.39	0.52
34:f:130:LEU:HD23	34:f:137:PHE:CD2	2.45	0.52
40:k:116:VAL:HG12	40:k:285:ALA:HB2	1.90	0.52
40:k:356:ARG:NH2	40:k:422:HIS:O	2.42	0.52
43:g:34:LEU:CB	43:g:46:TRP:HD1	2.23	0.52
1:2:815:G:C2	1:2:816:A:C8	2.98	0.52
1:2:1289:PSU:H2'	1:2:1290:G:C8	2.45	0.52
1:2:1657:A:H2'	1:2:1658:A:C8	2.44	0.52
2:A:143:VAL:CG2	2:A:156:VAL:HA	2.39	0.52
2:A:149:LEU:N	2:A:149:LEU:HD12	2.24	0.52
2:A:167:LYS:NZ	2:A:204:TYR:H	2.07	0.52
4:C:131:ARG:O	4:C:135:ILE:HG12	2.10	0.52
4:C:163:THR:HG21	4:C:226:THR:HG22	1.90	0.52
5:E:143:ASP:OD2	5:E:145:ARG:NH2	2.42	0.52
6:G:214:LYS:NZ	6:G:218:GLU:OE2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:62:GLN:O	11:N:65:VAL:HG12	2.09	0.52
15:X:63:GLN:HB2	15:X:64:PRO:HD3	1.91	0.52
21:D:106:LYS:HG3	21:D:175:VAL:HG22	1.91	0.52
24:M:56:VAL:HG11	24:M:85:ALA:HA	1.91	0.52
1:2:222:U:H2'	1:2:223:C:C6	2.44	0.52
1:2:445:A:N6	1:2:460:G:H21	2.07	0.52
1:2:1347:A:H2'	1:2:1348:G:C8	2.45	0.52
6:G:118:GLU:HG2	6:G:119:GLN:N	2.24	0.52
22:F:76:ALA:O	26:Q:122:ARG:NH2	2.42	0.52
26:Q:8:GLN:OE1	26:Q:21:HIS:ND1	2.32	0.52
43:g:124:ILE:CD1	43:g:134:VAL:HG22	2.40	0.52
1:2:1201:A:H61	1:2:1455:C:H5'	1.73	0.52
1:2:1474:C:H2'	1:2:1475:G:C8	2.45	0.52
14:W:11:LEU:HA	14:W:14:ILE:HG22	1.92	0.52
14:W:70:ASN:OD1	14:W:71:LYS:N	2.43	0.52
35:i:61:ILE:HG22	35:i:66:ARG:HG2	1.92	0.52
43:g:146:LEU:HG	43:g:147:GLY:H	1.74	0.52
1:2:189:C:N4	1:2:195:G:O6	2.43	0.52
1:2:357:U:H2'	1:2:359:A:C8	2.44	0.52
1:2:1480:C:OP2	1:2:1519:G:N1	2.36	0.52
1:2:1621:C:H2'	1:2:1622:C:C6	2.45	0.52
3:B:52:VAL:HG13	3:B:55:LYS:H	1.75	0.52
25:P:57:MET:HE2	25:P:61:ARG:CD	2.39	0.52
26:Q:45:ARG:HA	26:Q:48:VAL:HG12	1.91	0.52
1:2:700:C:O2'	1:2:701:U:OP1	2.27	0.52
4:C:93:LYS:CB	4:C:100:ARG:HG2	2.26	0.52
6:G:219:ARG:O	6:G:222:GLU:HG3	2.09	0.52
8:I:3:ILE:O	8:I:30:GLY:N	2.41	0.52
12:O:38:THR:HG21	12:O:41:ARG:HH21	1.74	0.52
23:K:21:LEU:HD23	23:K:46:LEU:HD11	1.92	0.52
28:S:29:VAL:O	28:S:33:THR:HG23	2.10	0.52
43:g:43:LEU:HD11	43:g:83:SER:HB3	1.92	0.52
43:g:171:ARG:HH12	43:g:193:TYR:H	1.57	0.52
1:2:330:A:H2'	1:2:331:U:C6	2.45	0.51
1:2:442:C:HO2'	1:2:444:A:H2	1.57	0.51
1:2:589:C:H2'	1:2:590:A:C8	2.44	0.51
2:A:143:VAL:HG23	2:A:156:VAL:HA	1.92	0.51
4:C:64:HIS:HD2	13:V:33:GLN:HE22	1.58	0.51
8:I:157:VAL:O	8:I:160:GLN:HG2	2.09	0.51
10:L:21:THR:HG22	10:L:32:LYS:HG2	1.92	0.51
14:W:18:GLU:OE2	14:W:18:GLU:C	2.53	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:107:PHE:CE2	15:X:114:LYS:HB3	2.45	0.51
21:D:24:PHE:HE2	23:K:65:TYR:CD2	2.28	0.51
22:F:85:ARG:O	22:F:87:ALA:N	2.43	0.51
1:2:1131:A:H2'	1:2:1132:A:C8	2.44	0.51
1:2:1610:U:H1'	22:F:101:MET:CE	2.40	0.51
2:A:207:PRO:HA	2:A:210:ILE:HG22	1.91	0.51
4:C:78:LEU:O	4:C:81:LEU:CD2	2.57	0.51
6:G:159:ARG:NE	6:G:172:ALA:HB2	2.25	0.51
9:J:133:HIS:HA	9:J:162:SER:HB3	1.91	0.51
22:F:198:GLU:HA	22:F:201:ILE:HG12	1.92	0.51
29:T:77:ASN:HB3	29:T:95:ASP:HB3	1.92	0.51
29:T:113:VAL:HG23	29:T:114:VAL:HG23	1.92	0.51
30:U:84:MET:HE1	33:d:52:PHE:CZ	2.45	0.51
36:m:30:ILE:HD11	36:m:85:ARG:HD3	1.91	0.51
38:l:13:C:O2'	38:l:14:A:O5'	2.18	0.51
40:k:102:ASN:OD1	40:k:190:SER:OG	2.27	0.51
1:2:765:G:C6	9:J:146:PHE:HE1	2.28	0.51
1:2:891:A:H2'	1:2:892:U:C6	2.46	0.51
2:A:59:LEU:O	2:A:63:ILE:HG12	2.11	0.51
2:A:97:PRO:O	2:A:98:ILE:HD13	2.10	0.51
14:W:87:GLU:HA	14:W:87:GLU:OE2	2.10	0.51
39:j:182:VAL:HG11	39:j:237:LYS:HE3	1.93	0.51
41:l:127:VAL:HG12	41:l:129:LEU:H	1.75	0.51
1:2:947:G:H2'	1:2:948:C:C6	2.45	0.51
1:2:1209:C:H2'	1:2:1210:A:C8	2.45	0.51
1:2:1407:G:N2	1:2:1410:G:OP2	2.35	0.51
1:2:1413:U:OP1	27:R:45:ARG:NH2	2.43	0.51
1:2:1427:G:H2'	1:2:1428:U:C6	2.45	0.51
1:2:1582:G:H22	1:2:1609:A:P	2.33	0.51
5:E:250:GLU:OE2	5:E:250:GLU:HA	2.09	0.51
14:W:106:THR:HG21	14:W:121:VAL:HG23	1.92	0.51
24:M:40:GLU:HA	24:M:43:LYS:HE3	1.92	0.51
35:i:38:ILE:HG13	35:i:77:ILE:HD13	1.91	0.51
35:i:46:ARG:HD3	35:i:58:MET:SD	2.51	0.51
1:2:1219:C:H2'	1:2:1220:A:C8	2.43	0.51
3:B:183:GLN:O	3:B:187:LYS:HG2	2.10	0.51
10:L:77:SER:HB3	10:L:85:VAL:HB	1.92	0.51
22:F:65:GLN:HE21	22:F:68:LYS:HG2	1.75	0.51
30:U:16:GLU:HB2	30:U:98:HIS:CD2	2.45	0.51
39:j:190:VAL:HG23	40:k:405:THR:HG21	1.91	0.51
41:l:233:TYR:O	41:l:257:MET:HE1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:3:LEU:HD23	6:G:109:LEU:HB2	1.93	0.51
6:G:163:THR:HG22	6:G:165:GLY:H	1.74	0.51
10:L:81:HIS:O	10:L:83:THR:HG22	2.09	0.51
11:N:46:THR:O	11:N:50:ILE:HG12	2.10	0.51
12:O:19:ILE:HB	12:O:83:ILE:HD13	1.93	0.51
17:a:11:ASN:O	17:a:11:ASN:ND2	2.43	0.51
21:D:35:SER:OG	21:D:51:ARG:O	2.18	0.51
40:k:457:GLU:HG2	40:k:460:GLU:HG3	1.92	0.51
1:2:1716:A:H2'	1:2:1717:A:C8	2.46	0.51
6:G:147:LEU:HD13	6:G:156:TYR:CD2	2.45	0.51
19:e:14:VAL:O	19:e:18:THR:HG23	2.11	0.51
22:F:167:LEU:HG	22:F:171:ASN:HD21	1.76	0.51
23:K:25:LYS:HB3	23:K:62:GLN:HG2	1.92	0.51
28:S:87:ASN:HD22	28:S:100:SER:HB2	1.76	0.51
43:g:7:MET:HE3	43:g:8:LEU:N	2.20	0.51
1:2:763:G:OP2	9:J:79:ARG:NH2	2.44	0.51
1:2:1471:U:H5	22:F:192:ILE:HG21	1.76	0.51
5:E:200:ARG:HD2	5:E:200:ARG:O	2.10	0.51
10:L:146:THR:O	10:L:150:ASN:ND2	2.44	0.51
11:N:33:VAL:O	11:N:37:ILE:HG12	2.10	0.51
35:i:37:GLN:NE2	35:i:76:ILE:HD13	2.26	0.51
36:m:39:LEU:HB3	36:m:79:GLN:HE22	1.76	0.51
43:g:10:LEU:N	43:g:320:TRP:CE3	2.78	0.51
1:2:406:A:H2'	1:2:407:C:H6	1.74	0.51
1:2:631:U:P	10:L:102:LYS:NZ	2.84	0.51
1:2:635:A:H5''	14:W:31:SER:HB3	1.93	0.51
1:2:1613:C:O2'	1:2:1614:G:OP2	2.25	0.51
4:C:61:ILE:CD1	4:C:66:LEU:HD23	2.41	0.51
4:C:174:LEU:HD13	4:C:203:THR:HG22	1.92	0.51
7:H:70:TYR:HE2	7:H:92:PHE:HE2	1.58	0.51
9:J:57:ARG:O	9:J:61:THR:HG23	2.11	0.51
25:P:83:MET:HB2	25:P:116:LEU:HD13	1.93	0.51
29:T:22:LEU:HD22	29:T:28:LEU:HD21	1.92	0.51
38:1:66:C:H2'	38:1:67:G:C8	2.45	0.51
1:2:90:C:H2'	1:2:91:G:H8	1.74	0.51
1:2:220:A:H2'	1:2:221:A:C8	2.46	0.51
1:2:586:C:H2'	1:2:587:U:C6	2.46	0.51
1:2:789:U:H5	1:2:790:A:C5	2.29	0.51
1:2:1067:C:H2'	1:2:1068:A:H8	1.76	0.51
1:2:1209:C:H2'	1:2:1210:A:H8	1.74	0.51
1:2:1736:U:H2'	1:2:1737:C:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:52:LYS:O	2:A:56:LYS:HG2	2.10	0.51
3:B:82:ARG:NH2	3:B:191:GLU:OE2	2.41	0.51
11:N:20:ARG:NH2	14:W:56:HIS:HB3	2.24	0.51
14:W:25:VAL:HG22	14:W:63:VAL:HB	1.93	0.51
16:Y:128:LYS:HD3	16:Y:131:ARG:HD3	1.92	0.51
21:D:8:LYS:CD	33:d:34:TYR:CE1	2.73	0.51
22:F:118:HIS:HA	22:F:121:GLU:CD	2.36	0.51
38:1:56:C:H41	39:j:114:TYR:HD1	1.59	0.51
1:2:1741:U:H2'	1:2:1742:A:H8	1.76	0.50
1:2:1773:U:P	20:h:11:ARG:HH22	2.34	0.50
2:A:30:GLN:HE22	2:A:34:GLU:HB2	1.76	0.50
23:K:20:VAL:HG12	23:K:67:THR:HG22	1.92	0.50
26:Q:100:GLN:HG2	43:g:58:PRO:HG2	1.92	0.50
39:j:54:ARG:NH2	39:j:57:ARG:HH11	2.07	0.50
40:k:84:PHE:HB3	40:k:309:PHE:HD2	1.77	0.50
40:k:322:ASP:HB2	40:k:324:ASN:OD1	2.11	0.50
1:2:103:A:H4'	1:2:105:A:C8	2.46	0.50
5:E:59:ARG:NH2	16:Y:87:PRO:HG3	2.26	0.50
5:E:173:ILE:HD11	5:E:235:TRP:CE2	2.46	0.50
6:G:69:LEU:HD12	6:G:70:PRO:HD2	1.91	0.50
6:G:200:ALA:O	6:G:203:GLU:HG3	2.12	0.50
12:O:111:ARG:HB3	17:a:58:VAL:CG1	2.41	0.50
22:F:162:VAL:HG11	32:c:25:VAL:HG21	1.94	0.50
28:S:112:ASP:O	28:S:115:ARG:HG2	2.11	0.50
40:k:260:LEU:O	40:k:263:GLN:HG2	2.11	0.50
1:2:639:U:H2'	1:2:640:G:O4'	2.12	0.50
1:2:753:A:OP2	5:E:187:ARG:NH2	2.44	0.50
1:2:1169:G:H5'	1:2:1573:7MG:HM71	1.92	0.50
1:2:1391:C:H2'	1:2:1392:G:H8	1.76	0.50
1:2:1604:C:OP2	26:Q:127:LYS:N	2.44	0.50
2:A:74:VAL:CG2	2:A:118:PRO:HG3	2.41	0.50
2:A:84:ARG:CZ	27:R:82:ASP:OD1	2.59	0.50
7:H:111:LYS:O	7:H:113:PRO:HD3	2.12	0.50
28:S:56:LYS:NZ	28:S:60:GLU:OE2	2.44	0.50
39:j:36:LEU:HD21	39:j:85:LEU:HD11	1.94	0.50
43:g:256:ARG:HH22	43:g:322:VAL:HG11	1.75	0.50
1:2:1159:A:H2'	1:2:1160:C:H6	1.74	0.50
1:2:1315:G:H2'	1:2:1316:C:H6	1.76	0.50
1:2:1332:C:H4'	21:D:162:GLN:OE1	2.11	0.50
11:N:87:ASP:N	11:N:87:ASP:OD1	2.43	0.50
16:Y:113:ASN:O	16:Y:117:LYS:HG2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:e:25:GLU:OE1	19:e:25:GLU:HA	2.12	0.50
22:F:86:LYS:O	22:F:86:LYS:HG2	2.10	0.50
25:P:114:HIS:HB3	25:P:118:GLU:CD	2.37	0.50
39:j:236:ASP:HB3	39:j:238:GLN:HE22	1.76	0.50
40:k:462:LEU:HD21	40:k:501:LEU:HB3	1.93	0.50
1:2:536:G:C6	9:J:171:ARG:HD2	2.46	0.50
1:2:1182:A:C5	25:P:100:LYS:HE2	2.46	0.50
1:2:1795:A:H61	17:a:85:ARG:H	1.60	0.50
4:C:86:MET:HG3	4:C:212:LEU:HD21	1.93	0.50
6:G:7:TYR:HD2	6:G:10:ASN:HB2	1.76	0.50
12:O:17:ALA:N	12:O:80:HIS:O	2.40	0.50
21:D:154:ASP:OD1	21:D:155:GLY:N	2.44	0.50
25:P:85:ILE:HA	25:P:89:MET:SD	2.52	0.50
26:Q:74:HIS:O	26:Q:78:VAL:HG23	2.12	0.50
30:U:96:PRO:HD2	30:U:99:ILE:HD11	1.94	0.50
40:k:60:THR:HG23	40:k:63:GLU:H	1.76	0.50
40:k:174:CYS:HA	40:k:183:TYR:CE2	2.45	0.50
40:k:416:VAL:HG21	40:k:492:CYS:HB2	1.93	0.50
41:l:230:ILE:HA	41:l:234:VAL:HB	1.93	0.50
1:2:1049:G:H5'	1:2:1050:G:OP2	2.12	0.50
1:2:1217:G:N2	1:2:1441:U:O3'	2.45	0.50
1:2:1421:U:H2'	1:2:1422:A:O4'	2.11	0.50
2:A:41:ARG:HH11	2:A:45:VAL:HB	1.77	0.50
10:L:80:MET:HE2	10:L:85:VAL:HG23	1.92	0.50
12:O:18:ARG:NH1	12:O:31:THR:HG21	2.26	0.50
15:X:121:ARG:C	15:X:122:PHE:CD1	2.90	0.50
22:F:135:VAL:HA	22:F:200:LEU:HD22	1.93	0.50
26:Q:35:PRO:CD	26:Q:38:LEU:HD22	2.21	0.50
28:S:118:LYS:C	28:S:118:LYS:HD3	2.37	0.50
33:d:21:CYS:C	33:d:23:ILE:H	2.19	0.50
40:k:337:VAL:HA	40:k:399:GLY:HA2	1.93	0.50
1:2:77:U:H1'	6:G:159:ARG:HH12	1.76	0.50
1:2:887:U:H2'	1:2:888:U:C6	2.47	0.50
1:2:1339:U:H1'	1:2:1376:U:H5'	1.94	0.50
1:2:1391:C:H2'	1:2:1392:G:C8	2.46	0.50
3:B:131:ASP:CG	3:B:132:ASP:H	2.19	0.50
5:E:121:TYR:CD2	5:E:161:LYS:HE3	2.47	0.50
8:I:170:ILE:HA	8:I:182:GLY:HA3	1.94	0.50
11:N:89:TYR:HE1	11:N:150:VAL:HA	1.77	0.50
23:K:3:ILE:HG21	23:K:8:ARG:NE	2.16	0.50
33:d:43:PHE:CZ	33:d:52:PHE:CD2	2.97	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:m:28:ILE:HG22	36:m:42:VAL:HG23	1.94	0.50
38:1:16:H2U:O3'	38:1:18:G:OP1	2.27	0.50
1:2:392:C:H2'	1:2:393:C:C6	2.46	0.50
1:2:899:A:C8	1:2:900:G:N2	2.79	0.50
1:2:1430:U:H4'	1:2:1431:G:O5'	2.11	0.50
26:Q:48:VAL:HG13	26:Q:49:TYR:CD2	2.46	0.50
26:Q:95:LYS:O	43:g:60:ARG:NH1	2.31	0.50
39:j:252:THR:HA	39:j:255:ILE:HG22	1.94	0.50
43:g:179:MET:HA	43:g:205:TYR:HB2	1.94	0.50
1:2:219:A:C8	1:2:831:U:H1'	2.47	0.50
1:2:444:A:H2'	1:2:445:A:H8	1.77	0.50
1:2:743:U:H2'	1:2:744:U:C6	2.47	0.50
1:2:1001:G:O3'	36:m:67:ASN:ND2	2.43	0.50
1:2:1529:G:H5'	31:Z:81:ARG:HH12	1.77	0.50
1:2:1655:U:OP1	1:2:1656:G:O2'	2.22	0.50
3:B:5:LYS:HG3	3:B:7:LYS:H	1.75	0.50
9:J:56:ALA:O	9:J:60:LEU:HD23	2.12	0.50
12:O:29:HIS:CD2	12:O:41:ARG:HA	2.47	0.50
12:O:102:LEU:CD2	17:a:53:LEU:HD21	2.41	0.50
36:m:89:CYS:O	36:m:93:ILE:HG23	2.11	0.50
38:1:9:IMG:O2'	38:1:45:U:O2	2.30	0.50
43:g:34:LEU:HB3	43:g:46:TRP:CD1	2.45	0.50
1:2:44:U:OP2	1:2:436:A:N6	2.45	0.49
1:2:267:C:H3'	6:G:186:ARG:HH22	1.77	0.49
1:2:404:C:O2'	6:G:92:ARG:O	2.23	0.49
5:E:175:PHE:HE2	5:E:222:LEU:HD11	1.76	0.49
6:G:180:THR:HG23	6:G:183:ARG:H	1.76	0.49
14:W:22:LYS:NZ	18:b:3:LEU:HA	2.26	0.49
32:c:66:LEU:CD2	32:c:67:ARG:H	2.25	0.49
38:1:12:G:C6	38:1:24:G:N1	2.80	0.49
1:2:3:U:H5'	4:C:184:VAL:HG12	1.94	0.49
1:2:938:A:H2'	1:2:939:A:C8	2.48	0.49
1:2:945:U:C5'	3:B:165:ARG:HH12	2.25	0.49
1:2:997:A:H2'	1:2:998:PSU:C6	2.47	0.49
1:2:1178:G:H2'	1:2:1179:C:C6	2.46	0.49
1:2:1522:A:N3	1:2:1588:G:O2'	2.33	0.49
6:G:3:LEU:HD22	6:G:111:LEU:CD2	2.42	0.49
6:G:150:GLU:N	6:G:150:GLU:OE1	2.45	0.49
9:J:32:GLY:HA3	19:e:40:TYR:CG	2.47	0.49
12:O:31:THR:CG2	12:O:35:GLY:HA2	2.43	0.49
21:D:105:MET:SD	21:D:122:VAL:HG11	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:D:116:ARG:HD2	21:D:152:PHE:HZ	1.77	0.49
43:g:36:SER:CB	43:g:46:TRP:HE1	2.25	0.49
1:2:786:G:C6	1:2:787:A:C6	3.00	0.49
1:2:1254:G:H2'	24:M:40:GLU:OE2	2.12	0.49
1:2:1323:G:O3'	2:A:113:ARG:NH2	2.45	0.49
1:2:1475:G:O2'	29:T:48:GLN:N	2.30	0.49
1:2:1581:A:H61	1:2:1609:A:H3'	1.77	0.49
6:G:155:ASP:OD1	6:G:156:TYR:CD1	2.65	0.49
9:J:141:VAL:HG12	9:J:143:ILE:H	1.74	0.49
15:X:107:PHE:HD1	15:X:123:LYS:HG3	1.77	0.49
34:f:105:TYR:HB3	34:f:129:PHE:CE2	2.48	0.49
34:f:128:ILE:HG23	34:f:128:ILE:O	2.12	0.49
34:f:130:LEU:HD23	34:f:137:PHE:HD2	1.77	0.49
34:f:130:LEU:HD12	34:f:139:CYS:HB2	1.92	0.49
40:k:432:ILE:HG13	40:k:485:LEU:HD12	1.93	0.49
1:2:784:U:H2'	1:2:785:C:C6	2.48	0.49
1:2:917:U:H4'	12:O:18:ARG:CZ	2.42	0.49
5:E:106:LYS:HG3	5:E:108:ARG:NH2	2.28	0.49
17:a:10:ARG:NH1	17:a:12:LYS:HD2	2.28	0.49
22:F:202:ASN:HA	22:F:205:LYS:NZ	2.27	0.49
25:P:83:MET:HE2	25:P:116:LEU:HD22	1.95	0.49
30:U:84:MET:SD	30:U:84:MET:N	2.85	0.49
30:U:98:HIS:CB	30:U:102:ARG:HH21	2.23	0.49
34:f:121:CYS:HB3	34:f:128:ILE:CG2	2.43	0.49
35:i:35:TYR:HE1	35:i:95:TYR:HE2	1.60	0.49
36:m:70:LYS:HD2	36:m:71:ASP:N	2.26	0.49
39:j:8:PHE:HA	39:j:127:TYR:CE2	2.46	0.49
1:2:160:U:O2'	1:2:161:A:OP2	2.30	0.49
1:2:1003:U:H5'	1:2:1004:A:H5''	1.94	0.49
1:2:1096:U:O2'	4:C:173:ARG:NH1	2.44	0.49
2:A:102:PHE:O	2:A:103:THR:OG1	2.28	0.49
5:E:159:THR:HG21	5:E:227:VAL:O	2.13	0.49
9:J:3:ARG:HD2	9:J:4:ALA:N	2.27	0.49
11:N:65:VAL:HG13	11:N:66:ILE:HG23	1.94	0.49
11:N:83:GLU:HG2	11:N:84:ILE:HG12	1.94	0.49
25:P:80:LEU:HB3	25:P:83:MET:SD	2.52	0.49
36:m:91:PHE:CE2	36:m:95:GLN:HG2	2.48	0.49
43:g:260:THR:HG23	43:g:269:ILE:HD13	1.95	0.49
1:2:890:A:H2'	1:2:891:A:C8	2.47	0.49
1:2:1173:C:O2'	1:2:1195:A:N6	2.45	0.49
1:2:1506:U:H2'	1:2:1507:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:184:LEU:O	3:B:188:LEU:HG	2.13	0.49
6:G:44:GLU:C	6:G:119:GLN:HE21	2.20	0.49
15:X:56:LYS:HG2	15:X:72:VAL:HG12	1.93	0.49
24:M:67:LEU:HA	34:f:108:VAL:HG11	1.93	0.49
25:P:21:ASP:OD1	25:P:22:LEU:N	2.41	0.49
26:Q:117:LEU:HD23	26:Q:117:LEU:H	1.77	0.49
39:j:187:ASP:OD1	39:j:265:THR:OG1	2.29	0.49
43:g:157:VAL:HA	43:g:174:PHE:CB	2.43	0.49
1:2:946:U:HO2'	1:2:947:G:H8	1.60	0.49
1:2:1554:A:H5''	25:P:40:ARG:NH2	2.28	0.49
1:2:1578:C:H2'	1:2:1579:C:C6	2.47	0.49
6:G:103:GLY:H	6:G:106:LEU:HD23	1.78	0.49
8:I:173:ARG:NH2	8:I:176:GLN:HE21	2.10	0.49
21:D:75:LYS:HD3	23:K:22:VAL:HG12	1.95	0.49
21:D:123:VAL:HG12	21:D:127:MET:CE	2.36	0.49
22:F:85:ARG:C	22:F:87:ALA:N	2.68	0.49
22:F:186:PHE:CD2	22:F:187:ARG:HG2	2.48	0.49
36:m:66:GLY:HA2	36:m:79:GLN:O	2.12	0.49
39:j:246:SER:O	39:j:250:LYS:HG2	2.13	0.49
43:g:212:SER:N	43:g:217:LEU:O	2.42	0.49
1:2:292:U:H2'	1:2:293:C:C6	2.48	0.49
1:2:387:G:OP2	1:2:422:G:O2'	2.31	0.49
1:2:1628:U:HO2'	1:2:1762:C:HO2'	1.59	0.49
8:I:78:ILE:HG23	8:I:102:VAL:HG21	1.95	0.49
15:X:102:VAL:HG23	15:X:127:VAL:HG12	1.93	0.49
15:X:107:PHE:HB2	15:X:121:ARG:O	2.13	0.49
21:D:161:GLY:O	21:D:164:VAL:HG12	2.13	0.49
23:K:29:GLN:NE2	23:K:31:LYS:O	2.37	0.49
33:d:52:PHE:C	33:d:53:TYR:HD1	2.21	0.49
36:m:65:ASN:O	36:m:81:GLN:HG2	2.12	0.49
39:j:204:ALA:HB1	39:j:251:ILE:HG13	1.95	0.49
40:k:342:ILE:HD12	40:k:396:ILE:HD12	1.95	0.49
1:2:72:A:OP1	1:2:72:A:H4'	2.13	0.49
1:2:854:A:O2'	1:2:855:A:H3'	2.13	0.49
1:2:1000:A:H2'	1:2:1001:G:C8	2.48	0.49
1:2:1218:A:H4'	23:K:47:GLN:HE22	1.75	0.49
1:2:1295:A:OP1	2:A:138:TYR:OH	2.26	0.49
1:2:1323:G:H4'	2:A:113:ARG:NH1	2.28	0.49
1:2:1492:C:H2'	1:2:1493:C:C6	2.47	0.49
3:B:33:LYS:O	3:B:98:THR:HG22	2.12	0.49
8:I:103:GLN:O	8:I:104:ILE:HD13	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:4:GLU:C	10:L:5:LEU:HD23	2.38	0.49
12:O:71:CYS:HB3	12:O:76:ILE:HB	1.95	0.49
16:Y:3:ASP:OD1	16:Y:32:ARG:HD2	2.13	0.49
16:Y:103:ALA:O	16:Y:108:ARG:NH1	2.45	0.49
22:F:139:ILE:HD11	22:F:174:ILE:HG13	1.95	0.49
25:P:108:ARG:H	25:P:111:MET:HG2	1.78	0.49
35:i:29:LYS:HB2	35:i:33:GLN:O	2.13	0.49
43:g:10:LEU:HD11	43:g:318:ARG:HB3	1.95	0.49
43:g:302:SER:HB3	43:g:307:THR:OG1	2.13	0.49
1:2:357:U:H2'	1:2:359:A:H8	1.76	0.49
1:2:563:G:H1	1:2:579:A:P	2.36	0.49
1:2:578:A:O2'	1:2:579:A:H5''	2.13	0.49
1:2:1316:C:H2'	1:2:1317:G:O4'	2.13	0.49
1:2:1353:G:H1'	1:2:1370:G:N2	2.28	0.49
1:2:1439:C:O2'	1:2:1445:C:N4	2.46	0.49
2:A:121:VAL:HG13	2:A:143:VAL:HG12	1.94	0.49
6:G:7:TYR:HD1	6:G:113:ILE:HG23	1.77	0.49
14:W:90:THR:OG1	14:W:94:LEU:HD12	2.13	0.49
15:X:62:LYS:NZ	15:X:118:PRO:CA	2.76	0.49
15:X:65:ASN:ND2	15:X:116:ASP:OD2	2.44	0.49
17:a:41:ILE:HG13	17:a:41:ILE:O	2.12	0.49
18:b:74:SER:HB3	18:b:77:THR:HG23	1.95	0.49
25:P:81:ARG:HB3	25:P:117:GLY:HA3	1.95	0.49
34:f:131:ALA:O	34:f:137:PHE:HA	2.12	0.49
39:j:170:LYS:HA	39:j:173:ILE:HG12	1.95	0.49
1:2:430:C:H2'	1:2:431:G:C8	2.48	0.48
1:2:1249:U:H5'	1:2:1250:U:OP2	2.12	0.48
1:2:1290:G:H1	1:2:1323:G:H22	1.61	0.48
1:2:1290:G:H22	1:2:1323:G:N2	2.11	0.48
1:2:1720:A:H5''	6:G:75:LEU:HD11	1.94	0.48
2:A:33:GLN:OE1	13:V:64:GLU:OE2	2.30	0.48
3:B:82:ARG:HG3	3:B:83:LYS:H	1.78	0.48
23:K:5:LYS:HD2	23:K:8:ARG:HH12	1.78	0.48
24:M:71:LEU:HD22	34:f:106:TYR:CE2	2.48	0.48
27:R:34:LEU:HD23	27:R:37:GLU:OE2	2.12	0.48
41:l:259:CYS:HB3	41:l:263:GLY:H	1.78	0.48
1:2:53:G:O3'	16:Y:110:GLN:OE1	2.31	0.48
1:2:446:U:O3'	5:E:11:ARG:NH2	2.46	0.48
1:2:705:U:H2'	1:2:706:A:H8	1.78	0.48
1:2:932:A:OP2	17:a:37:LYS:HE3	2.12	0.48
1:2:1344:A:O3'	30:U:53:LYS:NZ	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1730:A:H2'	1:2:1731:C:H6	1.77	0.48
2:A:88:LYS:HE2	2:A:202:TYR:CD1	2.48	0.48
6:G:64:LYS:HB2	6:G:97:VAL:HG21	1.95	0.48
21:D:184:ILE:C	21:D:184:ILE:CD1	2.85	0.48
27:R:17:ILE:CD1	27:R:58:MET:HE1	2.37	0.48
35:i:75:ASP:OD1	35:i:76:ILE:N	2.46	0.48
40:k:359:ILE:HB	40:k:371:LYS:HB2	1.95	0.48
1:2:194:G:H2'	1:2:195:G:H5'	1.94	0.48
1:2:926:C:H2'	1:2:927:U:C6	2.48	0.48
1:2:1612:A:OP2	22:F:86:LYS:NZ	2.46	0.48
1:2:1726:U:H2'	1:2:1727:C:C6	2.48	0.48
4:C:61:ILE:HD13	4:C:66:LEU:HD23	1.95	0.48
10:L:54:ILE:HG23	10:L:55:ASP:N	2.26	0.48
13:V:15:ARG:HH11	13:V:33:GLN:HE21	1.60	0.48
21:D:17:PHE:HE1	21:D:77:PHE:CE2	2.31	0.48
22:F:75:THR:O	22:F:77:GLY:N	2.41	0.48
33:d:33:LYS:HG2	33:d:34:TYR:CD2	2.49	0.48
39:j:104:LYS:HD2	39:j:142:TYR:CG	2.49	0.48
1:2:78:A:H8	6:G:154:ARG:HG3	1.77	0.48
1:2:200:G:H2'	1:2:201:A:C8	2.49	0.48
1:2:736:C:O2'	1:2:737:A:O5'	2.31	0.48
1:2:760:A:C2	1:2:761:G:H1'	2.48	0.48
1:2:789:U:C5	1:2:790:A:C5	3.01	0.48
1:2:884:G:N2	12:O:123:SER:OG	2.43	0.48
1:2:1019:A:OP1	11:N:106:ARG:NH2	2.46	0.48
1:2:1202:A:C2	1:2:1554:A:C4	3.02	0.48
1:2:1519:G:O2'	1:2:1521:G:OP2	2.18	0.48
1:2:1611:U:H3'	22:F:86:LYS:NZ	2.29	0.48
2:A:50:VAL:O	2:A:53:THR:OG1	2.22	0.48
2:A:54:TRP:CZ3	2:A:58:VAL:HB	2.48	0.48
4:C:58:ILE:HD12	4:C:62:PHE:HE2	1.79	0.48
6:G:49:VAL:HG12	6:G:115:LYS:H	1.78	0.48
9:J:106:GLU:O	9:J:111:THR:OG1	2.26	0.48
11:N:71:ILE:H	11:N:71:ILE:HD12	1.79	0.48
14:W:77:PRO:O	14:W:79:PHE:N	2.46	0.48
21:D:21:LEU:HD21	21:D:48:ILE:CD1	2.43	0.48
27:R:93:LEU:HG	27:R:98:ASP:OD1	2.13	0.48
35:i:48:GLU:C	35:i:48:GLU:OE1	2.57	0.48
39:j:248:ILE:HD13	39:j:264:ILE:HD13	1.96	0.48
40:k:111:HIS:CD2	40:k:217:LEU:HB3	2.49	0.48
1:2:418:G:O5'	6:G:72:ARG:NH2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:861:A:H5''	11:N:16:ILE:HG21	1.94	0.48
1:2:1085:A:H8	1:2:1085:A:OP1	1.97	0.48
1:2:1431:G:C2	33:d:41:GLN:HB3	2.48	0.48
1:2:1501:A:H8	1:2:1501:A:OP1	1.97	0.48
2:A:18:LEU:HG	2:A:23:HIS:CD2	2.49	0.48
3:B:132:ASP:HB3	3:B:221:PRO:CG	2.44	0.48
9:J:15:PRO:HD3	9:J:43:TYR:CE1	2.48	0.48
10:L:80:MET:HE2	10:L:85:VAL:CG2	2.44	0.48
17:a:82:ARG:NH2	17:a:85:ARG:NH1	2.61	0.48
19:e:35:TYR:CE1	19:e:39:LEU:HD11	2.47	0.48
22:F:97:ASN:HA	22:F:100:MET:HE3	1.94	0.48
22:F:217:ASP:OD2	22:F:221:ARG:NH2	2.47	0.48
39:j:12:LYS:CA	39:j:40:ASP:OD2	2.51	0.48
40:k:101:ILE:HD11	40:k:304:VAL:HG13	1.95	0.48
1:2:740:A:H2'	1:2:741:C:O4'	2.14	0.48
1:2:1212:G:O2'	1:2:1243:A:N6	2.47	0.48
1:2:1230:U:OP2	34:f:94:LYS:NZ	2.46	0.48
1:2:1280:G:O3'	30:U:76:SER:OG	2.28	0.48
1:2:1610:U:H2'	1:2:1611:U:O4'	2.14	0.48
1:2:1687:A:H2'	1:2:1688:G:N7	2.28	0.48
1:2:1749:C:H2'	1:2:1750:U:H6	1.78	0.48
3:B:161:ILE:O	3:B:165:ARG:HG3	2.14	0.48
5:E:87:MET:O	5:E:122:LYS:HE3	2.14	0.48
5:E:163:ASP:OD1	5:E:163:ASP:N	2.44	0.48
6:G:76:LEU:HD21	6:G:92:ARG:HG2	1.95	0.48
7:H:24:PHE:CE2	7:H:77:LEU:HD11	2.49	0.48
7:H:162:ILE:HG21	7:H:169:PHE:CZ	2.45	0.48
32:c:27:GLN:HG3	32:c:65:ARG:NH1	2.28	0.48
39:j:55:ARG:HD3	39:j:56:ILE:H	1.78	0.48
43:g:171:ARG:HH12	43:g:192:SER:HA	1.79	0.48
1:2:1492:C:H2'	1:2:1493:C:H6	1.78	0.48
6:G:215:ARG:HB3	6:G:219:ARG:HH21	1.77	0.48
7:H:62:VAL:HG11	7:H:67:LEU:HD13	1.96	0.48
8:I:72:VAL:HG11	8:I:112:TRP:CZ2	2.49	0.48
8:I:191:ALA:O	8:I:194:LEU:HG	2.14	0.48
9:J:49:LEU:HA	9:J:52:ILE:HG22	1.95	0.48
25:P:100:LYS:HG3	25:P:101:VAL:N	2.29	0.48
30:U:32:LYS:HA	30:U:32:LYS:HE3	1.95	0.48
30:U:65:ILE:CG1	33:d:52:PHE:HE2	2.27	0.48
38:l:27:C:H5'	41:l:170:LYS:HZ1	1.79	0.48
39:j:7:ARG:CB	39:j:40:ASP:OD1	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:j:72:VAL:HG11	39:j:89:ARG:HB3	1.96	0.48
43:g:245:ASP:HB2	43:g:263:THR:HB	1.96	0.48
1:2:2:A:C6	4:C:175:ILE:HD12	2.48	0.48
1:2:43:A:C2	1:2:377:A:C5	3.02	0.48
1:2:780:A:H62	16:Y:10:ARG:HH21	1.62	0.48
1:2:968:C:H4'	1:2:1103:U:O2'	2.13	0.48
1:2:1180:U:H2'	1:2:1181:U:O4'	2.14	0.48
1:2:1465:C:H1'	29:T:89:ARG:HH22	1.78	0.48
1:2:1549:U:H2'	1:2:1550:U:C6	2.49	0.48
1:2:1754:A:N6	35:i:66:ARG:O	2.47	0.48
2:A:167:LYS:CE	2:A:204:TYR:H	2.26	0.48
7:H:134:GLU:CD	11:N:21:ASN:ND2	2.72	0.48
12:O:103:ARG:NH2	17:a:48:ALA:C	2.72	0.48
26:Q:14:LYS:HB2	26:Q:76:SER:HB2	1.96	0.48
27:R:25:THR:O	27:R:58:MET:HG3	2.14	0.48
29:T:22:LEU:HD22	29:T:28:LEU:HD11	1.96	0.48
1:2:616:U:H2'	1:2:617:U:O2	2.13	0.48
1:2:860:U:O3'	11:N:20:ARG:NH2	2.43	0.48
1:2:1513:A:O2'	1:2:1514:A:OP1	2.26	0.48
1:2:1636:G:O6	1:2:1765:G:N2	2.46	0.48
1:2:1738:A:H2'	1:2:1739:U:C6	2.49	0.48
3:B:29:TRP:HE3	3:B:45:LYS:HG2	1.79	0.48
5:E:86:PHE:CD1	5:E:86:PHE:C	2.91	0.48
7:H:117:THR:HG23	7:H:120:ALA:H	1.77	0.48
8:I:43:ILE:HD11	8:I:55:PHE:HB3	1.95	0.48
8:I:186:GLU:OE1	10:L:23:PRO:HG2	2.14	0.48
25:P:81:ARG:HB3	25:P:117:GLY:CA	2.44	0.48
28:S:66:LEU:HD13	28:S:69:ILE:HD11	1.94	0.48
1:2:945:U:H5''	3:B:165:ARG:NH1	2.28	0.48
1:2:1169:G:C2	1:2:1170:A:C8	3.01	0.48
1:2:1549:U:H2'	1:2:1550:U:H6	1.79	0.48
1:2:1552:U:H2'	1:2:1553:A:O4'	2.14	0.48
1:2:1582:G:N2	1:2:1609:A:OP2	2.40	0.48
5:E:105:VAL:HG12	5:E:243:GLY:HA2	1.96	0.48
9:J:101:VAL:HG22	9:J:105:LEU:HD23	1.95	0.48
9:J:108:ARG:NH2	9:J:110:GLN:OE1	2.37	0.48
13:V:62:ARG:HH12	14:W:20:THR:HG22	1.78	0.48
16:Y:18:LEU:HA	16:Y:85:PHE:HE2	1.78	0.48
38:1:53:G:H2'	38:1:54:A:H8	1.79	0.48
39:j:226:PRO:HG3	40:k:408:ARG:HD3	1.95	0.48
1:2:163:A:H5'	6:G:112:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:430:C:H2'	1:2:431:G:H8	1.79	0.47
1:2:623:G:H2'	1:2:624:C:C6	2.48	0.47
1:2:1102:U:H2'	1:2:1103:U:C6	2.49	0.47
1:2:1353:G:H1'	1:2:1370:G:C2	2.49	0.47
2:A:64:ILE:HG23	2:A:73:VAL:HG21	1.97	0.47
3:B:99:ASN:OD1	3:B:100:PHE:N	2.48	0.47
10:L:33:ARG:NH1	10:L:48:ALA:O	2.46	0.47
16:Y:62:THR:HA	16:Y:69:SER:HA	1.95	0.47
21:D:91:VAL:HG21	21:D:94:ARG:HB3	1.96	0.47
26:Q:9:THR:HB	26:Q:87:LYS:HG2	1.94	0.47
30:U:53:LYS:HB2	30:U:92:ASP:OD1	2.14	0.47
35:i:68:LYS:HZ3	35:i:68:LYS:HB2	1.78	0.47
38:1:10:2MG:N2	38:1:26:M2G:H1'	2.29	0.47
41:l:138:PHE:O	41:l:141:ILE:HG22	2.14	0.47
1:2:15:U:H2'	1:2:16:G:O4'	2.14	0.47
1:2:383:G:H2'	1:2:384:A:H8	1.79	0.47
1:2:586:C:H5'	19:e:24:GLN:OE1	2.13	0.47
1:2:992:A:OP1	1:2:1775:G:N2	2.46	0.47
1:2:1535:C:H5''	1:2:1570:2MG:HN1	1.78	0.47
1:2:1559:U:H2'	1:2:1560:G:H8	1.79	0.47
1:2:1570:2MG:H8	1:2:1570:2MG:H2'	1.21	0.47
1:2:1742:A:H3'	1:2:1743:G:H8	1.79	0.47
4:C:103:PHE:O	4:C:122:THR:HA	2.14	0.47
5:E:122:LYS:NZ	5:E:143:ASP:OD2	2.37	0.47
14:W:46:TYR:HE2	14:W:130:TYR:HA	1.79	0.47
26:Q:7:VAL:HG11	26:Q:95:LYS:HG3	1.96	0.47
27:R:20:TYR:HD2	27:R:23:LYS:HD2	1.79	0.47
39:j:183:LYS:HD3	39:j:185:ARG:HD2	1.96	0.47
1:2:70:C:H2'	1:2:71:A:O4'	2.14	0.47
1:2:303:U:H2'	1:2:304:C:H6	1.80	0.47
1:2:335:G:H2'	1:2:337:C:H5	1.79	0.47
1:2:624:C:H2'	1:2:625:U:H6	1.80	0.47
1:2:967:U:H2'	1:2:968:C:O4'	2.14	0.47
11:N:119:GLU:OE1	11:N:119:GLU:HA	2.14	0.47
22:F:113:VAL:HA	22:F:116:VAL:HG12	1.96	0.47
28:S:126:ARG:NH2	28:S:133:VAL:C	2.72	0.47
32:c:16:LEU:HB2	32:c:27:GLN:HB2	1.96	0.47
40:k:95:ILE:HD11	40:k:186:VAL:O	2.14	0.47
1:2:463:A:C2	1:2:464:G:C8	3.03	0.47
1:2:691:U:N3	1:2:692:C:N4	2.62	0.47
1:2:1339:U:O4	26:Q:9:THR:HA	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1387:C:H1'	27:R:28:PHE:CZ	2.49	0.47
4:C:238:GLN:HG3	4:C:239:ALA:N	2.29	0.47
8:I:48:THR:HG21	8:I:54:LYS:HD3	1.95	0.47
11:N:46:THR:HG23	11:N:49:GLN:H	1.78	0.47
28:S:33:THR:HG22	28:S:39:GLY:C	2.39	0.47
33:d:22:ARG:NE	33:d:36:LEU:O	2.47	0.47
35:i:88:GLN:N	35:i:88:GLN:CD	2.73	0.47
39:j:21:MET:HE2	39:j:68:ASN:CB	2.45	0.47
40:k:373:ILE:HD13	40:k:406:LEU:HD23	1.96	0.47
40:k:463:MET:HB3	40:k:502:SER:OG	2.14	0.47
1:2:92:A:H5''	1:2:93:A:H5''	1.96	0.47
1:2:140:A:H61	6:G:187:LYS:HB2	1.79	0.47
1:2:760:A:C6	1:2:761:G:C4	3.03	0.47
1:2:1234:C:C2	1:2:1235:A:C8	3.03	0.47
1:2:1315:G:H2'	1:2:1316:C:C6	2.49	0.47
1:2:1482:G:H8	1:2:1482:G:OP2	1.97	0.47
1:2:1795:A:H5'	17:a:95:ARG:HH12	1.80	0.47
2:A:167:LYS:CE	2:A:204:TYR:N	2.78	0.47
14:W:22:LYS:HZ2	18:b:3:LEU:HA	1.79	0.47
17:a:23:CYS:HB3	17:a:28:ARG:H	1.79	0.47
40:k:245:ILE:HG12	40:k:279:PRO:HG2	1.97	0.47
40:k:464:VAL:HG12	40:k:466:ILE:HG13	1.96	0.47
1:2:200:G:H2'	1:2:201:A:H8	1.80	0.47
1:2:346:G:H5'	10:L:80:MET:SD	2.54	0.47
1:2:621:A:O2'	1:2:1031:G:H5'	2.15	0.47
1:2:777:C:O2'	5:E:261:LEU:O	2.32	0.47
1:2:1250:U:O2'	34:f:131:ALA:HB1	2.14	0.47
1:2:1607:U:H5''	26:Q:75:VAL:HG12	1.97	0.47
2:A:168:HIS:HA	2:A:203:PHE:CE1	2.48	0.47
3:B:58:SER:O	3:B:62:LYS:HG2	2.15	0.47
4:C:95:THR:HG22	4:C:96:ARG:N	2.30	0.47
6:G:29:ASP:O	6:G:31:ARG:NH1	2.47	0.47
10:L:111:VAL:HG23	10:L:139:VAL:HG21	1.96	0.47
21:D:24:PHE:HE2	23:K:65:TYR:CZ	2.33	0.47
22:F:156:ALA:HB1	22:F:158:ARG:HG2	1.96	0.47
22:F:215:LYS:O	22:F:219:LEU:HD23	2.14	0.47
39:j:236:ASP:HB3	39:j:238:GLN:OE1	2.14	0.47
40:k:504:ARG:HG3	40:k:509:TRP:CE3	2.49	0.47
43:g:174:PHE:CE2	43:g:186:TRP:CD1	3.00	0.47
1:2:82:U:H2'	1:2:83:G:O4'	2.13	0.47
1:2:342:C:H2'	1:2:343:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:649:U:H2'	1:2:650:G:C8	2.50	0.47
1:2:711:G:N2	1:2:727:C:N3	2.61	0.47
1:2:771:A:HO2'	9:J:6:ARG:HH21	1.60	0.47
1:2:901:G:H2'	1:2:902:U:C6	2.49	0.47
1:2:901:G:N7	12:O:24:ASN:ND2	2.62	0.47
1:2:1065:C:H2'	1:2:1066:C:H6	1.80	0.47
1:2:1427:G:O2'	30:U:72:ASN:ND2	2.47	0.47
1:2:1581:A:N1	1:2:1609:A:H5''	2.30	0.47
1:2:1606:U:O3'	26:Q:73:GLY:HA3	2.15	0.47
1:2:1710:A:H2'	1:2:1711:G:H4'	1.97	0.47
1:2:1730:A:H2'	1:2:1731:C:C6	2.50	0.47
1:2:1787:G:OP2	12:O:132:ARG:NH2	2.48	0.47
2:A:89:TYR:CE1	2:A:93:THR:HG21	2.49	0.47
8:I:42:ARG:N	8:I:59:ARG:O	2.41	0.47
11:N:113:PHE:O	11:N:116:ILE:HG22	2.15	0.47
14:W:10:ALA:HA	14:W:27:ILE:HD12	1.96	0.47
16:Y:84:LYS:HG3	16:Y:85:PHE:CD1	2.50	0.47
22:F:85:ARG:HD3	22:F:88:GLN:CG	2.45	0.47
26:Q:13:LYS:HD3	26:Q:79:TYR:HB3	1.97	0.47
26:Q:103:ASN:O	26:Q:107:LYS:HG3	2.15	0.47
30:U:25:ASN:OD1	30:U:115:GLU:HB3	2.15	0.47
30:U:32:LYS:HD2	30:U:32:LYS:N	2.30	0.47
39:j:166:LEU:HD23	39:j:169:LEU:HD21	1.96	0.47
40:k:356:ARG:NE	40:k:424:PRO:HD2	2.30	0.47
41:l:254:LEU:HB3	41:l:256:PHE:CE1	2.50	0.47
43:g:49:THR:N	43:g:55:PHE:O	2.18	0.47
43:g:171:ARG:NE	43:g:187:SER:HB2	2.30	0.47
43:g:184:ARG:HD3	43:g:186:TRP:HH2	1.78	0.47
43:g:205:TYR:OH	43:g:223:LYS:HE2	2.15	0.47
1:2:113:U:O2'	1:2:115:G:O2'	2.28	0.47
1:2:337:C:H1'	8:I:5:ARG:HB2	1.96	0.47
1:2:590:A:H2'	1:2:591:G:H8	1.79	0.47
1:2:1029:A:OP1	17:a:3:LYS:NZ	2.47	0.47
1:2:1280:G:H5''	30:U:78:THR:HG21	1.97	0.47
1:2:1386:A:H5'	1:2:1387:C:C6	2.50	0.47
1:2:1689:A:N6	1:2:1708:U:O2'	2.48	0.47
4:C:86:MET:HG2	4:C:216:LEU:HD11	1.96	0.47
22:F:65:GLN:OE1	22:F:90:PRO:HA	2.13	0.47
30:U:20:HIS:HD2	30:U:96:PRO:HA	1.80	0.47
35:i:61:ILE:HD13	35:i:91:VAL:HG21	1.96	0.47
35:i:96:ASN:ND2	35:i:99:GLU:OE1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:609:G:N2	15:X:19:ARG:HH12	2.13	0.47
1:2:899:A:H1'	1:2:914:A:C2	2.50	0.47
1:2:1171:G:H2'	1:2:1172:C:C6	2.50	0.47
1:2:1243:A:H2'	1:2:1243:A:N3	2.29	0.47
1:2:1386:A:N6	1:2:1409:A:N7	2.63	0.47
1:2:1634:C:C2	1:2:1636:G:C6	3.03	0.47
4:C:234:LEU:O	4:C:234:LEU:HD23	2.15	0.47
21:D:55:VAL:HG23	21:D:88:ALA:HB1	1.97	0.47
21:D:59:VAL:HA	21:D:66:ILE:HG23	1.95	0.47
22:F:63:TYR:CE2	22:F:167:LEU:HB2	2.50	0.47
22:F:74:HIS:CD2	22:F:109:LYS:HD3	2.49	0.47
22:F:86:LYS:HG2	22:F:94:ARG:HH22	1.80	0.47
25:P:33:PHE:O	25:P:37:ALA:N	2.47	0.47
26:Q:40:GLN:O	26:Q:42:GLU:OE1	2.33	0.47
30:U:30:LYS:HE2	30:U:33:GLN:HB2	1.97	0.47
39:j:198:ILE:HG22	39:j:202:LYS:HE3	1.97	0.47
39:j:236:ASP:C	39:j:238:GLN:OE1	2.58	0.47
39:j:244:LEU:O	39:j:248:ILE:HG13	2.15	0.47
40:k:208:ALA:HA	40:k:211:MET:HG2	1.97	0.47
40:k:249:ASN:ND2	46:k:601:GCP:O6	2.47	0.47
1:2:5:U:O2'	1:2:552:G:H4'	2.14	0.47
1:2:434:C:H2'	1:2:435:A:O4'	2.14	0.47
1:2:1198:G:H4'	1:2:1199:G:O5'	2.14	0.47
1:2:1331:C:H4'	21:D:203:PRO:HB3	1.96	0.47
2:A:57:ILE:HD11	2:A:173:ILE:HD11	1.97	0.47
4:C:46:LEU:HG	4:C:73:ILE:HD13	1.97	0.47
21:D:7:LYS:HG2	30:U:27:THR:HG21	1.96	0.47
22:F:114:ARG:HD3	26:Q:43:ILE:CD1	2.44	0.47
25:P:40:ARG:HD2	25:P:40:ARG:HA	1.69	0.47
26:Q:129:PHE:O	26:Q:137:ARG:NH1	2.43	0.47
1:2:7:G:O6	4:C:210:ARG:NH1	2.39	0.46
1:2:92:A:OP2	1:2:397:G:N1	2.45	0.46
1:2:765:G:C6	9:J:149:ARG:HG2	2.50	0.46
1:2:906:A:N3	1:2:996:G:O2'	2.40	0.46
1:2:1107:G:H4'	1:2:1108:G:H5''	1.97	0.46
1:2:1234:C:OP2	1:2:1244:G:H8	1.97	0.46
1:2:1343:A:H2'	1:2:1344:A:C8	2.50	0.46
1:2:1457:C:N4	28:S:139:LYS:HG3	2.31	0.46
1:2:1522:A:O3'	29:T:93:HIS:ND1	2.48	0.46
4:C:111:ASP:OD2	4:C:115:HIS:HD2	1.97	0.46
5:E:49:ARG:NE	5:E:50:ASN:OD1	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:18:ARG:HA	12:O:82:LYS:HB2	1.98	0.46
14:W:111:MET:CE	14:W:115:GLU:HB2	2.46	0.46
16:Y:16:PRO:HA	16:Y:19:ALA:HA	1.96	0.46
17:a:82:ARG:HH22	17:a:85:ARG:CZ	2.27	0.46
22:F:207:SER:O	22:F:213:ILE:HG21	2.15	0.46
27:R:33:ARG:HG3	43:g:128:ARG:HH11	1.75	0.46
29:T:13:ASP:OD1	29:T:13:ASP:C	2.57	0.46
39:j:190:VAL:O	40:k:405:THR:HG21	2.14	0.46
40:k:149:LYS:HE3	40:k:184:LYS:HB3	1.97	0.46
40:k:352:GLU:HB3	40:k:374:PHE:CZ	2.49	0.46
1:2:911:U:H2'	3:B:9:LEU:HD21	1.97	0.46
6:G:147:LEU:CD1	6:G:156:TYR:CD2	2.98	0.46
9:J:123:HIS:NE2	19:e:37:ARG:HG3	2.29	0.46
11:N:70:LYS:O	11:N:74:ILE:HG12	2.14	0.46
11:N:88:LEU:O	11:N:92:ILE:HG12	2.15	0.46
18:b:31:HIS:O	18:b:48:SER:OG	2.25	0.46
22:F:68:LYS:NZ	22:F:88:GLN:O	2.48	0.46
22:F:74:HIS:CD2	26:Q:79:TYR:OH	2.68	0.46
23:K:3:ILE:CG2	23:K:8:ARG:HE	2.15	0.46
25:P:28:MET:SD	25:P:29:PRO:HD2	2.55	0.46
29:T:6:VAL:HG13	29:T:14:PHE:CE2	2.50	0.46
35:i:68:LYS:HB2	35:i:68:LYS:HE2	1.57	0.46
39:j:203:ASP:OD1	39:j:204:ALA:N	2.48	0.46
40:k:512:ILE:HG13	40:k:513:GLY:N	2.31	0.46
41:l:170:LYS:HG2	41:l:170:LYS:O	2.15	0.46
1:2:886:A:H2'	1:2:887:U:H6	1.81	0.46
1:2:1097:U:P	4:C:173:ARG:HH12	2.37	0.46
1:2:1544:G:H5'	28:S:123:ARG:NH1	2.31	0.46
5:E:120:SER:O	5:E:164:LEU:HB3	2.15	0.46
12:O:103:ARG:HE	17:a:49:ALA:CB	2.29	0.46
17:a:4:LYS:HG3	17:a:5:ARG:CD	2.45	0.46
25:P:28:MET:HE3	25:P:32:ASP:HB3	1.96	0.46
27:R:28:PHE:HA	27:R:55:THR:HG21	1.97	0.46
28:S:112:ASP:HA	28:S:115:ARG:NE	2.31	0.46
41:l:131:TYR:CE2	41:l:135:LEU:HD11	2.50	0.46
43:g:187:SER:HB3	43:g:196:GLU:OE2	2.16	0.46
1:2:519:A:H3'	1:2:520:A:H8	1.80	0.46
1:2:686:C:H4'	14:W:118:ARG:NH1	2.31	0.46
1:2:958:U:H5''	11:N:15:ALA:O	2.14	0.46
1:2:1047:G:O3'	18:b:69:GLY:HA3	2.16	0.46
1:2:1064:A:OP1	3:B:160:HIS:NE2	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1199:G:H3'	1:2:1199:G:P	2.55	0.46
1:2:1364:C:H2'	1:2:1365:C:C6	2.50	0.46
1:2:1374:C:H2'	1:2:1375:U:C6	2.51	0.46
1:2:1431:G:H2'	1:2:1432:U:C6	2.51	0.46
1:2:1551:G:H4'	33:d:14:PHE:CE2	2.51	0.46
1:2:1756:U:H2'	1:2:1757:C:H6	1.80	0.46
4:C:87:ASN:HB2	4:C:212:LEU:HD23	1.98	0.46
10:L:111:VAL:HA	10:L:139:VAL:HG22	1.97	0.46
11:N:142:GLU:HG2	11:N:143:SER:N	2.30	0.46
12:O:13:VAL:N	12:O:77:THR:OG1	2.48	0.46
21:D:163:PRO:HD3	21:D:203:PRO:HG2	1.97	0.46
22:F:115:ILE:O	22:F:119:THR:HG23	2.16	0.46
29:T:9:VAL:HG23	29:T:10:PRO:HD2	1.92	0.46
29:T:89:ARG:NH1	29:T:90:PRO:HD3	2.31	0.46
31:Z:91:PRO:HA	31:Z:101:TYR:HD1	1.81	0.46
35:i:87:ASP:HB3	35:i:88:GLN:OE1	2.16	0.46
39:j:22:VAL:HG12	39:j:36:LEU:HD23	1.98	0.46
40:k:84:PHE:HB3	40:k:309:PHE:CD2	2.51	0.46
43:g:10:LEU:HB2	43:g:320:TRP:CE2	2.50	0.46
1:2:141:U:P	6:G:139:ASN:HD21	2.38	0.46
1:2:163:A:H1'	6:G:13:GLN:HE21	1.80	0.46
1:2:181:A:H2'	1:2:182:U:C6	2.51	0.46
1:2:330:A:OP2	8:I:176:GLN:NE2	2.49	0.46
1:2:1056:U:H5''	3:B:202:LYS:HE3	1.97	0.46
1:2:1226:A:O4'	1:2:1255:A:N6	2.47	0.46
1:2:1233:A:C2	34:f:138:TYR:HE2	2.34	0.46
1:2:1240:G:O3'	25:P:77:ARG:NH1	2.46	0.46
1:2:1251:C:OP1	34:f:118:ARG:NH1	2.47	0.46
1:2:1495:U:C2	1:2:1496:G:C8	3.03	0.46
1:2:1526:U:H5'	22:F:110:LEU:HD11	1.97	0.46
6:G:44:GLU:HA	6:G:119:GLN:HE21	1.80	0.46
11:N:49:GLN:HA	11:N:52:VAL:HG12	1.98	0.46
12:O:133:ARG:HH21	12:O:136:ARG:CZ	2.29	0.46
21:D:136:VAL:HG23	21:D:184:ILE:CD1	2.45	0.46
22:F:45:PHE:HB2	22:F:48:TRP:CZ3	2.50	0.46
33:d:36:LEU:HB3	33:d:38:ILE:HG12	1.97	0.46
43:g:308:LEU:O	43:g:319:VAL:HA	2.15	0.46
1:2:211:U:H2'	1:2:212:A:H8	1.79	0.46
1:2:643:U:H2'	1:2:644:C:H6	1.80	0.46
1:2:921:G:H2'	1:2:922:A:C8	2.49	0.46
1:2:1293:G:H1	1:2:1302:U:H3	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1573:7MG:O2'	1:2:1574:A:O4'	2.33	0.46
1:2:1679:A:H8	6:G:65:GLN:HG3	1.81	0.46
5:E:44:LEU:HD21	5:E:70:VAL:HG11	1.98	0.46
14:W:40:VAL:HG11	14:W:103:ILE:HD12	1.96	0.46
16:Y:46:GLU:C	16:Y:46:GLU:OE1	2.59	0.46
26:Q:109:PHE:HD1	26:Q:116:LEU:HD13	1.80	0.46
29:T:109:GLU:OE2	29:T:122:ARG:HG2	2.15	0.46
30:U:99:ILE:O	30:U:102:ARG:HG2	2.15	0.46
31:Z:79:ALA:O	31:Z:83:LEU:HG	2.16	0.46
35:i:87:ASP:CA	35:i:88:GLN:OE1	2.63	0.46
39:j:156:GLU:C	39:j:156:GLU:OE1	2.59	0.46
43:g:30:GLN:HE22	43:g:78:GLY:CA	2.28	0.46
1:2:210:U:OP1	10:L:20:PHE:HB2	2.16	0.46
1:2:267:C:H3'	6:G:186:ARG:NH2	2.31	0.46
1:2:284:G:H2'	1:2:285:C:C6	2.51	0.46
1:2:385:G:H2'	1:2:386:A:C8	2.50	0.46
1:2:880:A:N1	1:2:947:G:C6	2.83	0.46
1:2:959:U:H2'	1:2:960:U:H6	1.80	0.46
1:2:1086:A:OP2	1:2:1086:A:H8	1.97	0.46
1:2:1460:G:H2'	1:2:1461:C:C6	2.50	0.46
1:2:1471:U:O2	22:F:105:ASN:ND2	2.41	0.46
1:2:1556:U:H5''	1:2:1557:A:H4'	1.96	0.46
1:2:1737:C:H2'	1:2:1738:A:C8	2.49	0.46
3:B:27:LYS:HD2	3:B:47:LEU:CD2	2.46	0.46
5:E:86:PHE:CZ	5:E:87:MET:HE3	2.49	0.46
11:N:36:GLN:O	11:N:39:LYS:HG2	2.16	0.46
22:F:210:SER:HB3	22:F:213:ILE:HG22	1.98	0.46
27:R:71:PHE:O	27:R:74:GLN:HG2	2.15	0.46
35:i:71:MET:HA	35:i:94:LYS:HZ3	1.80	0.46
39:j:36:LEU:HD12	39:j:42:ILE:HG22	1.96	0.46
39:j:52:SER:O	39:j:88:ARG:NH2	2.49	0.46
40:k:128:PHE:O	40:k:132:LEU:HB2	2.15	0.46
40:k:133:GLU:HB3	41:l:256:PHE:HE2	1.81	0.46
40:k:140:LEU:HD23	40:k:140:LEU:H	1.81	0.46
40:k:359:ILE:O	40:k:370:CYS:HA	2.15	0.46
1:2:223:C:H2'	1:2:224:A:H8	1.81	0.46
1:2:643:U:H2'	1:2:644:C:C6	2.50	0.46
1:2:978:A:H4'	1:2:1784:G:H21	1.81	0.46
1:2:1622:C:H2'	1:2:1623:C:H6	1.81	0.46
1:2:1716:A:H2'	1:2:1717:A:H8	1.80	0.46
1:2:1736:U:H2'	1:2:1737:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:39:GLU:HG3	6:G:46:LYS:CE	2.44	0.46
8:I:27:PHE:CD1	8:I:28:GLU:HG3	2.51	0.46
11:N:45:LEU:HD23	11:N:49:GLN:HB3	1.97	0.46
12:O:84:ARG:HG2	12:O:85:ALA:O	2.15	0.46
15:X:107:PHE:CD2	15:X:114:LYS:HB3	2.51	0.46
17:a:4:LYS:NZ	17:a:92:ARG:NH2	2.64	0.46
22:F:167:LEU:O	22:F:171:ASN:ND2	2.49	0.46
23:K:88:PRO:HD2	23:K:91:TYR:CD2	2.48	0.46
30:U:65:ILE:O	30:U:81:THR:HA	2.15	0.46
34:f:130:LEU:HG	34:f:137:PHE:HB3	1.98	0.46
1:2:328:G:H5''	8:I:98:LYS:HB3	1.97	0.46
1:2:358:A:N7	15:X:38:PHE:HE2	2.14	0.46
1:2:494:C:H3'	1:2:495:G:C8	2.51	0.46
1:2:697:C:O2'	1:2:699:U:OP1	2.32	0.46
1:2:914:A:N3	1:2:914:A:H2'	2.31	0.46
1:2:1660:G:H2'	1:2:1661:G:H8	1.81	0.46
2:A:121:VAL:HG12	2:A:142:PRO:O	2.16	0.46
12:O:104:ALA:O	12:O:108:SER:HB2	2.15	0.46
29:T:131:ASP:O	29:T:135:ILE:HG12	2.15	0.46
43:g:304:ASP:OD1	43:g:305:GLY:N	2.49	0.46
1:2:331:U:O2'	8:I:5:ARG:NH2	2.49	0.46
1:2:576:G:H1'	35:i:64:LYS:HD3	1.98	0.46
1:2:700:C:HO2'	1:2:701:U:P	2.39	0.46
1:2:960:U:H2'	1:2:961:C:C6	2.51	0.46
1:2:998:PSU:O5'	1:2:998:PSU:H6	1.99	0.46
1:2:1108:G:H1	1:2:1135:U:H3	1.64	0.46
1:2:1220:A:H2'	1:2:1221:C:C6	2.51	0.46
1:2:1590:A:H2'	1:2:1591:A:C8	2.51	0.46
4:C:58:ILE:HD11	4:C:115:HIS:CE1	2.51	0.46
4:C:106:VAL:HG13	4:C:120:ILE:HG22	1.97	0.46
8:I:167:TYR:HB3	8:I:185:LEU:HD12	1.98	0.46
12:O:51:ASP:OD1	12:O:51:ASP:O	2.34	0.46
14:W:11:LEU:HD12	14:W:72:CYS:HB2	1.98	0.46
21:D:122:VAL:O	21:D:126:VAL:HG23	2.16	0.46
22:F:138:ALA:HB1	22:F:203:ALA:HB3	1.98	0.46
24:M:28:SER:HB2	24:M:33:GLY:HA3	1.98	0.46
26:Q:40:GLN:N	26:Q:41:PRO:CD	2.77	0.46
27:R:33:ARG:HD3	27:R:33:ARG:HA	1.69	0.46
28:S:36:ARG:HG3	28:S:105:LEU:HD23	1.98	0.46
32:c:29:ARG:HH21	32:c:40:ILE:C	2.24	0.46
34:f:138:TYR:CE1	34:f:143:HIS:HA	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:649:U:O2'	1:2:650:G:OP1	2.19	0.45
1:2:701:U:H3	1:2:737:A:H2	1.64	0.45
1:2:816:A:H2'	1:2:817:C:C6	2.51	0.45
1:2:861:A:H4'	1:2:862:A:O5'	2.16	0.45
1:2:917:U:H5''	12:O:18:ARG:HD3	1.98	0.45
1:2:933:C:C4	1:2:1076:C:H4'	2.51	0.45
1:2:1078:U:OP1	17:a:93:ARG:NH2	2.50	0.45
1:2:1415:A:O2'	26:Q:125:GLU:OE2	2.30	0.45
1:2:1557:A:O5'	28:S:135:GLY:HA3	2.16	0.45
1:2:1794:C:OP2	17:a:92:ARG:HD3	2.16	0.45
4:C:131:ARG:O	4:C:134:ILE:HG22	2.16	0.45
14:W:10:ALA:CA	14:W:27:ILE:HD12	2.46	0.45
22:F:29:THR:HG23	26:Q:28:LEU:HD12	1.99	0.45
34:f:100:LEU:HB3	34:f:103:LEU:HD23	1.98	0.45
34:f:124:CYS:SG	34:f:141:LYS:CG	3.04	0.45
43:g:250:LEU:HA	43:g:260:THR:O	2.17	0.45
1:2:273:G:H2'	1:2:274:C:C6	2.52	0.45
1:2:460:G:OP1	9:J:2:PRO:HG2	2.16	0.45
1:2:977:A:C4	1:2:978:A:C8	3.04	0.45
1:2:1100:G:H5''	14:W:76:SER:HB3	1.98	0.45
1:2:1659:U:H2'	1:2:1660:G:C8	2.51	0.45
2:A:154:GLU:HB3	2:A:155:TYR:HD1	1.81	0.45
7:H:80:GLU:HA	7:H:83:LYS:HD2	1.99	0.45
17:a:46:GLU:HG2	17:a:48:ALA:H	1.81	0.45
22:F:118:HIS:HA	22:F:121:GLU:OE2	2.15	0.45
22:F:123:ILE:HG13	22:F:197:ALA:HB1	1.97	0.45
32:c:19:THR:CG2	32:c:27:GLN:NE2	2.70	0.45
36:m:28:ILE:HD11	36:m:105:ILE:HG23	1.97	0.45
40:k:198:ASP:OD1	40:k:199:ILE:HD12	2.16	0.45
40:k:215:LEU:HD23	40:k:245:ILE:HB	1.98	0.45
43:g:148:HIS:NE2	43:g:184:ARG:HD2	2.32	0.45
1:2:677:G:H2'	1:2:678:G:C8	2.52	0.45
1:2:1395:U:O2'	1:2:1398:A:N6	2.47	0.45
1:2:1522:A:H2'	1:2:1523:A:C8	2.52	0.45
2:A:89:TYR:CD1	2:A:89:TYR:C	2.92	0.45
2:A:127:ARG:CZ	2:A:152:PRO:HD3	2.47	0.45
5:E:36:HIS:ND1	5:E:85:GLY:HA3	2.31	0.45
7:H:44:LYS:HA	7:H:44:LYS:HE3	1.98	0.45
8:I:64:ASN:HB2	8:I:181:ASP:OD1	2.16	0.45
11:N:141:TYR:HE1	11:N:146:ALA:HB2	1.82	0.45
19:e:23:LYS:HD3	19:e:23:LYS:HA	1.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:K:13:GLN:OE1	23:K:17:GLN:NE2	2.49	0.45
26:Q:49:TYR:O	26:Q:52:LEU:HG	2.15	0.45
26:Q:99:GLU:OE1	26:Q:103:ASN:ND2	2.49	0.45
32:c:9:LEU:HD12	32:c:54:LEU:O	2.16	0.45
33:d:42:SER:HA	33:d:45:GLU:HG3	1.99	0.45
34:f:141:LYS:HA	34:f:141:LYS:HD2	1.36	0.45
40:k:286:GLN:HB3	41:l:262:CYS:HB2	1.98	0.45
43:g:62:TYR:CE2	43:g:93:TRP:HB3	2.52	0.45
43:g:157:VAL:HA	43:g:174:PHE:HB3	1.99	0.45
1:2:28:A:C6	1:2:29:U:C4	3.05	0.45
1:2:467:A:N1	1:2:593:A:O2'	2.37	0.45
1:2:594:G:H2'	1:2:595:C:H6	1.81	0.45
1:2:1061:A:H2'	1:2:1062:U:O4'	2.16	0.45
1:2:1205:U:H2'	1:2:1206:C:C5	2.51	0.45
1:2:1292:U:H1'	2:A:111:ILE:HD12	1.98	0.45
1:2:1417:G:H2'	1:2:1418:C:C6	2.51	0.45
1:2:1554:A:H1'	1:2:1558:U:OP2	2.17	0.45
3:B:105:PHE:HE1	3:B:213:ARG:CA	2.27	0.45
4:C:40:TRP:HH2	4:C:50:VAL:HG13	1.81	0.45
4:C:166:LYS:HG3	4:C:171:SER:HB3	1.99	0.45
5:E:23:LEU:HD12	9:J:3:ARG:NH2	2.31	0.45
5:E:183:VAL:HG11	5:E:188:ASN:HB2	1.98	0.45
8:I:103:GLN:HA	8:I:166:LEU:O	2.16	0.45
9:J:28:LEU:HD23	19:e:43:ARG:HD2	1.98	0.45
12:O:80:HIS:HA	12:O:113:GLY:O	2.15	0.45
22:F:82:LYS:HB2	22:F:85:ARG:HB3	1.99	0.45
28:S:64:GLU:HA	28:S:67:GLU:OE1	2.16	0.45
41:l:241:SER:OG	41:l:243:ASN:ND2	2.40	0.45
43:g:173:THR:HA	43:g:186:TRP:O	2.16	0.45
1:2:86:A:H2'	1:2:87:C:H6	1.82	0.45
1:2:358:A:N7	15:X:38:PHE:CE2	2.84	0.45
1:2:381:C:C2	1:2:382:G:C8	3.04	0.45
1:2:473:A:N6	1:2:593:A:H5'	2.31	0.45
1:2:659:G:O6	1:2:660:A:N6	2.50	0.45
1:2:787:A:C2	5:E:19:MET:HE2	2.52	0.45
1:2:1031:G:H2'	1:2:1032:C:H6	1.81	0.45
1:2:1623:C:H2'	1:2:1624:U:C6	2.50	0.45
3:B:156:ALA:HB3	3:B:161:ILE:HD11	1.99	0.45
3:B:205:PHE:CG	3:B:206:PRO:HD2	2.52	0.45
4:C:49:LEU:HD11	4:C:248:TYR:HB2	1.97	0.45
8:I:3:ILE:HB	8:I:30:GLY:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:a:70:LYS:HD3	17:a:72:HIS:HE2	1.81	0.45
26:Q:125:GLU:OE1	26:Q:125:GLU:C	2.59	0.45
33:d:36:LEU:O	33:d:38:ILE:HG23	2.17	0.45
36:m:33:ARG:HG2	36:m:34:ASN:H	1.81	0.45
39:j:167:ASP:O	39:j:170:LYS:HG2	2.17	0.45
43:g:20:TRP:HD1	43:g:313:THR:C	2.24	0.45
1:2:747:C:O3'	14:W:80:ASN:ND2	2.49	0.45
1:2:884:G:H2'	1:2:885:U:C6	2.52	0.45
1:2:1146:A:O2'	1:2:1634:C:OP2	2.33	0.45
1:2:1246:U:OP1	34:f:92:ARG:HA	2.16	0.45
3:B:179:SER:HB2	3:B:183:GLN:HB2	1.98	0.45
4:C:152:ASN:O	13:V:4:ASP:HB3	2.17	0.45
5:E:260:GLY:C	5:E:261:LEU:HD12	2.42	0.45
6:G:1:MET:HE3	6:G:109:LEU:HD23	1.99	0.45
8:I:196:ARG:O	8:I:200:LYS:HG2	2.17	0.45
11:N:36:GLN:NE2	11:N:40:TYR:CE2	2.84	0.45
15:X:56:LYS:HD2	15:X:93:LEU:HD21	1.99	0.45
24:M:25:LEU:HD13	24:M:92:ALA:HA	1.99	0.45
25:P:98:ASN:OD1	25:P:122:THR:HA	2.16	0.45
38:1:64:RIA:H2A	38:1:65:G:H8	1.81	0.45
1:2:1040:G:H2'	1:2:1041:G:C8	2.51	0.45
1:2:1319:U:O2'	1:2:1321:A:OP1	2.19	0.45
4:C:58:ILE:HD12	4:C:62:PHE:CE2	2.51	0.45
5:E:17:HIS:HB2	5:E:108:ARG:HA	1.99	0.45
8:I:90:LEU:HB3	8:I:95:THR:HB	1.99	0.45
9:J:80:LEU:HA	9:J:83:ILE:HG22	1.99	0.45
9:J:93:LEU:C	9:J:96:VAL:HG12	2.42	0.45
10:L:17:PRO:O	10:L:19:ILE:HD12	2.17	0.45
12:O:69:ALA:HA	12:O:72:LYS:HG2	1.99	0.45
26:Q:16:ALA:HB2	26:Q:72:GLY:HA3	1.97	0.45
26:Q:100:GLN:HA	26:Q:103:ASN:HD22	1.82	0.45
32:c:10:ALA:HB2	32:c:32:PHE:CD1	2.50	0.45
35:i:59:ALA:HA	35:i:89:CYS:O	2.17	0.45
35:i:87:ASP:C	35:i:88:GLN:CD	2.82	0.45
39:j:104:LYS:HD2	39:j:142:TYR:CD2	2.51	0.45
40:k:213:ALA:HB1	40:k:302:ILE:HD13	1.99	0.45
40:k:356:ARG:NH2	40:k:423:LEU:HD23	2.31	0.45
40:k:430:ILE:HG13	40:k:485:LEU:HB2	1.99	0.45
1:2:300:A:H4'	8:I:27:PHE:CE1	2.51	0.45
1:2:325:G:H2'	1:2:326:U:H6	1.79	0.45
1:2:380:C:H1'	1:2:756:A:C2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1069:C:O2'	18:b:17:ARG:HD3	2.16	0.45
1:2:1167:U:H2'	1:2:1168:G:C8	2.51	0.45
1:2:1329:G:C2	1:2:1330:A:H1'	2.52	0.45
1:2:1350:G:H2'	1:2:1351:U:C6	2.51	0.45
1:2:1586:G:N2	1:2:1606:U:O2	2.44	0.45
2:A:154:GLU:HB3	2:A:155:TYR:CD1	2.51	0.45
6:G:151:ASP:OD2	6:G:156:TYR:HE2	2.00	0.45
7:H:33:GLU:CD	7:H:33:GLU:N	2.75	0.45
17:a:51:ARG:NH1	17:a:55:GLU:OE1	2.50	0.45
23:K:3:ILE:CG2	23:K:8:ARG:NH2	2.68	0.45
23:K:40:LEU:HB3	23:K:44:LYS:HZ2	1.82	0.45
25:P:111:MET:HE2	28:S:119:ILE:HG13	1.99	0.45
41:l:228:ARG:HA	41:l:231:LEU:HG	1.99	0.45
1:2:289:G:H3'	1:2:290:G:H8	1.82	0.45
1:2:1248:U:H3'	1:2:1249:U:C6	2.52	0.45
1:2:1559:U:H2'	1:2:1560:G:C8	2.52	0.45
1:2:1741:U:H2'	1:2:1742:A:C8	2.51	0.45
3:B:90:GLU:OE1	3:B:97:LEU:HB2	2.17	0.45
3:B:108:ASP:OD2	17:a:65:PRO:CG	2.65	0.45
3:B:133:TYR:CE2	3:B:181:LEU:HB3	2.52	0.45
4:C:70:GLU:HB3	4:C:72:GLN:OE1	2.17	0.45
9:J:136:VAL:CG2	9:J:156:ILE:CD1	2.87	0.45
13:V:4:ASP:OD1	13:V:5:LYS:N	2.48	0.45
14:W:75:ILE:O	14:W:75:ILE:HG22	2.16	0.45
21:D:20:GLU:O	21:D:23:GLU:HG3	2.17	0.45
28:S:66:LEU:O	28:S:69:ILE:HG13	2.16	0.45
28:S:126:ARG:HG2	28:S:131:LEU:HB2	1.99	0.45
35:i:65:LEU:O	35:i:65:LEU:HD23	2.16	0.45
36:m:65:ASN:H	36:m:81:GLN:HG3	1.81	0.45
36:m:70:LYS:NZ	36:m:72:PRO:HA	2.32	0.45
39:j:155:TRP:HE3	39:j:158:ILE:HD11	1.82	0.45
40:k:347:PHE:O	40:k:390:ALA:N	2.50	0.45
43:g:80:TYR:HB3	43:g:92:LEU:HD11	1.99	0.45
43:g:243:ALA:O	43:g:268:LYS:NZ	2.44	0.45
1:2:116:U:H2'	1:2:117:U:C6	2.52	0.45
1:2:393:C:C4	1:2:394:U:C4	3.05	0.45
1:2:842:U:H2'	1:2:843:A:C8	2.52	0.45
1:2:967:U:H1'	1:2:1102:U:O2'	2.17	0.45
1:2:1077:C:H2'	1:2:1078:U:C6	2.51	0.45
1:2:1181:U:H4'	25:P:124:THR:OG1	2.17	0.45
1:2:1688:G:N2	1:2:1689:A:N1	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:163:ASN:OD1	2:A:165:ARG:N	2.49	0.45
7:H:13:PRO:HD2	7:H:17:GLU:OE2	2.17	0.45
7:H:70:TYR:CE2	7:H:92:PHE:HE2	2.35	0.45
14:W:94:LEU:HD13	14:W:100:GLY:O	2.17	0.45
21:D:162:GLN:N	21:D:163:PRO:HD2	2.31	0.45
22:F:25:VAL:HB	22:F:36:GLN:HE21	1.81	0.45
26:Q:50:GLU:N	26:Q:51:PRO:CD	2.80	0.45
35:i:57:ARG:NH1	35:i:81:LEU:HD22	2.31	0.45
40:k:106:ILE:HD13	40:k:236:ILE:HD12	1.98	0.45
1:2:138:A:O2'	6:G:187:LYS:NZ	2.45	0.44
1:2:431:G:H2'	1:2:432:C:C6	2.52	0.44
1:2:756:A:C4	1:2:757:A:C8	3.05	0.44
1:2:1038:A:O2'	1:2:1039:G:H8	2.00	0.44
1:2:1523:A:N3	1:2:1587:C:O2'	2.45	0.44
1:2:1794:C:C2	17:a:5:ARG:HG3	2.52	0.44
8:I:78:ILE:HG23	8:I:102:VAL:CG2	2.47	0.44
10:L:14:GLN:HB3	10:L:54:ILE:HG12	1.99	0.44
17:a:36:ILE:O	17:a:36:ILE:HG13	2.17	0.44
18:b:23:THR:OG1	18:b:25:VAL:O	2.35	0.44
21:D:76:ARG:NE	21:D:76:ARG:O	2.49	0.44
22:F:93:GLU:O	22:F:96:THR:OG1	2.28	0.44
22:F:97:ASN:HA	22:F:100:MET:HE2	1.99	0.44
22:F:137:ASP:O	22:F:141:ASN:ND2	2.50	0.44
26:Q:125:GLU:HG2	26:Q:126:PRO:HD2	1.98	0.44
28:S:17:LEU:O	28:S:20:THR:OG1	2.28	0.44
29:T:18:TYR:HD1	29:T:135:ILE:HG13	1.82	0.44
30:U:55:PRO:HA	30:U:91:ILE:HG12	1.99	0.44
30:U:64:LYS:HA	30:U:82:TYR:O	2.16	0.44
36:m:85:ARG:NH1	36:m:107:GLY:HA2	2.31	0.44
39:j:8:PHE:HE1	39:j:108:VAL:HG11	1.81	0.44
39:j:190:VAL:HG12	39:j:262:CYS:SG	2.56	0.44
40:k:79:PRO:HG2	40:k:82:PRO:HG3	1.99	0.44
1:2:155:A:O2'	1:2:156:A:O5'	2.30	0.44
1:2:721:U:H4'	1:2:722:G:C8	2.52	0.44
1:2:958:U:OP2	18:b:20:LYS:NZ	2.49	0.44
1:2:1385:G:N7	27:R:44:LYS:NZ	2.60	0.44
1:2:1403:G:H2'	1:2:1404:A:H8	1.83	0.44
1:2:1435:U:H2'	1:2:1436:G:H8	1.81	0.44
1:2:1544:G:H5'	28:S:123:ARG:HH12	1.81	0.44
1:2:1601:U:H2'	1:2:1602:U:C6	2.52	0.44
3:B:127:VAL:HG13	3:B:176:VAL:HG11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:151:ASP:OD2	5:E:153:ASN:OD1	2.36	0.44
6:G:21:GLU:O	6:G:24:VAL:HG12	2.17	0.44
7:H:162:ILE:HG23	7:H:162:ILE:HD12	1.60	0.44
12:O:49:LYS:HD3	39:j:91:SER:N	2.32	0.44
21:D:116:ARG:HD3	21:D:150:MET:HE1	1.99	0.44
23:K:14:HIS:CE1	23:K:34:GLU:OE1	2.70	0.44
36:m:55:LEU:O	36:m:59:LYS:HG2	2.16	0.44
43:g:230:TRP:CD1	43:g:237:ALA:HA	2.50	0.44
43:g:260:THR:HG23	43:g:301:TRP:CZ2	2.52	0.44
1:2:99:C:OP2	1:2:377:A:O2'	2.24	0.44
1:2:253:A:H2'	1:2:254:U:C6	2.52	0.44
1:2:477:A:OP1	19:e:37:ARG:NH2	2.50	0.44
1:2:816:A:H2'	1:2:817:C:H6	1.82	0.44
1:2:916:U:C3'	1:2:917:U:H5'	2.47	0.44
1:2:1065:C:C2	1:2:1066:C:C5	3.05	0.44
1:2:1065:C:H4'	3:B:149:GLN:HG2	1.99	0.44
1:2:1587:C:H2'	1:2:1588:G:C8	2.52	0.44
1:2:1717:A:H2'	1:2:1718:G:O4'	2.16	0.44
1:2:1735:G:H2'	1:2:1736:U:C6	2.53	0.44
9:J:117:GLY:O	9:J:118:LEU:HB2	2.18	0.44
12:O:20:PHE:O	12:O:27:PHE:N	2.38	0.44
12:O:29:HIS:CE1	12:O:38:THR:HB	2.53	0.44
21:D:121:GLY:O	21:D:124:ARG:HG2	2.17	0.44
26:Q:30:LYS:HD2	26:Q:34:SER:C	2.42	0.44
27:R:17:ILE:HD13	27:R:58:MET:CE	2.43	0.44
38:l:53:G:H2'	38:l:54:A:C8	2.52	0.44
39:j:96:ILE:O	39:j:99:GLU:HG2	2.17	0.44
1:2:10:G:C4	1:2:11:A:C8	3.06	0.44
1:2:661:C:H4'	1:2:662:U:O4'	2.17	0.44
1:2:843:A:H2'	1:2:844:G:H8	1.79	0.44
1:2:955:C:H2'	1:2:956:G:H8	1.82	0.44
21:D:64:ARG:O	21:D:67:ASN:HB2	2.18	0.44
41:l:167:ARG:NH2	41:l:217:PHE:O	2.50	0.44
43:g:183:VAL:HB	43:g:199:PHE:HB2	1.98	0.44
1:2:218:A:C6	1:2:842:U:H1'	2.53	0.44
1:2:220:A:H2'	1:2:221:A:H8	1.83	0.44
1:2:263:G:H5''	1:2:264:A:H5'	1.99	0.44
1:2:592:U:H3'	9:J:38:ASN:ND2	2.33	0.44
1:2:880:A:H2'	1:2:881:U:O4'	2.17	0.44
1:2:958:U:O4'	11:N:17:PRO:HD3	2.18	0.44
1:2:1488:A:OP1	21:D:9:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:33:GLU:OE2	9:J:33:GLU:HA	2.18	0.44
9:J:65:LYS:HA	9:J:65:LYS:HD3	1.74	0.44
22:F:65:GLN:NE2	22:F:68:LYS:HG2	2.33	0.44
22:F:123:ILE:HB	22:F:131:PRO:HB3	2.00	0.44
27:R:100:LEU:O	27:R:120:SER:OG	2.34	0.44
37:3:27[B]:A:H8	37:3:27[B]:A:OP2	2.01	0.44
40:k:104:GLY:HA3	40:k:211:MET:SD	2.58	0.44
40:k:314:ARG:HH21	40:k:343:LEU:HB2	1.83	0.44
1:2:179:A:H2'	1:2:180:A:O4'	2.18	0.44
1:2:196:A:H61	8:I:139:ASN:HD22	1.65	0.44
1:2:220:A:C6	1:2:840:U:C4	3.05	0.44
1:2:387:G:C6	1:2:409:A:C6	3.06	0.44
1:2:654:G:O6	1:2:676:U:O2	2.36	0.44
1:2:919:U:H1'	12:O:36:ARG:HH22	1.83	0.44
1:2:1357:G:H5'	29:T:126:ASP:OD1	2.18	0.44
3:B:91:VAL:HG12	3:B:93:GLY:H	1.83	0.44
4:C:115:HIS:HE1	13:V:11:LEU:HD11	1.81	0.44
5:E:35:PRO:HB2	5:E:36:HIS:CD2	2.52	0.44
7:H:143:LEU:HA	14:W:49:GLU:OE2	2.18	0.44
18:b:20:LYS:O	18:b:21:LEU:HB2	2.18	0.44
20:h:22:ALA:HA	20:h:25:LYS:HG2	2.00	0.44
23:K:46:LEU:HD13	23:K:66:TYR:CD2	2.53	0.44
27:R:14:LYS:O	27:R:18:GLU:HG2	2.17	0.44
35:i:37:GLN:NE2	35:i:76:ILE:CD1	2.81	0.44
39:j:14:PRO:HG3	39:j:39:TYR:CD2	2.53	0.44
39:j:134:LEU:HD23	39:j:144:ALA:CB	2.46	0.44
1:2:91:G:H2'	1:2:92:A:O4'	2.18	0.44
1:2:277:U:O5'	1:2:278:G:N2	2.51	0.44
1:2:1067:C:H2'	1:2:1068:A:C8	2.53	0.44
1:2:1144:U:H4'	4:C:93:LYS:HZ2	1.83	0.44
1:2:1340:A:H4'	43:g:91:ARG:HH22	1.82	0.44
1:2:1398:A:H2'	1:2:1399:A:C8	2.53	0.44
4:C:216:LEU:HA	4:C:216:LEU:HD23	1.83	0.44
5:E:102:VAL:HG21	5:E:239:PRO:HD3	1.99	0.44
7:H:62:VAL:HG13	7:H:63:PRO:HD2	2.00	0.44
11:N:102:LEU:HD23	11:N:102:LEU:HA	1.84	0.44
14:W:7:LEU:HG	14:W:11:LEU:HD23	1.99	0.44
22:F:205:LYS:HG3	22:F:207:SER:H	1.81	0.44
24:M:44:ALA:O	24:M:50:GLY:N	2.50	0.44
24:M:50:GLY:O	24:M:76:ASN:ND2	2.50	0.44
26:Q:38:LEU:O	26:Q:39:VAL:O	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:43:ILE:HD12	26:Q:43:ILE:H	1.83	0.44
27:R:52:GLY:O	27:R:55:THR:OG1	2.33	0.44
27:R:102:VAL:HB	27:R:106:THR:HG21	1.99	0.44
35:i:78:LEU:HB3	35:i:93:HIS:HB3	1.99	0.44
39:j:56:ILE:HD11	39:j:59:ILE:HG13	2.00	0.44
43:g:14:LEU:O	43:g:316:VAL:HB	2.17	0.44
1:2:90:C:O2'	1:2:450:A:H5''	2.17	0.44
1:2:157:U:O2'	1:2:158:U:H5'	2.18	0.44
1:2:228:U:H2'	1:2:229:C:C6	2.53	0.44
1:2:808:G:H2'	1:2:809:G:C8	2.53	0.44
1:2:1056:U:C4	1:2:1059:U:H5''	2.52	0.44
1:2:1066:C:C2	1:2:1067:C:C5	3.06	0.44
1:2:1169:G:H21	1:2:1569:C:H4'	1.83	0.44
1:2:1247:C:OP2	34:f:93:HIS:ND1	2.51	0.44
1:2:1646:A:C2	1:2:1751:A:C2	3.06	0.44
2:A:7:PHE:HA	2:A:191:ARG:HH22	1.82	0.44
2:A:147:THR:HG21	2:A:159:ALA:HB1	2.00	0.44
2:A:175:TYR:CD2	2:A:199:PRO:HA	2.53	0.44
3:B:105:PHE:HZ	3:B:211:HIS:HB3	1.82	0.44
8:I:143:LYS:HB3	8:I:147:ARG:NH1	2.33	0.44
11:N:115:LEU:O	11:N:119:GLU:HG2	2.18	0.44
15:X:43:PHE:HE1	15:X:49:ALA:CB	2.31	0.44
30:U:63:LEU:HD12	33:d:34:TYR:CZ	2.53	0.44
41:l:236:CYS:HB2	41:l:239:CYS:SG	2.55	0.44
1:2:472:A:H2'	1:2:473:A:O4'	2.18	0.44
1:2:1101:G:H2'	1:2:1102:U:O4'	2.17	0.44
1:2:1681:U:H2'	1:2:1682:U:O4'	2.17	0.44
2:A:163:ASN:HB3	2:A:169:SER:CB	2.48	0.44
3:B:39:GLU:OE1	3:B:39:GLU:N	2.42	0.44
5:E:42:LEU:HD21	5:E:47:PHE:HB2	2.00	0.44
5:E:148:ARG:HH11	6:G:201:GLN:NE2	2.16	0.44
6:G:149:LYS:HA	6:G:149:LYS:HD3	1.87	0.44
17:a:12:LYS:HG3	17:a:13:LYS:H	1.81	0.44
24:M:96:LYS:O	24:M:103:ALA:HB3	2.18	0.44
28:S:65:GLU:O	28:S:69:ILE:HG12	2.18	0.44
28:S:88:ARG:HE	28:S:91:ASP:HB2	1.83	0.44
28:S:113:LEU:O	28:S:117:LYS:HG3	2.18	0.44
28:S:113:LEU:C	28:S:117:LYS:HZ3	2.25	0.44
31:Z:75:LEU:C	31:Z:75:LEU:HD12	2.43	0.44
32:c:10:ALA:HA	32:c:32:PHE:HA	2.00	0.44
43:g:94:ASN:ND2	43:g:97:THR:OG1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:14:C:H5'	4:C:169:SER:OG	2.18	0.43
1:2:107:C:H5''	1:2:382:G:O2'	2.18	0.43
1:2:221:A:OP2	1:2:832:U:H1'	2.17	0.43
1:2:594:G:H2'	1:2:595:C:C6	2.53	0.43
1:2:914:A:H3'	1:2:915:U:C6	2.53	0.43
1:2:1548:A:C6	1:2:1560:G:C6	3.05	0.43
1:2:1671:G:H2'	1:2:1672:C:C6	2.53	0.43
8:I:65:PHE:HA	8:I:182:GLY:O	2.18	0.43
9:J:140:ILE:HG21	16:Y:65:GLY:HA3	2.00	0.43
15:X:62:LYS:NZ	15:X:118:PRO:N	2.66	0.43
16:Y:16:PRO:C	16:Y:19:ALA:H	2.26	0.43
21:D:192:PRO:HG2	21:D:202:LEU:HD12	2.00	0.43
22:F:75:THR:C	22:F:77:GLY:N	2.76	0.43
22:F:119:THR:HG22	22:F:193:ALA:O	2.17	0.43
23:K:9:LYS:HZ3	23:K:13:GLN:HG2	1.83	0.43
25:P:83:MET:CE	25:P:116:LEU:HD22	2.48	0.43
26:Q:87:LYS:HA	26:Q:90:VAL:HG22	1.99	0.43
27:R:34:LEU:O	27:R:37:GLU:HG2	2.17	0.43
27:R:58:MET:O	27:R:62:GLN:HG2	2.18	0.43
35:i:82:ARG:HD2	35:i:84:PHE:CZ	2.53	0.43
40:k:320:SER:OG	40:k:409:ALA:O	2.23	0.43
43:g:30:GLN:HG2	43:g:30:GLN:O	2.18	0.43
1:2:114:C:N4	1:2:244:U:O2	2.51	0.43
1:2:328:G:N3	1:2:329:G:C8	2.86	0.43
1:2:565:C:OP2	35:i:62:ARG:NH2	2.47	0.43
1:2:1105:U:H2'	1:2:1106:G:C8	2.53	0.43
1:2:1317:G:H2'	1:2:1318:A:C8	2.54	0.43
1:2:1652:G:H22	1:2:1743:G:H2'	1.83	0.43
12:O:30:VAL:HG11	12:O:71:CYS:SG	2.57	0.43
17:a:15:ARG:O	17:a:17:HIS:N	2.46	0.43
22:F:195:THR:O	22:F:198:GLU:HG3	2.18	0.43
29:T:39:THR:HA	29:T:100:ILE:HD13	2.00	0.43
30:U:72:ASN:OD1	30:U:73:GLY:N	2.51	0.43
35:i:38:ILE:HG23	35:i:47:VAL:HG13	2.00	0.43
38:l:71:C:H2'	38:l:72:U:H6	1.83	0.43
40:k:163:SER:HB3	40:k:295:ASN:OD1	2.19	0.43
41:l:247:LYS:HD2	41:l:258:VAL:HG21	2.00	0.43
43:g:25:SER:HB3	43:g:74:VAL:HG13	2.00	0.43
43:g:94:ASN:HB2	43:g:101:GLU:OE2	2.18	0.43
1:2:98:U:H2'	1:2:99:C:C6	2.53	0.43
1:2:106:U:H2'	1:2:107:C:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1241:A:P	25:P:77:ARG:HH12	2.41	0.43
1:2:1732:U:H2'	1:2:1733:U:C6	2.54	0.43
1:2:1733:U:H2'	1:2:1734:G:O4'	2.19	0.43
2:A:170:ILE:O	2:A:173:ILE:HG22	2.18	0.43
3:B:105:PHE:CZ	3:B:211:HIS:HB3	2.53	0.43
7:H:75:ILE:O	7:H:78:THR:OG1	2.28	0.43
12:O:70:LYS:O	12:O:74:VAL:HG23	2.18	0.43
14:W:111:MET:HE2	14:W:116:ALA:CA	2.48	0.43
15:X:90:ASP:HB3	19:e:12:GLY:HA2	2.01	0.43
21:D:48:ILE:HG23	21:D:86:LEU:HA	2.00	0.43
27:R:71:PHE:CE1	27:R:74:GLN:HB3	2.53	0.43
32:c:8:THR:OG1	32:c:56:LEU:O	2.33	0.43
33:d:21:CYS:HB3	33:d:25:GLY:N	2.31	0.43
34:f:138:TYR:HE1	34:f:143:HIS:HA	1.83	0.43
38:1:72:U:H3'	38:1:73:A:H8	1.83	0.43
40:k:104:GLY:HA2	40:k:192:VAL:O	2.18	0.43
1:2:257:C:H2'	1:2:258:U:C6	2.53	0.43
1:2:1227:G:H5''	1:2:1228:G:C8	2.53	0.43
1:2:1437:C:H2'	1:2:1438:C:H6	1.82	0.43
1:2:1585:A:H2'	1:2:1586:G:H8	1.84	0.43
1:2:1585:A:O2'	22:F:106:ASN:OD1	2.36	0.43
1:2:1607:U:H2'	1:2:1608:G:O4'	2.19	0.43
4:C:175:ILE:CG1	4:C:202:TYR:HB2	2.49	0.43
11:N:54:LEU:HD13	11:N:58:HIS:CD2	2.53	0.43
16:Y:20:ARG:NH1	16:Y:76:TYR:OH	2.46	0.43
21:D:209:ILE:H	21:D:209:ILE:HD12	1.83	0.43
24:M:87:GLN:O	24:M:91:TRP:CD1	2.71	0.43
31:Z:95:HIS:HB3	31:Z:98:GLN:NE2	2.30	0.43
35:i:55:ASN:ND2	35:i:57:ARG:HE	2.16	0.43
37:3:28[A]:A:O2'	37:3:29[A]:A:O4'	2.28	0.43
43:g:221:ALA:HB1	43:g:247:VAL:CG1	2.48	0.43
1:2:13:C:H5''	4:C:211:THR:HG21	2.00	0.43
1:2:71:A:H5''	1:2:72:A:OP2	2.18	0.43
1:2:262:C:H2'	1:2:263:G:C8	2.53	0.43
1:2:687:C:H5'	14:W:119:LYS:NZ	2.33	0.43
1:2:1290:G:H1	1:2:1323:G:H1	1.65	0.43
1:2:1332:C:H1'	21:D:162:GLN:CD	2.43	0.43
1:2:1380:A:O2'	1:2:1381:G:H8	2.01	0.43
1:2:1643:G:H2'	1:2:1644:C:C6	2.53	0.43
2:A:63:ILE:HG22	2:A:120:LEU:HD11	2.01	0.43
2:A:179:ARG:HD3	2:A:183:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:104:ASP:OD1	5:E:110:ALA:HB2	2.18	0.43
7:H:24:PHE:HE2	7:H:77:LEU:HD11	1.83	0.43
10:L:16:GLN:CB	10:L:19:ILE:HD13	2.48	0.43
12:O:18:ARG:HG2	12:O:18:ARG:O	2.18	0.43
13:V:32:VAL:HG12	13:V:55:LEU:HB2	2.01	0.43
17:a:10:ARG:HA	17:a:34:LYS:HB2	2.00	0.43
21:D:72:LEU:O	21:D:75:LYS:HG3	2.17	0.43
21:D:99:VAL:O	21:D:103:GLU:HG2	2.18	0.43
22:F:111:LYS:O	22:F:115:ILE:HG12	2.18	0.43
25:P:57:MET:HE3	25:P:57:MET:O	2.18	0.43
26:Q:118:ILE:HD12	26:Q:118:ILE:HA	1.70	0.43
35:i:41:MET:SD	35:i:41:MET:O	2.77	0.43
40:k:466:ILE:HG12	40:k:499:ILE:HG12	2.01	0.43
43:g:20:TRP:CD1	43:g:313:THR:C	2.95	0.43
43:g:93:TRP:CD1	43:g:100:SER:HA	2.51	0.43
43:g:185:SER:O	43:g:196:GLU:HB2	2.18	0.43
1:2:79:C:OP1	6:G:159:ARG:NH2	2.52	0.43
1:2:152:G:H2'	1:2:153:G:H8	1.83	0.43
1:2:208:U:H2'	1:2:209:A:H8	1.84	0.43
1:2:452:U:H2'	1:2:453:U:H5''	2.00	0.43
1:2:989:C:H2'	1:2:990:G:O4'	2.19	0.43
1:2:1006:5MC:O3'	12:O:135:ARG:NH1	2.52	0.43
1:2:1347:A:H2'	1:2:1348:G:H8	1.83	0.43
1:2:1391:C:O2'	1:2:1392:G:H5'	2.19	0.43
1:2:1396:U:H3'	1:2:1397:C:H5'	1.99	0.43
1:2:1540:G:N2	1:2:1567:A:OP2	2.47	0.43
1:2:1659:U:H2'	1:2:1660:G:H8	1.83	0.43
1:2:1673:C:H2'	1:2:1674:U:O4'	2.19	0.43
1:2:1683:G:C6	1:2:1715:G:C6	3.06	0.43
3:B:132:ASP:O	3:B:132:ASP:OD1	2.36	0.43
4:C:178:PRO:HG3	9:J:57:ARG:HE	1.82	0.43
6:G:186:ARG:O	6:G:189:GLN:HG3	2.19	0.43
8:I:154:GLU:OE2	8:I:156:ALA:HB3	2.18	0.43
15:X:38:PHE:CD1	15:X:38:PHE:C	2.92	0.43
22:F:117:LYS:HA	22:F:120:LEU:HD12	2.00	0.43
29:T:78:LYS:HG3	29:T:93:HIS:NE2	2.33	0.43
40:k:98:GLN:HE22	40:k:391:VAL:H	1.65	0.43
40:k:117:VAL:HG21	40:k:193:ASP:OD1	2.19	0.43
40:k:218:ILE:HD13	40:k:266:ILE:HD12	2.01	0.43
1:2:3:U:C6	4:C:184:VAL:HG13	2.54	0.43
1:2:307:C:OP1	10:L:103:ARG:NH1	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:751:G:N3	1:2:752:A:C8	2.87	0.43
1:2:978:A:N3	1:2:1773:U:O2'	2.51	0.43
1:2:995:U:H2'	1:2:996:G:C8	2.54	0.43
1:2:1044:C:N3	1:2:1073:G:N1	2.67	0.43
1:2:1119:U:H2'	1:2:1120:C:C6	2.53	0.43
1:2:1501:A:H2'	1:2:1502:G:C8	2.53	0.43
2:A:18:LEU:HA	2:A:23:HIS:CD2	2.54	0.43
2:A:26:ALA:HB2	2:A:149:LEU:HD22	2.01	0.43
4:C:147:GLY:HA3	4:C:160:ALA:HA	1.99	0.43
6:G:49:VAL:O	6:G:113:ILE:HD12	2.17	0.43
7:H:85:PHE:HB3	7:H:88:ARG:HD3	2.01	0.43
7:H:130:VAL:HG13	7:H:130:VAL:O	2.18	0.43
7:H:134:GLU:CD	11:N:21:ASN:HD21	2.26	0.43
14:W:66:ASN:HB3	14:W:68:ARG:HG3	2.01	0.43
22:F:45:PHE:HB3	22:F:117:LYS:HE3	2.01	0.43
24:M:126:ILE:HG23	24:M:130:HIS:CE1	2.53	0.43
26:Q:45:ARG:HG3	26:Q:49:TYR:CD2	2.53	0.43
29:T:108:LEU:HB3	29:T:114:VAL:CG2	2.48	0.43
35:i:96:ASN:N	35:i:99:GLU:OE2	2.43	0.43
38:l:7:G:O2'	38:l:49:5MC:O5'	2.32	0.43
40:k:311:ILE:HG21	40:k:344:ASN:HB2	2.00	0.43
43:g:52:GLU:OE1	43:g:53:GLN:N	2.52	0.43
43:g:89:THR:HG22	43:g:105:VAL:HG12	2.01	0.43
43:g:145:LEU:HD23	43:g:145:LEU:C	2.44	0.43
43:g:164:ASP:HA	43:g:167:VAL:N	2.33	0.43
1:2:284:G:H2'	1:2:285:C:H6	1.84	0.43
1:2:497:G:H1'	1:2:499:C:H41	1.84	0.43
1:2:631:U:P	10:L:102:LYS:HZ1	2.42	0.43
1:2:646:G:C6	1:2:688:G:C6	3.07	0.43
1:2:785:C:H2'	1:2:786:G:O4'	2.19	0.43
1:2:1203:A:N3	1:2:1203:A:H2'	2.34	0.43
1:2:1379:U:O4	1:2:1380:A:N6	2.50	0.43
1:2:1460:G:H2'	1:2:1461:C:H6	1.83	0.43
2:A:84:ARG:NH2	27:R:82:ASP:O	2.51	0.43
4:C:158:SER:OG	4:C:159:LEU:N	2.52	0.43
6:G:142:ARG:HD2	6:G:149:LYS:NZ	2.34	0.43
8:I:4:SER:OG	8:I:24:LYS:HD3	2.19	0.43
8:I:143:LYS:HB3	8:I:147:ARG:HH12	1.82	0.43
8:I:165:ARG:HA	8:I:165:ARG:HD3	1.88	0.43
9:J:83:ILE:HD11	9:J:147:MET:HG2	2.01	0.43
36:m:95:GLN:CD	36:m:96:LEU:N	2.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:j:16:ILE:HD12	39:j:16:ILE:HA	1.70	0.43
39:j:236:ASP:HB3	39:j:238:GLN:NE2	2.33	0.43
41:l:244:THR:HB	41:l:266:ARG:HH22	1.83	0.43
1:2:366:A:H2'	1:2:367:U:O4'	2.19	0.43
1:2:625:U:H2'	1:2:626:C:H6	1.83	0.43
1:2:813:A:C8	1:2:815:G:C8	3.07	0.43
1:2:946:U:O2'	1:2:947:G:H8	2.01	0.43
1:2:1203:A:C8	1:2:1553:A:N1	2.86	0.43
1:2:1239:U:H1'	1:2:1243:A:H2	1.84	0.43
1:2:1387:C:H6	27:R:28:PHE:CE2	2.37	0.43
1:2:1502:G:OP1	29:T:98:GLY:N	2.52	0.43
1:2:1739:U:H2'	1:2:1740:U:H6	1.83	0.43
1:2:1750:U:H2'	1:2:1751:A:C8	2.54	0.43
2:A:9:LEU:HD21	2:A:14:ALA:HB2	2.01	0.43
2:A:18:LEU:HG	2:A:23:HIS:HD2	1.83	0.43
3:B:124:ASN:OD1	3:B:125:VAL:N	2.52	0.43
6:G:7:TYR:CE2	6:G:9:ILE:HB	2.53	0.43
6:G:204:ALA:O	6:G:207:GLU:HG2	2.19	0.43
15:X:43:PHE:CE1	15:X:49:ALA:HB3	2.51	0.43
19:e:56:MET:HE3	19:e:56:MET:HB2	1.67	0.43
21:D:54:LYS:O	21:D:58:VAL:HG23	2.18	0.43
22:F:50:PHE:CE2	22:F:69:PRO:HA	2.52	0.43
25:P:90:ILE:HD11	25:P:109:PRO:HG3	2.01	0.43
34:f:116:LYS:HZ3	34:f:119:LYS:C	2.27	0.43
34:f:121:CYS:HB3	34:f:128:ILE:HG23	2.00	0.43
39:j:54:ARG:O	39:j:55:ARG:C	2.48	0.43
39:j:236:ASP:CB	39:j:238:GLN:OE1	2.67	0.43
40:k:105:THR:OG1	40:k:193:ASP:OD1	2.35	0.43
43:g:308:LEU:C	43:g:319:VAL:HG23	2.43	0.43
1:2:30:G:H4'	15:X:131:SER:HB3	2.01	0.43
1:2:760:A:C6	1:2:789:U:O4	2.72	0.43
1:2:833:G:H2'	1:2:834:U:C6	2.53	0.43
1:2:873:C:H2'	1:2:874:G:C8	2.53	0.43
1:2:1084:G:H5'	1:2:1085:A:OP2	2.19	0.43
1:2:1240:G:H5''	25:P:77:ARG:HG2	2.01	0.43
1:2:1279:C:H5'	33:d:44:ARG:NH1	2.31	0.43
1:2:1443:G:C4	34:f:89:LYS:HE2	2.54	0.43
5:E:108:ARG:H	5:E:108:ARG:HG2	1.59	0.43
10:L:42:PHE:CD2	10:L:140:LEU:HD23	2.54	0.43
25:P:18:LYS:NZ	28:S:90:LYS:O	2.51	0.43
28:S:114:GLU:HA	28:S:117:LYS:HZ3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:104:LYS:NZ	35:i:111:GLU:HA	2.34	0.43
38:1:11:C:H2'	38:1:12:G:H8	1.81	0.43
39:j:212:SER:OG	39:j:217:GLN:HA	2.19	0.43
40:k:172:PRO:HD2	40:k:183:TYR:HB2	2.01	0.43
1:2:24:U:OP1	9:J:10:LYS:NZ	2.33	0.42
1:2:69:G:H2'	1:2:70:C:C6	2.54	0.42
1:2:278:G:C6	1:2:280:G:C6	3.07	0.42
1:2:396:A:H4'	8:I:50:GLY:HA2	2.00	0.42
1:2:969:A:H2'	1:2:970:A:H5'	2.01	0.42
1:2:1025:A:H4'	1:2:1027:C:C5	2.54	0.42
1:2:1206:C:H4'	1:2:1207:A:O5'	2.19	0.42
1:2:1713:G:H2'	1:2:1714:C:C6	2.53	0.42
2:A:70:PRO:HB2	2:A:94:GLY:HA3	2.01	0.42
2:A:208:GLU:O	2:A:212:GLN:HG2	2.19	0.42
3:B:27:LYS:HD3	3:B:49:ASN:HA	2.00	0.42
5:E:66:MET:HE3	5:E:66:MET:HB2	1.87	0.42
6:G:7:TYR:CD2	6:G:10:ASN:HB2	2.53	0.42
6:G:31:ARG:HD2	6:G:101:ILE:HG13	2.01	0.42
7:H:70:TYR:O	7:H:74:GLN:N	2.52	0.42
9:J:29:LYS:NZ	19:e:44:PHE:CE1	2.87	0.42
16:Y:57:VAL:HB	16:Y:60:PHE:CE1	2.53	0.42
23:K:32:HIS:N	23:K:37:THR:O	2.29	0.42
25:P:28:MET:CE	25:P:32:ASP:HB3	2.49	0.42
29:T:100:ILE:HG13	29:T:101:ASN:N	2.35	0.42
33:d:21:CYS:SG	33:d:23:ILE:HB	2.59	0.42
38:1:76:A:N3	40:k:337:VAL:HG21	2.34	0.42
40:k:102:ASN:OD1	40:k:394:GLY:HA2	2.19	0.42
40:k:364:ASP:OD1	40:k:364:ASP:N	2.51	0.42
43:g:11:ARG:HB3	43:g:55:PHE:HZ	1.82	0.42
43:g:36:SER:HG	43:g:46:TRP:HE1	1.59	0.42
43:g:136:ASN:ND2	43:g:140:ASP:OD1	2.52	0.42
1:2:14:C:OP1	4:C:169:SER:OG	2.18	0.42
1:2:707:A:N6	1:2:730:G:H1	2.13	0.42
1:2:740:A:OP2	10:L:43:LYS:HE2	2.19	0.42
1:2:899:A:C5	1:2:900:G:C2	3.06	0.42
1:2:1165:A:H2'	1:2:1166:G:O4'	2.19	0.42
1:2:1386:A:C6	1:2:1409:A:N7	2.86	0.42
1:2:1511:G:O2'	1:2:1513:A:N3	2.45	0.42
1:2:1582:G:N9	26:Q:122:ARG:HD2	2.35	0.42
8:I:47:ARG:HH12	8:I:51:GLY:H	1.67	0.42
21:D:72:LEU:HD23	23:K:20:VAL:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:D:177:LEU:HD23	21:D:179:GLN:HE21	1.84	0.42
22:F:60:LEU:O	22:F:64:ILE:HG12	2.19	0.42
22:F:95:LEU:HD23	22:F:174:ILE:HG23	2.01	0.42
25:P:89:MET:O	25:P:92:SER:OG	2.24	0.42
1:2:88:U:C2	1:2:89:G:C8	3.07	0.42
1:2:104:A:N6	1:2:307:C:O4'	2.53	0.42
1:2:367:U:O2'	1:2:602:U:O2'	2.28	0.42
1:2:506:U:H3'	1:2:507:U:H5''	2.01	0.42
1:2:855:A:N6	7:H:96:ARG:HB3	2.34	0.42
1:2:1295:A:H2'	1:2:1296:G:O4'	2.18	0.42
1:2:1348:G:O2'	1:2:1377:C:N3	2.37	0.42
3:B:86:LEU:HD13	3:B:98:THR:HG21	2.02	0.42
3:B:134:VAL:HG12	3:B:218:LEU:HB2	2.01	0.42
4:C:63:LEU:HD23	4:C:63:LEU:HA	1.90	0.42
8:I:171:SER:H	8:I:182:GLY:HA2	1.85	0.42
10:L:75:VAL:HG23	10:L:84:ILE:HG23	2.01	0.42
15:X:87:VAL:HG13	15:X:132:LEU:HD21	2.01	0.42
15:X:107:PHE:CD1	15:X:123:LYS:HG3	2.54	0.42
22:F:85:ARG:HA	22:F:85:ARG:HE	1.85	0.42
22:F:181:ALA:N	22:F:199:GLU:OE1	2.52	0.42
23:K:33:GLU:O	23:K:34:GLU:HG3	2.19	0.42
24:M:56:VAL:HG23	24:M:59:VAL:HG13	2.01	0.42
26:Q:67:VAL:HG11	26:Q:81:ILE:HG23	2.01	0.42
28:S:69:ILE:O	28:S:73:MET:N	2.48	0.42
29:T:116:ILE:HD12	29:T:116:ILE:H	1.84	0.42
30:U:22:ILE:HD13	30:U:100:VAL:HG11	2.00	0.42
30:U:99:ILE:O	30:U:103:ILE:HG12	2.19	0.42
32:c:50:GLU:OE2	32:c:50:GLU:N	2.53	0.42
33:d:22:ARG:NH2	33:d:36:LEU:O	2.52	0.42
34:f:130:LEU:HD12	34:f:139:CYS:CA	2.50	0.42
36:m:54:ILE:O	36:m:58:LEU:HG	2.19	0.42
38:1:39:C:HO2'	39:j:57:ARG:NH2	2.18	0.42
38:1:44:A:O2'	38:1:45:U:O4'	2.33	0.42
1:2:208:U:C2	1:2:209:A:C8	3.07	0.42
1:2:303:U:H2'	1:2:304:C:C6	2.54	0.42
1:2:369:A:H3'	1:2:370:G:C8	2.54	0.42
1:2:445:A:C6	1:2:446:U:C4	3.08	0.42
1:2:446:U:H2'	1:2:447:C:O4'	2.19	0.42
1:2:766:PSU:H5'	1:2:767:U:H5''	2.00	0.42
1:2:1201:A:H3'	1:2:1201:A:N3	2.34	0.42
1:2:1415:A:H2'	1:2:1416:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1540:G:O3'	1:2:1541:A:H8	2.02	0.42
1:2:1680:U:O4	1:2:1718:G:N2	2.52	0.42
2:A:93:THR:OG1	2:A:94:GLY:N	2.51	0.42
5:E:101:LEU:HA	5:E:101:LEU:HD23	1.84	0.42
5:E:208:VAL:HG21	5:E:225:VAL:HG21	2.01	0.42
10:L:15:LYS:NZ	10:L:19:ILE:O	2.46	0.42
22:F:55:VAL:HG21	22:F:64:ILE:HG13	2.01	0.42
22:F:124:ASN:O	22:F:128:ASP:HA	2.20	0.42
24:M:42:ALA:O	24:M:46:THR:HG22	2.18	0.42
27:R:6:THR:O	27:R:9:VAL:HG22	2.19	0.42
28:S:100:SER:HB3	28:S:105:LEU:HB2	2.01	0.42
30:U:98:HIS:CB	30:U:102:ARG:NH2	2.82	0.42
37:3:30[A]:U:O2'	37:3:31[A]:C:H5'	2.19	0.42
38:1:62:C:H2'	38:1:63:G:C8	2.54	0.42
40:k:147:ILE:O	40:k:185:LEU:HD12	2.19	0.42
1:2:780:A:H8	16:Y:9:THR:O	2.02	0.42
1:2:976:A:N6	1:2:1023:U:C2	2.88	0.42
1:2:1080:A:HO2'	1:2:1081:C:H2'	1.83	0.42
1:2:1265:U:H2'	1:2:1266:G:C8	2.54	0.42
1:2:1304:U:H5''	1:2:1305:C:H5	1.84	0.42
1:2:1517:U:H2'	1:2:1518:U:C5	2.55	0.42
1:2:1532:G:O2'	31:Z:72:GLY:O	2.37	0.42
2:A:22:VAL:HG22	2:A:169:SER:HB2	2.01	0.42
3:B:35:PRO:HD3	3:B:98:THR:HG23	2.00	0.42
3:B:74:GLN:NE2	3:B:189:ILE:HG23	2.34	0.42
3:B:94:LYS:HA	3:B:94:LYS:HD3	1.78	0.42
5:E:63:ALA:HA	5:E:66:MET:HE3	2.01	0.42
6:G:1:MET:N	6:G:18:ILE:O	2.44	0.42
7:H:143:LEU:O	14:W:42:GLN:NE2	2.53	0.42
10:L:4:GLU:O	10:L:5:LEU:HD23	2.20	0.42
11:N:11:MET:HG3	11:N:11:MET:O	2.19	0.42
13:V:71:ARG:HG3	13:V:83:TRP:CZ2	2.54	0.42
14:W:22:LYS:HA	14:W:22:LYS:HE3	2.01	0.42
21:D:13:ALA:HA	21:D:16:VAL:HG12	2.02	0.42
22:F:33:VAL:O	22:F:37:GLN:N	2.47	0.42
26:Q:38:LEU:O	26:Q:39:VAL:C	2.61	0.42
31:Z:49:ARG:HA	31:Z:52:LYS:HG2	2.01	0.42
33:d:33:LYS:O	33:d:36:LEU:HD23	2.20	0.42
1:2:273:G:H2'	1:2:274:C:H6	1.85	0.42
1:2:414:C:O2'	1:2:417:G:O6	2.35	0.42
1:2:898:G:C4	1:2:899:A:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1611:U:H3'	22:F:86:LYS:HZ3	1.83	0.42
1:2:1773:U:P	20:h:11:ARG:HH12	2.42	0.42
2:A:126:PRO:HG3	2:A:145:ALA:HB1	2.00	0.42
4:C:172:VAL:HG11	4:C:219:ALA:HA	2.02	0.42
6:G:121:ILE:O	6:G:126:ASN:ND2	2.52	0.42
9:J:106:GLU:HA	9:J:106:GLU:OE1	2.19	0.42
14:W:24:GLN:HE22	18:b:5:GLN:H	1.64	0.42
22:F:60:LEU:HD12	22:F:140:ILE:HG12	2.00	0.42
23:K:85:HIS:CD2	23:K:86:ILE:HG12	2.55	0.42
24:M:81:LYS:HG3	24:M:82:VAL:N	2.35	0.42
24:M:82:VAL:CG1	24:M:83:ALA:H	2.07	0.42
26:Q:131:GLY:HA3	26:Q:136:SER:O	2.19	0.42
35:i:59:ALA:HB1	35:i:91:VAL:HG13	2.02	0.42
40:k:76:PRO:HG2	40:k:170:ILE:HD11	2.02	0.42
41:l:236:CYS:HB2	41:l:239:CYS:O	2.20	0.42
43:g:24:LEU:HD23	43:g:36:SER:HB3	2.00	0.42
1:2:69:G:H2'	1:2:70:C:H6	1.84	0.42
1:2:223:C:H2'	1:2:224:A:C8	2.55	0.42
1:2:960:U:C2	1:2:961:C:C5	3.08	0.42
1:2:1208:C:N3	1:2:1453:G:N2	2.67	0.42
1:2:1300:U:H5'	4:C:93:LYS:HD2	2.02	0.42
1:2:1689:A:O2'	1:2:1690:G:O4'	2.34	0.42
4:C:100:ARG:CG	4:C:100:ARG:O	2.68	0.42
7:H:162:ILE:O	7:H:162:ILE:HG22	2.20	0.42
8:I:60:ILE:HG12	8:I:180:CYS:HB2	2.00	0.42
9:J:41:GLU:O	9:J:45:ILE:HG12	2.19	0.42
10:L:125:VAL:HG22	10:L:137:PHE:HB3	2.01	0.42
15:X:50:LYS:HG2	15:X:51:GLY:N	2.35	0.42
15:X:107:PHE:CE2	15:X:114:LYS:HD2	2.55	0.42
16:Y:57:VAL:HB	16:Y:60:PHE:HE1	1.84	0.42
18:b:67:THR:CG2	18:b:68:GLY:H	2.30	0.42
20:h:2:ARG:HB2	20:h:5:TRP:CD1	2.55	0.42
20:h:7:LYS:HE2	20:h:11:ARG:HH21	1.84	0.42
21:D:57:ASP:O	21:D:65:ARG:NE	2.53	0.42
28:S:31:ALA:O	28:S:34:THR:OG1	2.22	0.42
28:S:116:LEU:O	28:S:119:ILE:HG22	2.19	0.42
36:m:26:ILE:HB	36:m:103:ILE:HG13	2.02	0.42
1:2:199:A:H2'	1:2:200:G:C8	2.55	0.42
1:2:261:U:H2'	1:2:262:C:C6	2.55	0.42
1:2:373:U:H2'	1:2:374:U:C6	2.54	0.42
1:2:454:C:H3'	1:2:455:A:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:567:G:OP2	15:X:70:LYS:NZ	2.45	0.42
1:2:700:C:O2'	1:2:701:U:P	2.78	0.42
1:2:877:G:O2'	11:N:108:ASP:OD1	2.33	0.42
1:2:1013:G:H2'	1:2:1014:U:O4'	2.20	0.42
1:2:1086:A:H2'	1:2:1087:A:C8	2.55	0.42
1:2:1329:G:H2'	1:2:1330:A:O4'	2.20	0.42
1:2:1601:U:H2'	1:2:1602:U:H6	1.84	0.42
2:A:148:ASP:CG	2:A:149:LEU:N	2.76	0.42
5:E:80:THR:HG23	5:E:81:THR:HG23	2.02	0.42
6:G:12:THR:HG21	6:G:124:ILE:HA	2.02	0.42
8:I:139:ASN:O	8:I:143:LYS:HG3	2.20	0.42
12:O:70:LYS:O	12:O:73:GLU:HG3	2.20	0.42
16:Y:86:GLU:OE1	16:Y:86:GLU:CA	2.59	0.42
22:F:50:PHE:HD1	22:F:132:LEU:HD21	1.83	0.42
27:R:53:TYR:CE2	27:R:57:LEU:HD11	2.54	0.42
29:T:84:LYS:HE3	29:T:86:ARG:HG2	2.01	0.42
30:U:33:GLN:O	30:U:37:VAL:HG23	2.19	0.42
30:U:53:LYS:HG3	30:U:92:ASP:OD2	2.20	0.42
33:d:22:ARG:NH2	33:d:36:LEU:CA	2.76	0.42
36:m:58:LEU:HD11	36:m:78:ILE:HD12	2.01	0.42
39:j:104:LYS:HG3	39:j:140:HIS:CE1	2.55	0.42
1:2:96:G:OP1	5:E:10:LYS:NZ	2.53	0.42
1:2:411:A:C8	1:2:421:G:C2	3.08	0.42
1:2:513:G:C2	1:2:514:A:C8	3.07	0.42
1:2:584:A:OP1	19:e:15:LYS:NZ	2.53	0.42
1:2:588:C:H2'	1:2:589:C:C6	2.55	0.42
1:2:778:G:C6	1:2:780:A:H1'	2.55	0.42
1:2:845:G:H2'	1:2:846:A:O4'	2.19	0.42
1:2:1306:U:H3	1:2:1317:G:H21	1.67	0.42
1:2:1334:U:H2'	1:2:1335:A:C8	2.55	0.42
1:2:1401:C:H2'	1:2:1402:C:H6	1.85	0.42
1:2:1562:U:HO2'	28:S:84:TRP:HZ3	1.67	0.42
1:2:1777:U:H2'	1:2:1779:A:OP2	2.20	0.42
6:G:39:GLU:HG2	6:G:46:LYS:HZ3	1.68	0.42
7:H:38:LEU:HD21	7:H:73:VAL:HG11	2.02	0.42
8:I:113:TYR:CE1	8:I:117:TYR:HB2	2.55	0.42
12:O:31:THR:HG21	12:O:35:GLY:HA2	2.01	0.42
22:F:66:ILE:HD11	22:F:91:ILE:HB	2.00	0.42
24:M:38:LEU:HB2	34:f:102:VAL:HG21	2.01	0.42
25:P:18:LYS:HE2	28:S:92:VAL:HG22	2.02	0.42
26:Q:44:LEU:HB3	26:Q:78:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:R:27:ASP:OD2	27:R:30:THR:HG23	2.19	0.42
31:Z:90:LYS:HG3	31:Z:104:ALA:HB2	2.02	0.42
34:f:137:PHE:HB2	34:f:148:THR:OG1	2.20	0.42
36:m:72:PRO:C	36:m:74:MET:H	2.28	0.42
43:g:20:TRP:HD1	43:g:313:THR:HA	1.79	0.42
43:g:69:VAL:HA	43:g:85:SER:HA	2.01	0.42
43:g:252:PHE:O	43:g:301:TRP:CD1	2.73	0.42
43:g:271:ASP:HB3	43:g:274:ASN:OD1	2.19	0.42
1:2:158:U:O2'	6:G:87:ARG:NH2	2.52	0.42
1:2:180:A:H2'	1:2:181:A:C8	2.55	0.42
1:2:930:C:H1'	3:B:120:LEU:HD22	2.02	0.42
1:2:1141:A:H2'	1:2:1142:A:O4'	2.19	0.42
1:2:1526:U:C2	1:2:1527:C:C5	3.08	0.42
1:2:1550:U:H2'	1:2:1551:G:O4'	2.20	0.42
1:2:1739:U:H2'	1:2:1740:U:C6	2.53	0.42
2:A:33:GLN:OE1	13:V:64:GLU:OE1	2.38	0.42
2:A:64:ILE:O	2:A:67:ILE:HG22	2.20	0.42
2:A:73:VAL:HG22	2:A:120:LEU:HB3	2.01	0.42
4:C:49:LEU:CD2	4:C:252:ALA:HB2	2.50	0.42
5:E:248:ILE:HA	5:E:251:GLU:HG3	2.02	0.42
12:O:29:HIS:CD2	12:O:40:ALA:O	2.72	0.42
15:X:77:ILE:HD12	15:X:77:ILE:HA	1.91	0.42
21:D:48:ILE:CG2	21:D:86:LEU:HA	2.50	0.42
22:F:92:VAL:O	22:F:96:THR:HG23	2.20	0.42
30:U:30:LYS:CE	30:U:33:GLN:HG3	2.50	0.42
32:c:29:ARG:HE	32:c:41:VAL:HA	1.85	0.42
38:1:66:C:H2'	38:1:67:G:H8	1.83	0.42
40:k:98:GLN:NE2	40:k:391:VAL:H	2.18	0.42
1:2:430:C:C2	1:2:431:G:C8	3.08	0.41
1:2:444:A:H1'	1:2:524:A:OP1	2.19	0.41
1:2:1178:G:H2'	1:2:1179:C:H6	1.84	0.41
1:2:1265:U:H2'	1:2:1266:G:H8	1.84	0.41
1:2:1270:G:H2'	1:2:1271:U:C6	2.55	0.41
1:2:1332:C:C4'	21:D:162:GLN:OE1	2.68	0.41
1:2:1332:C:H2'	1:2:1333:U:H6	1.85	0.41
1:2:1351:U:H2'	1:2:1352:U:O4'	2.20	0.41
2:A:189:PRO:HG2	2:A:193:GLN:HE22	1.85	0.41
5:E:111:VAL:O	5:E:111:VAL:HG13	2.20	0.41
7:H:14:THR:HG23	7:H:17:GLU:HG2	2.01	0.41
10:L:132:SER:OG	10:L:133:LYS:N	2.51	0.41
21:D:211:PRO:HD3	27:R:19:LYS:HZ2	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:140:LYS:HE2	26:Q:140:LYS:HB3	1.86	0.41
27:R:31:ASN:ND2	27:R:55:THR:HG22	2.35	0.41
28:S:56:LYS:HZ3	28:S:60:GLU:CD	2.28	0.41
29:T:64:HIS:O	29:T:67:LEU:HG	2.19	0.41
36:m:99:GLN:HG2	36:m:101:LYS:HB3	2.02	0.41
39:j:55:ARG:CG	39:j:56:ILE:H	2.33	0.41
40:k:146:LYS:HB3	40:k:148:TYR:CE2	2.55	0.41
1:2:6:G:C5	4:C:210:ARG:NH2	2.88	0.41
1:2:78:A:H2	6:G:174:LYS:HG3	1.85	0.41
1:2:279:U:H1'	1:2:280:G:OP2	2.20	0.41
1:2:317:U:C4'	8:I:11:ARG:HH21	2.28	0.41
1:2:545:C:H2'	1:2:546:U:C6	2.54	0.41
1:2:604:A:OP2	1:2:605:A:O2'	2.29	0.41
1:2:686:C:H2'	1:2:687:C:C6	2.55	0.41
1:2:715:U:H3	1:2:723:G:H22	1.66	0.41
1:2:822:G:H2'	1:2:823:G:O4'	2.20	0.41
1:2:932:A:C6	1:2:934:U:N3	2.88	0.41
1:2:1210:A:H2'	1:2:1211:G:O4'	2.20	0.41
1:2:1254:G:N7	24:M:39:ARG:NH2	2.63	0.41
1:2:1288:U:H2'	1:2:1289:PSU:C6	2.55	0.41
1:2:1343:A:H4'	1:2:1344:A:OP1	2.20	0.41
1:2:1356:G:H2'	1:2:1357:G:H8	1.85	0.41
1:2:1514:A:O2'	1:2:1515:U:H5'	2.19	0.41
1:2:1541:A:H2'	1:2:1542:U:O4'	2.19	0.41
1:2:1640:G:HO2'	1:2:1779:A:HO2'	1.61	0.41
1:2:1676:A:OP1	8:I:59:ARG:NH2	2.53	0.41
2:A:6:THR:C	2:A:191:ARG:HH12	2.27	0.41
4:C:153:LEU:CD2	13:V:4:ASP:OD2	2.68	0.41
6:G:37:ASP:HA	6:G:49:VAL:HG23	2.02	0.41
8:I:168:ALA:HA	8:I:185:LEU:H	1.84	0.41
12:O:18:ARG:H	12:O:82:LYS:HB2	1.85	0.41
13:V:17:CYS:HB3	13:V:22:ARG:H	1.85	0.41
14:W:52:TYR:CD1	14:W:52:TYR:C	2.98	0.41
24:M:45:LEU:HD21	24:M:72:ALA:HA	2.02	0.41
24:M:46:THR:HG21	34:f:127:GLY:HA3	2.02	0.41
27:R:70:SER:HA	27:R:74:GLN:HE22	1.78	0.41
32:c:18:ARG:NH1	32:c:26:THR:CG2	2.78	0.41
39:j:45:MET:HE2	39:j:45:MET:HB2	1.95	0.41
39:j:208:ALA:O	39:j:211:MET:HG2	2.19	0.41
43:g:34:LEU:CG	43:g:46:TRP:HD1	2.33	0.41
1:2:563:G:H21	1:2:576:G:P	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:601:U:H2'	1:2:602:U:C6	2.55	0.41
1:2:712:U:H3	1:2:726:G:H21	1.67	0.41
1:2:916:U:H3'	1:2:917:U:H5'	2.01	0.41
1:2:1173:C:H2'	1:2:1174:U:O4'	2.20	0.41
1:2:1262:G:H2'	1:2:1263:G:O4'	2.19	0.41
1:2:1760:A:C2	1:2:1761:A:C8	3.08	0.41
2:A:84:ARG:HH21	27:R:82:ASP:HA	1.85	0.41
15:X:93:LEU:C	15:X:93:LEU:HD23	2.45	0.41
19:e:54:ARG:CD	19:e:56:MET:HG2	2.49	0.41
22:F:224:LYS:HG2	22:F:227:ARG:NH2	2.33	0.41
26:Q:90:VAL:HA	26:Q:105:LEU:HD23	2.02	0.41
26:Q:143:ARG:NH1	38:1:33:U:O2'	2.53	0.41
35:i:60:HIS:O	35:i:91:VAL:HG22	2.20	0.41
36:m:49:TYR:CE2	36:m:53:ARG:NH1	2.88	0.41
38:1:16:H2U:HN3	38:1:59:A:H2	1.68	0.41
39:j:72:VAL:O	39:j:85:LEU:HA	2.21	0.41
40:k:111:HIS:NE2	40:k:217:LEU:HB3	2.36	0.41
40:k:128:PHE:HZ	40:k:139:LYS:HD2	1.86	0.41
40:k:146:LYS:HG3	40:k:188:HIS:HD2	1.85	0.41
40:k:282:PRO:HG3	41:l:135:LEU:HG	2.02	0.41
40:k:348:LYS:HA	40:k:389:PHE:HA	2.01	0.41
43:g:49:THR:OG1	43:g:54:GLN:OE1	2.35	0.41
43:g:81:ALA:HB2	43:g:95:LEU:HD21	2.01	0.41
1:2:72:A:H1'	1:2:73:U:C5	2.56	0.41
1:2:92:A:OP1	5:E:7:LYS:NZ	2.53	0.41
1:2:559:U:H2'	1:2:560:G:C8	2.52	0.41
1:2:708:C:C2	1:2:710:U:H5	2.38	0.41
1:2:1000:A:C4	36:m:33:ARG:NH1	2.89	0.41
1:2:1260:G:H2'	1:2:1261:U:C6	2.56	0.41
1:2:1314:U:H2'	1:2:1315:G:O4'	2.20	0.41
1:2:1471:U:C5	22:F:192:ILE:HG21	2.54	0.41
1:2:1568:A:H2'	1:2:1569:C:O4'	2.20	0.41
1:2:1608:G:P	26:Q:75:VAL:HG11	2.61	0.41
1:2:1658:A:H2'	1:2:1659:U:C6	2.55	0.41
4:C:45:LYS:O	4:C:49:LEU:HD23	2.21	0.41
4:C:231:THR:HG23	14:W:99:PHE:CE1	2.55	0.41
5:E:106:LYS:HG3	5:E:108:ARG:HH22	1.83	0.41
9:J:133:HIS:HD2	9:J:158:PHE:HD1	1.65	0.41
15:X:69:ARG:HG3	15:X:117:ILE:HG12	2.03	0.41
15:X:84:THR:HG23	15:X:120:VAL:HA	2.03	0.41
21:D:21:LEU:HD11	21:D:48:ILE:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:K:84:GLU:OE1	23:K:84:GLU:N	2.52	0.41
26:Q:45:ARG:C	26:Q:48:VAL:HG12	2.45	0.41
30:U:51:VAL:CG1	30:U:94:GLU:HB2	2.45	0.41
35:i:80:SER:HB3	35:i:90:ASP:OD1	2.20	0.41
38:1:39:C:H2'	38:1:40:C:C6	2.55	0.41
40:k:133:GLU:HB3	41:l:256:PHE:CE2	2.55	0.41
40:k:139:LYS:HG2	40:k:319:ARG:NH1	2.36	0.41
40:k:146:LYS:HG2	40:k:188:HIS:HB2	2.02	0.41
40:k:262:HIS:O	40:k:266:ILE:HG12	2.19	0.41
40:k:402:VAL:HG13	40:k:406:LEU:HD22	2.03	0.41
40:k:445:THR:HG21	40:k:450:GLN:HA	2.02	0.41
41:l:146:ASN:HD21	41:l:149:LEU:HD13	1.84	0.41
43:g:48:LEU:HA	43:g:56:GLY:HA2	2.03	0.41
43:g:216:SER:HB2	43:g:233:LYS:NZ	2.36	0.41
43:g:239:MET:HE3	43:g:239:MET:HB3	1.93	0.41
1:2:489:C:H5''	1:2:490:C:OP2	2.21	0.41
1:2:747:C:H4'	14:W:80:ASN:HD21	1.85	0.41
1:2:862:A:C8	1:2:864:A:N7	2.88	0.41
1:2:1276:G:C4	1:2:1434:A:C2	3.08	0.41
1:2:1390:U:H2'	1:2:1391:C:C6	2.56	0.41
1:2:1423:A:H2'	1:2:1424:C:C6	2.55	0.41
1:2:1464:G:H2'	1:2:1465:C:C6	2.55	0.41
1:2:1556:U:H4'	28:S:135:GLY:HA3	2.02	0.41
2:A:30:GLN:NE2	2:A:31:VAL:O	2.53	0.41
3:B:168:ILE:O	3:B:172:LEU:HD23	2.20	0.41
4:C:142:ILE:HD13	4:C:142:ILE:HA	1.88	0.41
4:C:230:LEU:HD12	4:C:230:LEU:HA	1.84	0.41
5:E:180:LEU:C	5:E:228:ILE:HG22	2.45	0.41
8:I:54:LYS:HB3	8:I:54:LYS:HE2	1.81	0.41
11:N:15:ALA:HB2	18:b:21:LEU:HD11	2.02	0.41
12:O:64:ALA:HB3	12:O:104:ALA:HB3	2.02	0.41
13:V:71:ARG:HG3	13:V:83:TRP:CH2	2.55	0.41
14:W:52:TYR:CD1	14:W:53:ILE:N	2.88	0.41
39:j:14:PRO:HB3	39:j:39:TYR:CZ	2.55	0.41
40:k:238:ILE:HD12	40:k:511:LEU:HD21	2.01	0.41
43:g:127:SER:HB3	43:g:129:ASP:OD1	2.20	0.41
1:2:161:A:H5'	6:G:82:SER:OG	2.20	0.41
1:2:335:G:O6	8:I:5:ARG:NH1	2.54	0.41
1:2:598:A:H2'	1:2:599:U:C6	2.56	0.41
1:2:735:C:O2'	1:2:736:C:H6	2.03	0.41
1:2:945:U:H5''	3:B:165:ARG:NH2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1082:G:H2'	1:2:1083:A:O4'	2.21	0.41
1:2:1317:G:H2'	1:2:1318:A:H8	1.86	0.41
1:2:1323:G:H4'	2:A:113:ARG:CZ	2.51	0.41
1:2:1679:A:N6	1:2:1718:G:O2'	2.38	0.41
1:2:1726:U:O2'	8:I:3:ILE:HD11	2.21	0.41
2:A:139:VAL:HG22	2:A:139:VAL:O	2.20	0.41
2:A:167:LYS:NZ	2:A:204:TYR:N	2.68	0.41
2:A:175:TYR:HB2	2:A:202:TYR:CD2	2.55	0.41
6:G:45:PHE:HA	6:G:48:TYR:HD2	1.86	0.41
6:G:132:ARG:CD	6:G:133:LEU:HD22	2.51	0.41
21:D:24:PHE:CE2	23:K:65:TYR:CZ	3.09	0.41
24:M:80:ILE:HG12	24:M:131:PHE:HD2	1.86	0.41
27:R:27:ASP:O	27:R:31:ASN:ND2	2.54	0.41
39:j:197:GLY:HA3	40:k:403:ASP:HB2	2.02	0.41
43:g:93:TRP:HE1	43:g:100:SER:HB2	1.85	0.41
43:g:252:PHE:CD2	43:g:259:LEU:HD21	2.56	0.41
43:g:260:THR:HG23	43:g:301:TRP:HZ2	1.85	0.41
43:g:281:LEU:HD23	43:g:320:TRP:CD1	2.55	0.41
1:2:203:G:H2'	1:2:204:U:O4'	2.20	0.41
1:2:357:U:O2'	1:2:359:A:OP1	2.35	0.41
1:2:464:G:C6	1:2:465:PSU:C2	3.08	0.41
1:2:1031:G:H2'	1:2:1032:C:C6	2.56	0.41
1:2:1127:C:C4	1:2:1128:U:C5	3.09	0.41
1:2:1203:A:C5	1:2:1204:C:C5	3.08	0.41
1:2:1276:G:H2'	1:2:1277:G:C8	2.55	0.41
1:2:1672:C:C2	1:2:1673:C:C5	3.08	0.41
5:E:54:TYR:O	16:Y:22:GLN:NE2	2.48	0.41
8:I:67:TRP:O	8:I:71:GLY:CA	2.69	0.41
9:J:96:VAL:HG22	9:J:96:VAL:O	2.21	0.41
21:D:8:LYS:HD2	33:d:34:TYR:HE1	1.74	0.41
21:D:65:ARG:HA	21:D:68:GLU:HG2	2.02	0.41
29:T:18:TYR:CE2	29:T:22:LEU:HD11	2.56	0.41
32:c:12:VAL:HG12	32:c:52:ASP:O	2.20	0.41
33:d:40:ARG:NH1	33:d:41:GLN:OE1	2.54	0.41
43:g:315:ASN:HD22	43:g:318:ARG:NH2	2.18	0.41
1:2:116:U:H3	1:2:299:A:H2	1.67	0.41
1:2:431:G:C5	1:2:432:C:C4	3.09	0.41
1:2:568:C:H2'	1:2:569:A:O4'	2.21	0.41
1:2:583:C:O2'	19:e:18:THR:HG21	2.20	0.41
1:2:955:C:P	11:N:11:MET:H	2.44	0.41
1:2:1172:C:OP1	28:S:141:THR:OG1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1588:G:H2'	1:2:1589:C:H6	1.86	0.41
5:E:128:LYS:HB3	5:E:140:VAL:HB	2.03	0.41
7:H:67:LEU:O	7:H:70:TYR:HB2	2.19	0.41
8:I:6:ASP:OD1	8:I:9:HIS:ND1	2.54	0.41
10:L:45:PRO:HG3	10:L:115:PHE:HE1	1.83	0.41
21:D:65:ARG:HG2	21:D:69:LEU:HD23	2.03	0.41
26:Q:99:GLU:HG2	26:Q:102:LYS:HE3	2.02	0.41
29:T:6:VAL:HB	29:T:66:TYR:CE2	2.56	0.41
30:U:65:ILE:HG13	33:d:43:PHE:CE2	2.56	0.41
36:m:70:LYS:HD2	36:m:70:LYS:C	2.46	0.41
39:j:96:ILE:H	39:j:96:ILE:HG13	1.74	0.41
40:k:139:LYS:HG2	40:k:319:ARG:HH11	1.85	0.41
43:g:8:LEU:HD11	43:g:281:LEU:HD21	2.02	0.41
43:g:296:ALA:HA	43:g:312:TYR:HA	2.01	0.41
1:2:157:U:C4	1:2:419:A:H4'	2.56	0.41
1:2:358:A:N3	1:2:358:A:H2'	2.34	0.41
1:2:423:C:O2'	1:2:425:G:OP1	2.31	0.41
1:2:591:G:H2'	1:2:592:U:O4'	2.21	0.41
1:2:602:U:H2'	1:2:603:A:C8	2.55	0.41
1:2:768:C:H2'	1:2:769:A:O4'	2.21	0.41
1:2:882:C:N3	1:2:945:U:C4	2.88	0.41
1:2:955:C:H2'	1:2:956:G:C8	2.56	0.41
1:2:1078:U:H2'	1:2:1079:U:C6	2.56	0.41
1:2:1121:G:N2	1:2:1124:A:OP2	2.51	0.41
1:2:1181:U:H3	1:2:1184:U:H5''	1.86	0.41
1:2:1206:C:H4'	1:2:1207:A:O4'	2.21	0.41
1:2:1227:G:OP2	24:M:38:LEU:HG	2.20	0.41
1:2:1238:U:H2'	1:2:1239:U:C6	2.56	0.41
1:2:1251:C:H41	34:f:95:HIS:HE1	1.67	0.41
1:2:1318:A:H2'	1:2:1319:U:O4'	2.20	0.41
1:2:1386:A:N7	1:2:1409:A:N6	2.68	0.41
1:2:1477:A:C2	1:2:1478:G:C8	3.09	0.41
1:2:1588:G:H2'	1:2:1589:C:C6	2.56	0.41
1:2:1595:A:P	33:d:19:ARG:HH22	2.44	0.41
1:2:1665:A:H2'	1:2:1666:G:C8	2.56	0.41
2:A:49:ASN:O	2:A:53:THR:HG23	2.21	0.41
2:A:143:VAL:HG23	2:A:143:VAL:O	2.21	0.41
3:B:142:PHE:O	3:B:207:LEU:HD12	2.21	0.41
4:C:87:ASN:OD1	4:C:88:ILE:N	2.54	0.41
6:G:9:ILE:H	6:G:9:ILE:HD12	1.86	0.41
6:G:142:ARG:NH1	6:G:149:LYS:HZ2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:182:GLN:HE22	6:G:186:ARG:NE	2.19	0.41
7:H:9:LEU:HD21	7:H:43:PHE:CB	2.25	0.41
7:H:64:VAL:HG22	7:H:94:ALA:HB1	2.02	0.41
7:H:139:ARG:HD3	7:H:153:LEU:HD13	2.02	0.41
7:H:162:ILE:CG2	7:H:169:PHE:CZ	3.03	0.41
8:I:114:GLU:OE1	8:I:120:SER:HA	2.21	0.41
8:I:169:ALA:HB2	8:I:185:LEU:HD21	2.02	0.41
9:J:84:GLY:C	9:J:107:ARG:HE	2.29	0.41
9:J:90:LYS:HD2	9:J:95:TYR:CD2	2.56	0.41
11:N:61:THR:OG1	11:N:62:GLN:N	2.54	0.41
14:W:111:MET:HE2	14:W:115:GLU:C	2.46	0.41
15:X:139:LYS:HB3	15:X:139:LYS:HE3	1.82	0.41
26:Q:40:GLN:HB2	26:Q:41:PRO:CD	2.50	0.41
26:Q:40:GLN:HB2	26:Q:41:PRO:HD3	2.03	0.41
27:R:6:THR:OG1	27:R:7:LYS:N	2.54	0.41
27:R:18:GLU:OE2	27:R:69:ILE:HB	2.21	0.41
28:S:65:GLU:HA	28:S:68:ARG:HG2	2.03	0.41
36:m:28:ILE:HA	36:m:41:THR:O	2.20	0.41
39:j:25:GLN:HG2	39:j:34:VAL:HA	2.03	0.41
39:j:38:GLU:OE2	39:j:105:SER:OG	2.37	0.41
41:l:175:SER:HA	41:l:210:ARG:HB3	2.03	0.41
43:g:10:LEU:HD12	43:g:319:VAL:O	2.20	0.41
43:g:229:VAL:HB	43:g:239:MET:SD	2.61	0.41
1:2:54:C:O3'	16:Y:109:LYS:HD3	2.21	0.41
1:2:606:G:OP2	1:2:612:G:N1	2.53	0.41
1:2:619:A:O2'	1:2:620:A:H5'	2.20	0.41
2:A:33:GLN:OE1	13:V:64:GLU:CD	2.64	0.41
2:A:105:GLY:H	2:A:135:GLU:CD	2.29	0.41
5:E:53:LYS:HG3	5:E:53:LYS:O	2.21	0.41
5:E:73:ASP:HB3	5:E:164:LEU:HD11	2.02	0.41
5:E:181:VAL:HG22	5:E:182:TYR:N	2.36	0.41
6:G:110:ALA:C	6:G:111:LEU:HD22	2.45	0.41
11:N:1:MET:SD	11:N:1:MET:N	2.79	0.41
14:W:32:LYS:HA	14:W:35:ILE:HD12	2.03	0.41
15:X:94:ASN:OD1	15:X:94:ASN:N	2.54	0.41
22:F:149:THR:O	22:F:151:VAL:HG23	2.20	0.41
26:Q:99:GLU:CD	43:g:58:PRO:HB2	2.46	0.41
38:1:10:2MG:C2	38:1:26:M2G:H1'	2.55	0.41
39:j:148:SER:HB3	39:j:154:VAL:HG21	2.02	0.41
40:k:268:LYS:HA	40:k:271:ARG:HE	1.85	0.41
43:g:153:THR:N	43:g:177:ALA:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:g:267:ILE:HB	43:g:281:LEU:HB2	2.02	0.41
1:2:121:U:H2'	1:2:122:U:C6	2.56	0.40
1:2:854:A:C2	1:2:856:U:H1'	2.57	0.40
1:2:1134:U:H2'	1:2:1135:U:C6	2.56	0.40
1:2:1201:A:N6	1:2:1455:C:O2	2.54	0.40
1:2:1332:C:H2'	1:2:1333:U:C6	2.56	0.40
1:2:1636:G:C6	1:2:1637:5MC:N3	2.89	0.40
5:E:100:ARG:NH2	5:E:121:TYR:O	2.54	0.40
5:E:136:ILE:HG23	5:E:149:TYR:CE1	2.56	0.40
8:I:38:ILE:HD11	8:I:78:ILE:HB	2.03	0.40
8:I:41:LYS:HG3	8:I:60:ILE:HD12	2.04	0.40
8:I:57:ALA:HB2	8:I:178:GLY:HA2	2.03	0.40
8:I:157:VAL:HG13	8:I:160:GLN:HE21	1.86	0.40
11:N:66:ILE:HG13	11:N:67:THR:N	2.36	0.40
20:h:1:MET:HE2	20:h:5:TRP:HB3	2.02	0.40
25:P:52:LYS:NZ	25:P:80:LEU:HD11	2.36	0.40
25:P:98:ASN:OD1	25:P:120:SER:O	2.39	0.40
26:Q:37:THR:CB	26:Q:49:TYR:OH	2.67	0.40
40:k:263:GLN:NE2	41:l:131:TYR:CE2	2.86	0.40
41:l:232:GLU:HG3	41:l:233:TYR:CD1	2.53	0.40
43:g:89:THR:HG21	43:g:103:ARG:NH2	2.36	0.40
1:2:251:U:H2'	1:2:252:A:C8	2.56	0.40
1:2:393:C:H2'	1:2:394:U:C6	2.56	0.40
1:2:765:G:O6	9:J:149:ARG:HG2	2.21	0.40
1:2:977:A:H2'	1:2:978:A:H8	1.86	0.40
1:2:1024:A:H2'	1:2:1026:A:OP1	2.21	0.40
1:2:1239:U:H1'	1:2:1243:A:C2	2.56	0.40
1:2:1278:C:O2	30:U:71:PRO:HG2	2.21	0.40
1:2:1475:G:C6	1:2:1529:G:N1	2.89	0.40
1:2:1502:G:H22	1:2:1547:C:H1'	1.85	0.40
1:2:1797:U:C3'	1:2:1798:A:H5''	2.51	0.40
8:I:84:HIS:HB3	8:I:87:ASN:O	2.20	0.40
8:I:173:ARG:HH21	8:I:176:GLN:HE21	1.70	0.40
9:J:114:TYR:HE2	9:J:121:SER:HA	1.85	0.40
11:N:52:VAL:HG23	11:N:55:ARG:NH2	2.37	0.40
11:N:66:ILE:HG13	11:N:67:THR:HG23	2.03	0.40
21:D:134:CYS:SG	21:D:135:GLU:N	2.94	0.40
23:K:28:ASN:OD1	33:d:7:TRP:NE1	2.37	0.40
24:M:33:GLY:O	24:M:115:LYS:N	2.53	0.40
28:S:63:GLN:O	28:S:66:LEU:HB2	2.21	0.40
28:S:66:LEU:HA	28:S:69:ILE:HG12	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:T:69:LYS:O	29:T:70:GLN:HG3	2.22	0.40
36:m:90:GLU:O	36:m:93:ILE:HG12	2.22	0.40
40:k:466:ILE:HG23	40:k:499:ILE:HG13	2.02	0.40
43:g:285:PHE:CE2	43:g:294:PRO:HD2	2.56	0.40
1:2:338:C:H2'	1:2:339:U:C6	2.56	0.40
1:2:345:G:P	10:L:79:ARG:HD3	2.61	0.40
1:2:670:G:H3'	1:2:672:G:C5	2.57	0.40
1:2:791:U:H2'	1:2:792:A:C1'	2.52	0.40
1:2:870:G:C6	1:2:956:G:C6	3.09	0.40
1:2:1168:G:C2	1:2:1575:A:C6	3.10	0.40
1:2:1474:C:O2'	29:T:45:LEU:HD21	2.22	0.40
1:2:1751:A:H2'	1:2:1752:A:O4'	2.22	0.40
4:C:182:GLY:N	4:C:200:ASP:OD1	2.52	0.40
4:C:227:TYR:O	13:V:23:ILE:HD13	2.21	0.40
16:Y:7:ILE:HG13	16:Y:27:VAL:HG12	2.03	0.40
22:F:163:ASP:OD1	32:c:44:VAL:HA	2.21	0.40
28:S:3:LEU:HD12	28:S:3:LEU:HA	1.93	0.40
35:i:87:ASP:HB2	35:i:88:GLN:OE1	2.19	0.40
38:1:12:G:C2	38:1:24:G:C2	3.09	0.40
38:1:14:A:H2	38:1:22:G:N1	2.18	0.40
39:j:236:ASP:CB	39:j:238:GLN:NE2	2.85	0.40
40:k:149:LYS:HZ2	40:k:151:GLN:HA	1.86	0.40
40:k:205:LEU:HD13	40:k:500:ALA:HB3	2.02	0.40
43:g:77:ASP:OD2	43:g:79:ASN:ND2	2.55	0.40
1:2:560:G:C2	1:2:561:G:C8	3.10	0.40
1:2:703:G:H3'	1:2:704:C:H3'	2.02	0.40
1:2:779:A:OP2	1:2:780:A:H2	2.05	0.40
1:2:865:G:H2'	1:2:866:G:H8	1.86	0.40
1:2:1231:U:H4'	23:K:2:LEU:HD21	2.02	0.40
1:2:1333:U:H2'	1:2:1334:U:C6	2.57	0.40
4:C:60:GLU:HA	4:C:63:LEU:HB2	2.04	0.40
4:C:187:PRO:O	4:C:191:LYS:HG3	2.21	0.40
5:E:35:PRO:HB3	5:E:143:ASP:O	2.21	0.40
6:G:12:THR:CB	6:G:124:ILE:HG13	2.47	0.40
8:I:160:GLN:OE1	8:I:167:TYR:HD1	2.04	0.40
11:N:86:GLU:CD	11:N:86:GLU:N	2.79	0.40
12:O:103:ARG:HH21	17:a:48:ALA:C	2.30	0.40
12:O:112:ILE:HD12	17:a:56:ALA:O	2.21	0.40
14:W:11:LEU:HD12	14:W:72:CYS:CB	2.51	0.40
26:Q:94:GLN:NE2	43:g:61:SER:O	2.54	0.40
26:Q:131:GLY:HA2	26:Q:138:PHE:CE1	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:R:44:LYS:HB2	27:R:47:ARG:NH2	2.35	0.40
29:T:14:PHE:C	29:T:14:PHE:CD1	2.97	0.40
36:m:67:ASN:O	36:m:78:ILE:HA	2.22	0.40
36:m:99:GLN:HG2	36:m:101:LYS:H	1.85	0.40
39:j:118:LYS:NZ	39:j:168:GLU:OE2	2.36	0.40
40:k:207:GLY:O	40:k:211:MET:HE2	2.22	0.40
40:k:246:ILE:HD12	40:k:280:ILE:HG12	2.04	0.40
40:k:359:ILE:H	40:k:359:ILE:HD12	1.87	0.40
1:2:245:G:H4'	5:E:202:GLU:OE1	2.21	0.40
1:2:728:A:H3'	1:2:729:G:H5''	2.03	0.40
1:2:748:U:O2'	14:W:122:SER:O	2.32	0.40
1:2:996:G:C6	1:2:997:A:N7	2.89	0.40
1:2:1040:G:C2	1:2:1077:C:C2	3.09	0.40
1:2:1277:G:H2'	1:2:1278:C:O4'	2.21	0.40
1:2:1401:C:H2'	1:2:1402:C:C6	2.56	0.40
1:2:1735:G:H2'	1:2:1736:U:H6	1.87	0.40
3:B:23:PRO:HA	3:B:26:ARG:NH1	2.37	0.40
5:E:35:PRO:C	5:E:36:HIS:CD2	3.00	0.40
7:H:37:ASP:N	7:H:37:ASP:OD1	2.53	0.40
8:I:46:VAL:HG12	8:I:54:LYS:O	2.21	0.40
9:J:77:ILE:HD11	9:J:91:LYS:HA	2.02	0.40
9:J:123:HIS:HB3	19:e:33:ARG:NH1	2.36	0.40
12:O:115:ILE:HD13	17:a:64:LEU:HD11	2.04	0.40
14:W:57:ARG:NH2	18:b:26:GLN:OE1	2.55	0.40
15:X:48:HIS:CD2	15:X:105:ALA:HB2	2.57	0.40
28:S:126:ARG:HH22	28:S:135:GLY:CA	2.32	0.40
40:k:355:ILE:O	40:k:372:PRO:HA	2.22	0.40
43:g:74:VAL:HA	43:g:81:ALA:HA	2.04	0.40
43:g:86:TRP:CA	43:g:110:ASP:HB2	2.51	0.40
43:g:223:LYS:HD2	43:g:246:GLU:OE1	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
2	A	217/254 (85%)	203 (94%)	14 (6%)	0	100	100
3	B	225/255 (88%)	215 (96%)	9 (4%)	1 (0%)	30	65
4	C	218/259 (84%)	206 (94%)	11 (5%)	1 (0%)	24	60
5	E	258/261 (99%)	245 (95%)	13 (5%)	0	100	100
6	G	228/236 (97%)	223 (98%)	5 (2%)	0	100	100
7	H	182/190 (96%)	174 (96%)	8 (4%)	0	100	100
8	I	184/201 (92%)	172 (94%)	12 (6%)	0	100	100
9	J	180/188 (96%)	176 (98%)	4 (2%)	0	100	100
10	L	151/156 (97%)	141 (93%)	9 (6%)	1 (1%)	18	54
11	N	149/151 (99%)	143 (96%)	6 (4%)	0	100	100
12	O	127/137 (93%)	122 (96%)	5 (4%)	0	100	100
13	V	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
14	W	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
15	X	142/145 (98%)	132 (93%)	10 (7%)	0	100	100
16	Y	132/135 (98%)	128 (97%)	4 (3%)	0	100	100
17	a	100/103 (97%)	91 (91%)	8 (8%)	1 (1%)	12	45
18	b	79/82 (96%)	78 (99%)	1 (1%)	0	100	100
19	e	58/63 (92%)	55 (95%)	3 (5%)	0	100	100
20	h	23/25 (92%)	23 (100%)	0	0	100	100
21	D	225/237 (95%)	218 (97%)	6 (3%)	1 (0%)	30	65
22	F	204/227 (90%)	183 (90%)	18 (9%)	3 (2%)	8	38
23	K	94/106 (89%)	88 (94%)	6 (6%)	0	100	100
24	M	113/134 (84%)	104 (92%)	8 (7%)	1 (1%)	14	48
25	P	115/142 (81%)	106 (92%)	8 (7%)	1 (1%)	14	48
26	Q	139/143 (97%)	122 (88%)	16 (12%)	1 (1%)	18	54
27	R	128/136 (94%)	122 (95%)	6 (5%)	0	100	100
28	S	143/146 (98%)	134 (94%)	9 (6%)	0	100	100
29	T	141/144 (98%)	133 (94%)	8 (6%)	0	100	100
30	U	104/117 (89%)	99 (95%)	5 (5%)	0	100	100
31	Z	76/108 (70%)	71 (93%)	5 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	c	62/67 (92%)	56 (90%)	6 (10%)	0	100	100
33	d	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
34	f	72/150 (48%)	55 (76%)	16 (22%)	1 (1%)	9	39
35	i	94/153 (61%)	84 (89%)	10 (11%)	0	100	100
36	m	84/108 (78%)	76 (90%)	8 (10%)	0	100	100
39	j	263/304 (86%)	246 (94%)	16 (6%)	1 (0%)	30	65
40	k	468/527 (89%)	437 (93%)	30 (6%)	1 (0%)	43	75
41	l	126/270 (47%)	123 (98%)	3 (2%)	0	100	100
42	n	87/812 (11%)	87 (100%)	0	0	100	100
43	g	314/326 (96%)	284 (90%)	30 (10%)	0	100	100
All	All	5970/7471 (80%)	5605 (94%)	351 (6%)	14 (0%)	44	75

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	j	55	ARG
3	B	21	VAL
22	F	86	LYS
26	Q	39	VAL
10	L	7	VAL
22	F	76	ALA
22	F	78	ARG
40	k	507	LYS
24	M	82	VAL
4	C	44	THR
17	a	36	ILE
34	f	118	ARG
25	P	121	ILE
21	D	4	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	
2	A	180/211 (85%)	180 (100%)	0	100	100
3	B	201/228 (88%)	201 (100%)	0	100	100
4	C	177/203 (87%)	177 (100%)	0	100	100
5	E	223/224 (100%)	223 (100%)	0	100	100
6	G	192/200 (96%)	192 (100%)	0	100	100
7	H	164/170 (96%)	164 (100%)	0	100	100
8	I	147/159 (92%)	147 (100%)	0	100	100
9	J	153/158 (97%)	153 (100%)	0	100	100
10	L	134/137 (98%)	134 (100%)	0	100	100
11	N	128/128 (100%)	128 (100%)	0	100	100
12	O	97/104 (93%)	97 (100%)	0	100	100
13	V	73/73 (100%)	73 (100%)	0	100	100
14	W	110/111 (99%)	109 (99%)	1 (1%)	70	76
15	X	119/120 (99%)	119 (100%)	0	100	100
16	Y	108/109 (99%)	108 (100%)	0	100	100
17	a	83/88 (94%)	83 (100%)	0	100	100
18	b	71/72 (99%)	71 (100%)	0	100	100
19	e	51/55 (93%)	51 (100%)	0	100	100
20	h	23/23 (100%)	23 (100%)	0	100	100
21	D	188/196 (96%)	187 (100%)	1 (0%)	81	82
22	F	174/194 (90%)	173 (99%)	1 (1%)	78	81
23	K	88/96 (92%)	88 (100%)	0	100	100
24	M	90/109 (83%)	90 (100%)	0	100	100
25	P	99/119 (83%)	98 (99%)	1 (1%)	68	76
26	Q	117/119 (98%)	113 (97%)	4 (3%)	32	55
27	R	116/124 (94%)	116 (100%)	0	100	100
28	S	127/129 (98%)	127 (100%)	0	100	100
29	T	117/118 (99%)	117 (100%)	0	100	100
30	U	96/107 (90%)	96 (100%)	0	100	100
31	Z	59/88 (67%)	59 (100%)	0	100	100
32	c	55/59 (93%)	54 (98%)	1 (2%)	51	68
33	d	47/48 (98%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	f	60/133 (45%)	57 (95%)	3 (5%)	22	45
35	i	80/130 (62%)	79 (99%)	1 (1%)	61	72
36	m	77/96 (80%)	77 (100%)	0	100	100
39	j	239/274 (87%)	238 (100%)	1 (0%)	84	84
40	k	393/449 (88%)	393 (100%)	0	100	100
41	l	125/234 (53%)	125 (100%)	0	100	100
43	g	264/272 (97%)	263 (100%)	1 (0%)	84	84
All	All	5045/5667 (89%)	5030 (100%)	15 (0%)	84	85

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	W	15	ASN
21	D	184	ILE
22	F	85	ARG
25	P	121	ILE
26	Q	37	THR
26	Q	38	LEU
26	Q	39	VAL
26	Q	48	VAL
32	c	22	ARG
34	f	130	LEU
34	f	139	CYS
34	f	141	LYS
35	i	88	GLN
39	j	233	GLN
43	g	54	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	40	ASN
3	B	124	ASN
4	C	99	GLN
4	C	115	HIS
5	E	142	HIS
5	E	157	ASN
6	G	13	GLN

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Mol	Chain	Res	Type
6	G	197	ASN
7	H	86	GLN
7	H	110	GLN
7	H	170	GLN
8	I	20	GLN
8	I	64	ASN
8	I	160	GLN
8	I	176	GLN
9	J	133	HIS
10	L	22	ASN
11	N	5	HIS
11	N	58	HIS
11	N	78	ASN
12	O	29	HIS
12	O	99	GLN
13	V	33	GLN
13	V	70	ASN
14	W	42	GLN
14	W	80	ASN
14	W	98	GLN
15	X	63	GLN
15	X	75	GLN
16	Y	22	GLN
17	a	8	ASN
18	b	9	HIS
22	F	36	GLN
22	F	74	HIS
23	K	14	HIS
23	K	17	GLN
24	M	134	GLN
26	Q	77	GLN
26	Q	100	GLN
26	Q	103	ASN
27	R	31	ASN
27	R	42	GLN
27	R	105	GLN
28	S	71	GLN
28	S	103	ASN
28	S	122	HIS
28	S	136	GLN
29	T	12	GLN
29	T	70	GLN

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Mol	Chain	Res	Type
30	U	20	HIS
30	U	87	HIS
31	Z	98	GLN
34	f	104	ASN
34	f	143	HIS
35	i	33	GLN
35	i	37	GLN
35	i	55	ASN
36	m	81	GLN
39	j	25	GLN
39	j	41	ASN
39	j	120	GLN
40	k	98	GLN
40	k	144	ASN
40	k	263	GLN
40	k	384	GLN
40	k	433	ASN
40	k	465	ASN
41	l	146	ASN
43	g	79	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1797/1798 (99%)	581 (32%)	29 (1%)
37	3	0/49	-	-
38	1	72/75 (96%)	26 (36%)	4 (5%)
All	All	1869/1922 (97%)	607 (32%)	33 (1%)

All (607) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	U
1	2	4	C
1	2	17	C
1	2	25	C
1	2	26	A
1	2	27	U
1	2	34	G
1	2	43	A

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Mol	Chain	Res	Type
1	2	45	U
1	2	47	A
1	2	50	C
1	2	57	G
1	2	59	C
1	2	66	U
1	2	67	A
1	2	68	A
1	2	69	G
1	2	72	A
1	2	73	U
1	2	74	U
1	2	75	U
1	2	77	U
1	2	78	A
1	2	79	C
1	2	84	A
1	2	104	A
1	2	111	U
1	2	114	C
1	2	115	G
1	2	116	U
1	2	124	A
1	2	127	G
1	2	129	U
1	2	130	C
1	2	131	C
1	2	132	U
1	2	134	U
1	2	135	A
1	2	136	C
1	2	137	U
1	2	139	C
1	2	140	A
1	2	146	A
1	2	150	G
1	2	155	A
1	2	158	U
1	2	159	C
1	2	160	U
1	2	161	A
1	2	166	U

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Mol	Chain	Res	Type
1	2	167	A
1	2	168	A
1	2	173	U
1	2	176	U
1	2	177	U
1	2	178	A
1	2	184	U
1	2	187	A
1	2	191	U
1	2	192	U
1	2	194	G
1	2	195	G
1	2	214	A
1	2	217	A
1	2	218	A
1	2	220	A
1	2	223	C
1	2	224	A
1	2	226	U
1	2	227	G
1	2	228	U
1	2	231	U
1	2	232	C
1	2	234	G
1	2	235	A
1	2	237	U
1	2	239	C
1	2	240	U
1	2	248	U
1	2	249	C
1	2	256	A
1	2	259	U
1	2	264	A
1	2	266	U
1	2	267	C
1	2	271	U
1	2	274	C
1	2	275	C
1	2	276	U
1	2	278	G
1	2	279	U
1	2	280	G

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Mol	Chain	Res	Type
1	2	286	G
1	2	300	A
1	2	301	U
1	2	307	C
1	2	308	C
1	2	311	A
1	2	313	C
1	2	314	A
1	2	315	A
1	2	319	U
1	2	320	C
1	2	321	G
1	2	332	A
1	2	336	G
1	2	337	C
1	2	358	A
1	2	359	A
1	2	360	C
1	2	379	U
1	2	389	G
1	2	399	A
1	2	400	A
1	2	401	C
1	2	403	G
1	2	405	U
1	2	411	A
1	2	412	U
1	2	415	A
1	2	416	A
1	2	418	G
1	2	421	G
1	2	422	G
1	2	423	C
1	2	424	A
1	2	425	G
1	2	427	A
1	2	433	G
1	2	436	A
1	2	438	U
1	2	439	U
1	2	440	A
1	2	443	C

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Mol	Chain	Res	Type
1	2	444	A
1	2	447	C
1	2	459	A
1	2	467	A
1	2	468	C
1	2	474	A
1	2	479	G
1	2	482	A
1	2	483	C
1	2	485	G
1	2	486	G
1	2	488	C
1	2	489	C
1	2	490	C
1	2	491	A
1	2	492	U
1	2	493	U
1	2	495	G
1	2	496	G
1	2	499	C
1	2	502	G
1	2	505	A
1	2	506	U
1	2	507	U
1	2	509	G
1	2	516	U
1	2	518	C
1	2	519	A
1	2	526	A
1	2	527	U
1	2	533	A
1	2	534	A
1	2	535	C
1	2	537	A
1	2	539	G
1	2	540	A
1	2	541	A
1	2	542	C
1	2	543	A
1	2	547	G
1	2	557	U
1	2	558	C

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Mol	Chain	Res	Type
1	2	564	C
1	2	565	C
1	2	567	G
1	2	576	G
1	2	578	A
1	2	584	A
1	2	587	U
1	2	593	A
1	2	594	G
1	2	605	A
1	2	610	U
1	2	618	A
1	2	619	A
1	2	620	A
1	2	621	A
1	2	622	A
1	2	623	G
1	2	634	A
1	2	637	U
1	2	638	U
1	2	641	G
1	2	650	G
1	2	651	U
1	2	652	C
1	2	657	C
1	2	659	G
1	2	660	A
1	2	661	C
1	2	663	U
1	2	664	U
1	2	671	C
1	2	672	G
1	2	675	C
1	2	676	U
1	2	679	U
1	2	680	U
1	2	681	U
1	2	684	A
1	2	685	A
1	2	686	C
1	2	693	U
1	2	694	U

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Mol	Chain	Res	Type
1	2	695	U
1	2	696	C
1	2	697	C
1	2	698	U
1	2	701	U
1	2	702	G
1	2	704	C
1	2	709	C
1	2	710	U
1	2	711	G
1	2	712	U
1	2	713	A
1	2	714	C
1	2	715	U
1	2	717	C
1	2	718	U
1	2	719	U
1	2	721	U
1	2	722	G
1	2	723	G
1	2	724	G
1	2	727	C
1	2	729	G
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	736	C
1	2	737	A
1	2	738	G
1	2	741	C
1	2	742	U
1	2	753	A
1	2	755	A
1	2	761	G
1	2	765	G
1	2	766	PSU
1	2	771	A
1	2	774	A
1	2	778	G
1	2	779	A
1	2	780	A

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Mol	Chain	Res	Type
1	2	782	G
1	2	783	C
1	2	788	A
1	2	789	U
1	2	792	A
1	2	793	U
1	2	794	U
1	2	809	G
1	2	811	A
1	2	812	U
1	2	813	A
1	2	814	G
1	2	817	C
1	2	819	U
1	2	820	U
1	2	821	U
1	2	822	G
1	2	826	C
1	2	827	U
1	2	828	A
1	2	829	U
1	2	830	U
1	2	832	U
1	2	837	G
1	2	839	U
1	2	840	U
1	2	845	G
1	2	848	C
1	2	859	U
1	2	862	A
1	2	864	A
1	2	875	G
1	2	876	G
1	2	885	U
1	2	895	U
1	2	896	C
1	2	897	A
1	2	898	G
1	2	905	A
1	2	911	U
1	2	912	G
1	2	913	G

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Mol	Chain	Res	Type
1	2	915	U
1	2	916	U
1	2	917	U
1	2	919	U
1	2	920	U
1	2	932	A
1	2	934	U
1	2	941	G
1	2	947	G
1	2	950	A
1	2	958	U
1	2	959	U
1	2	965	A
1	2	969	A
1	2	970	A
1	2	972	A
1	2	981	U
1	2	982	A
1	2	986	G
1	2	987	A
1	2	991	A
1	2	993	G
1	2	995	U
1	2	1003	U
1	2	1009	C
1	2	1011	U
1	2	1015	C
1	2	1025	A
1	2	1026	A
1	2	1027	C
1	2	1030	U
1	2	1031	G
1	2	1038	A
1	2	1039	G
1	2	1041	G
1	2	1042	A
1	2	1049	G
1	2	1050	G
1	2	1051	U
1	2	1052	G
1	2	1054	U
1	2	1055	U

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Mol	Chain	Res	Type
1	2	1056	U
1	2	1057	U
1	2	1058	C
1	2	1059	U
1	2	1062	U
1	2	1075	A
1	2	1081	C
1	2	1082	G
1	2	1084	G
1	2	1086	A
1	2	1091	A
1	2	1095	C
1	2	1096	U
1	2	1097	U
1	2	1099	G
1	2	1103	U
1	2	1104	C
1	2	1108	G
1	2	1110	G
1	2	1113	G
1	2	1137	A
1	2	1142	A
1	2	1149	G
1	2	1150	A
1	2	1153	G
1	2	1157	C
1	2	1158	C
1	2	1161	C
1	2	1162	A
1	2	1163	G
1	2	1166	G
1	2	1182	A
1	2	1184	U
1	2	1188	A
1	2	1189	C
1	2	1190	B8N
1	2	1193	A
1	2	1195	A
1	2	1198	G
1	2	1199	G
1	2	1201	A
1	2	1207	A

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Mol	Chain	Res	Type
1	2	1211	G
1	2	1213	U
1	2	1216	A
1	2	1217	G
1	2	1224	U
1	2	1226	A
1	2	1227	G
1	2	1228	G
1	2	1230	U
1	2	1236	G
1	2	1237	A
1	2	1241	A
1	2	1243	A
1	2	1244	G
1	2	1245	C
1	2	1247	C
1	2	1249	U
1	2	1250	U
1	2	1251	C
1	2	1254	G
1	2	1255	A
1	2	1256	U
1	2	1257	U
1	2	1258	U
1	2	1259	U
1	2	1260	G
1	2	1265	U
1	2	1268	U
1	2	1269	G
1	2	1272	G
1	2	1283	C
1	2	1284	U
1	2	1296	G
1	2	1297	U
1	2	1298	G
1	2	1306	U
1	2	1313	U
1	2	1314	U
1	2	1319	U
1	2	1320	A
1	2	1321	A
1	2	1323	G

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Mol	Chain	Res	Type
1	2	1324	A
1	2	1336	A
1	2	1337	C
1	2	1339	U
1	2	1343	A
1	2	1344	A
1	2	1345	A
1	2	1346	U
1	2	1347	A
1	2	1353	G
1	2	1355	U
1	2	1360	C
1	2	1361	U
1	2	1362	U
1	2	1363	G
1	2	1364	C
1	2	1366	G
1	2	1369	U
1	2	1370	G
1	2	1371	A
1	2	1376	U
1	2	1380	A
1	2	1383	G
1	2	1388	U
1	2	1390	U
1	2	1392	G
1	2	1396	U
1	2	1397	C
1	2	1398	A
1	2	1400	G
1	2	1401	C
1	2	1408	A
1	2	1409	A
1	2	1410	G
1	2	1411	U
1	2	1413	U
1	2	1414	G
1	2	1418	C
1	2	1425	A
1	2	1426	2MG
1	2	1429	C
1	2	1430	U

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Mol	Chain	Res	Type
1	2	1431	G
1	2	1442	A
1	2	1443	G
1	2	1444	A
1	2	1455	C
1	2	1456	G
1	2	1457	C
1	2	1458	A
1	2	1464	G
1	2	1469	A
1	2	1471	U
1	2	1475	G
1	2	1476	G
1	2	1481	A
1	2	1482	G
1	2	1484	G
1	2	1488	A
1	2	1489	C
1	2	1490	A
1	2	1491	A
1	2	1494	U
1	2	1498	C
1	2	1499	C
1	2	1510	G
1	2	1512	U
1	2	1513	A
1	2	1514	A
1	2	1518	U
1	2	1519	G
1	2	1521	G
1	2	1522	A
1	2	1523	A
1	2	1533	U
1	2	1534	G
1	2	1535	C
1	2	1538	G
1	2	1540	G
1	2	1554	A
1	2	1555	U
1	2	1556	U
1	2	1557	A
1	2	1558	U

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Mol	Chain	Res	Type
1	2	1566	C
1	2	1571	A
1	2	1572	G
1	2	1595	A
1	2	1597	C
1	2	1598	A
1	2	1599	G
1	2	1614	G
1	2	1617	C
1	2	1620	G
1	2	1624	U
1	2	1632	C
1	2	1633	A
1	2	1639	C
1	2	1647	G
1	2	1655	U
1	2	1656	G
1	2	1678	G
1	2	1679	A
1	2	1680	U
1	2	1682	U
1	2	1685	U
1	2	1686	U
1	2	1687	A
1	2	1688	G
1	2	1691	A
1	2	1692	A
1	2	1693	G
1	2	1694	G
1	2	1695	G
1	2	1697	G
1	2	1698	C
1	2	1699	A
1	2	1700	A
1	2	1702	U
1	2	1703	C
1	2	1704	C
1	2	1707	C
1	2	1709	C
1	2	1710	A
1	2	1711	G
1	2	1712	A

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Mol	Chain	Res	Type
1	2	1715	G
1	2	1725	G
1	2	1728	A
1	2	1734	G
1	2	1742	A
1	2	1743	G
1	2	1748	A
1	2	1754	A
1	2	1755	G
1	2	1758	G
1	2	1763	A
1	2	1764	A
1	2	1766	G
1	2	1767	U
1	2	1768	U
1	2	1778	G
1	2	1780	MA6
1	2	1781	C
1	2	1787	G
1	2	1790	G
1	2	1791	G
1	2	1792	A
1	2	1793	U
1	2	1794	C
1	2	1796	U
1	2	1798	A
38	1	8	U
38	1	9	1MG
38	1	10	2MG
38	1	13	C
38	1	14	A
38	1	15	G
38	1	16	H2U
38	1	18	G
38	1	19	G
38	1	20	A
38	1	21	A
38	1	22	G
38	1	23	C
38	1	26	M2G
38	1	33	U
38	1	34	C

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Mol	Chain	Res	Type
38	1	37	T6A
38	1	43	G
38	1	46	7MG
38	1	47	H2U
38	1	48	5MC
38	1	49	5MC
38	1	58	1MA
38	1	60	A
38	1	61	C
38	1	75	C

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	74	U
1	2	216	A
1	2	217	A
1	2	239	C
1	2	277	U
1	2	279	U
1	2	637	U
1	2	649	U
1	2	660	A
1	2	670	G
1	2	695	U
1	2	700	C
1	2	781	A
1	2	810	A
1	2	828	A
1	2	1080	A
1	2	1198	G
1	2	1206	C
1	2	1343	A
1	2	1430	U
1	2	1455	C
1	2	1470	C
1	2	1513	A
1	2	1571	A
1	2	1573	7MG
1	2	1613	C
1	2	1623	C
1	2	1765	G

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Mol	Chain	Res	Type
1	2	1797	U
38	1	8	U
38	1	47	H2U
38	1	58	1MA
38	1	74	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	B8N	2	1190	1	25,29,30	3.37	7 (28%)	28,42,45	1.98	9 (32%)
1	MA6	2	1780	1	23,26,27	1.36	4 (17%)	33,38,41	4.20	14 (42%)
38	5MC	1	49	38	19,22,23	3.62	8 (42%)	26,32,35	1.17	4 (15%)
38	1MA	1	58	38	21,25,26	2.91	5 (23%)	30,37,40	2.41	8 (26%)
1	7MG	2	1573	38,1	23,26,27	3.42	11 (47%)	27,39,42	2.17	10 (37%)
1	PSU	2	998	1	18,21,22	4.45	8 (44%)	21,30,33	2.00	6 (28%)
1	PSU	2	465	1	18,21,22	4.49	7 (38%)	21,30,33	1.95	5 (23%)
1	2MG	2	1570	1	23,26,27	2.90	8 (34%)	33,38,41	3.12	12 (36%)
38	T6A	1	37	38	31,34,35	2.03	8 (25%)	43,49,52	2.57	14 (32%)
38	H2U	1	47	38	18,21,22	3.16	5 (27%)	19,30,33	1.51	4 (21%)
38	RIA	1	64	38	35,38,39	4.30	20 (57%)	50,57,60	3.50	19 (38%)
38	H2U	1	16	38	18,21,22	3.13	5 (27%)	19,30,33	1.46	4 (21%)
38	2MG	1	10	38	23,26,27	2.87	9 (39%)	33,38,41	3.22	12 (36%)
1	5MC	2	1637	1	19,22,23	3.45	8 (42%)	26,32,35	0.98	2 (7%)
38	M2G	1	26	38	24,27,28	2.71	8 (33%)	33,40,43	2.52	10 (30%)
1	PSU	2	1289	1	18,21,22	4.50	7 (38%)	21,30,33	2.09	5 (23%)
38	1MG	1	9	38	23,26,27	3.04	7 (30%)	33,39,42	2.13	9 (27%)
38	7MG	1	46	38	23,26,27	3.64	11 (47%)	27,39,42	2.20	9 (33%)
1	5MC	2	1006	1	19,22,23	3.42	8 (42%)	26,32,35	0.98	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	2	120	1	18,21,22	4.53	7 (38%)	21,30,33	1.96	5 (23%)
1	PSU	2	766	1	18,21,22	4.41	8 (44%)	21,30,33	2.12	6 (28%)
1	2MG	2	1426	44,1	23,26,27	2.84	9 (39%)	33,38,41	3.23	12 (36%)
38	5MC	1	48	38	19,22,23	3.69	8 (42%)	26,32,35	1.00	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	B8N	2	1190	1	-	4/16/34/35	0/2/2/2
1	MA6	2	1780	1	-	3/11/29/30	0/3/3/3
38	5MC	1	49	38	-	3/7/25/26	0/2/2/2
38	1MA	1	58	38	-	2/7/25/26	0/3/3/3
1	7MG	2	1573	38,1	-	0/7/37/38	0/3/3/3
1	PSU	2	998	1	-	1/7/25/26	0/2/2/2
1	PSU	2	465	1	-	0/7/25/26	0/2/2/2
1	2MG	2	1570	1	-	1/9/27/28	0/3/3/3
38	T6A	1	37	38	-	5/23/41/42	0/3/3/3
38	H2U	1	47	38	-	1/7/38/39	0/2/2/2
38	RIA	1	64	38	-	6/17/51/52	0/4/4/4
38	H2U	1	16	38	-	7/7/38/39	0/2/2/2
38	2MG	1	10	38	-	4/9/27/28	0/3/3/3
1	5MC	2	1637	1	-	0/7/25/26	0/2/2/2
38	M2G	1	26	38	-	2/11/29/30	0/3/3/3
1	PSU	2	1289	1	-	0/7/25/26	0/2/2/2
38	1MG	1	9	38	-	3/7/25/26	0/3/3/3
38	7MG	1	46	38	-	2/7/37/38	0/3/3/3
1	5MC	2	1006	1	-	0/7/25/26	0/2/2/2
1	PSU	2	120	1	-	1/7/25/26	0/2/2/2
1	PSU	2	766	1	-	2/7/25/26	0/2/2/2
1	2MG	2	1426	44,1	-	1/9/27/28	0/3/3/3
38	5MC	1	48	38	-	3/7/25/26	0/2/2/2

All (186) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	64	RIA	C3A-C2A	-12.88	1.24	1.53
1	2	120	PSU	C6-C5	11.19	1.47	1.35
1	2	465	PSU	C6-C5	11.01	1.47	1.35
1	2	1289	PSU	C6-C5	10.95	1.47	1.35
1	2	998	PSU	C6-C5	10.89	1.47	1.35
1	2	766	PSU	C6-C5	10.78	1.47	1.35
38	1	64	RIA	C3'-C2'	-10.74	1.24	1.53
1	2	1289	PSU	C2-N1	10.04	1.49	1.36
1	2	465	PSU	C2-N1	9.94	1.49	1.36
1	2	120	PSU	C2-N1	9.92	1.49	1.36
38	1	47	H2U	C2-N1	9.78	1.49	1.35
38	1	16	H2U	C2-N1	9.74	1.49	1.35
38	1	64	RIA	C1'-C2'	9.73	1.65	1.52
1	2	766	PSU	C2-N1	9.61	1.49	1.36
1	2	998	PSU	C2-N1	9.57	1.49	1.36
38	1	58	1MA	C2-N3	9.07	1.47	1.30
38	1	46	7MG	C8-N9	8.76	1.51	1.45
1	2	1190	B8N	C6-N1	8.48	1.57	1.36
38	1	48	5MC	C5-C4	8.19	1.50	1.44
38	1	9	1MG	C2-N3	8.16	1.46	1.33
38	1	48	5MC	C6-C5	8.08	1.47	1.34
38	1	49	5MC	C6-C5	8.06	1.47	1.34
1	2	1573	7MG	C8-N9	7.83	1.51	1.45
38	1	37	T6A	C10-N6	7.79	1.54	1.37
1	2	1190	B8N	C4-N3	-7.74	1.26	1.40
1	2	1637	5MC	C6-C5	7.73	1.47	1.34
1	2	1570	2MG	C2-N3	7.62	1.46	1.32
1	2	1006	5MC	C6-C5	7.59	1.47	1.34
38	1	49	5MC	C5-C4	7.54	1.49	1.44
38	1	10	2MG	C2-N3	7.45	1.46	1.32
1	2	1190	B8N	C4-C5	7.42	1.64	1.47
38	1	46	7MG	C5-N7	7.30	1.44	1.35
1	2	998	PSU	C2-N3	7.29	1.49	1.37
1	2	1637	5MC	C5-C4	7.23	1.49	1.44
1	2	1426	2MG	C2-N3	7.22	1.45	1.32
38	1	9	1MG	C2-N2	7.22	1.46	1.34
1	2	1289	PSU	C2-N3	7.19	1.49	1.37
1	2	120	PSU	C2-N3	7.14	1.49	1.37
1	2	766	PSU	C2-N3	7.10	1.49	1.37
1	2	1006	5MC	C5-C4	7.08	1.49	1.44
1	2	465	PSU	C2-N3	6.97	1.49	1.37
38	1	58	1MA	C4-N3	6.80	1.49	1.35
1	2	1573	7MG	C5-N7	6.76	1.44	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1570	2MG	C4-N3	6.72	1.49	1.34
38	1	26	M2G	C4-N3	6.68	1.49	1.34
38	1	47	H2U	C2-N3	6.67	1.49	1.38
38	1	9	1MG	C4-N3	6.67	1.49	1.34
38	1	16	H2U	C2-N3	6.52	1.49	1.38
38	1	10	2MG	C4-N3	6.52	1.49	1.34
38	1	64	RIA	O4'-C4A	-6.34	1.30	1.45
1	2	1426	2MG	C4-N3	6.29	1.48	1.34
38	1	26	M2G	C2-N3	6.18	1.47	1.32
38	1	48	5MC	C4-N3	6.10	1.43	1.34
38	1	49	5MC	C4-N3	6.02	1.43	1.34
38	1	26	M2G	C2-N2	5.97	1.46	1.35
38	1	46	7MG	C2-N3	5.91	1.47	1.33
38	1	46	7MG	C4-N3	5.83	1.47	1.34
1	2	1006	5MC	C4-N3	5.76	1.43	1.34
1	2	1190	B8N	C2-N1	5.74	1.56	1.39
1	2	1637	5MC	C4-N3	5.73	1.43	1.34
38	1	64	RIA	O1'-C1'	-5.73	1.31	1.41
1	2	1573	7MG	C2-N3	5.72	1.47	1.33
38	1	48	5MC	C2-N3	5.67	1.47	1.36
38	1	10	2MG	C2-N2	5.65	1.45	1.33
1	2	766	PSU	O4-C4	-5.63	1.12	1.23
1	2	1426	2MG	C2-N2	5.63	1.45	1.33
1	2	1570	2MG	C2-N2	5.62	1.45	1.33
1	2	120	PSU	O4-C4	-5.62	1.12	1.23
38	1	49	5MC	C2-N3	5.60	1.47	1.36
1	2	1289	PSU	O4-C4	-5.60	1.12	1.23
1	2	465	PSU	O4-C4	-5.57	1.13	1.23
1	2	1573	7MG	C4-N3	5.50	1.46	1.34
1	2	998	PSU	O4-C4	-5.47	1.13	1.23
1	2	1006	5MC	C2-N3	5.45	1.47	1.36
38	1	64	RIA	C3A-C4A	5.44	1.66	1.53
1	2	120	PSU	C6-N1	5.37	1.45	1.36
1	2	1637	5MC	C2-N3	5.37	1.47	1.36
1	2	465	PSU	C6-N1	5.25	1.44	1.36
38	1	46	7MG	C4-N9	5.24	1.44	1.37
1	2	1289	PSU	C6-N1	5.20	1.44	1.36
1	2	998	PSU	C6-N1	5.11	1.44	1.36
1	2	1190	B8N	C6-C5	5.09	1.42	1.35
38	1	47	H2U	C4-N3	5.05	1.46	1.37
1	2	1573	7MG	C4-N9	4.99	1.44	1.37
38	1	10	2MG	C2-N1	4.98	1.44	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1426	2MG	C2-N1	4.95	1.44	1.36
1	2	1570	2MG	C2-N1	4.93	1.44	1.36
1	2	766	PSU	C6-N1	4.92	1.44	1.36
38	1	16	H2U	C4-N3	4.91	1.45	1.37
38	1	64	RIA	C6-N6	4.86	1.46	1.34
38	1	46	7MG	C2-N2	4.79	1.45	1.34
38	1	49	5MC	C2-N1	4.72	1.50	1.40
38	1	37	T6A	C10-N11	4.64	1.48	1.35
1	2	1573	7MG	C2-N2	4.60	1.44	1.34
38	1	64	RIA	C1A-N9	-4.45	1.34	1.46
38	1	48	5MC	C6-N1	4.45	1.45	1.38
38	1	48	5MC	C2-N1	4.45	1.49	1.40
38	1	49	5MC	C6-N1	4.41	1.45	1.38
1	2	1190	B8N	C1'-C5	-4.40	1.40	1.50
1	2	1637	5MC	C2-N1	4.29	1.49	1.40
38	1	58	1MA	C2-N1	4.26	1.44	1.35
1	2	1637	5MC	C6-N1	4.23	1.45	1.38
1	2	1006	5MC	C2-N1	4.22	1.48	1.40
1	2	998	PSU	C4-N3	4.18	1.46	1.38
1	2	1006	5MC	C6-N1	4.11	1.45	1.38
38	1	58	1MA	C5-C6	4.06	1.54	1.43
38	1	26	M2G	C2-N1	4.03	1.46	1.36
38	1	9	1MG	C2-N1	4.02	1.44	1.37
1	2	465	PSU	C4-N3	4.02	1.46	1.38
1	2	1289	PSU	C4-N3	3.99	1.46	1.38
1	2	120	PSU	C4-N3	3.98	1.46	1.38
1	2	1573	7MG	C2-N1	3.95	1.47	1.37
38	1	64	RIA	O4'-C1A	3.94	1.51	1.42
38	1	46	7MG	C2-N1	3.89	1.47	1.37
1	2	766	PSU	C4-N3	3.88	1.46	1.38
38	1	64	RIA	O2'-C2'	3.71	1.52	1.43
38	1	46	7MG	C5-C6	3.68	1.52	1.43
38	1	64	RIA	C2A-C1A	3.53	1.61	1.53
1	2	766	PSU	O2-C2	-3.50	1.15	1.23
1	2	465	PSU	O2-C2	-3.48	1.16	1.23
1	2	1289	PSU	O2-C2	-3.46	1.16	1.23
1	2	1573	7MG	C5-C6	3.46	1.52	1.43
1	2	998	PSU	O2-C2	-3.38	1.16	1.23
1	2	120	PSU	O2-C2	-3.37	1.16	1.23
38	1	64	RIA	O3'-C3'	3.35	1.51	1.43
38	1	46	7MG	C6-N1	3.33	1.45	1.38
1	2	1573	7MG	C6-N1	3.25	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	26	M2G	C5-N7	-3.23	1.32	1.39
1	2	1780	MA6	C5-N7	-3.20	1.33	1.39
1	2	1570	2MG	C5-N7	-3.06	1.32	1.39
38	1	64	RIA	C3'-C4'	3.06	1.60	1.53
38	1	64	RIA	O3A-C3A	3.04	1.50	1.43
38	1	49	5MC	CM5-C5	3.02	1.58	1.50
38	1	64	RIA	C5-C4	-3.00	1.33	1.39
38	1	48	5MC	CM5-C5	2.98	1.57	1.50
38	1	9	1MG	C5-C6	2.93	1.53	1.45
38	1	37	T6A	C5-C4	-2.91	1.33	1.39
1	2	1426	2MG	C5-N7	-2.89	1.33	1.39
1	2	1780	MA6	C5-C4	-2.87	1.34	1.39
1	2	1006	5MC	CM5-C5	2.87	1.57	1.50
38	1	10	2MG	C5-N7	-2.87	1.33	1.39
38	1	26	M2G	C5-C6	2.85	1.55	1.44
1	2	1637	5MC	CM5-C5	2.78	1.57	1.50
38	1	49	5MC	C4-N4	2.76	1.41	1.34
38	1	9	1MG	C5-N7	-2.73	1.33	1.39
38	1	64	RIA	C5'-C4'	-2.68	1.43	1.51
38	1	64	RIA	P'-O5'	2.67	1.68	1.60
38	1	58	1MA	C5-N7	-2.63	1.33	1.39
38	1	37	T6A	C6-N6	2.62	1.45	1.39
1	2	1006	5MC	C4-N4	2.61	1.40	1.34
38	1	26	M2G	C6-N1	2.61	1.43	1.38
38	1	46	7MG	O6-C6	-2.60	1.18	1.23
1	2	1426	2MG	C6-N1	2.59	1.43	1.38
1	2	1780	MA6	C6-N6	2.57	1.43	1.36
38	1	10	2MG	C5-C6	2.56	1.54	1.44
38	1	48	5MC	C4-N4	2.55	1.40	1.34
1	2	1637	5MC	C4-N4	2.55	1.40	1.34
1	2	1426	2MG	O6-C6	-2.54	1.18	1.23
1	2	1570	2MG	O6-C6	-2.51	1.18	1.23
38	1	10	2MG	C6-N1	2.50	1.43	1.38
1	2	1426	2MG	C5-C6	2.47	1.53	1.44
1	2	1570	2MG	C5-C6	2.46	1.53	1.44
1	2	1570	2MG	C6-N1	2.44	1.43	1.38
1	2	1573	7MG	O6-C6	-2.43	1.19	1.23
38	1	16	H2U	O2-C2	-2.42	1.18	1.23
38	1	10	2MG	O6-C6	-2.36	1.19	1.23
38	1	47	H2U	O2-C2	-2.35	1.18	1.23
1	2	1426	2MG	C4-N9	-2.33	1.32	1.38
38	1	64	RIA	C8-N9	-2.23	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	64	RIA	O2A-C2A	2.22	1.49	1.43
38	1	9	1MG	O6-C6	-2.22	1.18	1.23
38	1	64	RIA	C5-N7	-2.22	1.35	1.39
38	1	47	H2U	O4-C4	-2.18	1.18	1.23
38	1	16	H2U	O4-C4	-2.17	1.19	1.23
1	2	998	PSU	O4'-C1'	-2.14	1.40	1.43
38	1	37	T6A	C12-C13	-2.12	1.48	1.52
38	1	37	T6A	C8-N9	-2.11	1.33	1.37
38	1	26	M2G	C4-N9	-2.11	1.32	1.38
38	1	10	2MG	C4-N9	-2.11	1.32	1.38
1	2	1190	B8N	O2-C2	-2.07	1.18	1.22
38	1	37	T6A	C8-N7	2.06	1.35	1.31
1	2	1573	7MG	C5-C4	2.06	1.44	1.37
38	1	46	7MG	C5-C4	2.06	1.44	1.37
38	1	37	T6A	C5-C6	-2.02	1.37	1.41
1	2	766	PSU	O4'-C1'	-2.02	1.41	1.43
1	2	1780	MA6	C8-N9	-2.01	1.34	1.37

All (182) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	64	RIA	C1A-N9-C8	-12.96	98.34	127.09
1	2	1780	MA6	N1-C6-N6	-11.98	102.26	116.86
38	1	64	RIA	C4-N9-C1A	11.67	153.91	126.63
1	2	1780	MA6	C1'-N9-C8	-11.23	102.18	127.09
38	1	10	2MG	C1'-N9-C8	-10.42	97.13	126.73
1	2	1780	MA6	C4-N9-C1'	10.19	150.47	126.63
1	2	1426	2MG	C1'-N9-C8	-9.62	99.41	126.73
38	1	10	2MG	C1'-N9-C4	9.52	154.61	126.49
1	2	1570	2MG	C1'-N9-C8	-9.49	99.76	126.73
1	2	1570	2MG	C1'-N9-C4	9.02	153.13	126.49
1	2	1426	2MG	C1'-N9-C4	8.84	152.60	126.49
38	1	26	M2G	C1'-N9-C8	-8.11	103.70	126.73
38	1	64	RIA	N6-C6-N1	-7.98	100.60	118.38
1	2	1780	MA6	C5-C6-N6	7.97	137.94	125.33
38	1	37	T6A	C1'-N9-C8	-7.04	111.47	127.09
1	2	1426	2MG	C2-N3-C4	6.67	120.34	112.00
38	1	64	RIA	C5-C6-N6	6.52	139.43	123.29
1	2	1570	2MG	C2-N3-C4	6.46	120.08	112.00
38	1	26	M2G	C1'-N9-C4	6.44	145.50	126.49
38	1	58	1MA	C1'-N9-C4	-6.38	107.65	126.49
38	1	10	2MG	C2-N3-C4	6.23	119.79	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	58	1MA	C1'-N9-C8	6.08	144.02	126.73
38	1	37	T6A	N3-C2-N1	-5.78	119.84	128.58
38	1	64	RIA	N3-C2-N1	-5.69	119.96	128.58
1	2	1780	MA6	N1-C2-N3	-5.64	120.04	128.58
38	1	9	1MG	C1'-N9-C4	-5.49	110.26	126.49
38	1	37	T6A	N9-C8-N7	-5.46	106.18	113.94
1	2	1426	2MG	N1-C2-N2	5.43	122.11	116.56
1	2	1289	PSU	C4-N3-C2	-5.31	119.06	126.37
1	2	1570	2MG	C5-C4-N3	-5.22	120.09	128.39
1	2	1190	B8N	C5-C4-N3	5.20	125.59	116.15
38	1	9	1MG	C1'-N9-C8	5.19	141.48	126.73
1	2	766	PSU	C4-N3-C2	-5.11	119.33	126.37
38	1	46	7MG	C5-C6-N1	5.09	119.91	110.94
1	2	465	PSU	C4-N3-C2	-5.07	119.38	126.37
38	1	9	1MG	C5-C4-N3	-5.04	120.37	128.39
1	2	1780	MA6	C5-C4-N3	-4.99	119.84	126.72
38	1	64	RIA	C5-C4-N3	-4.93	119.92	126.72
38	1	37	T6A	C4-N9-C1'	4.92	138.15	126.63
38	1	58	1MA	N1-C2-N3	-4.91	120.16	126.00
38	1	58	1MA	C5-C4-N3	-4.87	120.10	127.27
1	2	120	PSU	C4-N3-C2	-4.82	119.73	126.37
38	1	10	2MG	C5-C4-N3	-4.79	120.77	128.39
1	2	1426	2MG	C5-C4-N3	-4.78	120.78	128.39
1	2	766	PSU	N1-C2-N3	4.74	120.17	115.17
38	1	37	T6A	N6-C10-N11	4.68	120.21	113.77
1	2	998	PSU	C4-N3-C2	-4.66	119.95	126.37
1	2	1573	7MG	C5-C6-N1	4.58	119.00	110.94
38	1	46	7MG	C2-N3-C4	4.55	120.14	112.30
1	2	1289	PSU	N1-C2-N3	4.53	119.95	115.17
38	1	26	M2G	C5-C4-N3	-4.46	121.30	128.39
38	1	37	T6A	C5-C4-N3	-4.43	120.62	126.72
38	1	37	T6A	C4-N9-C8	4.42	110.38	105.74
1	2	1190	B8N	C4-N3-C2	-4.40	120.20	125.62
1	2	1426	2MG	C2-N1-C6	-4.39	119.24	124.55
1	2	465	PSU	N1-C2-N3	4.34	119.74	115.17
38	1	64	RIA	C1'-C2'-C3'	4.33	107.68	102.29
1	2	120	PSU	N1-C2-N3	4.32	119.72	115.17
1	2	1570	2MG	C2-N1-C6	-4.21	119.46	124.55
38	1	26	M2G	N9-C8-N7	-4.20	105.62	113.40
1	2	998	PSU	N1-C2-N3	4.19	119.59	115.17
1	2	1573	7MG	C2-N3-C4	4.17	119.48	112.30
1	2	1780	MA6	C4-C5-C6	4.17	120.22	115.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1573	7MG	C5-C4-N3	-4.12	120.40	128.13
38	1	46	7MG	C5-C4-N3	-4.07	120.48	128.13
38	1	26	M2G	C2-N3-C4	4.00	119.90	112.51
38	1	64	RIA	N9-C8-N7	-3.97	108.31	113.94
38	1	10	2MG	C2-N1-C6	-3.92	119.81	124.55
1	2	1780	MA6	N9-C8-N7	-3.89	108.41	113.94
38	1	58	1MA	C2-N3-C4	3.89	120.16	112.53
38	1	46	7MG	C4-C5-N7	3.84	109.91	105.38
1	2	1573	7MG	C4-C5-N7	3.80	109.86	105.38
38	1	10	2MG	N1-C2-N2	3.77	120.41	116.56
1	2	1190	B8N	C1'-C5-C4	3.66	123.16	117.61
38	1	9	1MG	C2-N3-C4	3.61	120.09	111.98
38	1	16	H2U	N3-C2-N1	3.56	120.23	116.65
1	2	998	PSU	C6-N1-C2	-3.55	119.39	122.69
38	1	48	5MC	C5-C6-N1	-3.55	119.46	123.31
38	1	64	RIA	C1'-O2A-C2A	-3.54	109.60	117.98
1	2	1780	MA6	C2-N1-C6	3.45	120.26	111.83
1	2	1570	2MG	N1-C2-N2	3.43	120.06	116.56
38	1	64	RIA	C2-N3-C4	3.38	120.08	111.83
1	2	1190	B8N	N3-C2-N1	3.37	120.83	116.72
38	1	47	H2U	N3-C2-N1	3.36	120.03	116.65
38	1	37	T6A	C4-C5-C6	3.36	119.57	116.78
38	1	37	T6A	N3-C4-N9	3.33	132.83	127.17
1	2	766	PSU	C6-N1-C2	-3.32	119.61	122.69
1	2	766	PSU	C6-C5-C4	3.30	120.40	118.17
38	1	37	T6A	C5-N7-C8	3.29	108.62	103.45
1	2	1289	PSU	C6-C5-C4	3.29	120.39	118.17
1	2	1780	MA6	C2-N3-C4	3.28	119.84	111.83
1	2	120	PSU	C6-N1-C2	-3.21	119.71	122.69
1	2	1637	5MC	C5-C6-N1	-3.17	119.87	123.31
38	1	37	T6A	C2-N3-C4	3.12	119.45	111.83
38	1	47	H2U	C5-C4-N3	3.09	119.98	116.69
38	1	58	1MA	N9-C8-N7	-3.06	107.72	113.40
1	2	1426	2MG	N9-C8-N7	-3.05	107.74	113.40
1	2	766	PSU	O2-C2-N1	-3.05	119.65	122.79
38	1	46	7MG	C5-C4-N9	3.01	110.18	106.33
38	1	10	2MG	N9-C8-N7	-3.00	107.84	113.40
38	1	46	7MG	O6-C6-C5	-2.98	120.31	127.62
38	1	9	1MG	N9-C8-N7	-2.98	107.88	113.40
1	2	998	PSU	O2-C2-N1	-2.98	119.72	122.79
38	1	47	H2U	C5-C6-N1	2.96	120.48	111.52
38	1	64	RIA	N3-C4-N9	2.95	132.18	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	9	1MG	C5-C6-N1	2.93	120.43	115.02
38	1	26	M2G	N9-C4-N3	2.93	131.80	125.95
38	1	9	1MG	N9-C4-N3	2.92	131.79	125.95
1	2	1573	7MG	C5-C4-N9	2.91	110.07	106.33
1	2	1780	MA6	N3-C4-N9	2.90	132.10	127.17
38	1	64	RIA	C4A-O4'-C1A	-2.90	103.06	109.47
1	2	120	PSU	C6-C5-C4	2.89	120.12	118.17
1	2	465	PSU	C6-N1-C2	-2.88	120.02	122.69
1	2	1573	7MG	C2-N1-C6	-2.88	119.89	125.11
1	2	1780	MA6	C5-N7-C8	2.87	107.96	103.45
1	2	1190	B8N	O4-C4-N3	-2.86	115.34	119.99
38	1	64	RIA	C5-N7-C8	2.86	107.94	103.45
38	1	37	T6A	C12-N11-C10	2.85	126.73	121.99
38	1	16	H2U	C5-C6-N1	2.85	120.14	111.52
38	1	46	7MG	C2-N1-C6	-2.84	119.96	125.11
1	2	1289	PSU	C6-N1-C2	-2.82	120.07	122.69
1	2	1289	PSU	O2-C2-N1	-2.80	119.90	122.79
1	2	1426	2MG	C5-C6-N1	2.78	120.33	113.25
1	2	1573	7MG	N9-C4-N3	2.78	129.53	125.46
38	1	64	RIA	O4'-C1A-N9	2.77	113.42	108.09
1	2	1570	2MG	N9-C4-N3	2.76	131.48	125.95
1	2	1573	7MG	O6-C6-C5	-2.76	120.85	127.62
1	2	1570	2MG	C5-C6-N1	2.70	120.14	113.25
38	1	26	M2G	C5-C6-N1	2.70	120.12	113.25
38	1	37	T6A	O10-C10-N6	-2.69	118.86	123.64
38	1	26	M2G	C8-N7-C5	2.69	109.05	104.26
1	2	1006	5MC	C5-C6-N1	-2.66	120.42	123.31
1	2	1426	2MG	O6-C6-C5	-2.66	119.51	126.53
38	1	16	H2U	C5-C4-N3	2.65	119.50	116.69
38	1	46	7MG	N9-C4-N3	2.64	129.33	125.46
38	1	47	H2U	O2-C2-N1	-2.61	119.97	123.10
38	1	10	2MG	N9-C4-N3	2.60	131.16	125.95
1	2	465	PSU	O2-C2-N1	-2.55	120.16	122.79
38	1	10	2MG	C5-C6-N1	2.54	119.72	113.25
38	1	26	M2G	C8-N9-C4	2.54	110.78	106.03
1	2	1570	2MG	O6-C6-C5	-2.52	119.87	126.53
1	2	1573	7MG	O4'-C1'-N9	-2.51	105.87	109.30
1	2	1570	2MG	N9-C8-N7	-2.46	108.84	113.40
38	1	26	M2G	O6-C6-C5	-2.44	120.08	126.53
38	1	16	H2U	O2-C2-N1	-2.44	120.17	123.10
1	2	465	PSU	C6-C5-C4	2.43	119.81	118.17
1	2	120	PSU	O2-C2-N1	-2.42	120.29	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1573	7MG	N9-C8-N7	2.41	106.79	103.37
1	2	1190	B8N	C31-N3-C4	2.38	120.55	117.18
1	2	998	PSU	C6-C5-C4	2.37	119.78	118.17
1	2	1570	2MG	CM2-N2-C2	-2.36	118.58	123.65
38	1	49	5MC	C5-C6-N1	-2.33	120.78	123.31
38	1	49	5MC	O2-C2-N3	-2.33	118.66	122.33
38	1	10	2MG	O6-C6-C5	-2.31	120.43	126.53
38	1	64	RIA	O1'-C1'-C2'	2.29	107.90	104.98
1	2	1426	2MG	N9-C4-N3	2.29	130.53	125.95
1	2	998	PSU	O4'-C1'-C2'	2.26	108.28	105.15
1	2	1426	2MG	N1-C2-N3	-2.23	119.92	123.68
38	1	58	1MA	C8-N7-C5	2.22	108.22	104.26
38	1	64	RIA	C2A-C3A-C4A	2.22	106.77	101.99
38	1	46	7MG	N9-C8-N7	2.22	106.51	103.37
38	1	58	1MA	N9-C4-N3	2.22	131.95	126.90
38	1	49	5MC	C5-C4-N3	-2.20	119.50	121.75
1	2	766	PSU	O4'-C1'-C2'	2.19	108.19	105.15
38	1	64	RIA	C4-C5-N7	-2.16	108.12	110.58
1	2	1006	5MC	CM5-C5-C6	-2.13	119.97	122.85
38	1	10	2MG	C8-N7-C5	2.12	108.04	104.26
1	2	1426	2MG	C8-N7-C5	2.10	108.00	104.26
1	2	1570	2MG	N1-C2-N3	-2.10	120.15	123.68
38	1	10	2MG	N1-C2-N3	-2.09	120.16	123.68
1	2	1780	MA6	C4-C5-N7	-2.07	108.22	110.58
38	1	64	RIA	C6-C5-C4	2.06	119.99	117.18
1	2	1190	B8N	C32-C31-N3	-2.06	108.55	112.16
1	2	1780	MA6	C5-C4-N9	2.06	108.05	105.81
1	2	1637	5MC	CM5-C5-C6	-2.05	120.08	122.85
1	2	1190	B8N	O4'-C1'-C2'	2.04	107.98	105.15
38	1	49	5MC	C1'-N1-C2	2.03	122.93	118.44
1	2	1190	B8N	O4-C4-C5	-2.03	119.06	122.58
38	1	64	RIA	C2'-C3'-C4'	2.03	106.52	102.61
38	1	37	T6A	C4-C5-N7	-2.02	108.27	110.58
38	1	9	1MG	O6-C6-C5	-2.02	119.39	124.59
38	1	9	1MG	C8-N7-C5	2.02	107.85	104.26

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	766	PSU	O4'-C4'-C5'-O5'
1	2	1780	MA6	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
38	1	9	1MG	O4'-C4'-C5'-O5'
38	1	9	1MG	C3'-C4'-C5'-O5'
38	1	10	2MG	O4'-C4'-C5'-O5'
38	1	10	2MG	C3'-C4'-C5'-O5'
38	1	16	H2U	C4'-C5'-O5'-P
38	1	16	H2U	O4'-C1'-N1-C6
38	1	26	M2G	C3'-C4'-C5'-O5'
38	1	37	T6A	O4'-C4'-C5'-O5'
38	1	37	T6A	C14-C12-N11-C10
38	1	46	7MG	O4'-C4'-C5'-O5'
38	1	49	5MC	O4'-C4'-C5'-O5'
38	1	64	RIA	O1'-C4'-C5'-O5'
1	2	766	PSU	C3'-C4'-C5'-O5'
38	1	46	7MG	C3'-C4'-C5'-O5'
38	1	64	RIA	C3'-C4'-C5'-O5'
38	1	37	T6A	C13-C12-N11-C10
38	1	16	H2U	C2'-C1'-N1-C6
1	2	1780	MA6	C3'-C4'-C5'-O5'
38	1	26	M2G	O4'-C4'-C5'-O5'
38	1	64	RIA	C3A-C4A-C5A-O5A
38	1	16	H2U	C2'-C1'-N1-C2
38	1	16	H2U	C3'-C4'-C5'-O5'
38	1	49	5MC	C3'-C4'-C5'-O5'
38	1	37	T6A	C3'-C4'-C5'-O5'
38	1	48	5MC	C4'-C5'-O5'-P
38	1	58	1MA	O4'-C4'-C5'-O5'
1	2	1190	B8N	N34-C33-C34-O36
38	1	64	RIA	O4'-C4A-C5A-O5A
38	1	64	RIA	C4A-C5A-O5A-P
38	1	58	1MA	C3'-C4'-C5'-O5'
38	1	37	T6A	C13-C12-C14-C15
1	2	1190	B8N	N34-C33-C34-O35
38	1	16	H2U	O4'-C1'-N1-C2
38	1	48	5MC	O4'-C4'-C5'-O5'
38	1	47	H2U	C3'-C4'-C5'-O5'
38	1	10	2MG	C4'-C5'-O5'-P
1	2	998	PSU	O4'-C1'-C5-C4
38	1	16	H2U	O4'-C4'-C5'-O5'
1	2	1780	MA6	C5-C6-N6-C10
1	2	120	PSU	O4'-C4'-C5'-O5'
1	2	1426	2MG	O4'-C4'-C5'-O5'
38	1	10	2MG	C2'-C1'-N9-C8

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Mol	Chain	Res	Type	Atoms
38	1	49	5MC	C2'-C1'-N1-C6
38	1	64	RIA	C2A-C1A-N9-C8
38	1	48	5MC	C3'-C4'-C5'-O5'
1	2	1570	2MG	C2'-C1'-N9-C8
38	1	9	1MG	C4'-C5'-O5'-P
1	2	1190	B8N	N3-C31-C32-C33
1	2	1190	B8N	C4'-C5'-O5'-P

There are no ring outliers.

16 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	1780	MA6	4	0
38	1	49	5MC	1	0
1	2	1573	7MG	4	0
1	2	998	PSU	2	0
1	2	465	PSU	1	0
1	2	1570	2MG	3	0
38	1	64	RIA	1	0
38	1	16	H2U	3	0
38	1	10	2MG	2	0
1	2	1637	5MC	2	0
38	1	26	M2G	2	0
1	2	1289	PSU	2	0
38	1	9	1MG	2	0
1	2	1006	5MC	1	0
1	2	766	PSU	1	0
1	2	1426	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 102 ligands modelled in this entry, 100 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
47	MET	k	603	-	6,7,8	0.48	0	2,7,9	0.13	0
46	GCP	k	601	-	32,34,34	2.09	3 (9%)	49,54,54	0.88	2 (4%)

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
47	MET	k	603	-	-	2/5/6/8	-
46	GCP	k	601	-	-	3/19/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	k	601	GCP	PB-O3A	10.53	1.70	1.58
46	k	601	GCP	PA-O3A	2.90	1.62	1.59
46	k	601	GCP	PB-O2B	-2.20	1.51	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	k	601	GCP	O2B-PB-O1B	2.85	119.22	109.95
46	k	601	GCP	O1G-PG-C3B	-2.15	106.69	111.37

There are no chirality outliers.

All (5) torsion outliers are listed below:

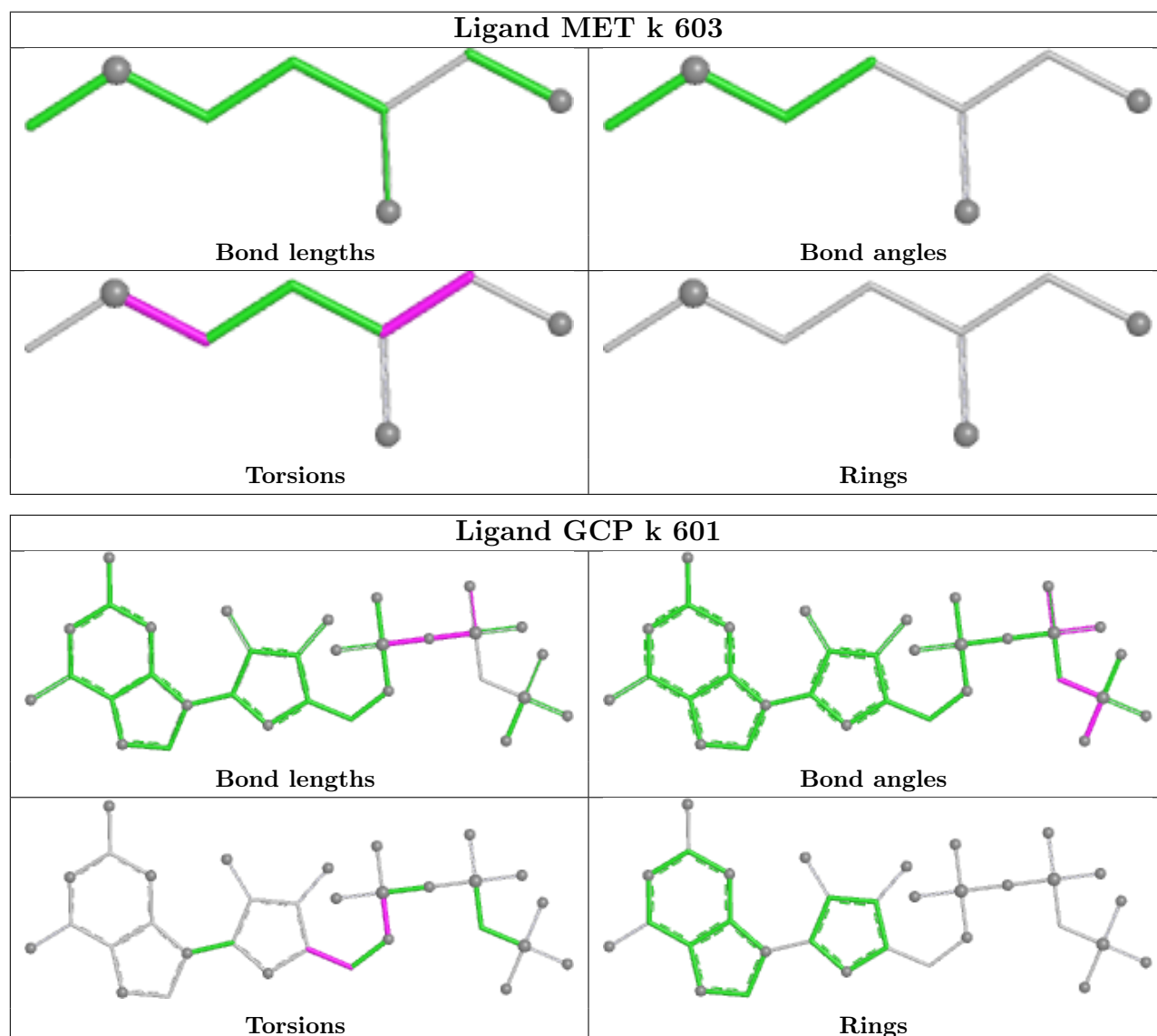
Mol	Chain	Res	Type	Atoms
46	k	601	GCP	C5'-O5'-PA-O3A
47	k	603	MET	O-C-CA-CB
46	k	601	GCP	O4'-C4'-C5'-O5'
46	k	601	GCP	C3'-C4'-C5'-O5'
47	k	603	MET	CB-CG-SD-CE

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	k	601	GCP	2	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	1	3
1	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	64:RIA	O3'	65:G	P	8.59
1	1	63:G	O3'	64:RIA	P	4.32
1	2	1190:B8N	O3'	1191:C	P	3.40
1	1	16:H2U	O3'	18:G	P	3.29

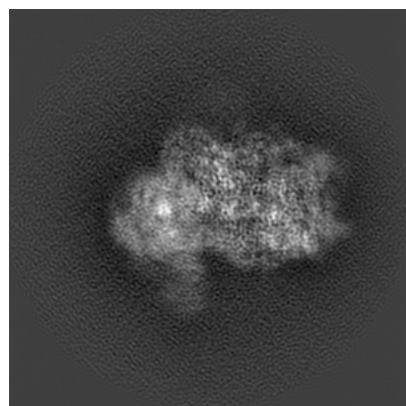
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19808. These allow visual inspection of the internal detail of the map and identification of artifacts.

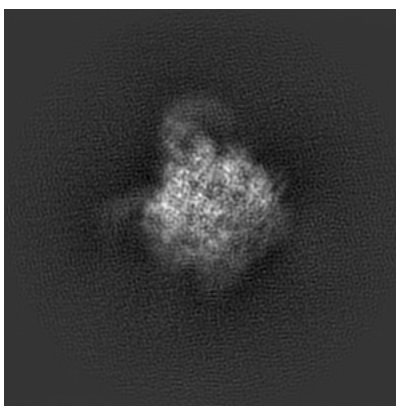
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

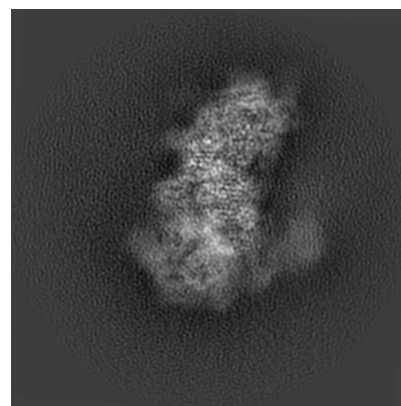
6.1.1 Primary map



X

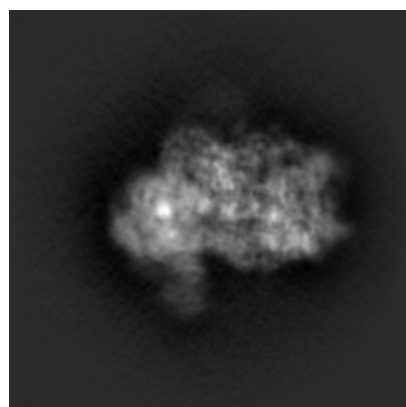


Y

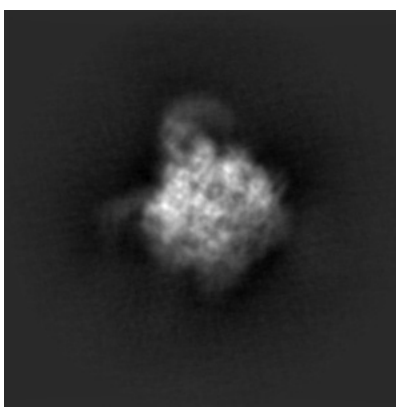


Z

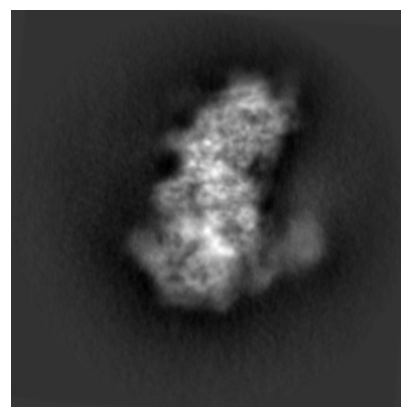
6.1.2 Raw map



X



Y

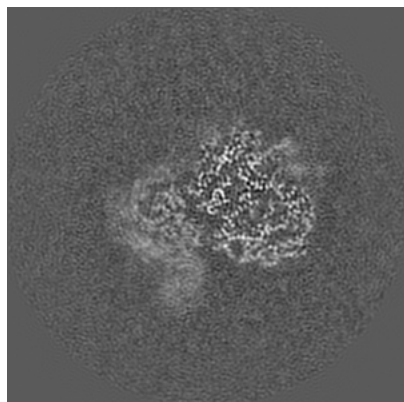


Z

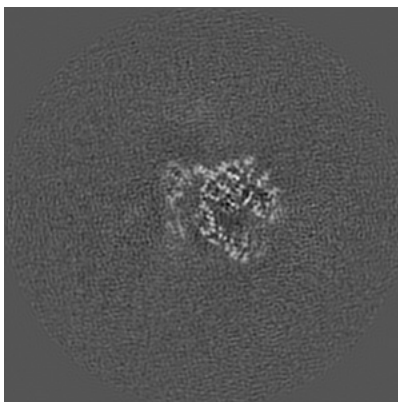
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

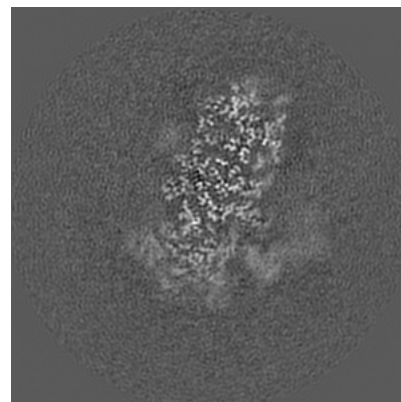
6.2.1 Primary map



X Index: 150

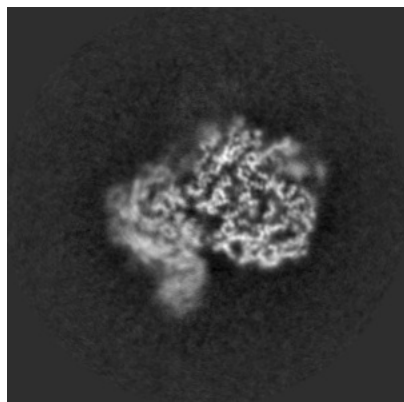


Y Index: 150

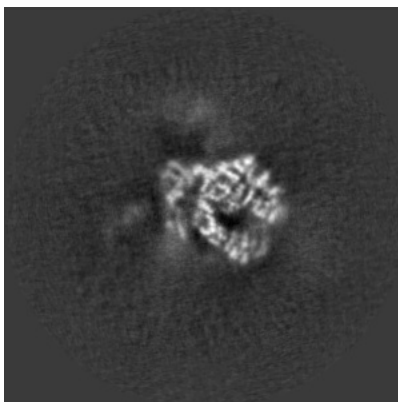


Z Index: 150

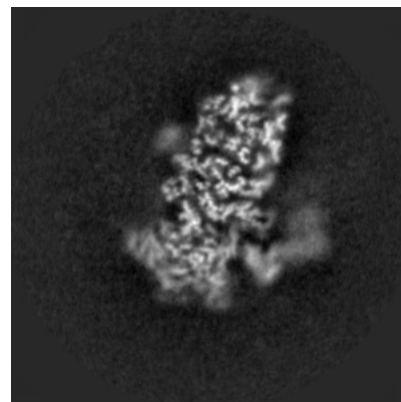
6.2.2 Raw map



X Index: 150



Y Index: 150

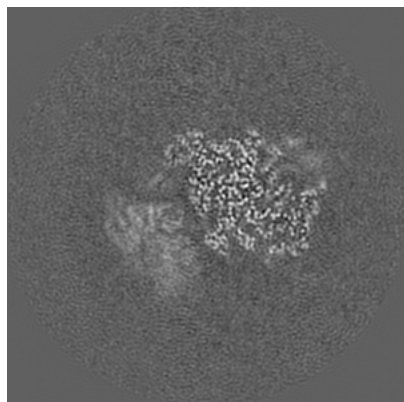


Z Index: 150

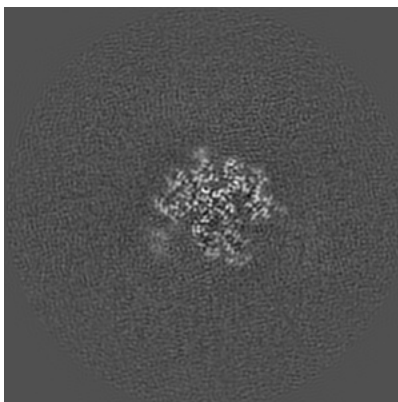
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

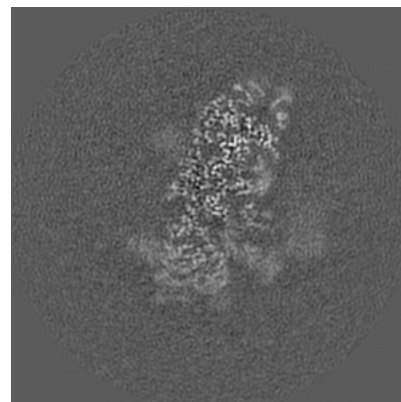
6.3.1 Primary map



X Index: 157

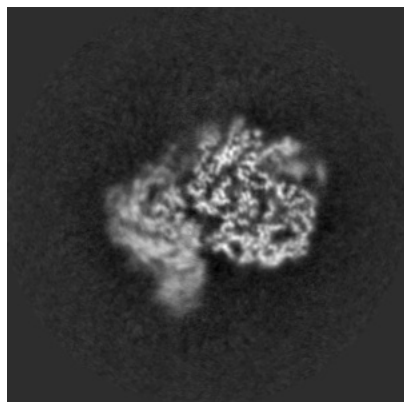


Y Index: 166

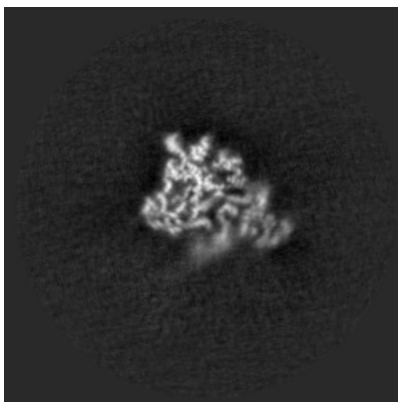


Z Index: 147

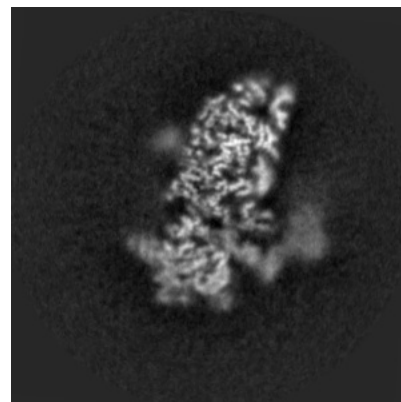
6.3.2 Raw map



X Index: 151



Y Index: 198

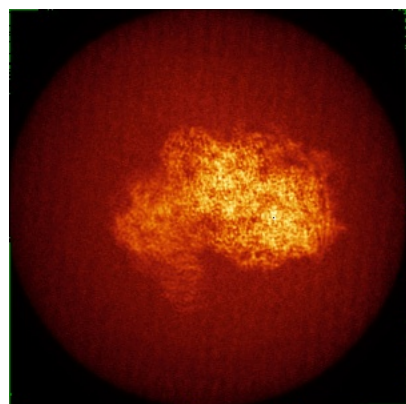


Z Index: 146

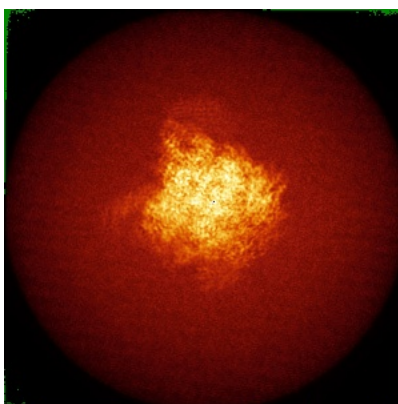
The images above show the largest variance slices of the map in three orthogonal directions.

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

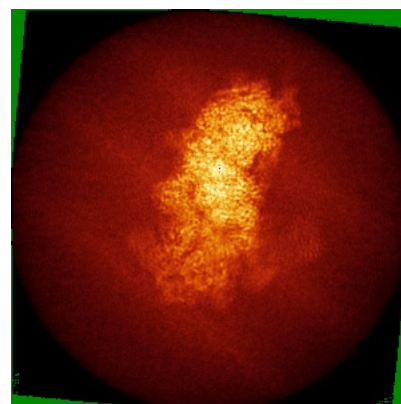
6.4.1 Primary map



X

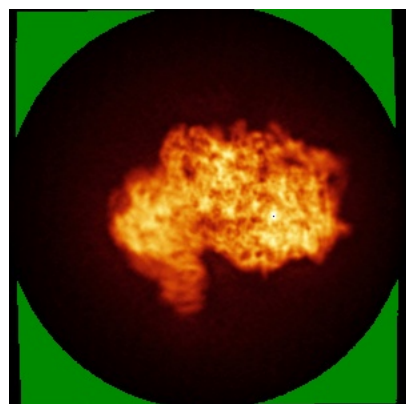


Y

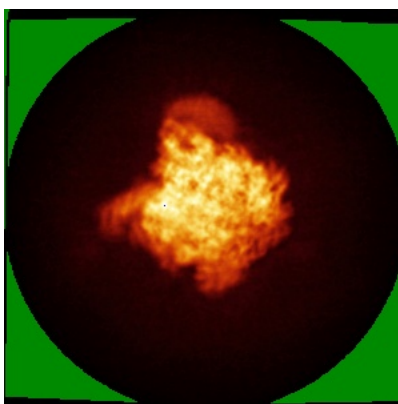


Z

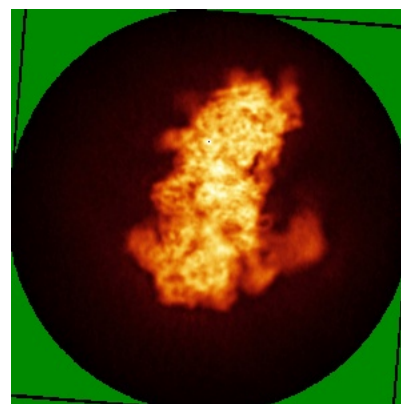
6.4.2 Raw map



X



Y

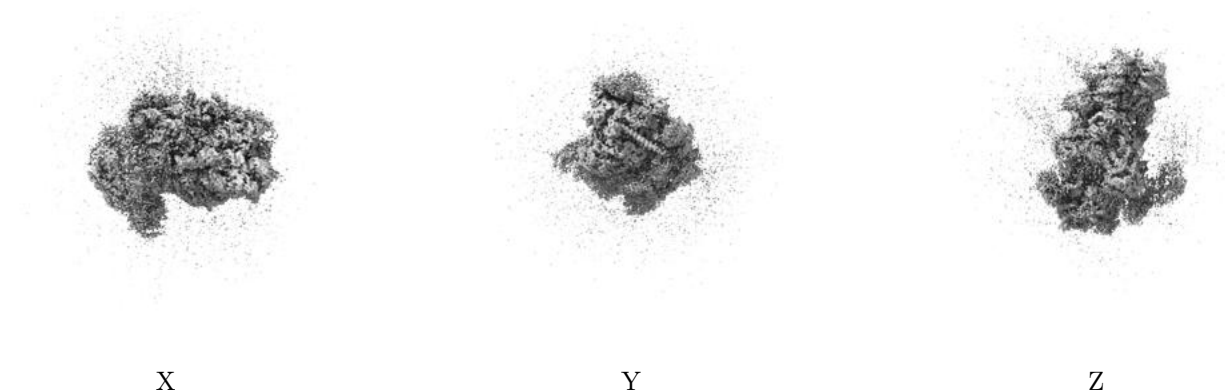


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

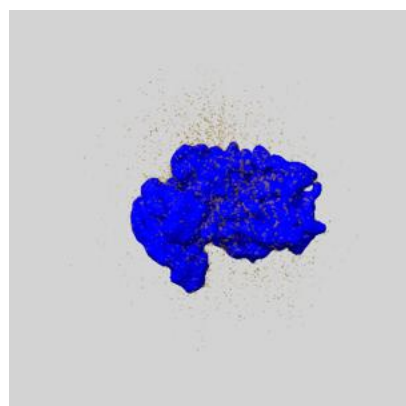
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

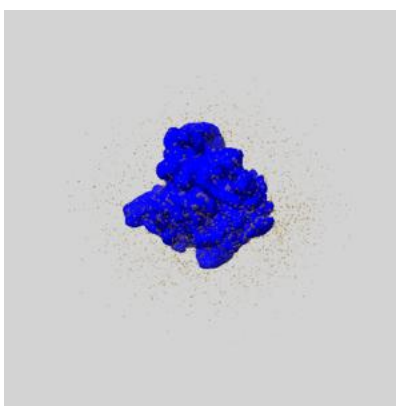
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

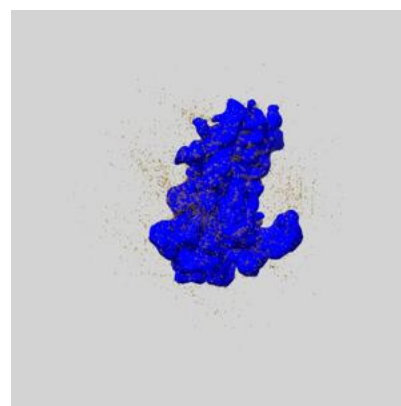
6.6.1 emd_19808_msk_1.map [i](#)



X



Y

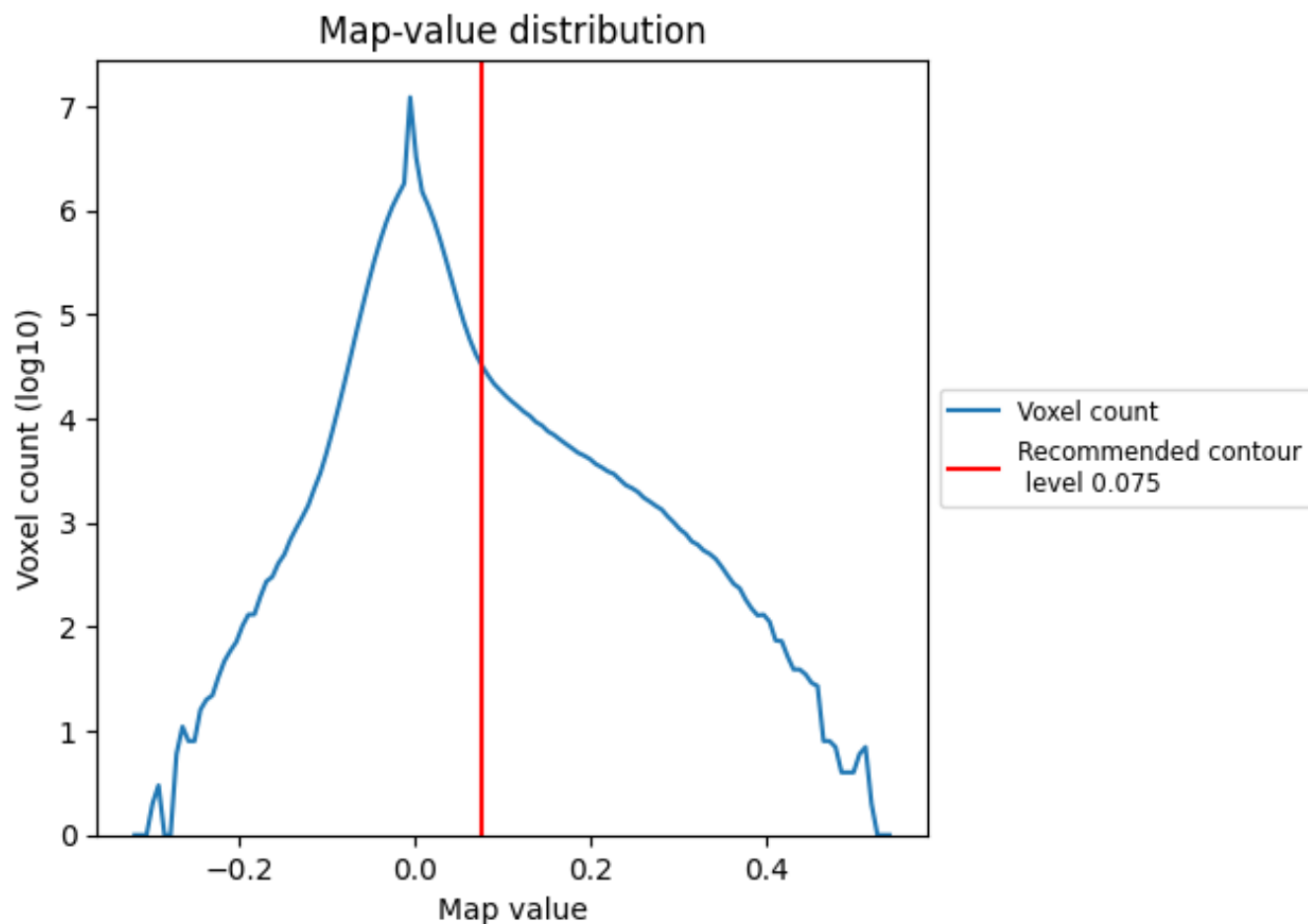


Z

7 Map analysis [i](#)

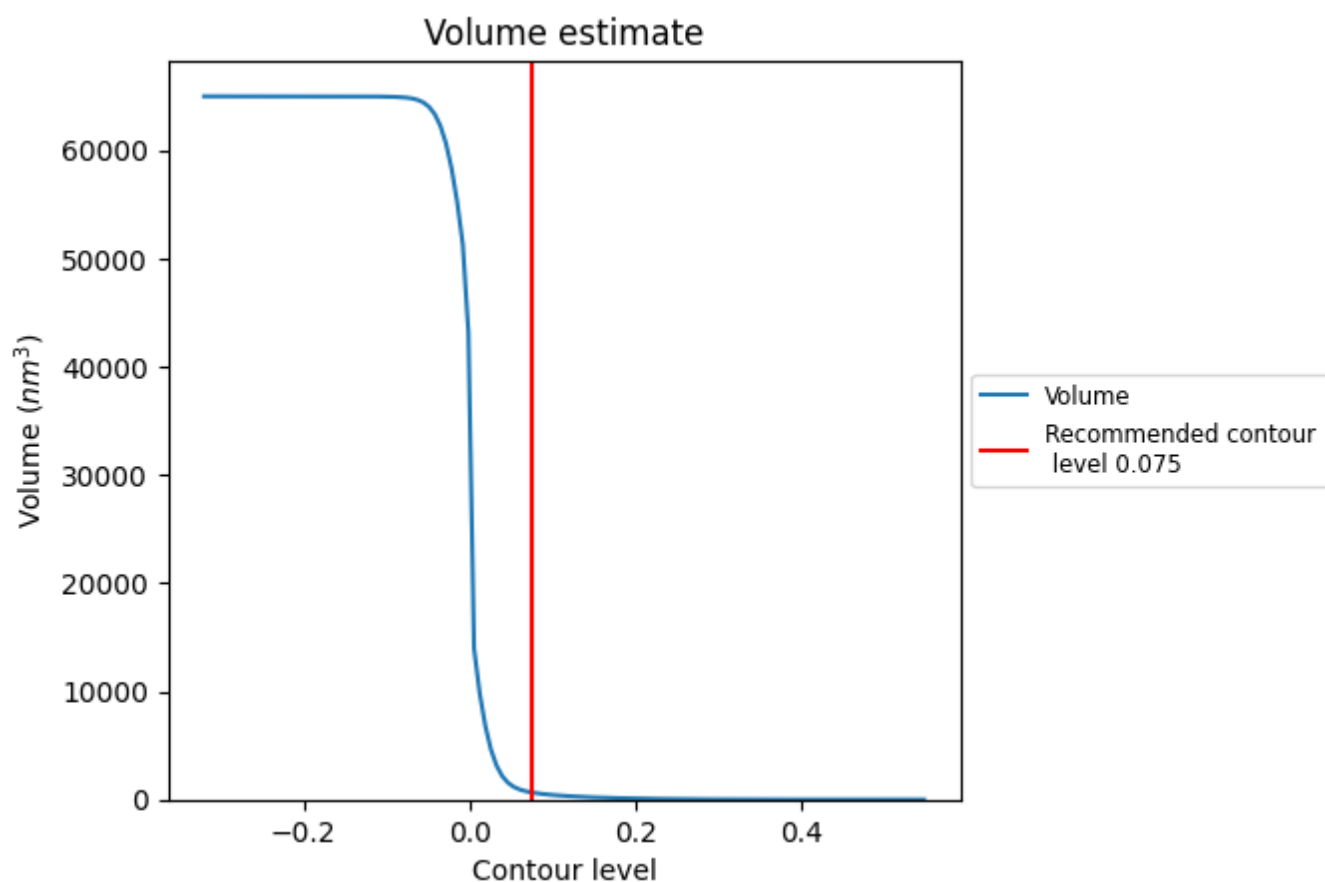
This section contains the results of statistical analysis of the map.

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.

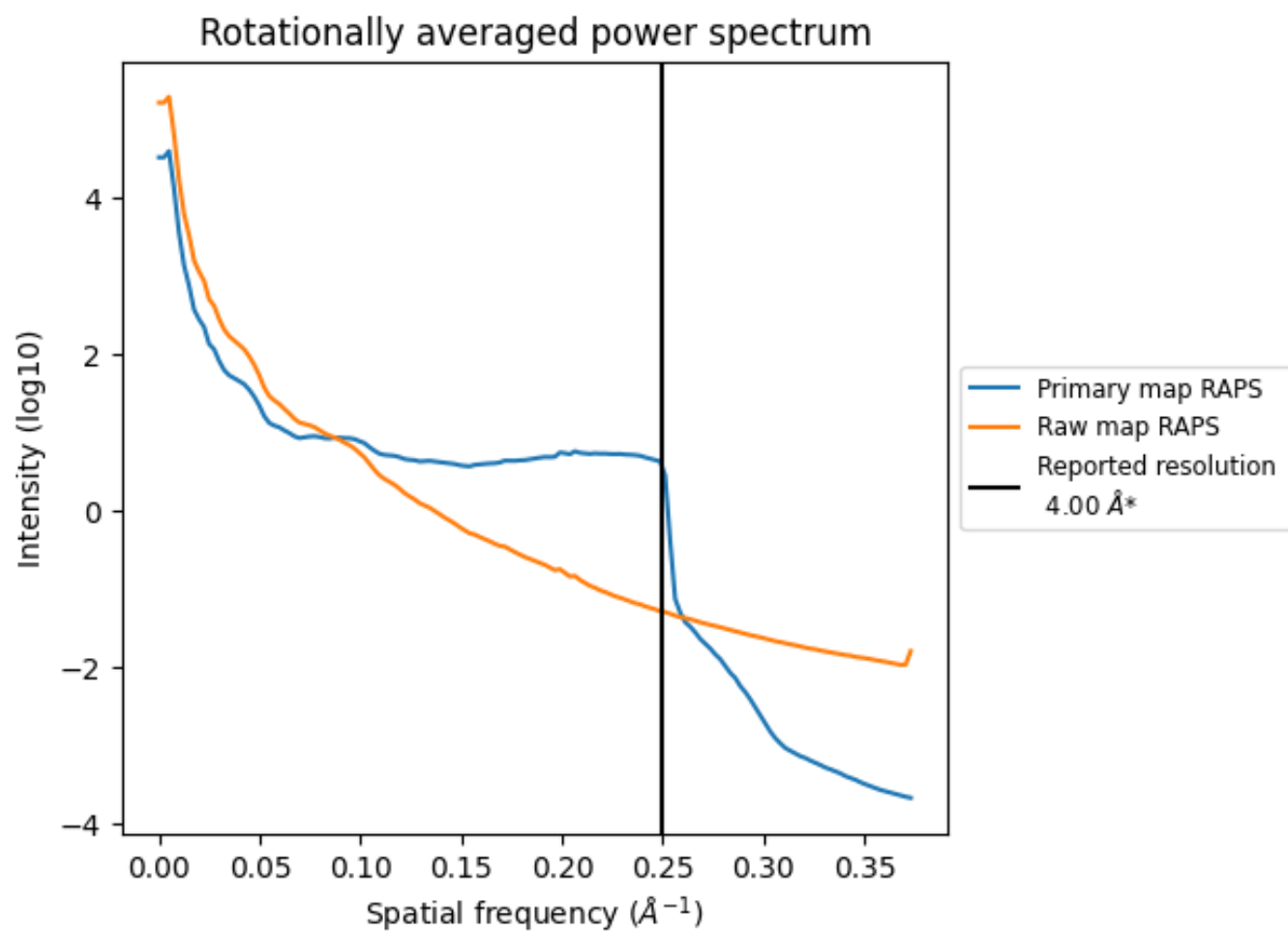
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 654 nm³; this corresponds to an approximate mass of 591 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 ⓘ

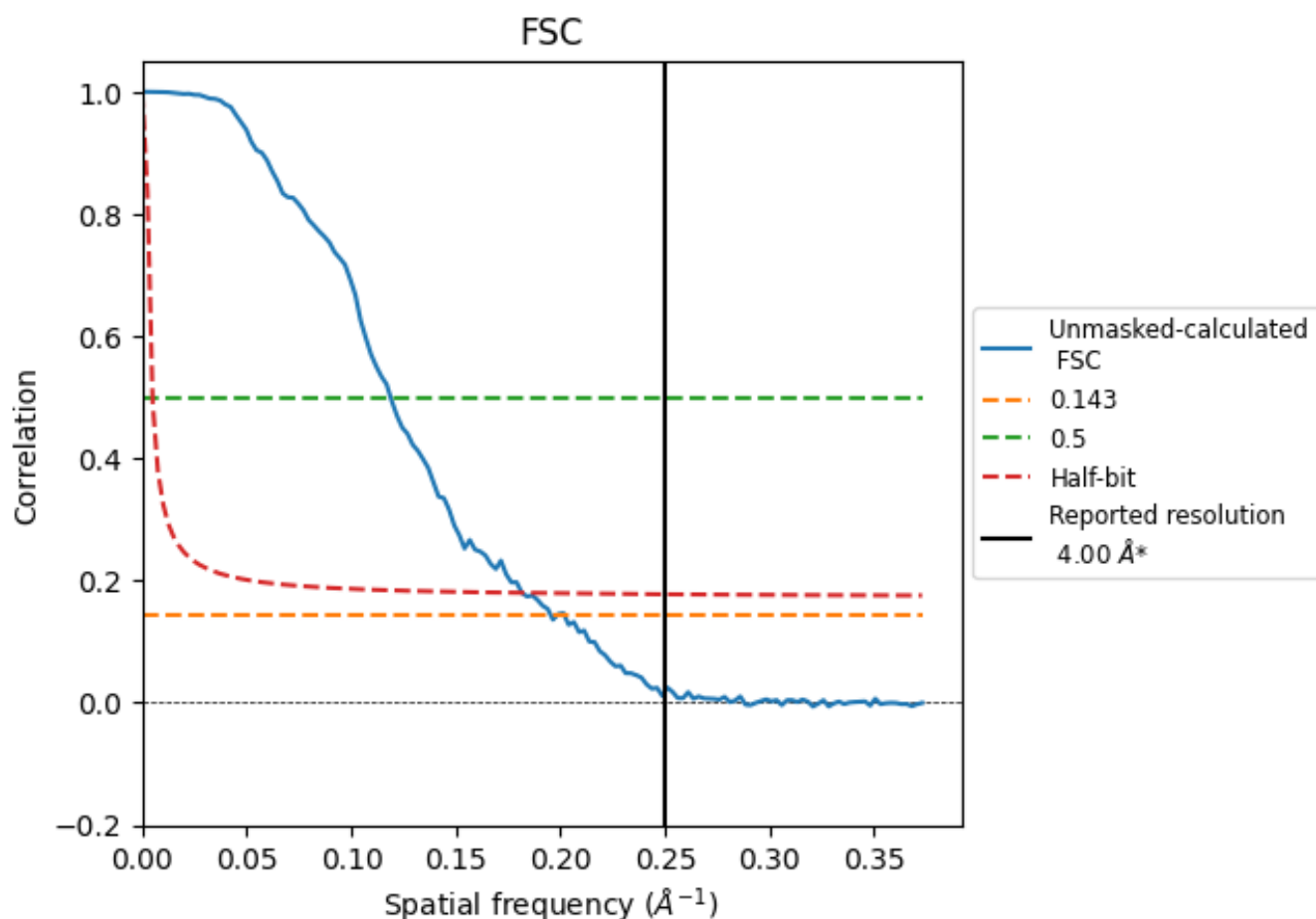


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

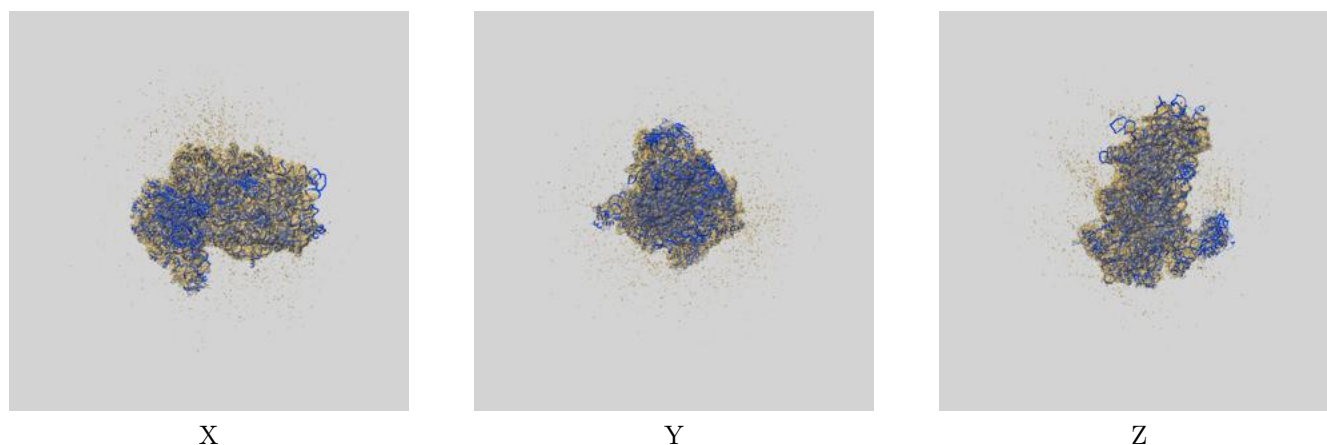
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.12	8.42	5.50

*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 5.12 differs from the reported value 4.0 by more than 10 %

9 Map-model fit [i](#)

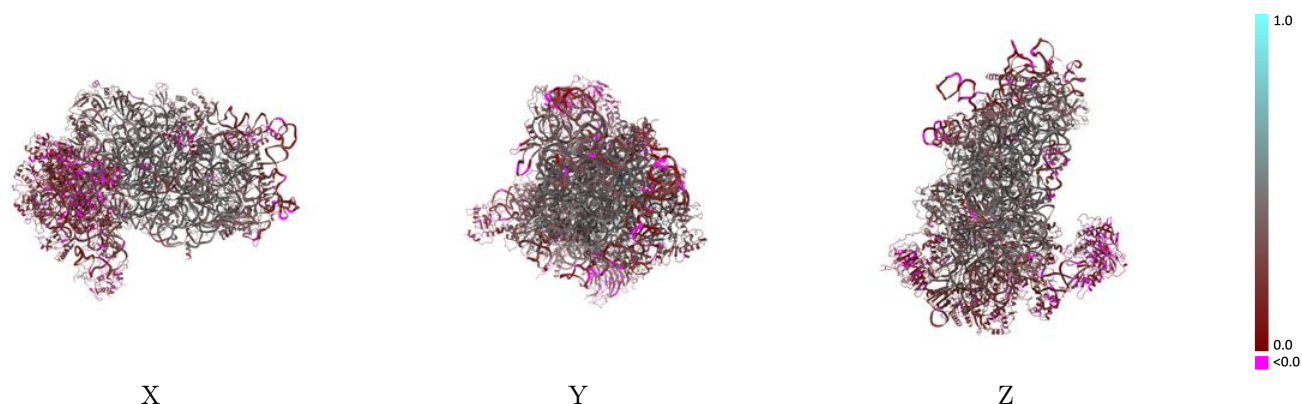
This section contains information regarding the fit between EMDB map EMD-19808 and PDB model 8S8K. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

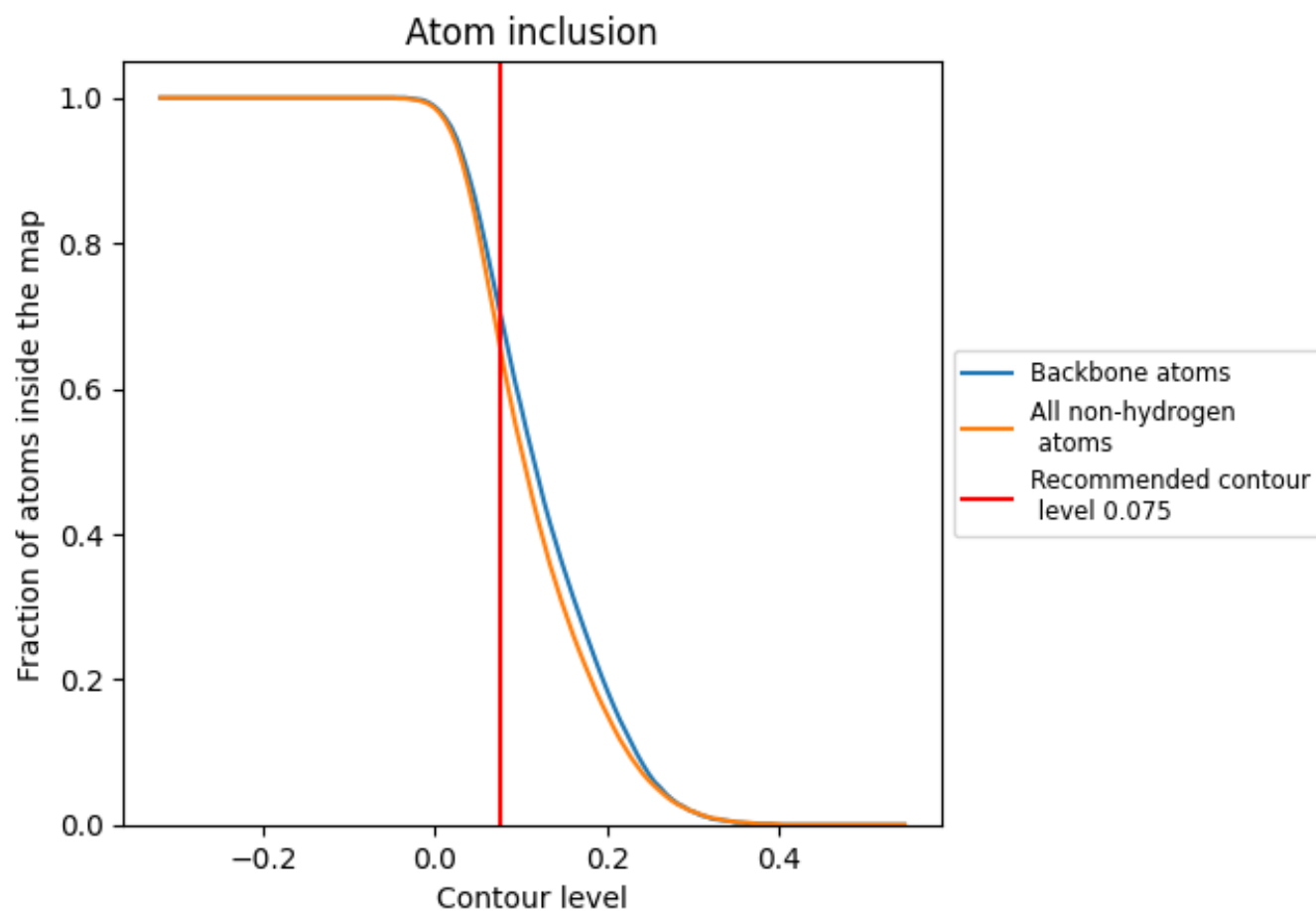


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6620	 0.3180
1	 0.4670	 0.1460
2	 0.8210	 0.3410
3	 0.0780	 0.2130
A	 0.7500	 0.3960
B	 0.7210	 0.3770
C	 0.7810	 0.4330
D	 0.5230	 0.2950
E	 0.8140	 0.4440
F	 0.5360	 0.2530
G	 0.7530	 0.3620
H	 0.6030	 0.3550
I	 0.7520	 0.4020
J	 0.8050	 0.4250
K	 0.4520	 0.2250
L	 0.7370	 0.4230
M	 0.1110	 0.1130
N	 0.7860	 0.4160
O	 0.7450	 0.3920
P	 0.3890	 0.1870
Q	 0.6170	 0.2770
R	 0.5210	 0.3110
S	 0.4530	 0.1950
T	 0.5610	 0.2320
U	 0.4810	 0.2990
V	 0.8130	 0.4260
W	 0.7960	 0.4530
X	 0.8000	 0.4530
Y	 0.8080	 0.4160
Z	 0.1500	 0.1930
a	 0.7870	 0.4330
b	 0.7080	 0.4110
c	 0.5260	 0.3150
d	 0.6020	 0.3040
e	 0.6790	 0.3990



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Chain	Atom inclusion	Q-score
f	 0.2250	 0.1520
g	 0.3520	 0.1570
h	 0.1840	 0.2910
i	 0.5530	 0.3620
j	 0.1580	 0.1750
k	 0.0610	 0.1030
l	 0.0990	 0.1340
m	 0.4830	 0.3130
n	 0.0350	 0.2020