



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 05:19 PM UTC

PDB ID : 8S8D / pdb_00008s8d
EMDB ID : EMD-19801
Title : Structure of a yeast 48S-AUC preinitiation complex in closed conformation (model py48S-AUC-2)
Authors : Villamayor-Belinchon, L.; Sharma, P.; Llacer, J.L.; Hussain, T.
Deposited on : 2024-03-06
Resolution : 3.45 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

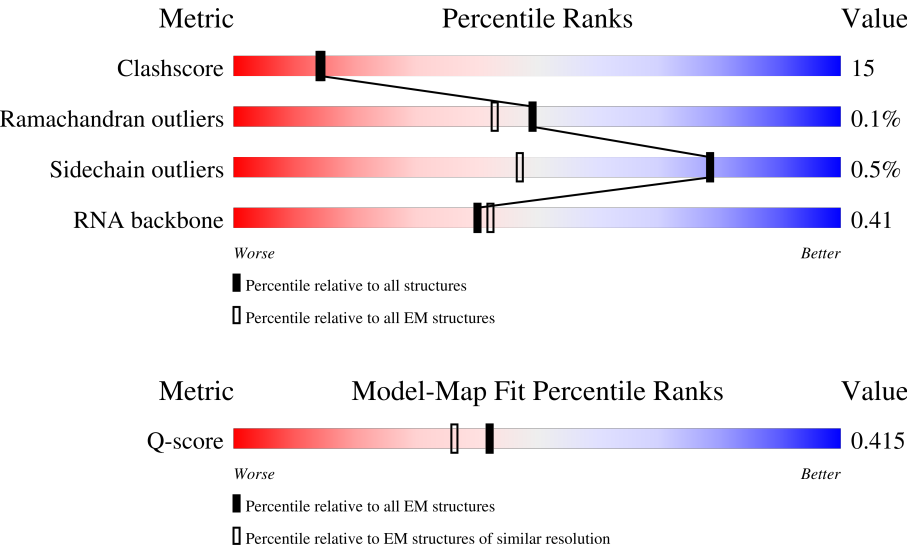
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.45 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.



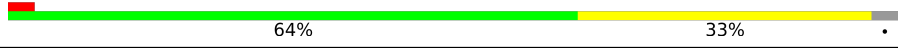
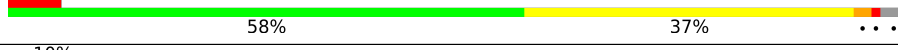
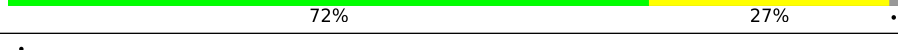
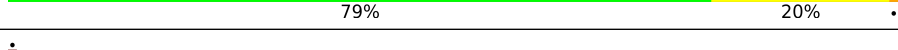
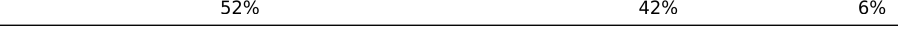
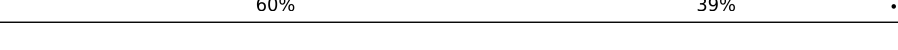
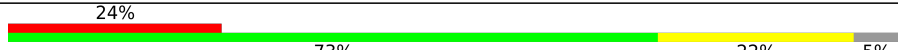
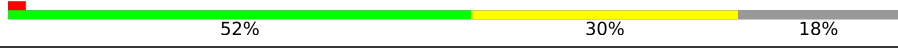
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13836 (2.95 - 3.95)

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	8% 33% 51% 15%
2	A	254	51% 34% 14%
3	B	255	56% 31% 12%

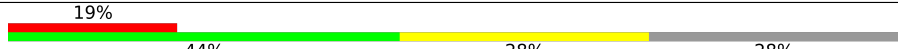
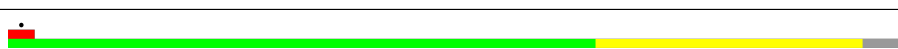
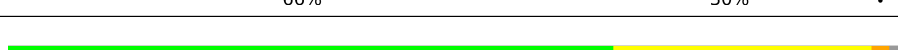
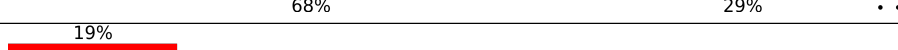
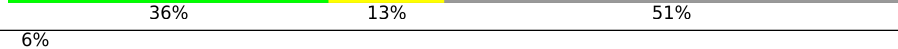
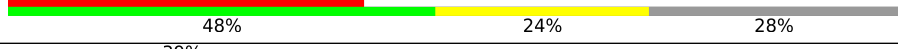
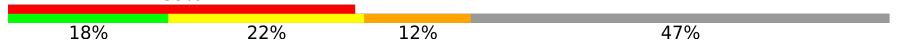
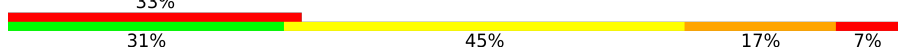
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Mol	Chain	Length	Quality of chain
4	C	259	
5	E	261	
6	G	236	
7	H	190	
8	I	201	
9	J	188	
10	L	156	
11	N	151	
12	O	137	
13	V	87	
14	W	130	
15	X	145	
16	Y	135	
17	a	119	
18	b	82	
19	e	63	
20	h	25	
21	D	237	
22	F	227	
23	K	106	
24	M	134	
25	P	142	
26	Q	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	g	326	
36	i	153	
37	3	49	
38	1	75	
39	j	304	
40	k	527	
41	l	285	

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 86108 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	225	Total	C	N	O	S	0	0
			1796	1135	330	328	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	155	Total	C	N	O	S	0	0
			1248	798	237	210	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 40S 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
			885	553	161	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	S	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
			595	376	111	107	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 KLLA0E12277p.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	110	Total	C	N	O	S	0	0
			870	534	167	164	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	3	26	Total	C	N	O	P	0	0
			536	242	84	184	26		

- 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	23	Total	C	N	O	0	0
			190	124	32	34		

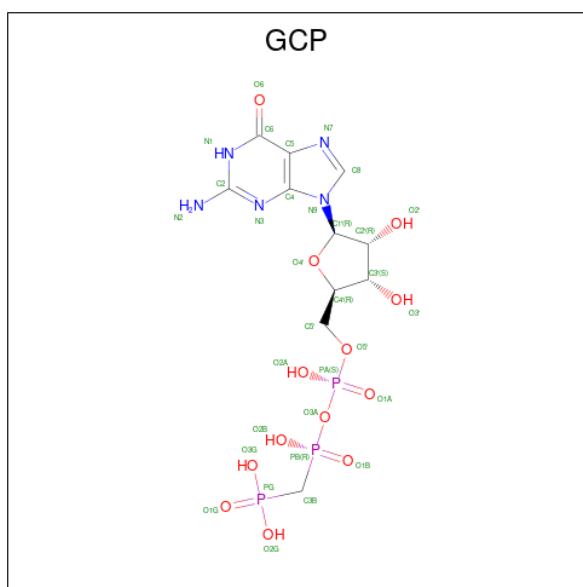
- Molecule 42 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
42	2	112	Total	Mg	0
			112	112	
42	T	1	Total	Mg	0
			1	1	
42	i	1	Total	Mg	0
			1	1	
42	3	1	Total	Mg	0
			1	1	
42	k	1	Total	Mg	0
			1	1	

- Molecule 43 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

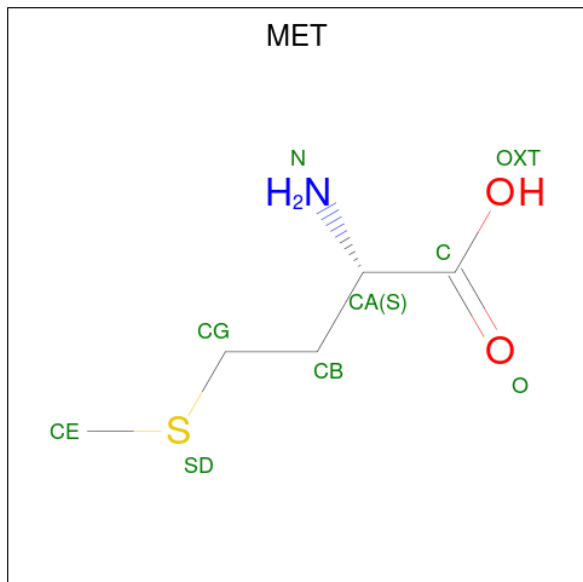
Mol	Chain	Residues	Atoms		AltConf
43	a	1	Total	Zn	0
			1	1	
43	b	1	Total	Zn	0
			1	1	
43	f	1	Total	Zn	0
			1	1	

- Molecule 44 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 45 is METHIONINE (CCD ID: MET) (formula: $C_5H_{11}NO_2S$) (labeled as "Ligand of Interest" by depositor).



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

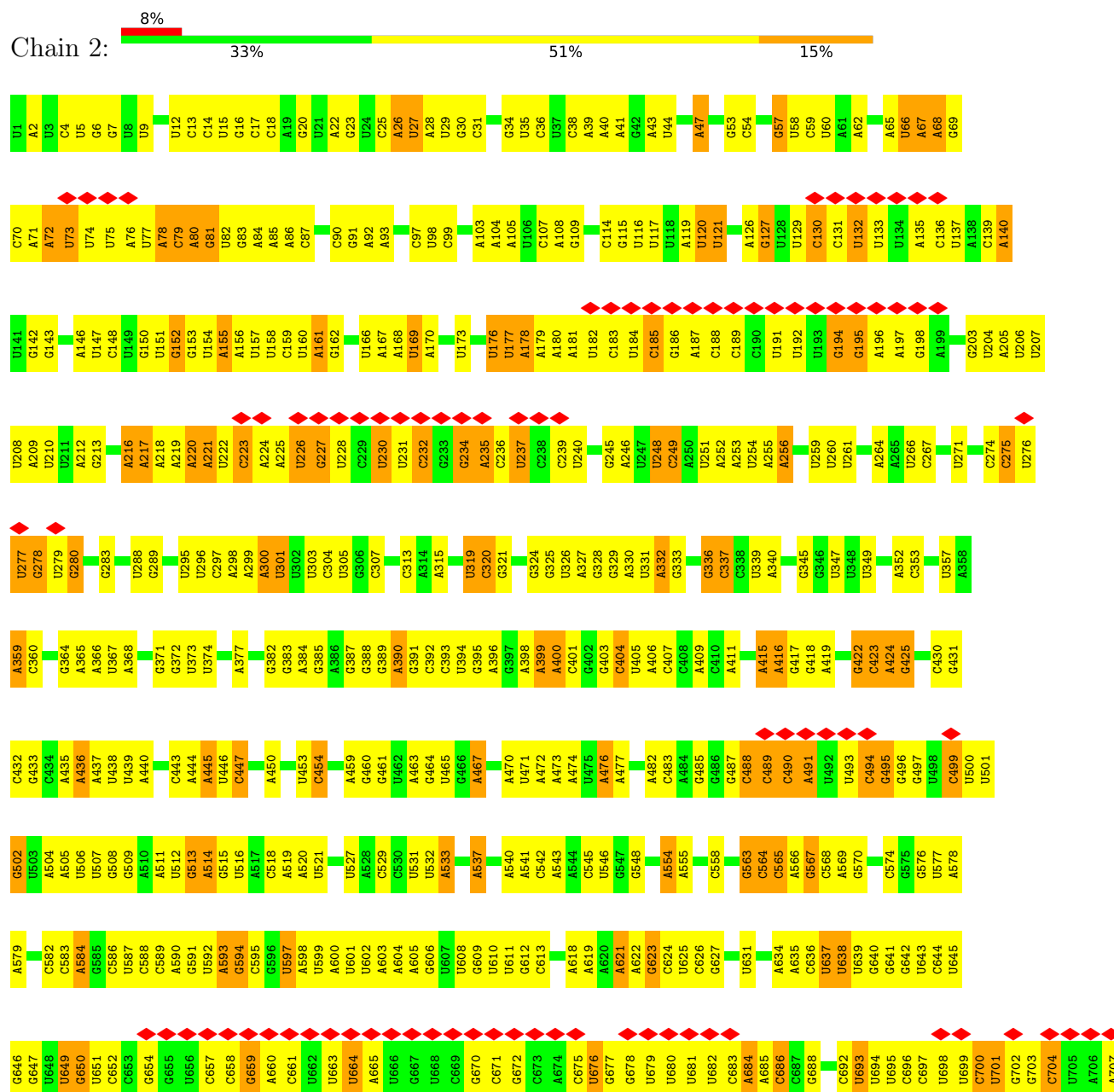
- Molecule 46 is water.

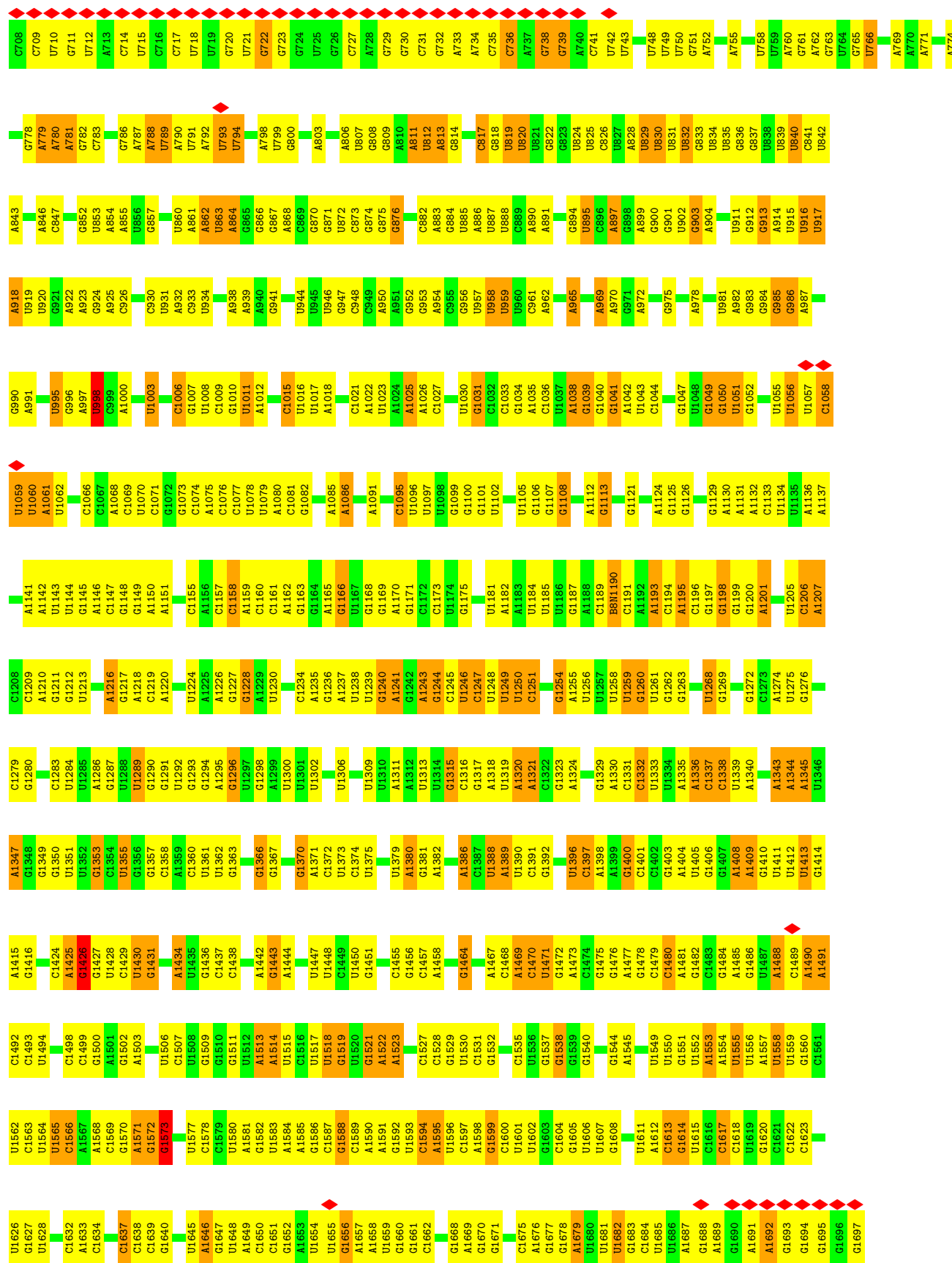
Mol	Chain	Residues	Atoms		AltConf
46	2	3	Total	O	0
			3	3	

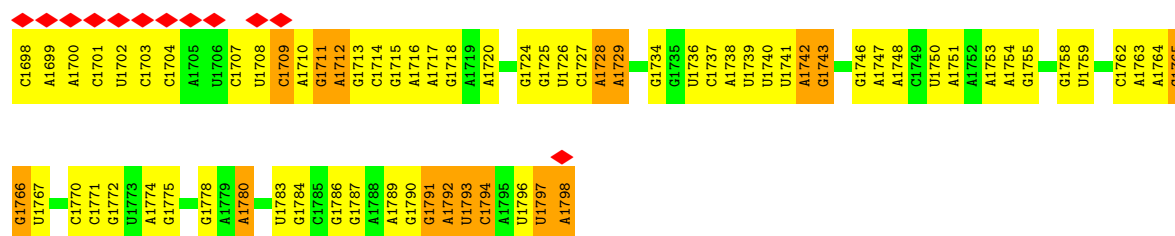
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 18S ribosomal RNA

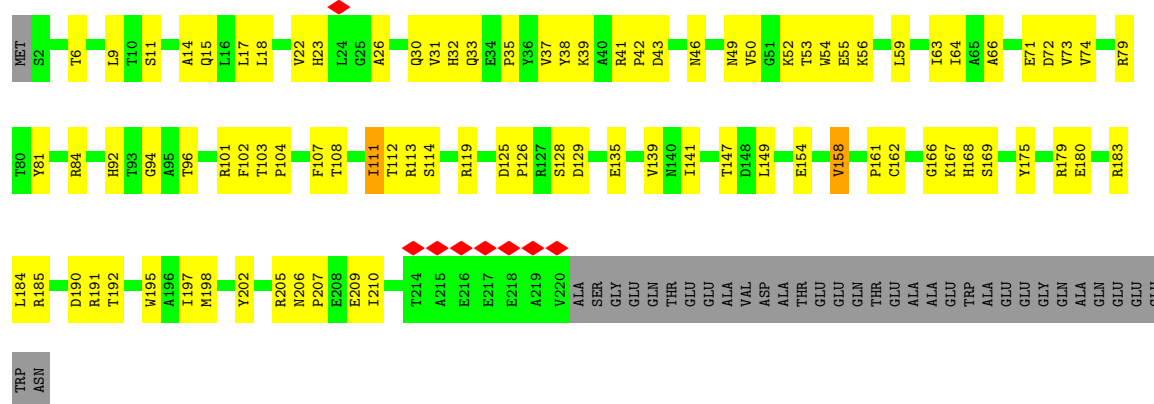






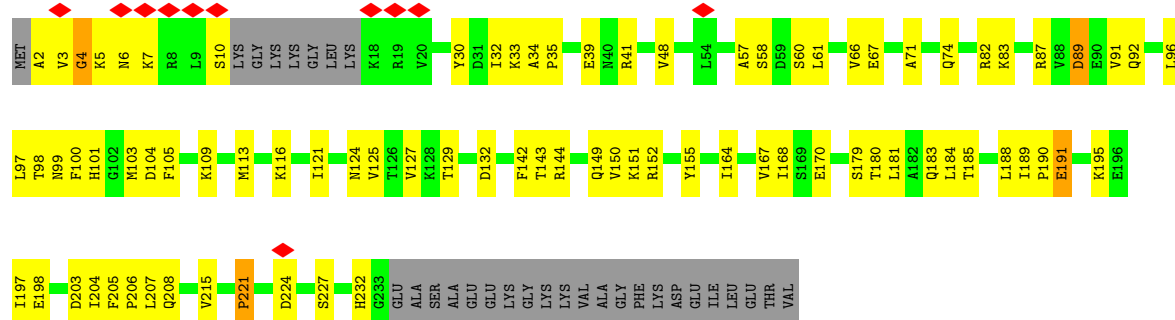
• Molecule 2: Small ribosomal subunit protein uS2

Chain A: 51% 34% 14%



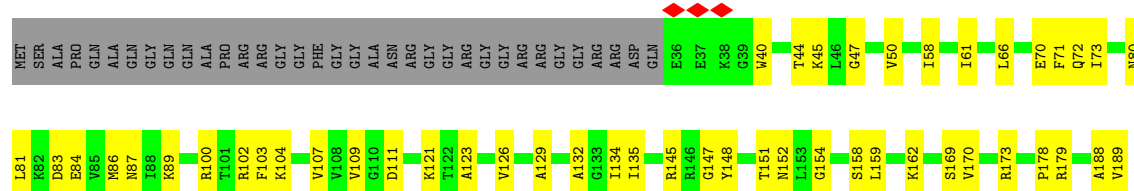
• Molecule 3: Small ribosomal subunit protein eS1

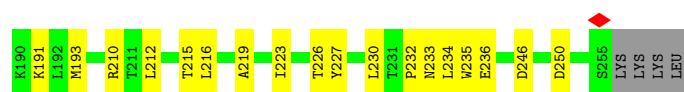
Chain B: 56% 31% 12%



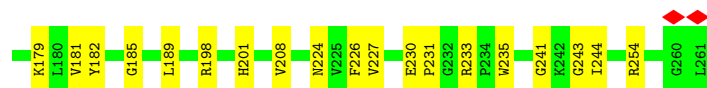
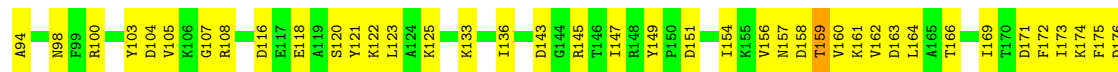
• Molecule 4: Small ribosomal subunit protein uS5

Chain C: 59% 26% 15%





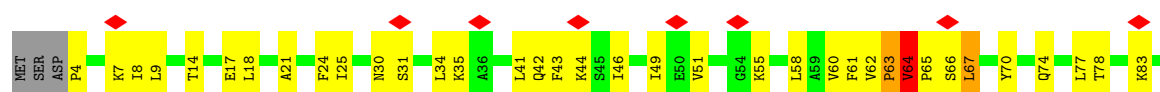
- Molecule 5: 40S ribosomal protein S4



- Molecule 6: Small ribosomal subunit protein eS6

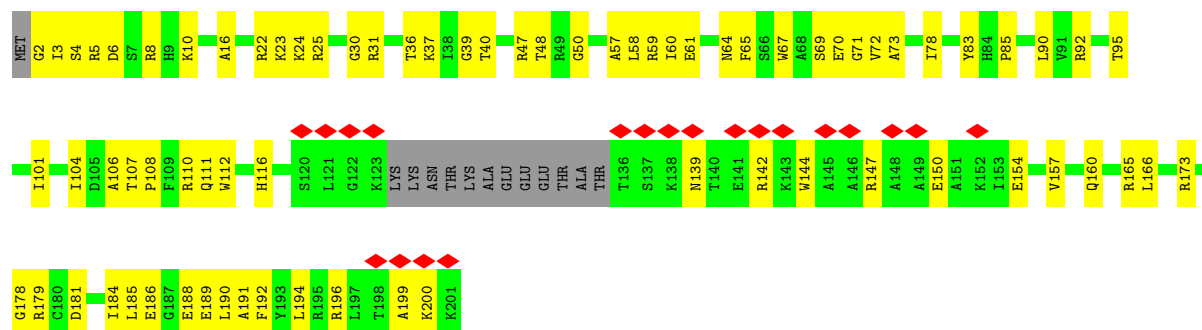


- Molecule 7: 40S ribosomal protein S7

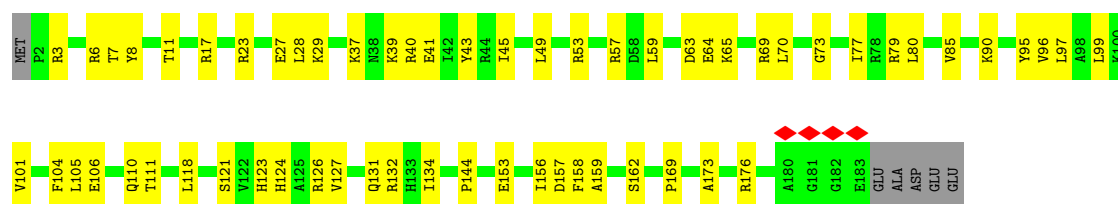


- Molecule 8: 40S ribosomal protein S8

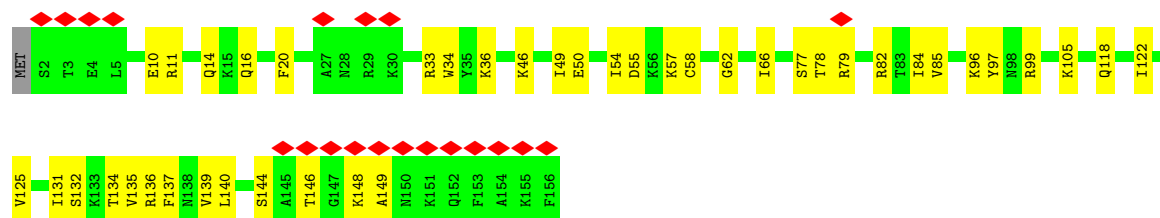




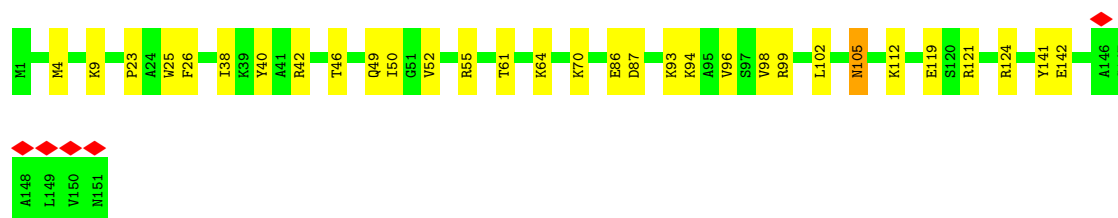
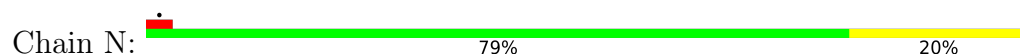
• Molecule 9: KLLA0E23673p



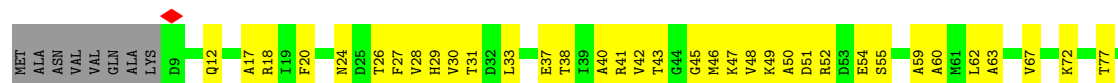
• Molecule 10: KLLA0A10483p



• Molecule 11: KLLA0F18040p



• Molecule 12: Small ribosomal subunit protein uS11





- Molecule 13: 40S ribosomal protein S21



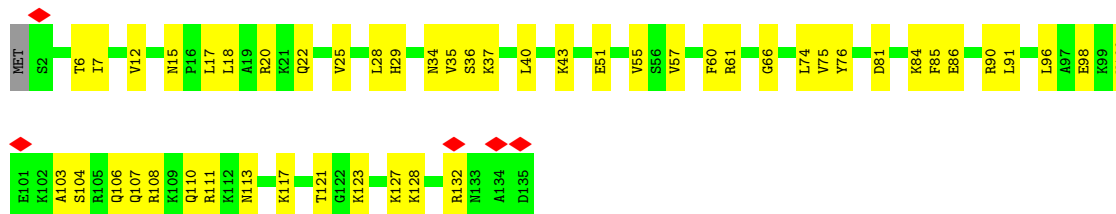
- Molecule 14: Small ribosomal subunit protein uS8



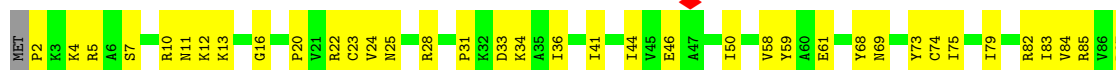
- Molecule 15: KLLA0B11231p

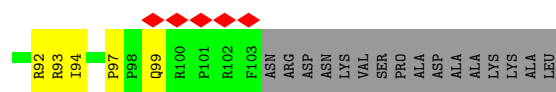


- Molecule 16: 40S ribosomal protein S24



- Molecule 17: 40S ribosomal protein S26

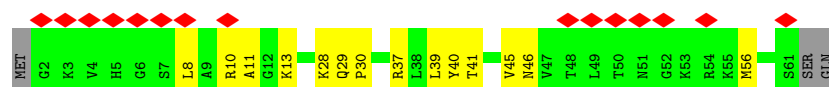




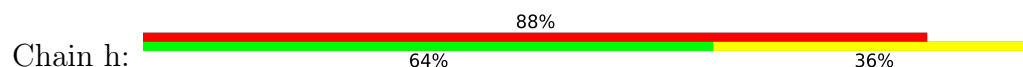
- Molecule 18: 40S ribosomal protein S27



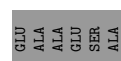
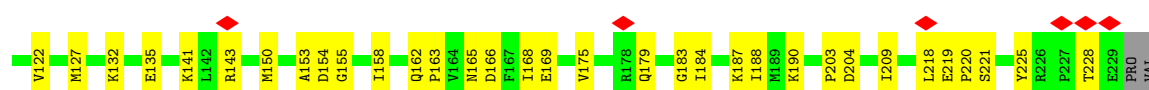
- Molecule 19: 40S ribosomal protein S30



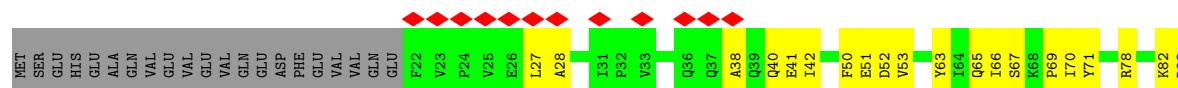
- Molecule 20: 40S ribosomal protein L41-A

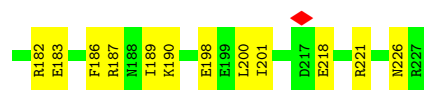


- Molecule 21: 40S ribosomal protein S3

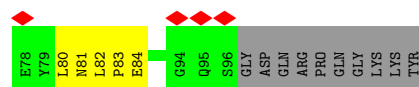


- Molecule 22: KLLA0D10659p

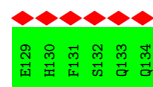
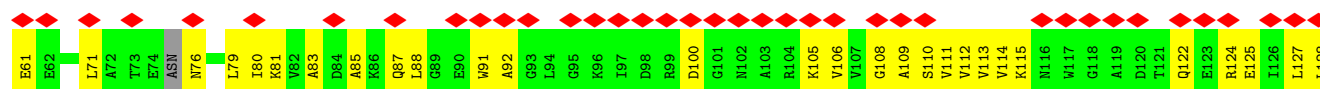
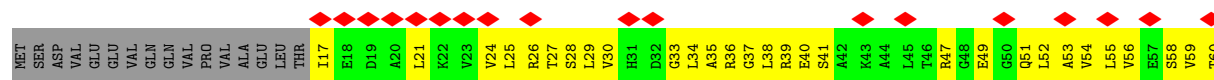




• Molecule 23: KLLA0B08173p



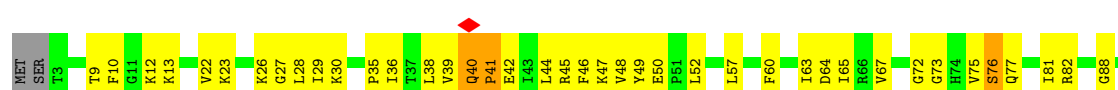
• Molecule 24: 40S ribosomal protein S12



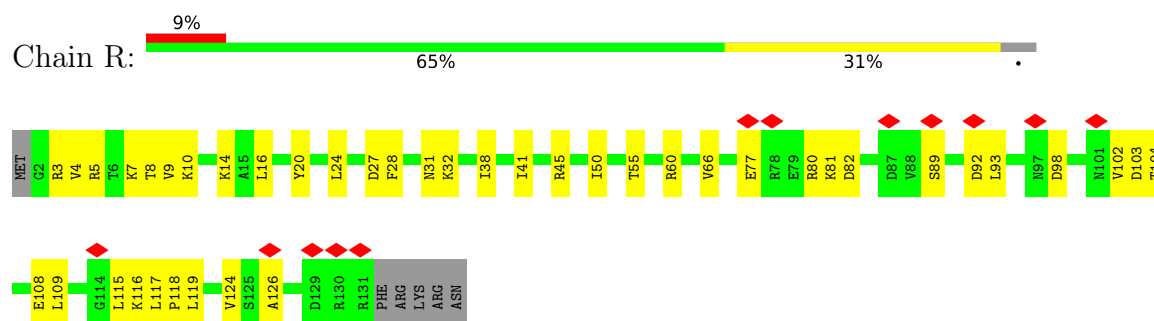
• Molecule 25: KLLA0F07843p



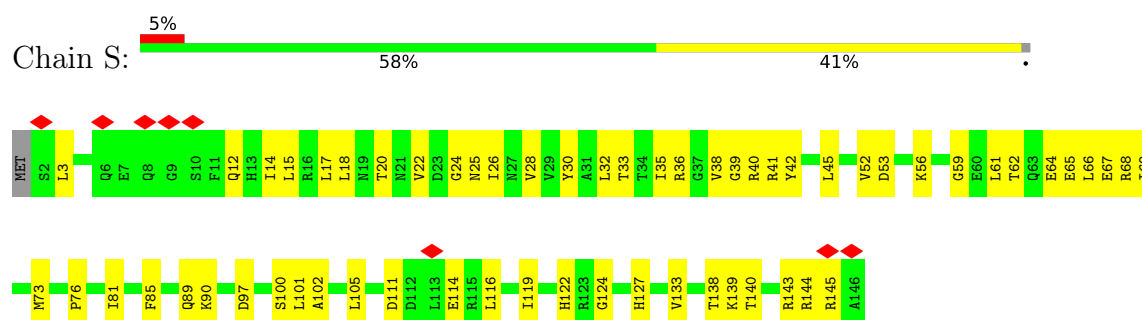
• Molecule 26: Small ribosomal subunit protein uS9



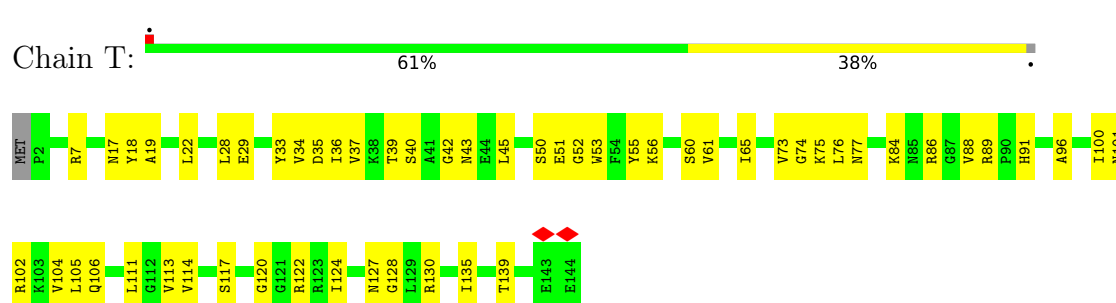
- Molecule 27: KLLA0B01474p



- Molecule 28: KLLA0B01562p



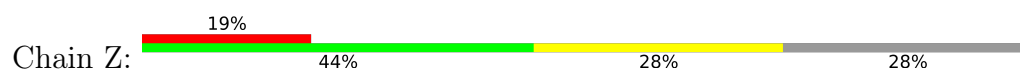
- Molecule 29: KLLA0A07194p

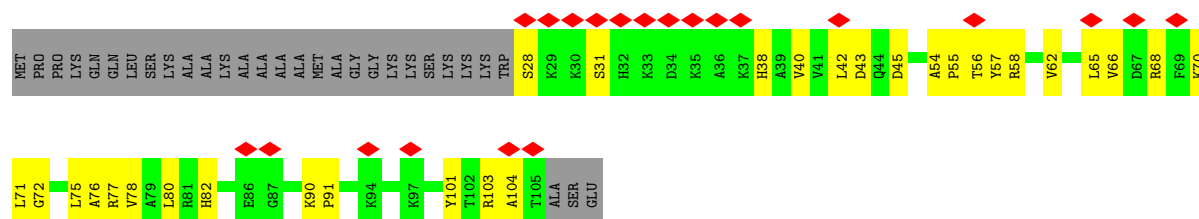


- Molecule 30: Small ribosomal subunit protein uS10

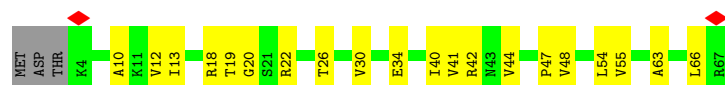


- Molecule 31: 40S ribosomal protein S25





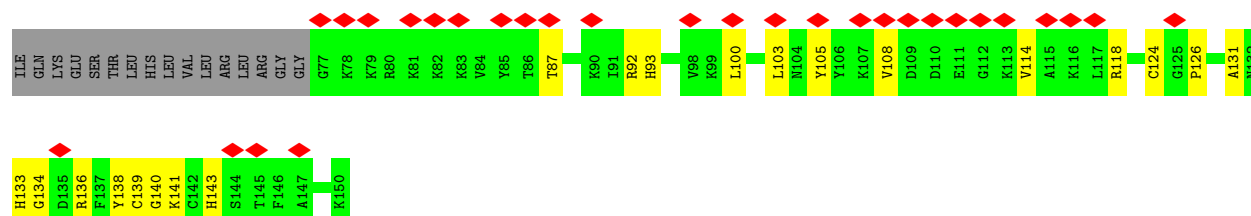
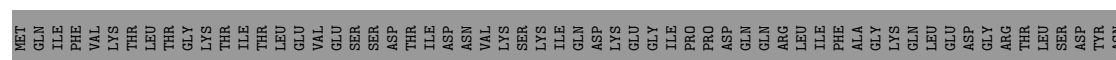
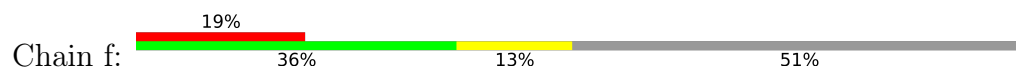
- Molecule 32: Small ribosomal subunit protein eS28



- Molecule 33: Small ribosomal subunit protein uS14



- Molecule 34: Small ribosomal subunit protein eS31

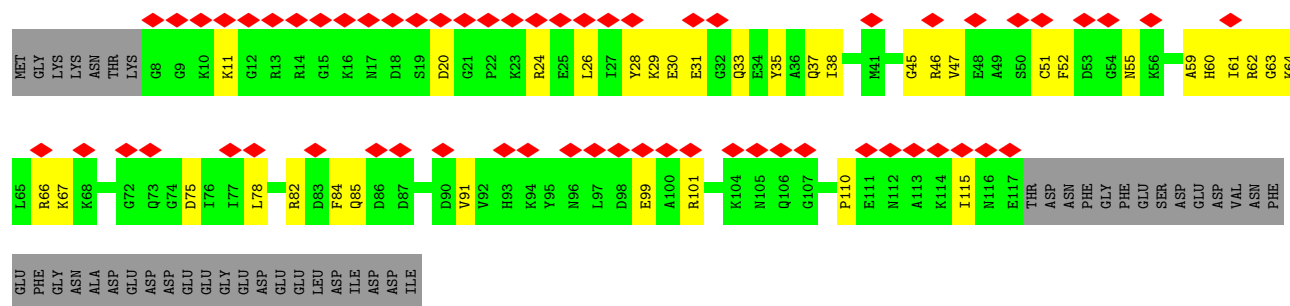
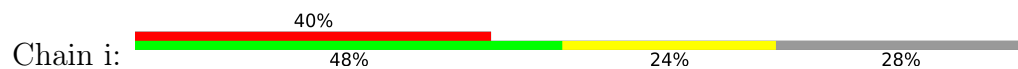


- Molecule 35: KLLA0E12277p

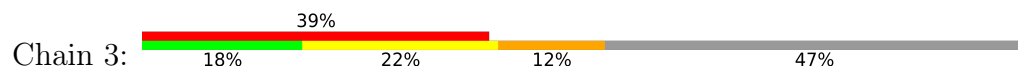




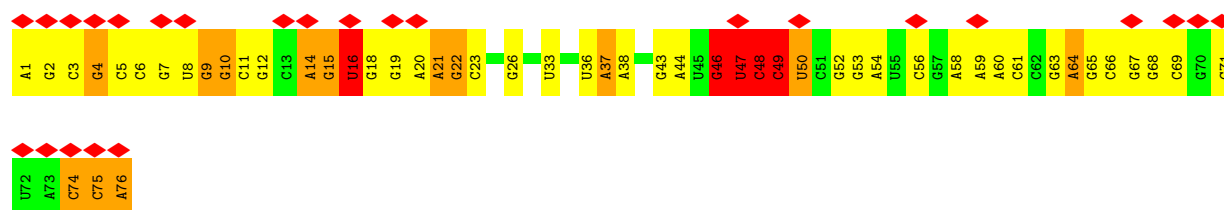
• Molecule 36: Eukaryotic translation initiation factor 1A



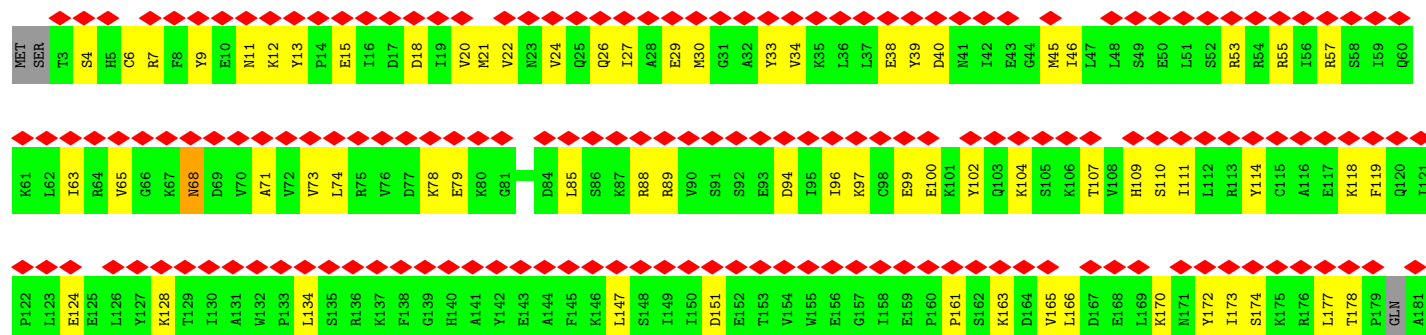
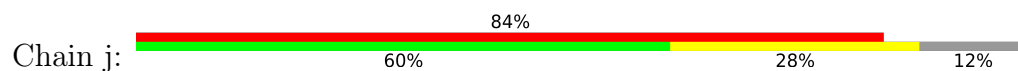
• Molecule 37: mRNA (5'-R(P*AP*AP*U)-3')

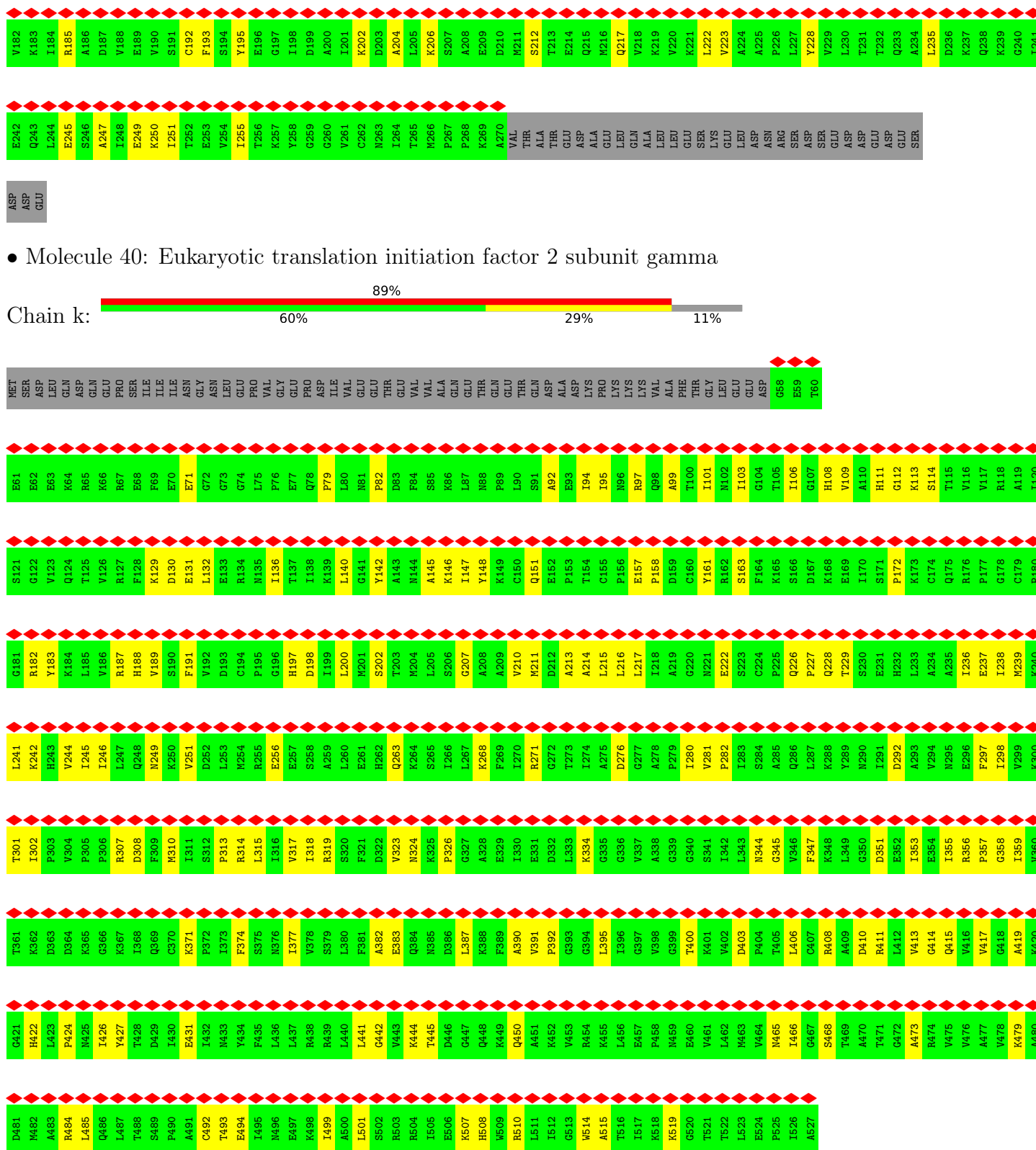


• Molecule 38: Met-tRNAi



• Molecule 39: Eukaryotic translation initiation factor 2 subunit alpha





- Molecule 41: Eukaryotic translation initiation factor 2 subunit beta





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	141338	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	0.670	Depositor
Minimum map value	-0.330	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.07	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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.12	0/42410	0.30	0/66079
2	A	0.19	0/1742	0.43	0/2383
3	B	0.19	0/1820	0.46	1/2448 (0.0%)
4	C	0.13	0/1678	0.36	0/2277
5	E	0.16	0/2122	0.43	0/2861
6	G	0.11	0/1855	0.33	0/2479
7	H	0.28	0/1507	0.57	3/2028 (0.1%)
8	I	0.16	0/1515	0.47	0/2029
9	J	0.16	0/1495	0.40	0/2001
10	L	0.13	0/1276	0.40	0/1718
11	N	0.13	0/1218	0.40	0/1638
12	O	0.18	0/966	0.48	0/1297
13	V	0.18	0/696	0.47	0/938
14	W	0.16	0/1039	0.39	0/1399
15	X	0.24	0/1137	0.43	0/1516
16	Y	0.16	0/1075	0.45	0/1433
17	a	0.15	0/810	0.48	0/1087
18	b	0.13	0/619	0.39	0/837
19	e	0.16	0/480	0.42	0/640
20	h	0.15	0/234	0.33	0/300
21	D	0.15	0/1800	0.41	0/2421
22	F	0.16	0/1628	0.48	0/2198
23	K	0.20	0/831	0.58	0/1123
24	M	0.16	0/891	0.50	0/1201
25	P	0.18	0/942	0.51	0/1269
26	Q	0.24	0/1125	0.51	0/1510
27	R	0.16	0/1044	0.40	0/1402
28	S	0.16	0/1208	0.51	0/1624
29	T	0.16	0/1129	0.44	0/1520
30	U	0.16	0/857	0.47	0/1158
31	Z	0.21	0/604	0.59	1/815 (0.1%)
32	c	0.13	0/501	0.39	0/673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.13	0/473	0.39	1/629 (0.2%)
34	f	0.12	0/597	0.41	0/795
35	g	0.14	0/2523	0.40	0/3434
36	i	0.17	0/880	0.49	0/1170
37	3	0.07	0/595	0.18	0/920
38	1	0.22	0/1529	0.37	0/2376
39	j	0.15	0/2171	0.40	0/2924
40	k	0.14	0/3657	0.35	0/4946
41	l	0.10	0/194	0.35	0/263
All	All	0.15	0/90873	0.37	6/131759 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	Z	31	SER	N-CA-C	6.82	118.80	111.36
7	H	63	PRO	N-CA-C	-5.83	106.26	113.84
7	H	101	LYS	CG-CD-CE	-5.49	98.67	111.30
33	d	23	ILE	N-CA-C	-5.43	107.33	111.62
7	H	64	VAL	N-CA-CB	5.19	118.48	111.21
3	B	191	GLU	CA-CB-CG	5.09	124.28	114.10

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	951	0
2	A	1702	0	1695	76	0
3	B	1796	0	1874	62	0
4	C	1648	0	1727	54	0
5	E	2078	0	2157	78	0
6	G	1832	0	1919	64	0
7	H	1483	0	1579	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	I	1489	0	1504	67	0
9	J	1471	0	1554	48	0
10	L	1248	0	1311	37	0
11	N	1195	0	1263	29	0
12	O	955	0	987	51	0
13	V	687	0	682	33	0
14	W	1021	0	1056	42	0
15	X	1119	0	1198	43	0
16	Y	1061	0	1111	41	0
17	a	797	0	835	34	0
18	b	609	0	630	22	0
19	e	472	0	508	14	0
20	h	233	0	284	11	0
21	D	1774	0	1855	57	0
22	F	1609	0	1679	61	0
23	K	809	0	810	41	0
24	M	885	0	917	45	0
25	P	923	0	960	45	0
26	Q	1105	0	1170	51	0
27	R	1033	0	1082	41	0
28	S	1189	0	1211	52	0
29	T	1110	0	1124	47	0
30	U	845	0	913	42	0
31	Z	595	0	593	30	0
32	c	499	0	536	14	0
33	d	461	0	448	21	0
34	f	584	0	600	19	0
35	g	2469	0	2403	88	0
36	i	870	0	869	39	0
37	3	536	0	277	11	0
38	1	1639	0	853	34	0
39	j	2139	0	2205	75	0
40	k	3596	0	3713	118	0
41	l	190	0	191	3	0
42	2	112	0	0	0	0
42	3	1	0	0	0	0
42	T	1	0	0	0	0
42	i	1	0	0	0	0
42	k	1	0	0	0	0
43	a	1	0	0	0	0
43	b	1	0	0	0	0
43	f	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	k	32	0	13	3	0
45	k	8	0	8	2	0
46	2	3	0	0	0	0
All	All	86108	0	67517	2336	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 15.

All (2336) 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)
1:2:824:U:H3	1:2:847:C:N4	1.56	1.02
1:2:1355:U:H3	1:2:1366:G:H1	1.09	0.98
1:2:1586:G:H1	1:2:1606:U:H3	1.04	0.98
1:2:975:G:H1	1:2:1022:A:HO2'	1.13	0.96
35:g:258:TRP:HB3	35:g:269:ILE:HD11	1.51	0.91
1:2:824:U:H3	1:2:847:C:H42	0.89	0.89
1:2:638:U:O5'	7:H:101:LYS:NZ	2.06	0.88
1:2:521:U:H5''	16:Y:37:LYS:HG3	1.55	0.88
1:2:485:G:H1	1:2:500:U:H3	0.88	0.87
38:1:47:H2U:H5''	38:1:47:H2U:H61	1.59	0.84
35:g:259:LEU:HG	35:g:272:LEU:HD21	1.60	0.82
8:I:196:ARG:HH12	10:L:11:ARG:HA	1.43	0.82
1:2:1124:A:H5''	20:h:15:ARG:HH12	1.45	0.81
40:k:210:VAL:HG21	40:k:318:ILE:HD11	1.63	0.80
39:j:46:ILE:HG12	39:j:85:LEU:HD22	1.63	0.80
1:2:899:A:H3'	1:2:900:G:H21	1.45	0.80
1:2:658:C:H2'	1:2:659:G:H8	1.44	0.79
30:U:34:LEU:HD21	30:U:89:ARG:HG3	1.61	0.79
3:B:181:LEU:HA	3:B:184:LEU:HB3	1.64	0.79
1:2:236:C:H5''	1:2:237:U:H5'	1.66	0.78
22:F:152:GLY:HA3	22:F:157:ALA:HA	1.63	0.78
1:2:1332:C:O4'	21:D:162:GLN:NE2	2.17	0.78
15:X:48:HIS:HB3	15:X:103:LEU:HD11	1.64	0.78
39:j:71:ALA:HB1	39:j:85:LEU:HD21	1.64	0.78
2:A:74:VAL:HG22	2:A:96:THR:HB	1.64	0.77
1:2:65:A:H2	1:2:84:A:H62	1.30	0.77
1:2:576:G:N3	36:i:64:LYS:NZ	2.33	0.77
1:2:635:A:H5''	14:W:31:SER:HB3	1.66	0.77
7:H:62:VAL:HG12	7:H:64:VAL:H	1.50	0.77
25:P:60:LEU:HD11	25:P:92:SER:HB3	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:887:U:H1'	12:O:126:THR:HG21	1.65	0.77
1:2:1338:C:O2'	1:2:1340:A:N7	2.16	0.77
12:O:60:ALA:HB1	12:O:101:ALA:HB2	1.66	0.77
1:2:760:A:N1	1:2:789:U:C4	2.53	0.77
15:X:87:VAL:HG12	15:X:132:LEU:HD21	1.64	0.77
12:O:47:LYS:HD3	12:O:62:LEU:HB3	1.66	0.76
1:2:1290:G:H1	1:2:1323:G:H22	1.29	0.76
36:i:62:ARG:HD2	36:i:63:GLY:H	1.51	0.76
1:2:904:A:H5''	12:O:52:ARG:HD2	1.67	0.76
24:M:54:VAL:HG12	24:M:80:ILE:HB	1.66	0.76
4:C:179:ARG:O	9:J:53:ARG:NH2	2.18	0.76
26:Q:67:VAL:HG11	26:Q:81:ILE:HG23	1.68	0.76
35:g:171:ARG:HH12	35:g:192:SER:HA	1.50	0.75
29:T:105:LEU:HD12	29:T:122:ARG:HD2	1.68	0.75
35:g:171:ARG:HE	35:g:187:SER:HB2	1.50	0.75
1:2:895:U:O2	12:O:41:ARG:NH1	2.20	0.75
35:g:210:GLN:NE2	35:g:211:PRO:O	2.20	0.75
5:E:64:ILE:HD11	16:Y:18:LEU:HG	1.66	0.75
12:O:24:ASN:HA	12:O:55:SER:HB3	1.69	0.75
1:2:353:C:H5''	8:I:16:ALA:HB2	1.68	0.74
1:2:995:U:H3	1:2:1007:G:H1	1.34	0.74
1:2:1798:A:N6	37:3:19:A:O2'	2.21	0.74
39:j:147:LEU:O	39:j:151:ASP:N	2.20	0.74
24:M:56:VAL:HG11	24:M:85:ALA:HB2	1.67	0.74
40:k:314:ARG:HD2	40:k:344:ASN:HD21	1.52	0.74
1:2:824:U:O2	1:2:847:C:N3	2.21	0.74
1:2:531:U:OP1	9:J:132:ARG:NH2	2.21	0.73
1:2:1095:C:OP2	14:W:71:LYS:NZ	2.21	0.73
40:k:466:ILE:HA	40:k:499:ILE:HG12	1.70	0.73
1:2:1675:C:H5''	8:I:59:ARG:HH12	1.52	0.73
4:C:152:ASN:ND2	13:V:2:GLU:O	2.21	0.73
14:W:24:GLN:NE2	18:b:5:GLN:O	2.21	0.73
9:J:59:LEU:HD12	9:J:69:ARG:HA	1.70	0.73
3:B:74:GLN:HE21	3:B:189:ILE:HG21	1.53	0.73
21:D:228:THR:HG21	35:g:194:ARG:HB2	1.70	0.73
29:T:76:LEU:HB3	29:T:101:ASN:HD22	1.54	0.73
35:g:179:MET:HA	35:g:205:TYR:HB2	1.70	0.73
1:2:97:C:H1'	1:2:425:G:H5'	1.70	0.72
1:2:226:U:O2	1:2:833:G:O6	2.06	0.72
1:2:1345:A:OP2	1:2:1347:A:N6	2.21	0.72
2:A:56:LYS:NZ	13:V:70:ASN:OD1	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:101:LYS:HE2	7:H:112:ARG:HH22	1.53	0.72
3:B:144:ARG:HB3	3:B:206:PRO:HB2	1.71	0.72
1:2:1170:A:H2'	1:2:1171:G:C8	2.24	0.72
5:E:100:ARG:NH1	5:E:118:GLU:OE2	2.23	0.72
1:2:1661:G:H1	1:2:1736:U:H3	1.35	0.72
26:Q:47:LYS:HB3	26:Q:82:ARG:HD2	1.72	0.72
1:2:566:A:OP1	15:X:70:LYS:NZ	2.23	0.71
1:2:1670:G:H2'	1:2:1671:G:H8	1.54	0.71
34:f:139:CYS:SG	34:f:140:GLY:N	2.63	0.71
1:2:150:G:O2'	6:G:13:GLN:NE2	2.23	0.71
1:2:642:G:O6	1:2:692:C:N4	2.23	0.71
30:U:82:TYR:HB3	33:d:52:PHE:HB3	1.73	0.71
1:2:952:G:H2'	1:2:953:G:H8	1.55	0.71
40:k:377:ILE:HA	40:k:400:THR:HG22	1.71	0.71
24:M:26:ARG:HH11	24:M:30:VAL:HG21	1.56	0.70
11:N:55:ARG:NH2	18:b:51:GLN:OE1	2.24	0.70
13:V:46:ILE:HD12	13:V:47:PRO:HD2	1.73	0.70
31:Z:71:LEU:HD23	31:Z:76:ALA:HA	1.73	0.70
4:C:100:ARG:HG2	4:C:100:ARG:HH11	1.56	0.70
5:E:175:PHE:HE1	5:E:198:ARG:HD2	1.57	0.70
38:1:74:C:H4'	38:1:75:C:H5'	1.74	0.70
27:R:103:ASP:OD1	27:R:104:THR:N	2.24	0.70
27:R:115:LEU:HB3	27:R:117:LEU:HD23	1.73	0.70
39:j:204:ALA:HB1	39:j:251:ILE:HG22	1.73	0.70
1:2:471:U:O2'	1:2:769:A:N3	2.25	0.70
1:2:1121:G:N2	1:2:1124:A:OP2	2.25	0.70
1:2:1480:C:OP2	1:2:1519:G:N2	2.24	0.70
13:V:7:GLN:OE1	13:V:7:GLN:N	2.25	0.70
24:M:105:LYS:HG2	24:M:106:VAL:HG23	1.73	0.70
35:g:43:LEU:HD11	35:g:83:SER:HB3	1.73	0.70
1:2:1033:C:HO2'	14:W:2:THR:N	1.89	0.70
21:D:105:MET:HE1	21:D:184:ILE:HD13	1.73	0.70
1:2:917:U:H2'	1:2:918:A:C8	2.26	0.69
1:2:139:C:N4	1:2:280:G:OP1	2.24	0.69
1:2:1213:U:HO2'	33:d:2:ALA:N	1.90	0.69
35:g:90:LEU:HB2	35:g:104:PHE:HB2	1.74	0.69
1:2:1443:G:N2	34:f:87:THR:O	2.25	0.69
1:2:1531:C:OP2	31:Z:77:ARG:NH2	2.25	0.69
6:G:50:PHE:HE1	6:G:113:ILE:HD12	1.57	0.69
16:Y:55:VAL:HG22	16:Y:75:VAL:HG22	1.73	0.69
35:g:54:GLN:OE1	35:g:54:GLN:N	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:j:7:ARG:HG2	39:j:12:LYS:HA	1.73	0.69
1:2:12:U:OP1	4:C:89:LYS:NZ	2.25	0.69
1:2:701:U:O2	1:2:738:G:N2	2.26	0.69
28:S:41:ARG:NH2	29:T:36:ILE:O	2.26	0.69
35:g:21:VAL:HG11	35:g:317:ILE:HD11	1.74	0.69
1:2:917:U:H2'	1:2:918:A:H8	1.56	0.68
13:V:3:ASN:OD1	13:V:4:ASP:N	2.26	0.68
29:T:17:ASN:ND2	29:T:139:THR:OG1	2.21	0.68
21:D:108:LYS:HB3	21:D:113:LEU:HD23	1.75	0.68
22:F:50:PHE:HE2	22:F:70:ILE:H	1.41	0.68
39:j:22:VAL:HB	39:j:34:VAL:HG21	1.75	0.68
1:2:923:A:H2'	1:2:924:G:C8	2.28	0.68
1:2:1464:G:O2'	1:2:1600:C:OP1	2.11	0.68
28:S:25:ASN:HB2	31:Z:40:VAL:HG21	1.76	0.68
30:U:22:ILE:HG21	30:U:100:VAL:HG11	1.75	0.68
1:2:798:A:H4'	5:E:201:HIS:CE1	2.28	0.68
5:E:151:ASP:HB3	5:E:154:ILE:HG13	1.76	0.68
25:P:34:VAL:HG22	25:P:45:PHE:HD2	1.59	0.68
1:2:1254:G:O6	24:M:39:ARG:NH1	2.24	0.68
1:2:326:U:H2'	1:2:327:A:C8	2.28	0.68
1:2:1564:U:H5''	28:S:39:GLY:H	1.58	0.68
26:Q:143:ARG:NH2	38:1:33:U:OP2	2.24	0.68
1:2:866:G:O6	1:2:961:C:N4	2.27	0.67
29:T:37:VAL:HG12	29:T:39:THR:H	1.58	0.67
35:g:210:GLN:HE22	35:g:252:PHE:HB2	1.59	0.67
1:2:1786:G:OP1	12:O:127:ARG:NH2	2.28	0.67
29:T:22:LEU:HD23	29:T:28:LEU:HD22	1.75	0.67
29:T:40:SER:HB2	29:T:96:ALA:HA	1.76	0.67
1:2:23:G:O6	1:2:601:U:O2	2.11	0.67
1:2:1592:G:OP2	1:2:1594:C:N4	2.27	0.67
40:k:351:ASP:HB2	40:k:377:ILE:HD12	1.76	0.67
1:2:1472:G:H2'	1:2:1473:A:C8	2.30	0.67
1:2:1797:U:O2	3:B:152:ARG:NH2	2.28	0.67
1:2:1076:C:OP1	17:a:13:LYS:NZ	2.27	0.67
3:B:97:LEU:HB3	3:B:232:HIS:HD2	1.60	0.67
1:2:437:A:H1'	1:2:464:G:H22	1.58	0.67
1:2:1682:U:O2	1:2:1715:G:O6	2.12	0.67
1:2:1289:PSU:H2'	1:2:1290:G:C8	2.30	0.67
9:J:85:VAL:HG11	9:J:104:PHE:HD1	1.60	0.67
21:D:116:ARG:HH21	21:D:150:MET:HE1	1.59	0.67
7:H:77:LEU:HD22	7:H:92:PHE:HZ	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:X:125:VAL:HG12	15:X:126:LYS:HG3	1.77	0.67
35:g:208:VAL:HG11	35:g:249:ALA:HA	1.75	0.67
1:2:234:G:H2'	1:2:235:A:C8	2.29	0.66
1:2:1033:C:OP1	11:N:9:LYS:NZ	2.28	0.66
1:2:12:U:H2'	1:2:13:C:C6	2.31	0.66
25:P:118:GLU:OE2	25:P:118:GLU:N	2.26	0.66
7:H:44:LYS:HD2	7:H:63:PRO:HA	1.77	0.66
30:U:23:ARG:HG3	30:U:92:ASP:HB3	1.77	0.66
1:2:447:C:OP1	5:E:49:ARG:NH2	2.24	0.66
9:J:41:GLU:O	9:J:45:ILE:HG12	1.94	0.66
25:P:110:GLU:HB2	28:S:119:ILE:HD13	1.78	0.66
8:I:57:ALA:HB2	8:I:178:GLY:HA2	1.75	0.66
21:D:169:GLU:HB3	21:D:190:LYS:HZ1	1.61	0.66
23:K:77:ARG:HD3	23:K:84:GLU:HA	1.75	0.66
25:P:93:VAL:HG22	25:P:106:GLU:HG2	1.76	0.66
1:2:1502:G:H2'	1:2:1503:A:C8	2.31	0.66
24:M:29:LEU:HD12	24:M:36:ARG:HH22	1.60	0.66
28:S:65:GLU:OE1	28:S:68:ARG:NH1	2.28	0.66
40:k:263:GLN:HE22	40:k:280:ILE:HD13	1.60	0.66
7:H:74:GLN:O	7:H:78:THR:OG1	2.13	0.66
1:2:162:G:OP2	1:2:162:G:N2	2.26	0.66
16:Y:86:GLU:OE2	16:Y:90:ARG:NH1	2.29	0.66
1:2:395:G:N7	8:I:47:ARG:NH1	2.43	0.65
1:2:1380:A:HO2'	1:2:1381:G:H8	1.44	0.65
3:B:67:GLU:HG3	3:B:83:LYS:HD3	1.76	0.65
11:N:105:ASN:HD22	11:N:105:ASN:C	2.02	0.65
1:2:862:A:O5'	14:W:57:ARG:NH2	2.30	0.65
7:H:9:LEU:HG	7:H:43:PHE:HB2	1.78	0.65
7:H:30:ASN:HB2	7:H:34:LEU:HD12	1.78	0.65
23:K:11:ILE:HD11	23:K:42:VAL:HG22	1.77	0.65
26:Q:77:GLN:O	26:Q:81:ILE:HG13	1.96	0.65
4:C:50:VAL:HG21	4:C:73:ILE:HG23	1.79	0.65
1:2:44:U:OP2	1:2:436:A:N6	2.26	0.65
22:F:221:ARG:HH12	39:j:45:MET:HG3	1.60	0.65
27:R:31:ASN:HD22	27:R:55:THR:HG22	1.61	0.65
35:g:151:TRP:HB2	35:g:179:MET:HE3	1.77	0.65
40:k:103:ILE:HG12	40:k:213:ALA:HB3	1.78	0.65
1:2:256:A:H1'	8:I:73:ALA:HB3	1.79	0.65
8:I:67:TRP:O	8:I:71:GLY:HA2	1.97	0.65
21:D:21:LEU:HD21	21:D:48:ILE:HD13	1.79	0.65
30:U:22:ILE:HG13	30:U:118:ILE:HA	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1198:G:N2	33:d:30:LEU:O	2.30	0.65
1:2:1589:C:H2'	1:2:1590:A:H8	1.62	0.65
4:C:72:GLN:OE1	4:C:72:GLN:N	2.26	0.65
10:L:46:LYS:HA	10:L:49:ILE:HB	1.78	0.65
11:N:86:GLU:N	11:N:86:GLU:OE2	2.29	0.65
14:W:6:VAL:HG22	14:W:34:ILE:HD11	1.79	0.65
27:R:77:GLU:OE1	27:R:80:ARG:NH2	2.29	0.65
40:k:71:GLU:O	40:k:182:ARG:NH1	2.30	0.65
1:2:156:A:H2	1:2:418:G:H21	1.43	0.65
1:2:326:U:H2'	1:2:327:A:H8	1.62	0.65
1:2:1182:A:N3	1:2:1209:C:O2'	2.28	0.65
2:A:175:TYR:OH	2:A:197:ILE:O	2.12	0.65
10:L:49:ILE:HG22	10:L:50:GLU:HG3	1.77	0.65
10:L:77:SER:HB3	10:L:85:VAL:HB	1.78	0.65
14:W:24:GLN:HG3	18:b:7:LEU:HD11	1.79	0.65
24:M:52:LEU:HB3	24:M:114:VAL:HB	1.78	0.65
36:i:52:PHE:HB3	36:i:110:PRO:HD2	1.79	0.65
40:k:202:SER:HA	40:k:465:ASN:HD21	1.62	0.65
1:2:502:G:O2'	19:e:46:ASN:ND2	2.30	0.64
21:D:71:LEU:HB3	23:K:20:VAL:HG21	1.79	0.64
25:P:90:ILE:HA	25:P:107:ILE:HG22	1.79	0.64
29:T:39:THR:HA	29:T:100:ILE:HD12	1.80	0.64
38:1:67:G:H2'	38:1:68:G:H8	1.61	0.64
1:2:337:C:H1'	8:I:5:ARG:HB2	1.79	0.64
1:2:1124:A:H5''	20:h:15:ARG:NH1	2.10	0.64
10:L:78:THR:HG21	10:L:118:GLN:HA	1.79	0.64
1:2:396:A:H4'	8:I:50:GLY:HA2	1.80	0.64
1:2:1523:A:N3	1:2:1587:C:O2'	2.30	0.64
8:I:166:LEU:HD13	8:I:184:ILE:HG21	1.78	0.64
21:D:143:ARG:NH2	37:3:38:C:O2	2.31	0.64
40:k:101:ILE:HD12	40:k:187:ARG:HD3	1.79	0.64
1:2:151:U:O2	6:G:4:ASN:ND2	2.29	0.64
2:A:30:GLN:NE2	2:A:31:VAL:O	2.30	0.64
7:H:140:VAL:HB	14:W:52:TYR:HB3	1.79	0.64
29:T:61:VAL:O	29:T:65:ILE:HG13	1.97	0.64
1:2:1472:G:H2'	1:2:1473:A:H8	1.62	0.64
1:2:1131:A:H2'	1:2:1132:A:H8	1.63	0.64
18:b:18:LYS:O	18:b:29:ARG:NH2	2.23	0.64
1:2:1564:U:H5''	28:S:39:GLY:N	2.13	0.64
3:B:33:LYS:O	3:B:98:THR:OG1	2.15	0.64
1:2:897:A:N6	1:2:913:G:O2'	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:F:78:ARG:HG2	26:Q:122:ARG:HD3	1.80	0.64
1:2:890:A:H2'	1:2:891:A:H8	1.63	0.63
35:g:246:GLU:HB3	35:g:264:ALA:HB2	1.79	0.63
40:k:308:ASP:HB2	40:k:310:MET:HE1	1.79	0.63
1:2:1617:C:O2	32:c:22:ARG:NH2	2.31	0.63
6:G:159:ARG:HE	6:G:170:THR:HG21	1.62	0.63
9:J:63:ASP:OD1	9:J:64:GLU:N	2.32	0.63
12:O:52:ARG:NH2	22:F:158:ARG:HD2	2.14	0.63
31:Z:65:LEU:HB3	31:Z:71:LEU:HD22	1.81	0.63
35:g:115:ALA:HB3	35:g:124:ILE:HB	1.80	0.63
36:i:67:LYS:HD2	37:3:33:C:H4'	1.78	0.63
40:k:313:PRO:HA	40:k:345:GLY:HA3	1.80	0.63
1:2:142:G:H2'	1:2:143:G:C8	2.33	0.63
1:2:715:U:H3	1:2:723:G:H1	1.46	0.63
1:2:1146:A:O2'	1:2:1634:C:OP2	2.16	0.63
2:A:41:ARG:HG2	2:A:43:ASP:H	1.62	0.63
1:2:277:U:O5'	1:2:278:G:N2	2.31	0.63
1:2:537:A:H5'	1:2:542:C:H41	1.63	0.63
1:2:779:A:O2'	1:2:781:A:N7	2.30	0.63
25:P:31:GLU:OE1	25:P:31:GLU:N	2.29	0.63
39:j:53:ARG:HA	39:j:88:ARG:HG2	1.80	0.63
1:2:66:U:H3	6:G:173:PRO:HD3	1.62	0.63
1:2:703:G:H3'	1:2:704:C:H3'	1.81	0.63
13:V:42:GLU:OE2	13:V:42:GLU:N	2.22	0.63
15:X:70:LYS:HG2	15:X:93:LEU:HD22	1.81	0.63
7:H:151:LYS:HE3	7:H:184:GLU:HG3	1.81	0.63
11:N:105:ASN:O	11:N:105:ASN:ND2	2.19	0.63
40:k:281:VAL:HG13	41:l:134:LEU:HD13	1.80	0.63
3:B:103:MET:HB3	3:B:215:VAL:HB	1.81	0.63
11:N:4:MET:SD	11:N:124:ARG:NH1	2.72	0.63
1:2:404:C:O2'	6:G:92:ARG:O	2.15	0.62
1:2:1500:G:N7	29:T:102:ARG:NH2	2.47	0.62
2:A:42:PRO:HB2	27:R:126:ALA:HB2	1.81	0.62
22:F:148:THR:OG1	22:F:159:ARG:NE	2.31	0.62
35:g:117:ASP:OD2	35:g:121:SER:OG	2.16	0.62
1:2:938:A:H2'	1:2:939:A:C8	2.33	0.62
24:M:60:THR:O	24:M:61:GLU:HG3	1.98	0.62
1:2:92:A:H5''	1:2:93:A:H5''	1.82	0.62
1:2:1571:A:H4'	1:2:1572:G:O5'	1.99	0.62
1:2:1639:C:H2'	1:2:1640:G:C8	2.35	0.62
4:C:162:LYS:HD3	4:C:173:ARG:HH21	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:159:THR:HG23	5:E:173:ILE:HB	1.81	0.62
11:N:94:LYS:O	11:N:98:VAL:HG23	1.98	0.62
39:j:222:LEU:HD21	40:k:324:ASN:HB2	1.80	0.62
40:k:356:ARG:HG3	40:k:424:PRO:HB2	1.81	0.62
1:2:91:G:OP1	1:2:396:A:N6	2.30	0.62
1:2:1292:U:H1'	2:A:111:ILE:HD12	1.81	0.62
1:2:1480:C:O2'	26:Q:72:GLY:O	2.16	0.62
1:2:1754:A:OP2	36:i:66:ARG:NH1	2.33	0.62
1:2:1765:G:H4'	1:2:1766:G:O5'	1.99	0.62
24:M:56:VAL:HG22	24:M:58:SER:H	1.62	0.62
1:2:99:C:OP2	1:2:377:A:O2'	2.14	0.62
1:2:563:G:N2	1:2:576:G:OP1	2.22	0.62
1:2:1279:C:H4'	30:U:69:LYS:HB3	1.81	0.62
1:2:1656:G:O6	1:2:1741:U:O2	2.18	0.62
30:U:63:LEU:O	30:U:83:GLU:HA	2.00	0.62
35:g:307:THR:HG22	35:g:321:GLN:HG3	1.82	0.62
3:B:87:ARG:HB2	3:B:101:HIS:HB2	1.82	0.62
7:H:8:ILE:HG13	7:H:9:LEU:HD12	1.80	0.62
39:j:124:GLU:OE1	39:j:128:LYS:NZ	2.27	0.62
40:k:112:GLY:HA3	44:k:601:GCP:H8	1.81	0.62
1:2:78:A:H2'	1:2:79:C:C6	2.34	0.62
1:2:1679:A:N6	1:2:1718:G:O2'	2.31	0.62
13:V:11:LEU:HD12	13:V:12:TYR:HD1	1.65	0.62
1:2:1170:A:H2'	1:2:1171:G:H8	1.64	0.62
1:2:1670:G:H2'	1:2:1671:G:C8	2.35	0.62
4:C:189:VAL:O	4:C:193:MET:HG2	2.00	0.62
10:L:131:ILE:HB	10:L:135:VAL:HG23	1.82	0.62
21:D:17:PHE:HE2	21:D:39:VAL:HG11	1.63	0.62
40:k:408:ARG:HH21	40:k:411:ARG:HE	1.48	0.62
1:2:924:G:H2'	1:2:925:A:H8	1.65	0.61
6:G:7:TYR:HE1	6:G:9:ILE:HB	1.65	0.61
28:S:64:GLU:HA	28:S:67:GLU:HG2	1.82	0.61
1:2:324:G:OP1	10:L:134:THR:OG1	2.17	0.61
1:2:554:A:N3	1:2:589:C:O2'	2.31	0.61
1:2:649:U:O2'	1:2:650:G:OP1	2.18	0.61
1:2:1522:A:H2'	1:2:1523:A:C8	2.35	0.61
5:E:105:VAL:HB	5:E:243:GLY:HA2	1.82	0.61
10:L:66:ILE:HG21	10:L:140:LEU:HD11	1.81	0.61
1:2:1158:C:O2'	26:Q:140:LYS:NZ	2.34	0.61
1:2:1159:A:H2'	1:2:1160:C:C6	2.34	0.61
27:R:9:VAL:HG23	27:R:50:ILE:HA	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:38:HIS:HB3	31:Z:72:GLY:HA2	1.82	0.61
38:1:47:H2U:H2'	38:1:50:U:OP1	2.00	0.61
1:2:638:U:H1'	1:2:639:U:C5	2.36	0.61
1:2:700:C:O2'	1:2:701:U:OP1	2.18	0.61
8:I:4:SER:HB2	8:I:24:LYS:HD2	1.82	0.61
24:M:28:SER:O	24:M:33:GLY:N	2.28	0.61
40:k:148:TYR:O	40:k:161:TYR:HA	2.01	0.61
1:2:329:G:OP2	8:I:173:ARG:NH1	2.34	0.61
1:2:392:C:OP1	8:I:2:GLY:N	2.33	0.61
1:2:1792:A:OP2	17:a:4:LYS:NZ	2.29	0.61
22:F:136:VAL:O	22:F:140:ILE:HG12	2.00	0.61
1:2:103:A:H4'	1:2:105:A:C8	2.36	0.61
1:2:1056:U:O2'	1:2:1058:C:OP2	2.17	0.61
2:A:79:ARG:NH1	2:A:125:ASP:OD2	2.32	0.61
12:O:52:ARG:HH22	22:F:158:ARG:HD2	1.66	0.61
25:P:111:MET:HE2	28:S:119:ILE:HD11	1.82	0.61
40:k:268:LYS:HA	40:k:271:ARG:HH12	1.64	0.61
1:2:512:U:H2'	1:2:513:G:C8	2.35	0.61
1:2:1315:G:OP1	27:R:7:LYS:N	2.33	0.61
1:2:1563:C:OP1	28:S:41:ARG:NH1	2.34	0.61
16:Y:7:ILE:HD11	16:Y:25:VAL:HG13	1.81	0.61
21:D:106:LYS:HG3	21:D:175:VAL:HG22	1.81	0.61
1:2:922:A:H2'	1:2:923:A:C8	2.36	0.61
25:P:110:GLU:OE1	25:P:110:GLU:N	2.30	0.61
21:D:179:GLN:OE1	21:D:179:GLN:N	2.34	0.61
9:J:73:GLY:O	9:J:77:ILE:HG12	2.00	0.61
12:O:31:THR:HG22	12:O:38:THR:HA	1.83	0.61
21:D:168:ILE:HD11	21:D:187:LYS:HB3	1.83	0.61
33:d:15:GLY:O	33:d:19:ARG:NH1	2.34	0.61
34:f:108:VAL:HA	34:f:114:VAL:HG12	1.82	0.61
40:k:479:LYS:HE3	40:k:484:ARG:HH22	1.65	0.61
1:2:704:C:N4	1:2:735:C:O2	2.34	0.60
1:2:1486:G:H3'	1:2:1513:A:H61	1.65	0.60
2:A:72:ASP:OD2	4:C:45:LYS:NZ	2.34	0.60
1:2:1197:G:O3'	33:d:40:ARG:NH2	2.33	0.60
1:2:1711:G:H3'	1:2:1712:A:C8	2.36	0.60
1:2:222:U:H2'	1:2:223:C:C6	2.36	0.60
3:B:129:THR:OG1	3:B:179:SER:O	2.19	0.60
6:G:85:ARG:O	6:G:87:ARG:NH1	2.34	0.60
9:J:157:ASP:OD1	9:J:158:PHE:N	2.34	0.60
12:O:49:LYS:HG3	39:j:74:LEU:HD23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:a:46:GLU:OE1	17:a:46:GLU:N	2.29	0.60
40:k:382:ALA:O	45:k:603:MET:N	2.35	0.60
1:2:924:G:H2'	1:2:925:A:C8	2.36	0.60
1:2:956:G:N2	18:b:51:GLN:HE21	1.99	0.60
23:K:84:GLU:N	23:K:84:GLU:OE1	2.35	0.60
34:f:100:LEU:HD13	34:f:103:LEU:HD21	1.82	0.60
1:2:345:G:P	10:L:79:ARG:HH22	2.24	0.60
1:2:686:C:H4'	14:W:118:ARG:HD2	1.82	0.60
1:2:1598:A:H2'	1:2:1599:G:H5''	1.83	0.60
3:B:89:ASP:OD1	3:B:89:ASP:N	2.35	0.60
15:X:60:GLU:OE1	36:i:60:HIS:NE2	2.34	0.60
26:Q:98:ASP:OD1	26:Q:100:GLN:N	2.35	0.60
1:2:508:G:H2'	1:2:509:G:C8	2.36	0.60
2:A:84:ARG:NH2	27:R:82:ASP:O	2.33	0.60
5:E:121:TYR:OH	5:E:235:TRP:O	2.19	0.60
9:J:106:GLU:O	9:J:111:THR:OG1	2.18	0.60
25:P:45:PHE:CD1	25:P:49:LEU:HD21	2.36	0.60
1:2:984:G:H1	1:2:1015:C:H5	1.49	0.60
1:2:1246:U:OP1	34:f:92:ARG:NH2	2.34	0.60
5:E:65:LEU:HD22	5:E:70:VAL:HG21	1.84	0.60
8:I:92:ARG:HG2	8:I:92:ARG:HH11	1.67	0.60
11:N:46:THR:HG22	11:N:49:GLN:HG3	1.82	0.60
22:F:94:ARG:NH2	22:F:171:ASN:OD1	2.31	0.60
1:2:17:C:O2'	1:2:1136:A:N1	2.35	0.60
1:2:445:A:OP1	5:E:57:ASN:ND2	2.35	0.60
1:2:763:G:OP2	9:J:79:ARG:NH2	2.33	0.60
1:2:1302:U:O2'	1:2:1321:A:OP2	2.18	0.60
1:2:1645:U:H2'	1:2:1646:A:C8	2.37	0.60
5:E:143:ASP:HB2	5:E:145:ARG:HG3	1.84	0.60
14:W:14:ILE:HD13	14:W:25:VAL:HG21	1.83	0.60
29:T:51:GLU:OE1	29:T:51:GLU:N	2.34	0.60
36:i:99:GLU:OE2	36:i:99:GLU:N	2.26	0.60
1:2:248:U:H3'	1:2:249:C:H5'	1.83	0.60
1:2:787:A:OP2	5:E:108:ARG:NH2	2.30	0.60
40:k:111:HIS:NE2	40:k:222:GLU:OE1	2.27	0.60
1:2:1000:A:OP1	38:1:38:A:O2'	2.17	0.60
12:O:49:LYS:HA	12:O:49:LYS:HE3	1.84	0.60
31:Z:56:THR:H	31:Z:103:ARG:HD3	1.66	0.60
4:C:84:GLU:N	4:C:84:GLU:OE2	2.35	0.59
8:I:37:LYS:H	8:I:59:ARG:H	1.49	0.59
12:O:17:ALA:N	12:O:80:HIS:O	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:D:162:GLN:O	21:D:166:ASP:N	2.35	0.59
12:O:26:THR:HG21	12:O:97:GLY:HA3	1.85	0.59
26:Q:29:ILE:HA	26:Q:65:ILE:HB	1.84	0.59
1:2:1069:C:H4'	18:b:17:ARG:HE	1.67	0.59
4:C:170:VAL:HG11	4:C:215:THR:HA	1.83	0.59
25:P:45:PHE:HD1	25:P:49:LEU:HD21	1.66	0.59
35:g:85:SER:OG	35:g:87:ASP:OD1	2.19	0.59
1:2:883:A:H4'	3:B:124:ASN:HD21	1.68	0.59
1:2:1595:A:OP1	33:d:19:ARG:NH1	2.31	0.59
24:M:25:LEU:HD13	24:M:92:ALA:HA	1.85	0.59
1:2:339:U:H2'	1:2:340:A:H8	1.66	0.59
1:2:1355:U:O4	1:2:1366:G:O6	2.20	0.59
11:N:99:ARG:NH2	11:N:141:TYR:OH	2.27	0.59
25:P:15:TYR:HB3	25:P:22:LEU:HD12	1.83	0.59
40:k:227:PRO:HG2	40:k:444:LYS:HG2	1.85	0.59
1:2:1035:A:H2'	1:2:1036:C:C6	2.38	0.59
1:2:1386:A:OP2	27:R:32:LYS:NZ	2.35	0.59
1:2:1469:A:OP1	22:F:187:ARG:NH2	2.34	0.59
14:W:81:VAL:O	14:W:122:SER:OG	2.19	0.59
22:F:155:GLY:HA2	39:j:55:ARG:HD2	1.85	0.59
28:S:56:LYS:HD3	28:S:61:LEU:HB3	1.84	0.59
40:k:473:ALA:HB1	40:k:485:LEU:HB3	1.85	0.59
1:2:148:C:OP1	16:Y:121:THR:OG1	2.21	0.59
1:2:367:U:O4	1:2:368:A:N6	2.35	0.59
12:O:12:GLN:OE1	12:O:77:THR:OG1	2.20	0.59
40:k:108:HIS:HB2	40:k:228:GLN:HE21	1.67	0.59
40:k:356:ARG:HE	40:k:424:PRO:HD2	1.66	0.59
1:2:29:U:H2'	1:2:30:G:H8	1.68	0.59
1:2:564:C:H2'	36:i:64:LYS:NZ	2.17	0.59
2:A:119:ARG:NE	4:C:246:ASP:OD1	2.35	0.59
1:2:152:G:OP1	6:G:2:LYS:NZ	2.36	0.59
1:2:606:G:H21	1:2:613:C:H5''	1.67	0.59
1:2:1469:A:H2	1:2:1472:G:N3	2.01	0.59
3:B:104:ASP:OD1	3:B:105:PHE:N	2.36	0.59
21:D:72:LEU:HD12	23:K:65:TYR:HD2	1.66	0.59
24:M:35:ALA:HB3	24:M:113:VAL:HB	1.83	0.59
32:c:41:VAL:HG13	32:c:63:ALA:HB3	1.84	0.59
4:C:100:ARG:HH12	4:C:102:ARG:HD2	1.67	0.59
21:D:76:ARG:NH1	21:D:76:ARG:O	2.35	0.59
35:g:156:ARG:HG3	35:g:156:ARG:HH11	1.68	0.59
1:2:590:A:H2'	1:2:591:G:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:638:U:P	7:H:101:LYS:HZ1	2.26	0.58
1:2:658:C:H2'	1:2:659:G:C8	2.33	0.58
1:2:758:U:H5''	9:J:7:THR:HG21	1.84	0.58
1:2:1162:A:N3	1:2:1611:U:O2'	2.33	0.58
1:2:1434:A:OP2	21:D:27:ARG:NH2	2.36	0.58
1:2:1613:C:O2'	1:2:1614:G:OP2	2.20	0.58
1:2:1648:U:H2'	1:2:1649:A:C8	2.38	0.58
4:C:61:ILE:HA	4:C:66:LEU:HD12	1.85	0.58
23:K:49:LEU:HB3	23:K:55:VAL:HG23	1.85	0.58
26:Q:63:ILE:HD12	26:Q:92:TYR:HE2	1.66	0.58
27:R:102:VAL:HG21	27:R:119:LEU:HD13	1.85	0.58
5:E:23:LEU:HD11	9:J:6:ARG:HD3	1.84	0.58
15:X:61:SER:OG	15:X:62:LYS:N	2.35	0.58
30:U:33:GLN:H	30:U:33:GLN:CD	2.12	0.58
35:g:271:ASP:OD2	35:g:274:ASN:ND2	2.36	0.58
1:2:548:G:H1	1:2:588:C:H5	1.49	0.58
1:2:1584:A:H5''	26:Q:136:SER:HB2	1.85	0.58
20:h:12:ARG:O	20:h:15:ARG:HB2	2.03	0.58
1:2:7:G:N7	4:C:210:ARG:NH2	2.51	0.58
1:2:297:C:H5''	5:E:38:LEU:HD23	1.84	0.58
1:2:861:A:O2'	1:2:962:A:N6	2.36	0.58
1:2:1256:U:O2'	23:K:1:MET:O	2.20	0.58
2:A:154:GLU:OE1	2:A:154:GLU:N	2.36	0.58
24:M:55:LEU:HD21	24:M:81:LYS:HZ3	1.67	0.58
28:S:32:LEU:O	28:S:35:ILE:HG22	2.03	0.58
39:j:161:PRO:HG2	39:j:165:VAL:HG21	1.85	0.58
1:2:1332:C:H2'	1:2:1333:U:H6	1.68	0.58
1:2:1741:U:H2'	1:2:1742:A:C8	2.39	0.58
15:X:60:GLU:OE2	15:X:60:GLU:N	2.25	0.58
16:Y:103:ALA:O	16:Y:108:ARG:NH1	2.36	0.58
24:M:100:ASP:OD1	24:M:100:ASP:N	2.37	0.58
27:R:16:LEU:HD22	27:R:38:ILE:HD11	1.84	0.58
35:g:115:ALA:N	35:g:124:ILE:O	2.33	0.58
35:g:183:VAL:HB	35:g:199:PHE:HB2	1.84	0.58
22:F:50:PHE:CD2	22:F:69:PRO:HA	2.38	0.58
22:F:190:LYS:NZ	22:F:198:GLU:OE2	2.26	0.58
24:M:125:GLU:HA	24:M:128:LEU:HG	1.84	0.58
40:k:353:ILE:HG12	40:k:417:VAL:HG12	1.85	0.58
1:2:490:C:H2'	1:2:491:A:H4'	1.86	0.58
1:2:1549:U:O4	25:P:40:ARG:NH2	2.36	0.58
3:B:97:LEU:HB3	3:B:232:HIS:CD2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:W:41:MET:HE2	14:W:47:ILE:HD12	1.86	0.58
1:2:883:A:H2'	1:2:884:G:C8	2.39	0.58
12:O:42:VAL:HG12	12:O:67:VAL:HG13	1.85	0.58
20:h:2:ARG:HH21	20:h:4:LYS:HD2	1.69	0.58
23:K:33:GLU:HG3	23:K:34:GLU:OE2	2.03	0.58
30:U:25:ASN:OD1	30:U:115:GLU:HB3	2.04	0.58
40:k:111:HIS:O	40:k:249:ASN:ND2	2.37	0.58
1:2:983:G:H1	1:2:1016:U:H5	1.52	0.58
1:2:1241:A:OP1	25:P:59:LYS:NZ	2.36	0.58
2:A:26:ALA:HB1	2:A:149:LEU:HB2	1.85	0.58
1:2:520:A:H2'	1:2:521:U:C6	2.39	0.58
1:2:735:C:O2'	1:2:736:C:O5'	2.19	0.58
1:2:857:G:OP1	7:H:116:ARG:NH2	2.37	0.58
1:2:1590:A:H2'	1:2:1591:A:H8	1.67	0.57
6:G:20:ASP:HB3	6:G:23:ARG:HG2	1.84	0.57
21:D:105:MET:HB2	21:D:122:VAL:HG21	1.84	0.57
1:2:1456:G:OP1	28:S:138:THR:N	2.35	0.57
1:2:1590:A:H2'	1:2:1591:A:C8	2.39	0.57
30:U:106:ILE:HG13	30:U:107:THR:HG23	1.85	0.57
1:2:303:U:OP1	10:L:136:ARG:NH1	2.38	0.57
1:2:598:A:N3	15:X:47:SER:OG	2.32	0.57
1:2:1381:G:H2'	1:2:1382:A:C8	2.39	0.57
5:E:158:ASP:OD1	5:E:174:LYS:HA	2.04	0.57
12:O:87:GLY:HA3	12:O:120:PRO:HD2	1.86	0.57
33:d:33:LYS:HG2	33:d:34:TYR:CE2	2.39	0.57
1:2:371:G:H1'	1:2:611:U:H3	1.69	0.57
1:2:1746:G:H2'	1:2:1747:A:C8	2.40	0.57
24:M:17:ILE:HG13	24:M:127:LEU:HD13	1.87	0.57
30:U:100:VAL:O	30:U:104:THR:HG23	2.05	0.57
39:j:11:ASN:HD21	39:j:15:GLU:HG3	1.70	0.57
1:2:196:A:N6	8:I:139:ASN:OD1	2.35	0.57
1:2:220:A:H2'	1:2:221:A:C8	2.39	0.57
4:C:233:ASN:HB2	13:V:1:MET:HE2	1.86	0.57
7:H:55:LYS:HD3	7:H:89:HIS:HE2	1.69	0.57
14:W:30:SER:OG	14:W:58:SER:O	2.23	0.57
23:K:16:PHE:HD2	23:K:80:LEU:HD23	1.69	0.57
35:g:188:LEU:HA	35:g:193:TYR:HA	1.87	0.57
21:D:7:LYS:HG2	30:U:27:THR:HG21	1.87	0.57
22:F:28:ALA:HB3	26:Q:28:LEU:HB2	1.87	0.57
22:F:125:VAL:O	31:Z:58:ARG:NH1	2.38	0.57
25:P:51:GLU:OE1	25:P:51:GLU:N	2.28	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:97:C:H2'	1:2:98:U:C6	2.40	0.57
1:2:230:U:O2'	1:2:232:C:OP2	2.23	0.57
1:2:1472:G:OP1	22:F:111:LYS:NZ	2.37	0.57
8:I:39:GLY:HA2	8:I:61:GLU:HB3	1.86	0.57
9:J:17:ARG:O	9:J:23:ARG:NH2	2.38	0.57
25:P:72:LYS:NZ	25:P:106:GLU:HG3	2.20	0.57
35:g:52:GLU:OE1	35:g:54:GLN:NE2	2.35	0.57
38:1:67:G:H2'	38:1:68:G:C8	2.40	0.57
1:2:467:A:N1	1:2:593:A:O2'	2.37	0.57
1:2:485:G:O6	1:2:500:U:O4	2.23	0.57
1:2:606:G:N2	1:2:613:C:H5''	2.19	0.57
13:V:53:TYR:CE2	13:V:72:LEU:HB3	2.40	0.57
22:F:137:ASP:O	22:F:141:ASN:ND2	2.38	0.57
35:g:210:GLN:OE1	35:g:252:PHE:N	2.37	0.57
40:k:357:PRO:HG2	40:k:415:GLN:HE21	1.69	0.57
1:2:372:G:H5'	10:L:96:LYS:HG3	1.87	0.57
2:A:59:LEU:HD22	13:V:79:LEU:HD21	1.87	0.57
2:A:206:ASN:HB3	2:A:209:GLU:HG2	1.87	0.57
4:C:121:LYS:HG2	4:C:132:ALA:HB3	1.87	0.57
27:R:28:PHE:HA	27:R:55:THR:HG21	1.87	0.57
31:Z:90:LYS:HD2	31:Z:104:ALA:HA	1.85	0.57
1:2:817:C:H2'	1:2:818:G:C8	2.39	0.56
5:E:64:ILE:HD12	16:Y:17:LEU:HB3	1.88	0.56
14:W:25:VAL:HG23	14:W:65:LEU:HD11	1.87	0.56
15:X:69:ARG:HG3	15:X:117:ILE:HG12	1.87	0.56
1:2:654:G:O6	1:2:676:U:O2	2.23	0.56
38:1:6:C:H2'	38:1:7:G:C8	2.40	0.56
1:2:31:C:OP1	15:X:140:LYS:NZ	2.32	0.56
1:2:327:A:H2'	1:2:328:G:H8	1.70	0.56
2:A:59:LEU:HB2	13:V:79:LEU:HD11	1.87	0.56
3:B:57:ALA:O	3:B:60:SER:N	2.39	0.56
6:G:215:ARG:O	6:G:219:ARG:HG2	2.05	0.56
28:S:12:GLN:N	28:S:59:GLY:O	2.38	0.56
40:k:151:GLN:H	40:k:151:GLN:CD	2.13	0.56
1:2:328:G:H2'	1:2:329:G:H8	1.71	0.56
1:2:946:U:H2'	1:2:947:G:H8	1.69	0.56
5:E:171:ASP:OD1	5:E:172:PHE:N	2.37	0.56
34:f:131:ALA:N	34:f:138:TYR:O	2.29	0.56
40:k:226:GLN:O	40:k:229:THR:OG1	2.23	0.56
1:2:108:A:H2'	1:2:109:G:C8	2.41	0.56
1:2:152:G:H2'	1:2:153:G:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:570:G:H5''	15:X:114:LYS:HD2	1.87	0.56
23:K:56:LYS:HB2	23:K:67:THR:HG23	1.87	0.56
25:P:37:ALA:O	25:P:42:ARG:NH1	2.39	0.56
14:W:11:LEU:HD13	14:W:73:GLY:H	1.71	0.56
15:X:41:SER:OG	15:X:43:PHE:O	2.24	0.56
28:S:24:GLY:O	28:S:59:GLY:N	2.39	0.56
1:2:1212:G:O2'	1:2:1243:A:N6	2.39	0.56
2:A:22:VAL:HG22	2:A:169:SER:HB2	1.88	0.56
9:J:127:VAL:O	9:J:131:GLN:HG2	2.05	0.56
22:F:96:THR:HG22	22:F:116:VAL:HG21	1.87	0.56
8:I:69:SER:OG	8:I:186:GLU:OE1	2.21	0.56
24:M:21:LEU:HB3	24:M:91:TRP:CH2	2.41	0.56
1:2:38:C:O3'	9:J:6:ARG:NH2	2.38	0.56
1:2:751:G:H2'	1:2:752:A:C8	2.41	0.56
8:I:70:GLU:N	8:I:70:GLU:OE2	2.38	0.56
1:2:283:G:N7	6:G:188:ARG:NH1	2.53	0.56
1:2:460:G:H2'	1:2:461:G:H8	1.71	0.56
4:C:87:ASN:HB2	4:C:212:LEU:HD23	1.87	0.56
6:G:78:ALA:HB2	6:G:92:ARG:HG3	1.87	0.56
40:k:358:GLY:HA3	40:k:371:LYS:O	2.06	0.56
1:2:38:C:H5''	9:J:6:ARG:HH21	1.71	0.55
4:C:107:VAL:HG11	4:C:134:ILE:HG13	1.88	0.55
14:W:24:GLN:HA	14:W:63:VAL:O	2.06	0.55
27:R:104:THR:O	27:R:108:GLU:HG3	2.05	0.55
40:k:147:ILE:HD12	40:k:187:ARG:HB3	1.88	0.55
4:C:83:ASP:HB3	4:C:109:VAL:HG23	1.88	0.55
17:a:23:CYS:HB2	17:a:74:CYS:HB3	1.89	0.55
21:D:113:LEU:HD12	21:D:114:ALA:H	1.71	0.55
32:c:44:VAL:HG22	32:c:54:LEU:HD21	1.87	0.55
39:j:7:ARG:NH1	39:j:9:TYR:O	2.36	0.55
40:k:95:ILE:HD11	40:k:187:ARG:HA	1.87	0.55
1:2:1205:U:OP2	1:2:1206:C:O2'	2.20	0.55
1:2:574:C:N4	15:X:65:ASN:OD1	2.37	0.55
1:2:638:U:H2'	7:H:101:LYS:HZ2	1.72	0.55
1:2:1661:G:N2	1:2:1736:U:O2	2.36	0.55
27:R:4:VAL:O	27:R:10:LYS:NZ	2.39	0.55
30:U:51:VAL:HG23	30:U:94:GLU:HB3	1.89	0.55
5:E:198:ARG:HG3	5:E:208:VAL:HG12	1.88	0.55
19:e:10:ARG:CZ	19:e:10:ARG:HA	2.36	0.55
39:j:26:GLN:HB2	39:j:33:TYR:HE1	1.72	0.55
1:2:699:U:H2'	1:2:700:C:H6	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:870:G:H2'	1:2:871:G:C8	2.41	0.55
1:2:1038:A:O2'	1:2:1039:G:O5'	2.23	0.55
39:j:24:VAL:HG13	39:j:65:VAL:HA	1.87	0.55
1:2:1079:U:H2'	1:2:1080:A:C8	2.41	0.55
1:2:1774:A:H2'	1:2:1775:G:C8	2.42	0.55
1:2:453:U:N1	5:E:66:MET:HE1	2.21	0.55
1:2:591:G:H2'	1:2:592:U:O4'	2.07	0.55
1:2:790:A:H2'	1:2:791:U:C6	2.42	0.55
1:2:23:G:N2	1:2:366:A:O2'	2.39	0.55
1:2:78:A:O2'	1:2:79:C:OP1	2.24	0.55
1:2:79:C:H2'	1:2:80:A:C4	2.42	0.55
1:2:627:G:OP1	11:N:124:ARG:NE	2.39	0.55
1:2:852:G:H2'	1:2:853:U:C6	2.42	0.55
1:2:867:G:OP1	11:N:121:ARG:NH1	2.39	0.55
1:2:886:A:H5''	12:O:120:PRO:HB3	1.89	0.55
1:2:952:G:H2'	1:2:953:G:C8	2.41	0.55
1:2:957:U:OP2	18:b:20:LYS:NZ	2.32	0.55
1:2:1320:A:N6	2:A:135:GLU:OE2	2.40	0.55
1:2:1357:G:H2'	1:2:1358:C:C6	2.42	0.55
1:2:1480:C:H4'	26:Q:77:GLN:NE2	2.22	0.55
6:G:48:TYR:CD1	6:G:113:ILE:HD11	2.42	0.55
10:L:34:TRP:HH2	10:L:36:LYS:HD3	1.72	0.55
28:S:36:ARG:HB2	28:S:102:ALA:HA	1.88	0.55
35:g:193:TYR:C	35:g:194:ARG:HE	2.15	0.55
1:2:245:G:H2'	1:2:246:A:C8	2.42	0.55
1:2:1490:A:O2'	1:2:1491:A:O4'	2.23	0.55
24:M:47:ARG:HD3	34:f:126:PRO:HG2	1.89	0.55
1:2:460:G:H2'	1:2:461:G:C8	2.42	0.54
1:2:97:C:H2'	1:2:98:U:H6	1.72	0.54
3:B:164:ILE:O	3:B:168:ILE:HG13	2.07	0.54
5:E:94:ALA:HB3	16:Y:17:LEU:HD12	1.89	0.54
1:2:824:U:H2'	1:2:825:U:C6	2.42	0.54
1:2:946:U:H2'	1:2:947:G:C8	2.42	0.54
1:2:1182:A:C8	25:P:100:LYS:HD2	2.42	0.54
1:2:1485:A:OP1	33:d:34:TYR:OH	2.20	0.54
3:B:32:ILE:HD12	3:B:96:LEU:HD11	1.89	0.54
16:Y:106:GLN:O	16:Y:110:GLN:HG2	2.07	0.54
18:b:67:THR:HG22	18:b:69:GLY:H	1.70	0.54
31:Z:80:LEU:HD21	31:Z:101:TYR:HE2	1.72	0.54
33:d:19:ARG:HE	33:d:32:ARG:HD2	1.72	0.54
34:f:124:CYS:SG	34:f:141:LYS:HB3	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:101:ILE:HB	40:k:189:VAL:HG12	1.88	0.54
1:2:1319:U:H2'	1:2:1321:A:H5'	1.89	0.54
6:G:31:ARG:HB3	6:G:101:ILE:HD13	1.90	0.54
6:G:142:ARG:HD3	6:G:149:LYS:HA	1.90	0.54
31:Z:57:TYR:OH	31:Z:68:ARG:NH1	2.41	0.54
31:Z:91:PRO:HA	31:Z:101:TYR:CD1	2.42	0.54
32:c:12:VAL:HG12	32:c:30:VAL:HG12	1.89	0.54
40:k:114:SER:N	44:k:601:GCP:O1A	2.41	0.54
1:2:154:U:OP2	16:Y:132:ARG:NH2	2.40	0.54
1:2:513:G:O2'	1:2:514:A:OP1	2.21	0.54
1:2:1143:U:HO2'	1:2:1300:U:HO2'	1.56	0.54
9:J:41:GLU:OE1	9:J:41:GLU:N	2.40	0.54
40:k:172:PRO:HD2	40:k:183:TYR:HB2	1.88	0.54
40:k:323:VAL:HG11	40:k:334:LYS:HD2	1.90	0.54
1:2:166:U:H5''	6:G:135:PRO:HA	1.88	0.54
1:2:332:A:H2'	1:2:333:G:C8	2.43	0.54
1:2:990:G:H21	1:2:1012:A:H62	1.56	0.54
7:H:113:PRO:HG2	7:H:116:ARG:HG3	1.89	0.54
14:W:17:ALA:HB3	14:W:25:VAL:HG22	1.89	0.54
29:T:73:VAL:O	29:T:77:ASN:ND2	2.41	0.54
29:T:74:GLY:HA2	29:T:77:ASN:HD22	1.72	0.54
29:T:102:ARG:O	29:T:106:GLN:HG3	2.07	0.54
40:k:431:GLU:HG3	40:k:484:ARG:NE	2.23	0.54
1:2:1035:A:H2'	1:2:1036:C:H6	1.72	0.54
2:A:179:ARG:HD2	2:A:183:ARG:HD2	1.90	0.54
16:Y:18:LEU:HA	16:Y:85:PHE:HE2	1.73	0.54
21:D:72:LEU:HD12	23:K:65:TYR:CD2	2.42	0.54
21:D:162:GLN:N	21:D:162:GLN:OE1	2.41	0.54
35:g:184:ARG:HH11	35:g:195:ILE:HD11	1.73	0.54
40:k:426:ILE:HG22	40:k:492:CYS:SG	2.48	0.54
1:2:1657:A:H2'	1:2:1658:A:C8	2.43	0.54
1:2:1660:G:H2'	1:2:1661:G:H8	1.73	0.54
6:G:43:ASP:HA	6:G:46:LYS:HE3	1.89	0.54
9:J:96:VAL:HA	9:J:99:LEU:HD23	1.90	0.54
12:O:18:ARG:HA	12:O:82:LYS:HB2	1.90	0.54
19:e:41:THR:HA	19:e:45:VAL:HG22	1.89	0.54
21:D:113:LEU:HD12	21:D:114:ALA:N	2.23	0.54
21:D:168:ILE:HA	21:D:188:ILE:O	2.08	0.54
21:D:218:LEU:HG	21:D:221:SER:HB2	1.90	0.54
25:P:107:ILE:HG12	25:P:111:MET:HG3	1.89	0.54
1:2:639:U:H2'	1:2:640:G:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1216:A:C6	23:K:40:LEU:HD11	2.43	0.54
1:2:1647:G:H2'	1:2:1648:U:C6	2.42	0.54
9:J:27:GLU:HB3	9:J:39:LYS:HD3	1.90	0.54
26:Q:100:GLN:NE2	35:g:57:VAL:HG13	2.23	0.54
27:R:5:ARG:O	27:R:10:LYS:NZ	2.41	0.54
39:j:24:VAL:HA	39:j:34:VAL:HG23	1.89	0.54
1:2:472:A:H2'	1:2:473:A:O4'	2.07	0.54
1:2:1175:G:HO2'	1:2:1194:C:HO2'	1.55	0.54
1:2:1332:C:H2'	1:2:1333:U:C6	2.43	0.54
7:H:31:SER:HA	7:H:35:LYS:HE3	1.90	0.54
10:L:99:ARG:HB2	15:X:12:ALA:HB2	1.90	0.54
17:a:46:GLU:H	17:a:46:GLU:CD	2.15	0.54
23:K:6:GLU:OE2	23:K:6:GLU:N	2.30	0.54
29:T:113:VAL:HA	29:T:128:GLY:HA3	1.89	0.54
1:2:339:U:H2'	1:2:340:A:C8	2.44	0.53
1:2:683:C:H3'	1:2:684:A:H8	1.74	0.53
1:2:1097:U:H1'	14:W:71:LYS:HD2	1.88	0.53
3:B:48:VAL:HG21	3:B:61:LEU:HD11	1.89	0.53
21:D:105:MET:HE1	21:D:184:ILE:HG21	1.90	0.53
22:F:189:ILE:HG21	31:Z:66:VAL:HG21	1.90	0.53
35:g:156:ARG:NH2	35:g:210:GLN:HG3	2.23	0.53
39:j:55:ARG:HH22	39:j:57:ARG:HD3	1.73	0.53
1:2:5:U:H2'	1:2:6:G:H8	1.72	0.53
1:2:169:U:N3	1:2:288:U:O2'	2.41	0.53
17:a:24:VAL:HG23	17:a:25:ASN:OD1	2.08	0.53
26:Q:46:PHE:HA	26:Q:49:TYR:HD2	1.73	0.53
35:g:86:TRP:HA	35:g:110:ASP:HB2	1.89	0.53
39:j:114:TYR:CZ	39:j:118:LYS:HD3	2.43	0.53
1:2:399:A:H5'	8:I:25:ARG:HA	1.89	0.53
1:2:738:G:N1	1:2:739:G:O6	2.41	0.53
7:H:21:ALA:O	7:H:25:ILE:HG12	2.09	0.53
7:H:99:LEU:O	7:H:112:ARG:NH1	2.40	0.53
10:L:146:THR:HB	10:L:149:ALA:HB3	1.88	0.53
12:O:20:PHE:HE1	12:O:86:THR:HA	1.72	0.53
13:V:12:TYR:O	13:V:12:TYR:CG	2.61	0.53
28:S:62:THR:OG1	28:S:64:GLU:OE1	2.25	0.53
1:2:12:U:H2'	1:2:13:C:H6	1.73	0.53
1:2:1794:C:N4	17:a:93:ARG:HH12	2.07	0.53
7:H:83:LYS:O	7:H:86:GLN:NE2	2.38	0.53
16:Y:18:LEU:HB2	16:Y:20:ARG:HG2	1.90	0.53
17:a:23:CYS:HB3	17:a:28:ARG:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:D:143:ARG:HE	37:3:37:U:H3	1.57	0.53
21:D:221:SER:HB3	35:g:200:ILE:O	2.08	0.53
33:d:30:LEU:HD12	33:d:31:ILE:H	1.73	0.53
1:2:593:A:OP2	9:J:37:LYS:NZ	2.41	0.53
1:2:1657:A:H2'	1:2:1658:A:H8	1.74	0.53
1:2:1774:A:H2'	1:2:1775:G:H8	1.74	0.53
8:I:150:GLU:OE2	8:I:150:GLU:N	2.39	0.53
31:Z:91:PRO:HA	31:Z:101:TYR:HD1	1.74	0.53
1:2:624:C:H2'	1:2:625:U:H6	1.73	0.53
5:E:65:LEU:HD12	5:E:80:THR:HA	1.90	0.53
35:g:14:LEU:HB2	35:g:317:ILE:HB	1.89	0.53
1:2:1280:G:O3'	30:U:76:SER:OG	2.27	0.53
15:X:14:LYS:HA	15:X:17:VAL:HG22	1.90	0.53
24:M:71:LEU:HD22	34:f:114:VAL:HG21	1.90	0.53
26:Q:22:VAL:HG12	26:Q:65:ILE:CD1	2.38	0.53
38:1:18:G:O6	39:j:110:SER:OG	2.26	0.53
40:k:237:GLU:HA	40:k:242:LYS:HZ1	1.74	0.53
1:2:107:C:H2'	1:2:108:A:H8	1.73	0.53
4:C:81:LEU:HD23	4:C:111:ASP:HB3	1.90	0.53
4:C:232:PRO:HA	4:C:235:TRP:CE2	2.43	0.53
9:J:53:ARG:NH2	9:J:97:LEU:O	2.34	0.53
31:Z:76:ALA:O	31:Z:80:LEU:HB2	2.09	0.53
38:1:74:C:H41	40:k:130:ASP:HB2	1.74	0.53
39:j:222:LEU:HD11	40:k:324:ASN:HB2	1.91	0.53
1:2:624:C:H2'	1:2:625:U:C6	2.44	0.53
1:2:1034:G:H2'	1:2:1035:A:H8	1.73	0.53
1:2:1145:G:H2'	1:2:1146:A:C8	2.43	0.53
23:K:11:ILE:HD13	23:K:35:ILE:HG12	1.91	0.53
23:K:24:LYS:HG2	23:K:26:ASP:H	1.74	0.53
1:2:1519:G:O2'	1:2:1521:G:OP2	2.26	0.53
4:C:227:TYR:OH	13:V:11:LEU:O	2.25	0.53
15:X:86:PHE:HE1	15:X:88:PRO:HA	1.74	0.53
24:M:51:GLN:NE2	24:M:76:ASN:OD1	2.42	0.53
1:2:85:A:N3	1:2:147:U:O2'	2.42	0.52
1:2:1049:G:OP1	18:b:70:LYS:NZ	2.26	0.52
1:2:1146:A:H2'	1:2:1147:C:C6	2.45	0.52
1:2:1240:G:OP1	25:P:77:ARG:NH1	2.41	0.52
12:O:63:ALA:O	12:O:67:VAL:HG22	2.09	0.52
22:F:50:PHE:HD2	22:F:69:PRO:HA	1.73	0.52
1:2:223:C:H2'	1:2:224:A:C8	2.44	0.52
1:2:1066:C:H5''	3:B:150:VAL:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:166:LEU:O	7:H:169:PHE:HB2	2.08	0.52
8:I:104:ILE:HB	8:I:166:LEU:HB2	1.91	0.52
29:T:50:SER:OG	29:T:51:GLU:OE1	2.26	0.52
32:c:19:THR:OG1	32:c:20:GLY:N	2.41	0.52
1:2:882:C:H2'	1:2:883:A:C8	2.44	0.52
1:2:1559:U:H2'	1:2:1560:G:H8	1.73	0.52
16:Y:12:VAL:HA	16:Y:22:GLN:O	2.09	0.52
24:M:53:ALA:HB3	24:M:79:LEU:HG	1.91	0.52
30:U:50:LEU:HD11	30:U:99:ILE:HD12	1.90	0.52
31:Z:45:ASP:OD1	31:Z:45:ASP:N	2.42	0.52
36:i:26:LEU:HD13	36:i:99:GLU:HB2	1.90	0.52
1:2:603:A:H2'	1:2:604:A:O4'	2.10	0.52
1:2:1349:G:H2'	1:2:1350:G:H8	1.74	0.52
22:F:78:ARG:HH11	26:Q:122:ARG:HD3	1.74	0.52
25:P:18:LYS:NZ	28:S:90:LYS:O	2.43	0.52
35:g:109:GLY:O	35:g:127:SER:OG	2.28	0.52
1:2:609:G:HO2'	1:2:612:G:HO2'	1.58	0.52
1:2:1290:G:H22	1:2:1323:G:N2	2.08	0.52
1:2:1380:A:H1'	30:U:57:ARG:HG2	1.92	0.52
1:2:1559:U:H4'	1:2:1597:C:H4'	1.92	0.52
4:C:236:GLU:N	4:C:236:GLU:OE2	2.40	0.52
12:O:45:GLY:HA2	12:O:54:GLU:HG2	1.92	0.52
26:Q:57:LEU:H	26:Q:57:LEU:HD12	1.72	0.52
26:Q:100:GLN:N	26:Q:100:GLN:OE1	2.41	0.52
28:S:45:LEU:HD11	29:T:36:ILE:HD13	1.91	0.52
38:1:53:G:H2'	38:1:54:A:H8	1.75	0.52
39:j:4:SER:OG	39:j:109:HIS:NE2	2.39	0.52
39:j:223:VAL:HA	40:k:326:PRO:HB3	1.92	0.52
1:2:1132:A:N3	1:2:1648:U:O2'	2.42	0.52
1:2:1471:U:H1'	22:F:105:ASN:HD22	1.74	0.52
1:2:1522:A:N3	1:2:1588:G:O2'	2.40	0.52
1:2:1586:G:O6	1:2:1606:U:O4	2.28	0.52
5:E:163:ASP:OD2	5:E:166:THR:OG1	2.27	0.52
8:I:116:HIS:O	8:I:147:ARG:NH1	2.43	0.52
12:O:84:ARG:HG3	12:O:119:THR:HA	1.91	0.52
21:D:154:ASP:OD1	21:D:155:GLY:N	2.43	0.52
38:1:36:U:H2'	38:1:37:T6A:H8	1.75	0.52
39:j:96:ILE:HA	39:j:99:GLU:OE2	2.09	0.52
40:k:466:ILE:O	40:k:468:SER:N	2.42	0.52
1:2:613:C:OP2	15:X:5:LYS:NZ	2.33	0.52
1:2:760:A:N1	1:2:789:U:O4	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:788:A:C2	1:2:789:U:H1'	2.45	0.52
2:A:102:PHE:HE2	2:A:135:GLU:HG3	1.74	0.52
7:H:91:ILE:HG21	7:H:129:LEU:HD12	1.92	0.52
26:Q:127:LYS:HA	26:Q:134:ALA:HA	1.91	0.52
28:S:100:SER:HB2	28:S:105:LEU:HA	1.92	0.52
38:1:1:A:H2'	38:1:2:G:C8	2.45	0.52
38:1:53:G:H2'	38:1:54:A:C8	2.45	0.52
39:j:27:ILE:HD11	39:j:63:ILE:HG21	1.92	0.52
40:k:97:ARG:HB3	40:k:387:LEU:HD21	1.90	0.52
1:2:14:C:H2'	1:2:15:U:C6	2.45	0.52
1:2:383:G:H2'	1:2:384:A:C8	2.44	0.52
1:2:833:G:H8	1:2:833:G:OP2	1.93	0.52
7:H:41:LEU:HG	7:H:70:TYR:CE1	2.45	0.52
36:i:38:ILE:HD12	36:i:75:ASP:HB2	1.92	0.52
1:2:14:C:H5'	4:C:169:SER:OG	2.09	0.52
1:2:147:U:H3	6:G:132:ARG:NH2	2.07	0.52
1:2:206:U:H2'	1:2:207:U:C6	2.45	0.52
1:2:327:A:H2'	1:2:328:G:C8	2.45	0.52
1:2:922:A:H2'	1:2:923:A:H8	1.74	0.52
1:2:1335:A:H2'	1:2:1336:A:O4'	2.09	0.52
28:S:139:LYS:O	28:S:143:ARG:NH2	2.43	0.52
35:g:134:VAL:HB	35:g:143:TYR:HB2	1.92	0.52
1:2:26:A:O2'	1:2:27:U:OP1	2.26	0.52
1:2:299:A:H2'	1:2:300:A:C8	2.44	0.52
1:2:1201:A:N6	1:2:1455:C:OP1	2.43	0.52
2:A:207:PRO:HA	2:A:210:ILE:HG22	1.92	0.52
5:E:103:TYR:O	5:E:182:TYR:OH	2.27	0.52
21:D:93:ASP:N	21:D:93:ASP:OD1	2.40	0.52
22:F:145:ARG:HG2	32:c:55:VAL:HG11	1.91	0.52
23:K:71:GLU:OE2	23:K:71:GLU:N	2.29	0.52
26:Q:45:ARG:HG2	26:Q:49:TYR:CE2	2.45	0.52
28:S:111:ASP:HA	28:S:114:GLU:HG3	1.91	0.52
35:g:171:ARG:NH1	35:g:189:ASN:OD1	2.39	0.52
40:k:297:PHE:O	40:k:301:THR:OG1	2.27	0.52
1:2:646:G:H2'	1:2:647:G:C8	2.46	0.51
1:2:1498:C:OP1	29:T:122:ARG:NH2	2.38	0.51
2:A:71:GLU:OE1	2:A:71:GLU:N	2.43	0.51
17:a:41:ILE:HG12	17:a:68:TYR:CD2	2.45	0.51
28:S:15:LEU:HB2	28:S:22:VAL:HG13	1.92	0.51
40:k:276:ASP:OD1	40:k:276:ASP:N	2.43	0.51
1:2:1143:U:H2'	1:2:1144:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1726:U:H2'	1:2:1727:C:C6	2.45	0.51
3:B:82:ARG:HG2	3:B:103:MET:HE3	1.92	0.51
3:B:99:ASN:OD1	3:B:100:PHE:N	2.43	0.51
5:E:162:VAL:HG12	5:E:164:LEU:H	1.75	0.51
7:H:141:ARG:HB3	14:W:51:GLU:OE1	2.10	0.51
34:f:134:GLY:O	34:f:136:ARG:HG3	2.10	0.51
1:2:1396:U:H3'	1:2:1397:C:H5'	1.92	0.51
1:2:1569:C:OP2	31:Z:28:SER:HB3	2.10	0.51
5:E:18:TRP:HH2	5:E:31:PRO:HD3	1.75	0.51
6:G:14:LYS:HB2	6:G:124:ILE:HD11	1.91	0.51
14:W:24:GLN:NE2	18:b:5:GLN:H	2.09	0.51
26:Q:10:PHE:HE2	26:Q:12:LYS:HD2	1.74	0.51
1:2:509:G:OP1	9:J:176:ARG:NH1	2.39	0.51
1:2:598:A:H2'	1:2:599:U:C6	2.46	0.51
3:B:58:SER:HA	3:B:61:LEU:HD23	1.93	0.51
5:E:104:ASP:O	5:E:107:GLY:N	2.27	0.51
10:L:16:GLN:HE22	10:L:33:ARG:HG3	1.75	0.51
22:F:102:ASN:OD1	22:F:182:ARG:HD3	2.11	0.51
30:U:45:ALA:HA	30:U:50:LEU:HD22	1.91	0.51
38:1:1:A:H2'	38:1:2:G:H8	1.74	0.51
39:j:170:LYS:HA	39:j:173:ILE:HG22	1.92	0.51
1:2:1279:C:H2'	1:2:1280:G:H8	1.75	0.51
1:2:1628:U:O2'	1:2:1762:C:O2'	2.25	0.51
5:E:11:ARG:HA	5:E:28:ALA:HB2	1.93	0.51
7:H:99:LEU:HB2	7:H:112:ARG:HD2	1.91	0.51
13:V:15:ARG:HH21	13:V:24:ILE:HG21	1.76	0.51
36:i:11:LYS:HD3	37:3:33:C:N4	2.26	0.51
1:2:91:G:H2'	1:2:92:A:O4'	2.11	0.51
1:2:520:A:N3	16:Y:34:ASN:ND2	2.36	0.51
1:2:638:U:H2'	7:H:101:LYS:NZ	2.25	0.51
1:2:1040:G:H2'	1:2:1041:G:C8	2.45	0.51
1:2:1043:U:H2'	1:2:1044:C:C6	2.45	0.51
1:2:1073:G:H2'	1:2:1074:C:C6	2.46	0.51
1:2:1594:C:O2'	1:2:1596:U:OP2	2.16	0.51
2:A:126:PRO:HG2	2:A:147:THR:HG22	1.92	0.51
3:B:35:PRO:HA	3:B:232:HIS:CE1	2.45	0.51
6:G:58:LYS:HA	6:G:107:ALA:HB2	1.92	0.51
8:I:160:GLN:HE22	8:I:190:LEU:HD21	1.76	0.51
10:L:99:ARG:HH21	14:W:79:PHE:HZ	1.59	0.51
11:N:102:LEU:HD11	11:N:112:LYS:HA	1.93	0.51
13:V:4:ASP:OD1	13:V:5:LYS:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:128:ARG:HD3	35:g:151:TRP:CE3	2.46	0.51
40:k:282:PRO:HD3	41:l:131:TYR:CD2	2.45	0.51
1:2:17:C:H2'	1:2:18:C:C6	2.46	0.51
1:2:319:U:H5''	1:2:320:C:H5''	1.91	0.51
1:2:367:U:O2'	1:2:602:U:O2'	2.19	0.51
1:2:1240:G:O2'	1:2:1241:A:O5'	2.28	0.51
1:2:1291:G:H2'	1:2:1292:U:O2	2.11	0.51
1:2:1742:A:H3'	1:2:1743:G:H8	1.75	0.51
13:V:49:GLU:OE2	13:V:49:GLU:HA	2.11	0.51
18:b:49:HIS:HA	18:b:70:LYS:HA	1.93	0.51
39:j:68:ASN:HD22	39:j:68:ASN:N	2.08	0.51
1:2:383:G:H2'	1:2:384:A:H8	1.76	0.51
1:2:1391:C:H2'	1:2:1392:G:H8	1.75	0.51
1:2:1759:U:O2'	37:3:30:U:OP1	2.21	0.51
5:E:66:MET:HG3	5:E:67:GLN:N	2.26	0.51
7:H:24:PHE:CE1	7:H:77:LEU:HD21	2.45	0.51
29:T:18:TYR:HD1	29:T:135:ILE:HD13	1.75	0.51
4:C:104:LYS:HA	4:C:121:LYS:O	2.11	0.51
4:C:159:LEU:HD22	4:C:226:THR:HG21	1.92	0.51
5:E:163:ASP:OD1	5:E:163:ASP:N	2.36	0.51
12:O:20:PHE:O	12:O:27:PHE:N	2.34	0.51
28:S:69:ILE:O	28:S:73:MET:HG3	2.10	0.51
34:f:118:ARG:HG2	34:f:118:ARG:HH11	1.75	0.51
39:j:21:MET:HB3	39:j:38:GLU:HB2	1.92	0.51
1:2:1141:A:H5''	17:a:2:PRO:HB3	1.93	0.50
1:2:1144:U:C2	1:2:1145:G:C8	2.99	0.50
1:2:1582:G:H22	1:2:1608:G:H3'	1.75	0.50
1:2:1595:A:H8	33:d:14:PHE:HB2	1.76	0.50
2:A:18:LEU:HG	2:A:23:HIS:CD2	2.45	0.50
23:K:24:LYS:HE2	23:K:63:TYR:CE1	2.46	0.50
26:Q:101:SER:O	26:Q:105:LEU:HG	2.11	0.50
35:g:39:ARG:HD2	35:g:68:ILE:HG23	1.93	0.50
40:k:94:ILE:HG23	40:k:391:VAL:HG21	1.93	0.50
1:2:1712:A:H2'	1:2:1713:G:H8	1.77	0.50
2:A:112:THR:HG22	2:A:114:SER:H	1.75	0.50
16:Y:81:ASP:HA	16:Y:84:LYS:HG2	1.92	0.50
25:P:30:THR:O	25:P:34:VAL:HG23	2.11	0.50
1:2:157:U:O2'	1:2:159:C:OP2	2.26	0.50
1:2:419:A:OP1	6:G:96:SER:OG	2.22	0.50
3:B:168:ILE:HG23	3:B:197:ILE:HD13	1.92	0.50
4:C:250:ASP:N	4:C:250:ASP:OD1	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:24:VAL:HG13	6:G:28:TYR:HE1	1.76	0.50
12:O:80:HIS:ND1	12:O:113:GLY:O	2.44	0.50
15:X:93:LEU:HD23	19:e:11:ALA:HB2	1.93	0.50
35:g:68:ILE:O	35:g:86:TRP:N	2.43	0.50
38:1:7:G:O2'	38:1:49:5MC:O5'	2.28	0.50
39:j:34:VAL:HG11	39:j:46:ILE:HD11	1.93	0.50
1:2:326:U:OP2	10:L:57:LYS:NZ	2.34	0.50
1:2:864:A:OP1	14:W:28:ARG:NH2	2.45	0.50
1:2:1259:U:O2'	1:2:1260:G:H8	1.95	0.50
3:B:91:VAL:HG22	3:B:96:LEU:HB3	1.94	0.50
35:g:45:SER:O	35:g:59:VAL:N	2.41	0.50
40:k:314:ARG:HH11	40:k:344:ASN:ND2	2.10	0.50
40:k:501:LEU:HD11	40:k:515:ALA:HB2	1.94	0.50
1:2:646:G:H2'	1:2:647:G:H8	1.77	0.50
1:2:863:U:C5	14:W:28:ARG:HD2	2.47	0.50
1:2:1386:A:N6	1:2:1409:A:N7	2.60	0.50
1:2:1389:A:H2'	1:2:1390:U:C6	2.46	0.50
3:B:109:LYS:O	3:B:113:MET:HG2	2.11	0.50
10:L:55:ASP:HA	10:L:82:ARG:HH12	1.75	0.50
23:K:82:LEU:HG	23:K:83:PRO:HD2	1.94	0.50
27:R:27:ASP:OD1	35:g:39:ARG:NH2	2.44	0.50
40:k:251:VAL:HG21	40:k:282:PRO:HB3	1.94	0.50
7:H:43:PHE:HE1	7:H:60:VAL:HB	1.76	0.50
7:H:51:VAL:HB	7:H:55:LYS:HB3	1.93	0.50
10:L:125:VAL:HG23	10:L:139:VAL:HA	1.93	0.50
1:2:248:U:OP1	10:L:34:TRP:NE1	2.32	0.50
1:2:433:G:N2	1:2:436:A:OP2	2.38	0.50
4:C:162:LYS:NZ	14:W:91:ALA:O	2.45	0.50
16:Y:20:ARG:HD3	16:Y:74:LEU:HD23	1.93	0.50
25:P:86:VAL:H	25:P:89:MET:HE3	1.77	0.50
1:2:494:C:H3'	1:2:495:G:C8	2.47	0.50
1:2:638:U:OP1	7:H:117:THR:HB	2.12	0.50
1:2:1604:C:H2'	1:2:1605:G:C8	2.47	0.50
3:B:30:TYR:HD2	3:B:48:VAL:HG21	1.77	0.50
3:B:180:THR:O	3:B:184:LEU:N	2.34	0.50
5:E:98:ASN:HD22	5:E:116:ASP:HA	1.77	0.50
6:G:84:TYR:OH	6:G:91:GLU:O	2.21	0.50
8:I:70:GLU:HG3	8:I:112:TRP:CH2	2.46	0.50
8:I:139:ASN:O	8:I:142:ARG:HG2	2.12	0.50
11:N:4:MET:HE1	11:N:121:ARG:HG3	1.93	0.50
21:D:162:GLN:O	21:D:165:ASN:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:P:34:VAL:HG22	25:P:45:PHE:CD2	2.45	0.50
25:P:81:ARG:HH21	25:P:120:SER:HG	1.53	0.50
1:2:97:C:O2	1:2:424:A:O2'	2.30	0.50
1:2:453:U:O2'	1:2:454:C:O4'	2.30	0.50
1:2:1251:C:H5''	34:f:105:TYR:OH	2.12	0.50
1:2:1380:A:H5''	30:U:60:THR:HG23	1.94	0.50
1:2:1412:U:O2'	1:2:1414:G:OP2	2.28	0.50
1:2:1430:U:H4'	1:2:1431:G:O5'	2.10	0.50
1:2:1754:A:N7	36:i:61:ILE:HG21	2.27	0.50
2:A:107:PHE:HB2	2:A:135:GLU:HB3	1.93	0.50
2:A:205:ARG:HE	2:A:210:ILE:HD13	1.76	0.50
3:B:2:ALA:HA	39:j:89:ARG:NH1	2.27	0.50
4:C:145:ARG:NH1	13:V:10:GLU:OE1	2.45	0.50
7:H:42:GLN:O	7:H:70:TYR:OH	2.30	0.50
8:I:67:TRP:O	8:I:71:GLY:CA	2.60	0.50
23:K:58:GLN:HA	23:K:58:GLN:HE21	1.77	0.50
28:S:18:LEU:O	28:S:20:THR:HG23	2.12	0.50
35:g:48:LEU:HA	35:g:56:GLY:HA2	1.93	0.50
1:2:855:A:N6	7:H:96:ARG:HB3	2.26	0.49
1:2:978:A:H4'	1:2:1784:G:N2	2.26	0.49
1:2:1168:G:N1	1:2:1573:7MG:OP2	2.45	0.49
4:C:148:TYR:OH	4:C:154:GLY:O	2.26	0.49
6:G:180:THR:HG22	6:G:182:GLN:H	1.76	0.49
22:F:150:ARG:HG2	22:F:159:ARG:HH12	1.76	0.49
1:2:17:C:H2'	1:2:18:C:H6	1.77	0.49
1:2:840:U:C4	1:2:841:C:C4	3.00	0.49
1:2:1101:G:OP1	14:W:76:SER:OG	2.29	0.49
1:2:1250:U:H1'	34:f:133:HIS:CD2	2.47	0.49
1:2:1738:A:H2'	1:2:1739:U:C6	2.47	0.49
3:B:144:ARG:HB2	3:B:208:GLN:CB	2.41	0.49
8:I:112:TRP:O	8:I:116:HIS:HB2	2.11	0.49
9:J:159:ALA:O	9:J:162:SER:OG	2.25	0.49
12:O:91:SER:O	12:O:92:LYS:HG2	2.12	0.49
14:W:115:GLU:O	14:W:119:LYS:HG2	2.13	0.49
22:F:42:ILE:HG12	22:F:71:TYR:CZ	2.46	0.49
22:F:78:ARG:HG2	22:F:78:ARG:HH11	1.77	0.49
25:P:81:ARG:NH2	25:P:120:SER:OG	2.33	0.49
30:U:19:ILE:HG22	30:U:21:LYS:H	1.77	0.49
40:k:148:TYR:HB3	40:k:183:TYR:HB3	1.94	0.49
40:k:307:ARG:HG2	40:k:392:PRO:HB2	1.93	0.49
1:2:1318:A:H2'	1:2:1319:U:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1683:G:H2'	1:2:1684:C:C6	2.47	0.49
8:I:22:ARG:HG3	8:I:22:ARG:O	2.12	0.49
22:F:165:SER:HB2	32:c:48:VAL:HG13	1.92	0.49
23:K:38:LYS:O	23:K:42:VAL:HG23	2.12	0.49
29:T:61:VAL:HG21	29:T:104:VAL:HG11	1.93	0.49
35:g:71:ASP:OD1	35:g:72:VAL:N	2.45	0.49
40:k:214:ALA:HB3	40:k:244:VAL:HG22	1.94	0.49
1:2:861:A:N7	11:N:70:LYS:NZ	2.58	0.49
1:2:1159:A:H2'	1:2:1160:C:H6	1.74	0.49
1:2:1357:G:H2'	1:2:1358:C:H6	1.76	0.49
1:2:1589:C:H2'	1:2:1590:A:C8	2.46	0.49
8:I:144:TRP:HA	8:I:147:ARG:HD2	1.93	0.49
15:X:37:ALA:O	15:X:41:SER:OG	2.18	0.49
16:Y:7:ILE:HD13	16:Y:40:LEU:HD11	1.94	0.49
39:j:26:GLN:HB2	39:j:33:TYR:CE1	2.48	0.49
40:k:356:ARG:NH2	40:k:422:HIS:O	2.39	0.49
7:H:133:THR:OG1	7:H:154:LEU:HD23	2.12	0.49
22:F:179:ILE:O	22:F:183:GLU:HG2	2.11	0.49
22:F:218:GLU:OE1	39:j:30:MET:HE3	2.13	0.49
23:K:24:LYS:O	23:K:39:ASN:ND2	2.45	0.49
28:S:42:TYR:HD1	28:S:85:PHE:HE1	1.60	0.49
39:j:195:TYR:CG	40:k:374:PHE:HB3	2.47	0.49
40:k:292:ASP:N	40:k:292:ASP:OD1	2.44	0.49
1:2:299:A:H2'	1:2:300:A:H8	1.78	0.49
1:2:444:A:H62	1:2:461:G:H1'	1.78	0.49
1:2:911:U:OP2	3:B:10:SER:N	2.46	0.49
4:C:162:LYS:HD2	14:W:95:PRO:HA	1.94	0.49
5:E:185:GLY:O	5:E:224:ASN:ND2	2.34	0.49
7:H:77:LEU:HD22	7:H:92:PHE:CZ	2.45	0.49
7:H:143:LEU:HB2	7:H:147:ASN:OD1	2.13	0.49
10:L:54:ILE:HG23	10:L:55:ASP:H	1.77	0.49
11:N:99:ARG:NH2	11:N:119:GLU:OE2	2.42	0.49
30:U:71:PRO:HB3	33:d:41:GLN:HG2	1.94	0.49
38:1:3:C:H2'	38:1:4:G:H8	1.78	0.49
38:1:36:U:H2'	38:1:37:T6A:C8	2.48	0.49
40:k:113:LYS:N	44:k:601:GCP:O1A	2.44	0.49
40:k:207:GLY:O	40:k:211:MET:HG2	2.12	0.49
1:2:38:C:H2'	1:2:39:A:C8	2.47	0.49
4:C:71:PHE:CD1	4:C:135:ILE:HD12	2.48	0.49
4:C:151:THR:O	4:C:151:THR:HG22	2.13	0.49
8:I:60:ILE:HD12	8:I:61:GLU:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:D:109:LEU:HD11	21:D:115:ILE:HG12	1.93	0.49
25:P:18:LYS:NZ	28:S:90:LYS:HB3	2.27	0.49
39:j:222:LEU:HD12	39:j:228:TYR:HE1	1.77	0.49
40:k:99:ALA:HA	40:k:188:HIS:HB3	1.95	0.49
40:k:507:LYS:O	40:k:508:HIS:ND1	2.45	0.49
1:2:388:G:H2'	1:2:389:G:O4'	2.12	0.49
1:2:623:G:H2'	1:2:624:C:C6	2.48	0.49
1:2:1125:G:H2'	1:2:1126:G:H8	1.78	0.49
1:2:1506:U:H2'	1:2:1507:C:C6	2.48	0.49
1:2:1771:C:H2'	1:2:1772:G:H8	1.77	0.49
1:2:1793:U:C6	17:a:75:ILE:HD11	2.47	0.49
5:E:173:ILE:HD11	5:E:235:TRP:CE2	2.47	0.49
6:G:137:ARG:HB3	6:G:140:ASN:HB2	1.94	0.49
13:V:17:CYS:HB2	13:V:56:SER:HB2	1.94	0.49
18:b:20:LYS:HG2	18:b:21:LEU:HG	1.94	0.49
22:F:70:ILE:HA	26:Q:112:TYR:OH	2.13	0.49
26:Q:36:ILE:HD13	26:Q:52:LEU:HD11	1.94	0.49
40:k:355:ILE:HG13	40:k:417:VAL:HG13	1.95	0.49
1:2:5:U:H2'	1:2:6:G:C8	2.48	0.49
1:2:384:A:H5''	8:I:22:ARG:HB2	1.95	0.49
1:2:513:G:HO2'	1:2:514:A:P	2.36	0.49
1:2:965:A:OP2	11:N:124:ARG:NH1	2.46	0.49
1:2:1645:U:H2'	1:2:1646:A:H8	1.76	0.49
1:2:1647:G:H2'	1:2:1648:U:H6	1.78	0.49
6:G:191:LYS:O	6:G:195:ILE:HG12	2.12	0.49
16:Y:98:GLU:N	16:Y:98:GLU:OE2	2.45	0.49
25:P:33:PHE:O	25:P:37:ALA:N	2.45	0.49
28:S:17:LEU:HD11	28:S:66:LEU:HB3	1.95	0.49
28:S:97:ASP:N	28:S:97:ASP:OD1	2.44	0.49
34:f:140:GLY:O	34:f:143:HIS:ND1	2.45	0.49
35:g:302:SER:HG	35:g:306:GLN:H	1.61	0.49
36:i:62:ARG:HH11	36:i:63:GLY:N	2.11	0.49
38:1:76:A:H62	40:k:334:LYS:HD3	1.78	0.49
1:2:698:U:H2'	1:2:699:U:C6	2.48	0.49
1:2:1626:U:H2'	1:2:1627:G:C8	2.48	0.49
2:A:15:GLN:HB2	27:R:117:LEU:HD11	1.95	0.49
2:A:190:ASP:OD2	2:A:192:THR:OG1	2.31	0.49
5:E:49:ARG:NE	5:E:50:ASN:OD1	2.40	0.49
6:G:10:ASN:HA	6:G:128:THR:HG22	1.95	0.49
16:Y:20:ARG:NH2	16:Y:76:TYR:OH	2.46	0.49
34:f:133:HIS:HE1	34:f:138:TYR:HB3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1:11:C:H2'	38:1:12:G:C8	2.48	0.49
1:2:1017:U:C2	1:2:1018:A:C8	3.01	0.48
1:2:1479:C:H5'	26:Q:40:GLN:OE1	2.13	0.48
1:2:1677:G:H21	1:2:1720:A:H62	1.61	0.48
1:2:1712:A:H2'	1:2:1713:G:C8	2.47	0.48
5:E:11:ARG:HD3	5:E:21:ASP:O	2.14	0.48
5:E:31:PRO:HG3	5:E:43:PRO:HG3	1.95	0.48
16:Y:18:LEU:HD13	16:Y:20:ARG:CZ	2.43	0.48
22:F:92:VAL:O	22:F:96:THR:HG23	2.13	0.48
29:T:18:TYR:HD1	29:T:135:ILE:HG21	1.78	0.48
1:2:220:A:C6	1:2:840:U:C4	3.01	0.48
1:2:1427:G:H2'	1:2:1428:U:C6	2.47	0.48
1:2:1607:U:H5''	26:Q:75:VAL:HG22	1.94	0.48
5:E:136:ILE:HG23	5:E:149:TYR:CE1	2.49	0.48
7:H:14:THR:O	7:H:17:GLU:HG2	2.13	0.48
8:I:83:TYR:HD2	8:I:101:ILE:HD12	1.77	0.48
8:I:188:GLU:O	8:I:191:ALA:HB3	2.12	0.48
16:Y:29:HIS:ND1	16:Y:29:HIS:O	2.46	0.48
20:h:1:MET:HE3	20:h:9:ARG:HH21	1.77	0.48
26:Q:9:THR:HG21	26:Q:88:GLY:HA2	1.95	0.48
35:g:68:ILE:HB	35:g:86:TRP:CG	2.49	0.48
40:k:314:ARG:HE	40:k:494:GLU:HG2	1.78	0.48
40:k:347:PHE:H	40:k:390:ALA:HB3	1.79	0.48
1:2:80:A:H5''	1:2:81:G:C8	2.48	0.48
1:2:476:A:OP2	19:e:28:LYS:NZ	2.45	0.48
1:2:1737:C:H2'	1:2:1738:A:H8	1.78	0.48
5:E:179:LYS:NZ	5:E:230:GLU:OE1	2.37	0.48
15:X:43:PHE:HB3	15:X:46:SER:HB3	1.95	0.48
22:F:175:ALA:O	22:F:179:ILE:HG12	2.13	0.48
25:P:107:ILE:HG23	25:P:111:MET:HG3	1.94	0.48
26:Q:60:PHE:HB2	26:Q:63:ILE:HB	1.94	0.48
38:1:18:G:N7	39:j:107:THR:HG22	2.28	0.48
1:2:329:G:H2'	1:2:330:A:C8	2.49	0.48
1:2:643:U:H2'	1:2:644:C:C6	2.47	0.48
1:2:986:G:N2	1:2:1012:A:OP2	2.46	0.48
1:2:1047:G:O3'	18:b:69:GLY:HA3	2.12	0.48
1:2:1521:G:C2	29:T:75:LYS:NZ	2.81	0.48
1:2:1668:G:O2'	1:2:1729:A:N6	2.46	0.48
4:C:158:SER:OG	4:C:159:LEU:N	2.46	0.48
14:W:24:GLN:HE22	18:b:5:GLN:H	1.61	0.48
25:P:85:ILE:HG21	25:P:111:MET:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:P:88:GLU:OE1	25:P:88:GLU:N	2.42	0.48
31:Z:80:LEU:HD21	31:Z:101:TYR:CE2	2.48	0.48
35:g:172:ILE:HB	35:g:188:LEU:HB2	1.95	0.48
1:2:23:G:O6	1:2:601:U:C2	2.66	0.48
1:2:126:A:O2'	1:2:127:G:H5'	2.13	0.48
1:2:197:A:C5	1:2:198:G:H1'	2.48	0.48
1:2:1200:G:N7	1:2:1593:U:H2'	2.28	0.48
1:2:1711:G:H3'	1:2:1712:A:H8	1.78	0.48
2:A:17:LEU:HD11	2:A:54:TRP:HD1	1.79	0.48
4:C:103:PHE:CE1	37:3:38:C:H2'	2.49	0.48
6:G:64:LYS:HB2	6:G:97:VAL:HG21	1.95	0.48
7:H:162:ILE:HG23	7:H:165:LYS:HB2	1.94	0.48
17:a:87:ARG:NH2	17:a:94:ILE:O	2.41	0.48
31:Z:54:ALA:HB3	31:Z:55:PRO:HD3	1.95	0.48
1:2:107:C:H2'	1:2:108:A:C8	2.49	0.48
1:2:1554:A:O2'	25:P:40:ARG:NH1	2.47	0.48
9:J:118:LEU:HB2	9:J:158:PHE:CZ	2.49	0.48
25:P:71:GLU:N	25:P:71:GLU:OE2	2.46	0.48
1:2:116:U:O2'	1:2:332:A:N3	2.46	0.48
1:2:151:U:H5'	6:G:13:GLN:HE22	1.79	0.48
1:2:155:A:N6	1:2:417:G:N7	2.62	0.48
1:2:637:U:H4'	1:2:638:U:OP2	2.14	0.48
1:2:1007:G:H2'	1:2:1008:U:C6	2.49	0.48
1:2:1043:U:H5	1:2:1073:G:H1	1.60	0.48
1:2:1086:A:OP2	1:2:1086:A:H8	1.96	0.48
1:2:1171:G:H21	29:T:88:VAL:HG21	1.77	0.48
1:2:1234:C:C2	1:2:1235:A:C8	3.02	0.48
1:2:1737:C:H2'	1:2:1738:A:C8	2.49	0.48
8:I:78:ILE:HD12	8:I:78:ILE:H	1.78	0.48
9:J:101:VAL:HG22	9:J:105:LEU:HD23	1.96	0.48
11:N:38:ILE:O	11:N:42:ARG:HG3	2.14	0.48
21:D:204:ASP:HB2	27:R:8:THR:HG21	1.96	0.48
23:K:16:PHE:CD2	23:K:80:LEU:HD23	2.47	0.48
25:P:21:ASP:OD1	25:P:22:LEU:N	2.47	0.48
31:Z:62:VAL:O	31:Z:66:VAL:HG22	2.13	0.48
35:g:64:GLY:HA3	35:g:91:ARG:HH12	1.78	0.48
1:2:29:U:H2'	1:2:30:G:C8	2.47	0.48
1:2:365:A:OP1	1:2:758:U:O2'	2.28	0.48
1:2:444:A:H61	1:2:460:G:N2	2.11	0.48
1:2:497:G:H1'	1:2:499:C:H41	1.78	0.48
1:2:1216:A:H4'	23:K:44:LYS:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1488:A:OP1	21:D:9:ARG:NH2	2.46	0.48
5:E:156:VAL:HG12	5:E:157:ASN:OD1	2.14	0.48
18:b:35:VAL:HG12	18:b:79:PHE:HB3	1.96	0.48
25:P:22:LEU:HA	25:P:25:LEU:HB2	1.96	0.48
35:g:110:ASP:N	35:g:110:ASP:OD1	2.45	0.48
36:i:30:GLU:HB3	36:i:31:GLU:OE2	2.13	0.48
39:j:15:GLU:OE1	39:j:39:TYR:OH	2.32	0.48
39:j:100:GLU:O	39:j:104:LYS:HG2	2.14	0.48
1:2:194:G:O6	1:2:195:G:O6	2.31	0.48
1:2:1219:C:H2'	1:2:1220:A:H8	1.79	0.48
1:2:1287:G:OP1	1:2:1622:C:O2'	2.32	0.48
1:2:1415:A:H2'	1:2:1416:G:O4'	2.13	0.48
1:2:1622:C:H2'	1:2:1623:C:H6	1.79	0.48
2:A:63:ILE:HG12	13:V:36:ILE:HG13	1.96	0.48
9:J:153:GLU:O	9:J:156:ILE:HD12	2.14	0.48
28:S:3:LEU:HD22	31:Z:82:HIS:CG	2.48	0.48
35:g:101:GLU:OE2	35:g:101:GLU:N	2.47	0.48
36:i:64:LYS:HD3	36:i:64:LYS:N	2.27	0.48
40:k:197:HIS:HB3	40:k:200:LEU:HD12	1.96	0.48
1:2:798:A:H4'	5:E:201:HIS:HE1	1.76	0.48
1:2:1350:G:H2'	1:2:1351:U:C6	2.49	0.48
2:A:175:TYR:HE1	2:A:195:TRP:CE3	2.32	0.48
5:E:185:GLY:C	5:E:224:ASN:HD21	2.21	0.48
9:J:90:LYS:HB3	9:J:95:TYR:CG	2.48	0.48
17:a:12:LYS:HZ2	17:a:16:GLY:H	1.61	0.48
22:F:172:GLN:O	22:F:176:LEU:HD22	2.14	0.48
28:S:53:ASP:HB3	28:S:56:LYS:HB2	1.95	0.48
1:2:208:U:H2'	1:2:209:A:H8	1.79	0.47
1:2:227:G:H2'	1:2:228:U:C6	2.49	0.47
1:2:405:U:H2'	1:2:406:A:C8	2.49	0.47
1:2:529:C:O2	16:Y:61:ARG:NH2	2.47	0.47
1:2:1038:A:O2'	1:2:1039:G:H8	1.97	0.47
1:2:1659:U:H2'	1:2:1660:G:C8	2.49	0.47
3:B:167:VAL:HA	3:B:170:GLU:OE2	2.14	0.47
6:G:1:MET:HE1	6:G:24:VAL:HG21	1.96	0.47
16:Y:43:LYS:HB3	16:Y:43:LYS:HE3	1.67	0.47
1:2:1309:U:O2'	1:2:1400:G:O2'	2.27	0.47
1:2:1651:C:H2'	1:2:1652:G:O4'	2.14	0.47
2:A:49:ASN:O	2:A:53:THR:HG23	2.14	0.47
2:A:128:SER:OG	2:A:129:ASP:OD1	2.32	0.47
4:C:80:ASN:OD1	4:C:80:ASN:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Y:35:VAL:HG11	16:Y:40:LEU:HD13	1.96	0.47
40:k:298:ILE:HA	40:k:302:ILE:HD12	1.96	0.47
1:2:127:G:N2	6:G:195:ILE:HD12	2.29	0.47
1:2:430:C:C2	1:2:431:G:C8	3.02	0.47
1:2:867:G:H2'	1:2:868:A:H8	1.79	0.47
1:2:1486:G:O2'	1:2:1492:C:O2	2.29	0.47
3:B:34:ALA:HB3	3:B:41:ARG:HA	1.95	0.47
5:E:160:VAL:HG21	5:E:169:ILE:HD12	1.96	0.47
10:L:34:TRP:CH2	10:L:36:LYS:HD3	2.48	0.47
19:e:8:LEU:HD21	36:i:62:ARG:NH2	2.28	0.47
1:2:221:A:OP2	1:2:832:U:H1'	2.13	0.47
1:2:347:U:HO2'	1:2:352:A:HO2'	1.56	0.47
1:2:373:U:H2'	1:2:374:U:C6	2.49	0.47
1:2:1532:G:N7	31:Z:77:ARG:NH1	2.50	0.47
4:C:147:GLY:N	4:C:158:SER:O	2.39	0.47
25:P:52:LYS:HB3	25:P:80:LEU:HD11	1.95	0.47
27:R:77:GLU:HG3	27:R:81:LYS:HE2	1.96	0.47
35:g:149:THR:N	35:g:180:ASP:OD2	2.47	0.47
1:2:328:G:H2'	1:2:329:G:C8	2.50	0.47
1:2:567:G:H4'	15:X:90:ASP:HA	1.96	0.47
1:2:599:U:H1'	15:X:47:SER:HB2	1.95	0.47
1:2:811:A:H4'	1:2:812:U:H5''	1.97	0.47
1:2:1588:G:H2'	1:2:1589:C:C6	2.50	0.47
1:2:1646:A:H2'	1:2:1647:G:C8	2.49	0.47
8:I:90:LEU:HB3	8:I:95:THR:HB	1.95	0.47
8:I:157:VAL:HA	8:I:160:GLN:NE2	2.30	0.47
17:a:97:PRO:O	17:a:99:GLN:N	2.42	0.47
26:Q:45:ARG:O	26:Q:48:VAL:HG12	2.14	0.47
36:i:46:ARG:HD3	36:i:60:HIS:CD2	2.48	0.47
40:k:256:GLU:HA	41:l:139:PHE:HE2	1.80	0.47
1:2:1070:U:H2'	1:2:1071:C:C6	2.50	0.47
1:2:1580:U:O2'	1:2:1612:A:N6	2.48	0.47
1:2:1691:A:H3'	1:2:1692:A:H4'	1.96	0.47
2:A:38:TYR:CE1	27:R:109:LEU:HB2	2.49	0.47
4:C:234:LEU:HD11	13:V:14:PRO:HD2	1.95	0.47
5:E:32:SER:OG	5:E:81:THR:OG1	2.28	0.47
6:G:7:TYR:CE1	6:G:9:ILE:HB	2.47	0.47
23:K:46:LEU:HD12	23:K:55:VAL:HG11	1.96	0.47
28:S:116:LEU:HA	28:S:119:ILE:HG22	1.97	0.47
30:U:84:MET:HE3	33:d:52:PHE:CE1	2.50	0.47
36:i:84:PHE:CD2	36:i:85:GLN:HG2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:j:7:ARG:HB3	39:j:40:ASP:N	2.29	0.47
1:2:78:A:N6	6:G:178:LEU:HD23	2.30	0.47
1:2:251:U:OP1	5:E:133:LYS:NZ	2.47	0.47
1:2:405:U:H2'	1:2:406:A:H8	1.78	0.47
1:2:432:C:H2'	1:2:433:G:C8	2.49	0.47
1:2:576:G:H1'	36:i:64:LYS:NZ	2.30	0.47
1:2:631:U:O2'	1:2:1102:U:OP1	2.31	0.47
1:2:824:U:H2'	1:2:825:U:H6	1.78	0.47
1:2:842:U:H2'	1:2:843:A:C8	2.49	0.47
1:2:861:A:HO2'	1:2:962:A:N6	2.11	0.47
1:2:933:C:C4	1:2:1076:C:H4'	2.49	0.47
1:2:1160:C:H2'	1:2:1161:C:H6	1.79	0.47
1:2:1562:U:H2'	1:2:1563:C:C6	2.50	0.47
1:2:1593:U:H5'	1:2:1594:C:OP2	2.14	0.47
1:2:1646:A:H2'	1:2:1647:G:H8	1.79	0.47
1:2:1741:U:H2'	1:2:1742:A:H8	1.76	0.47
5:E:19:MET:SD	5:E:108:ARG:HD2	2.54	0.47
6:G:50:PHE:CD2	6:G:111:LEU:HD13	2.49	0.47
9:J:29:LYS:HD2	19:e:40:TYR:HE1	1.79	0.47
11:N:23:PRO:HG2	11:N:26:PHE:HB2	1.95	0.47
12:O:131:GLY:O	17:a:22:ARG:NH2	2.48	0.47
13:V:74:GLN:NE2	13:V:83:TRP:O	2.47	0.47
16:Y:15:ASN:ND2	16:Y:18:LEU:HD12	2.30	0.47
21:D:225:TYR:H	35:g:197:ALA:HA	1.79	0.47
23:K:6:GLU:O	23:K:10:LYS:HG3	2.15	0.47
24:M:24:VAL:O	24:M:27:THR:HG22	2.15	0.47
24:M:87:GLN:O	24:M:91:TRP:CD1	2.68	0.47
29:T:28:LEU:H	29:T:111:LEU:HD21	1.80	0.47
30:U:58:LEU:HD21	30:U:90:TYR:CD2	2.50	0.47
36:i:82:ARG:NH2	36:i:85:GLN:OE1	2.33	0.47
39:j:11:ASN:OD1	39:j:11:ASN:N	2.48	0.47
40:k:315:LEU:HB3	40:k:417:VAL:HB	1.96	0.47
1:2:251:U:H2'	1:2:252:A:H8	1.80	0.47
1:2:1151:A:O3'	17:a:82:ARG:NH1	2.31	0.47
1:2:1555:U:O2'	1:2:1556:U:H2'	2.15	0.47
1:2:1637:5MC:H2'	1:2:1638:C:O4'	2.15	0.47
35:g:43:LEU:HB2	35:g:62:TYR:HB2	1.97	0.47
36:i:45:GLY:O	36:i:61:ILE:HB	2.14	0.47
40:k:197:HIS:HD2	40:k:198:ASP:H	1.63	0.47
40:k:427:TYR:HE2	40:k:493:THR:HB	1.78	0.47
1:2:295:U:H2'	1:2:296:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:812:U:O2'	1:2:814:G:OP1	2.29	0.47
1:2:1791:G:O6	17:a:34:LYS:NZ	2.48	0.47
2:A:94:GLY:H	2:A:185:ARG:HH12	1.62	0.47
4:C:100:ARG:HG2	4:C:100:ARG:NH1	2.27	0.47
6:G:195:ILE:O	6:G:199:GLN:HG2	2.15	0.47
15:X:8:GLY:O	15:X:11:SER:OG	2.33	0.47
16:Y:57:VAL:HB	16:Y:60:PHE:CE1	2.50	0.47
25:P:75:VAL:HG21	25:P:104:GLN:HE22	1.79	0.47
27:R:116:LYS:HD2	27:R:118:PRO:HD3	1.97	0.47
39:j:173:ILE:HA	39:j:177:LEU:HD13	1.96	0.47
40:k:238:ILE:HG23	40:k:514:TRP:HB3	1.97	0.47
1:2:93:A:O4'	5:E:3:ARG:NH1	2.48	0.47
1:2:357:U:O2'	1:2:359:A:OP1	2.31	0.47
1:2:446:U:O2'	5:E:27:TYR:O	2.32	0.47
1:2:1331:C:H4'	21:D:203:PRO:HB3	1.96	0.47
1:2:1513:A:O2'	1:2:1515:U:OP2	2.32	0.47
2:A:63:ILE:HD12	2:A:158:VAL:HG11	1.96	0.47
24:M:88:LEU:O	24:M:92:ALA:HB2	2.15	0.47
28:S:40:ARG:HD3	29:T:45:LEU:HD11	1.97	0.47
40:k:217:LEU:HD22	40:k:249:ASN:HB2	1.97	0.47
1:2:564:C:H2'	36:i:64:LYS:HZ1	1.80	0.46
1:2:643:U:H2'	1:2:644:C:H6	1.79	0.46
1:2:834:U:H2'	1:2:835:U:C6	2.50	0.46
1:2:1469:A:H2'	1:2:1469:A:N3	2.31	0.46
1:2:1564:U:H2'	1:2:1565:U:C5	2.49	0.46
2:A:41:ARG:HD3	27:R:124:VAL:HG11	1.96	0.46
15:X:92:CYS:HG	15:X:136:TRP:CD1	2.32	0.46
16:Y:57:VAL:HB	16:Y:60:PHE:HE1	1.80	0.46
30:U:58:LEU:HB2	30:U:88:LYS:HB2	1.98	0.46
39:j:29:GLU:HG3	39:j:30:MET:SD	2.55	0.46
40:k:151:GLN:HE22	40:k:182:ARG:N	2.13	0.46
1:2:78:A:C6	6:G:178:LEU:HD23	2.51	0.46
1:2:799:U:H2'	1:2:800:G:C8	2.51	0.46
1:2:1009:C:H2'	1:2:1010:G:O4'	2.15	0.46
1:2:1169:G:C2	1:2:1170:A:C8	3.03	0.46
1:2:1424:C:H3'	1:2:1425:A:H4'	1.96	0.46
13:V:25:LYS:HB2	13:V:28:ASP:HB2	1.95	0.46
27:R:41:ILE:H	27:R:41:ILE:HD12	1.81	0.46
29:T:52:GLY:HA2	29:T:55:TYR:HD1	1.79	0.46
1:2:67:A:C6	1:2:84:A:C8	3.03	0.46
1:2:181:A:H2'	1:2:182:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:387:G:O3'	1:2:424:A:N6	2.48	0.46
1:2:748:U:O2'	14:W:122:SER:O	2.25	0.46
1:2:1195:A:H4'	1:2:1196:C:H5''	1.97	0.46
2:A:64:ILE:HG23	2:A:73:VAL:HG21	1.96	0.46
36:i:47:VAL:HG23	36:i:61:ILE:HG12	1.97	0.46
38:1:64:RIA:H3A	38:1:65:G:H8	1.81	0.46
1:2:277:U:P	1:2:278:G:H21	2.38	0.46
1:2:592:U:OP1	9:J:40:ARG:HB2	2.14	0.46
1:2:874:G:O2'	1:2:876:G:OP2	2.31	0.46
1:2:902:U:O2'	1:2:904:A:N7	2.42	0.46
1:2:1349:G:H2'	1:2:1350:G:C8	2.51	0.46
1:2:1467:A:H2'	1:2:1468:C:C6	2.51	0.46
1:2:1480:C:H4'	26:Q:77:GLN:HE21	1.81	0.46
3:B:188:LEU:HD21	3:B:215:VAL:HG21	1.98	0.46
12:O:118:VAL:O	12:O:118:VAL:HG22	2.15	0.46
18:b:36:LYS:O	18:b:36:LYS:HG3	2.16	0.46
26:Q:30:LYS:HE3	26:Q:35:PRO:HD3	1.97	0.46
1:2:947:G:H2'	1:2:948:C:C6	2.51	0.46
1:2:1244:G:OP1	33:d:3:HIS:NE2	2.48	0.46
1:2:1336:A:P	26:Q:123:ARG:HH12	2.39	0.46
1:2:1717:A:H2'	1:2:1718:G:O4'	2.16	0.46
3:B:5:LYS:HG2	3:B:7:LYS:HD2	1.97	0.46
3:B:92:GLN:HG3	3:B:97:LEU:HD11	1.97	0.46
7:H:131:PHE:CD1	7:H:131:PHE:C	2.93	0.46
24:M:56:VAL:HG23	24:M:83:ALA:HA	1.98	0.46
36:i:26:LEU:HD23	36:i:26:LEU:H	1.79	0.46
38:1:66:C:H2'	38:1:67:G:C8	2.51	0.46
40:k:445:THR:HG21	40:k:450:GLN:HA	1.96	0.46
1:2:140:A:H61	6:G:187:LYS:HB2	1.81	0.46
1:2:1389:A:H2'	1:2:1390:U:H6	1.81	0.46
1:2:1514:A:OP2	30:U:88:LYS:NZ	2.46	0.46
2:A:9:LEU:HG	2:A:14:ALA:HB2	1.97	0.46
4:C:188:ALA:HB1	4:C:216:LEU:HD21	1.98	0.46
25:P:72:LYS:HZ2	25:P:106:GLU:HG3	1.80	0.46
29:T:33:TYR:O	29:T:36:ILE:HB	2.15	0.46
31:Z:91:PRO:HB3	31:Z:101:TYR:HE1	1.79	0.46
40:k:431:GLU:HB3	40:k:519:LYS:HB3	1.97	0.46
1:2:423:C:O2'	1:2:424:A:O5'	2.34	0.46
1:2:444:A:N6	1:2:461:G:H1'	2.31	0.46
1:2:453:U:O2'	1:2:454:C:O5'	2.34	0.46
1:2:1437:C:H2'	1:2:1438:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:59:LEU:O	2:A:63:ILE:HG13	2.16	0.46
6:G:32:ILE:HG23	6:G:53:ALA:HA	1.97	0.46
24:M:29:LEU:HD12	24:M:36:ARG:NH2	2.30	0.46
30:U:56:VAL:O	30:U:89:ARG:HA	2.16	0.46
39:j:79:GLU:N	39:j:79:GLU:OE2	2.49	0.46
1:2:155:A:H2'	1:2:156:A:O4'	2.15	0.46
1:2:332:A:OP2	8:I:48:THR:OG1	2.34	0.46
1:2:1069:C:H4'	18:b:17:ARG:NE	2.28	0.46
1:2:1124:A:C5'	20:h:15:ARG:HH12	2.23	0.46
1:2:1219:C:H2'	1:2:1220:A:C8	2.50	0.46
1:2:1261:U:H2'	1:2:1262:G:C8	2.51	0.46
1:2:1403:G:H2'	1:2:1404:A:C8	2.50	0.46
4:C:40:TRP:NE1	4:C:70:GLU:OE1	2.49	0.46
4:C:232:PRO:HA	4:C:235:TRP:CD2	2.51	0.46
6:G:2:LYS:O	6:G:108:VAL:HA	2.16	0.46
6:G:199:GLN:OE1	6:G:202:ARG:NH2	2.49	0.46
7:H:164:ASN:O	7:H:164:ASN:ND2	2.48	0.46
12:O:80:HIS:ND1	12:O:114:ARG:HB2	2.30	0.46
13:V:74:GLN:OE1	13:V:83:TRP:N	2.41	0.46
21:D:26:THR:HA	21:D:34:TYR:HD2	1.81	0.46
22:F:137:ASP:OD1	22:F:141:ASN:ND2	2.48	0.46
24:M:21:LEU:HB3	24:M:91:TRP:CZ3	2.50	0.46
26:Q:44:LEU:O	26:Q:47:LYS:HB2	2.16	0.46
35:g:52:GLU:N	35:g:52:GLU:OE2	2.49	0.46
35:g:88:LYS:HG2	35:g:109:GLY:C	2.41	0.46
35:g:243:ALA:O	35:g:268:LYS:NZ	2.49	0.46
40:k:108:HIS:CE1	40:k:109:VAL:HG12	2.50	0.46
1:2:22:A:H2'	1:2:23:G:O4'	2.16	0.46
1:2:26:A:HO2'	1:2:27:U:P	2.38	0.46
1:2:203:G:H2'	1:2:204:U:O4'	2.15	0.46
1:2:582:C:C2	1:2:583:C:C5	3.04	0.46
1:2:841:C:H2'	1:2:842:U:C6	2.50	0.46
1:2:1173:C:O2'	1:2:1195:A:N6	2.49	0.46
1:2:1239:U:O3'	1:2:1240:G:N2	2.31	0.46
1:2:1537:G:H4'	28:S:40:ARG:HH21	1.80	0.46
3:B:144:ARG:HB3	3:B:206:PRO:CB	2.44	0.46
3:B:185:THR:O	3:B:189:ILE:HG12	2.16	0.46
16:Y:51:GLU:H	16:Y:51:GLU:CD	2.22	0.46
29:T:18:TYR:CD1	29:T:135:ILE:HG21	2.51	0.46
35:g:35:VAL:HG12	35:g:72:VAL:HG11	1.98	0.46
38:1:66:C:H2'	38:1:67:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:86:A:H2'	1:2:87:C:H6	1.81	0.46
1:2:254:U:H2'	1:2:255:A:H8	1.81	0.46
1:2:255:A:H2'	1:2:256:A:O4'	2.16	0.46
1:2:627:G:N1	1:2:969:A:OP2	2.29	0.46
1:2:817:C:H2'	1:2:818:G:H8	1.79	0.46
1:2:1078:U:H2'	1:2:1079:U:C6	2.51	0.46
1:2:1100:G:O2'	14:W:4:THR:OG1	2.28	0.46
1:2:1783:U:H2'	1:2:1784:G:H8	1.80	0.46
3:B:132:ASP:HB2	3:B:221:PRO:HB3	1.98	0.46
3:B:144:ARG:HB2	3:B:208:GLN:HB2	1.98	0.46
8:I:72:VAL:HG11	8:I:112:TRP:CZ2	2.51	0.46
24:M:122:GLN:O	24:M:125:GLU:HG2	2.16	0.46
36:i:30:GLU:OE1	36:i:30:GLU:N	2.49	0.46
1:2:121:U:H1'	5:E:33:ALA:O	2.16	0.45
1:2:868:A:H61	1:2:957:U:H5	1.64	0.45
1:2:890:A:H2'	1:2:891:A:C8	2.48	0.45
1:2:931:U:OP2	3:B:155:TYR:OH	2.32	0.45
1:2:1021:C:O2'	1:2:1124:A:N1	2.43	0.45
1:2:1650:C:H2'	1:2:1651:C:H6	1.81	0.45
1:2:1658:A:H2'	1:2:1659:U:C6	2.50	0.45
6:G:32:ILE:HD12	6:G:54:GLY:H	1.81	0.45
12:O:28:VAL:HG11	12:O:67:VAL:HG21	1.98	0.45
21:D:74:GLU:HA	21:D:79:TYR:HB2	1.98	0.45
24:M:34:LEU:HD22	24:M:36:ARG:CZ	2.46	0.45
29:T:76:LEU:HB3	29:T:101:ASN:ND2	2.27	0.45
35:g:13:THR:HG22	35:g:318:ARG:HG2	1.98	0.45
38:1:63:G:H2'	38:1:64:RIA:H1A	1.98	0.45
1:2:638:U:C6	7:H:118:LEU:HB2	2.51	0.45
1:2:1131:A:H2'	1:2:1132:A:C8	2.46	0.45
1:2:1405:U:H2'	1:2:1406:G:C8	2.51	0.45
6:G:37:ASP:HA	6:G:49:VAL:HG23	1.97	0.45
10:L:54:ILE:HG23	10:L:55:ASP:N	2.30	0.45
10:L:58:CYS:HB3	10:L:62:GLY:H	1.81	0.45
22:F:91:ILE:HD11	22:F:139:ILE:HD13	1.98	0.45
23:K:59:PHE:CE1	23:K:62:GLN:HA	2.51	0.45
26:Q:39:VAL:O	26:Q:40:GLN:C	2.60	0.45
1:2:20:G:H5'	1:2:570:G:C8	2.51	0.45
1:2:453:U:C2	5:E:66:MET:HE1	2.52	0.45
1:2:846:A:H2'	1:2:847:C:C6	2.51	0.45
1:2:1040:G:OP2	2:A:32:HIS:HE1	1.99	0.45
1:2:1262:G:H2'	1:2:1263:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:100:ARG:NH2	5:E:122:LYS:HA	2.31	0.45
7:H:49:ILE:HD12	7:H:175:LYS:HG2	1.97	0.45
11:N:142:GLU:N	11:N:142:GLU:OE2	2.49	0.45
17:a:46:GLU:O	17:a:50:ILE:HG23	2.16	0.45
17:a:75:ILE:O	17:a:79:ILE:HG12	2.16	0.45
24:M:124:ARG:HH11	24:M:128:LEU:HD21	1.81	0.45
30:U:50:LEU:HD23	30:U:93:LEU:HD13	1.98	0.45
32:c:18:ARG:HA	32:c:26:THR:HA	1.97	0.45
33:d:21:CYS:C	33:d:23:ILE:H	2.25	0.45
39:j:6:CYS:SG	39:j:124:GLU:HA	2.56	0.45
39:j:94:ASP:O	39:j:97:LYS:HG2	2.16	0.45
39:j:163:LYS:HE2	39:j:163:LYS:HA	1.97	0.45
40:k:383:GLU:H	40:k:383:GLU:CD	2.25	0.45
1:2:234:G:H2'	1:2:235:A:H8	1.77	0.45
1:2:387:G:C6	1:2:409:A:C6	3.05	0.45
1:2:568:C:H41	15:X:69:ARG:HH12	1.63	0.45
1:2:887:U:H2'	1:2:888:U:C6	2.52	0.45
1:2:1247:C:C2	1:2:1248:U:C5	3.04	0.45
1:2:1335:A:C2	1:2:1414:G:C5	3.05	0.45
1:2:1679:A:O2'	6:G:31:ARG:NH1	2.49	0.45
1:2:1797:U:H3	3:B:152:ARG:CZ	2.29	0.45
2:A:166:GLY:O	2:A:167:LYS:HB3	2.15	0.45
2:A:166:GLY:C	2:A:168:HIS:H	2.25	0.45
5:E:77:ARG:HD2	5:E:82:PHE:CE1	2.52	0.45
5:E:121:TYR:CD2	5:E:161:LYS:HG3	2.51	0.45
7:H:55:LYS:HD3	7:H:89:HIS:NE2	2.32	0.45
7:H:131:PHE:C	7:H:131:PHE:HD1	2.24	0.45
10:L:97:TYR:O	10:L:99:ARG:HG2	2.17	0.45
23:K:81:ASN:ND2	24:M:30:VAL:HG13	2.31	0.45
27:R:60:ARG:HH21	27:R:66:VAL:HG21	1.80	0.45
40:k:202:SER:HA	40:k:465:ASN:ND2	2.31	0.45
1:2:178:A:H2'	1:2:179:A:O4'	2.17	0.45
1:2:194:G:C2'	1:2:195:G:H5'	2.46	0.45
1:2:366:A:H2'	1:2:367:U:O4'	2.17	0.45
1:2:682:U:C4	1:2:683:C:H1'	2.52	0.45
1:2:1274:A:O2'	21:D:141:LYS:HD3	2.16	0.45
1:2:1477:A:H5''	29:T:60:SER:HB3	1.98	0.45
1:2:1614:G:H2'	1:2:1615:U:C6	2.51	0.45
2:A:53:THR:HA	2:A:161:PRO:HD2	1.99	0.45
2:A:190:ASP:OD1	2:A:191:ARG:N	2.49	0.45
5:E:75:LYS:HD2	5:E:77:ARG:NH2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:154:GLU:OE1	8:I:157:VAL:HG13	2.16	0.45
14:W:77:PRO:HB2	14:W:79:PHE:CE1	2.52	0.45
15:X:112:LYS:HB2	15:X:112:LYS:HE2	1.86	0.45
22:F:93:GLU:O	22:F:96:THR:OG1	2.30	0.45
26:Q:131:GLY:HA3	26:Q:136:SER:O	2.17	0.45
31:Z:42:LEU:HD12	31:Z:43:ASP:N	2.31	0.45
35:g:117:ASP:OD1	35:g:118:ALA:N	2.50	0.45
39:j:245:GLU:O	39:j:249:GLU:HG3	2.16	0.45
1:2:182:U:H2'	1:2:183:C:H6	1.80	0.45
1:2:332:A:H8	1:2:332:A:OP1	1.99	0.45
1:2:854:A:O2'	1:2:855:A:H3'	2.17	0.45
1:2:996:G:H1	1:2:1006:5MC:HN41	1.63	0.45
1:2:1043:U:H2'	1:2:1044:C:H6	1.82	0.45
1:2:1187:G:O2'	1:2:1428:U:OP1	2.33	0.45
1:2:1228:G:N1	24:M:40:GLU:OE2	2.47	0.45
2:A:39:LYS:HA	2:A:39:LYS:HD2	1.68	0.45
12:O:48:VAL:HG11	12:O:59:ALA:HB2	1.99	0.45
23:K:25:LYS:HD2	23:K:59:PHE:CZ	2.52	0.45
35:g:25:SER:HB3	35:g:74:VAL:HG13	1.99	0.45
1:2:393:C:H2'	1:2:394:U:C6	2.51	0.45
1:2:855:A:P	7:H:97:ARG:HH21	2.40	0.45
1:2:1588:G:OP1	29:T:91:HIS:HB2	2.16	0.45
9:J:49:LEU:HB2	9:J:104:PHE:HE2	1.81	0.45
16:Y:123:LYS:O	16:Y:127:LYS:NZ	2.47	0.45
22:F:148:THR:HA	22:F:160:GLN:O	2.16	0.45
24:M:37:GLY:O	24:M:41:SER:OG	2.28	0.45
35:g:267:ILE:HB	35:g:281:LEU:HB2	1.99	0.45
38:1:52:G:H2'	38:1:53:G:H8	1.80	0.45
39:j:20:VAL:HG23	39:j:71:ALA:HB3	1.99	0.45
39:j:193:PHE:HA	40:k:406:LEU:HD12	1.99	0.45
1:2:623:G:H2'	1:2:624:C:H6	1.82	0.45
1:2:700:C:HO2'	1:2:701:U:P	2.40	0.45
1:2:1017:U:N3	1:2:1018:A:N7	2.64	0.45
1:2:1077:C:H2'	1:2:1078:U:C6	2.52	0.45
9:J:28:LEU:HD21	19:e:39:LEU:HB3	1.98	0.45
9:J:65:LYS:HA	9:J:70:LEU:HD21	1.97	0.45
23:K:9:LYS:O	23:K:9:LYS:HD3	2.16	0.45
23:K:61:TRP:N	23:K:61:TRP:CD1	2.85	0.45
27:R:93:LEU:HB3	27:R:98:ASP:HA	1.99	0.45
37:3:39:U:H2'	37:3:40:C:H4'	1.98	0.45
1:2:997:A:N6	1:2:1003:U:OP2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1344:A:H5'	30:U:53:LYS:HE2	1.99	0.45
3:B:179:SER:HB2	3:B:183:GLN:HB2	1.98	0.45
11:N:87:ASP:N	11:N:87:ASP:OD1	2.50	0.45
16:Y:15:ASN:OD1	16:Y:17:LEU:HB2	2.17	0.45
16:Y:36:SER:O	16:Y:36:SER:OG	2.30	0.45
28:S:35:ILE:HG13	28:S:102:ALA:HB2	1.98	0.45
40:k:353:ILE:HG13	40:k:419:ALA:HA	1.98	0.45
1:2:131:C:H4'	1:2:132:U:H4'	1.98	0.45
1:2:180:A:H2'	1:2:181:A:C8	2.52	0.45
1:2:903:G:H4'	37:3:25:A:H5'	1.99	0.45
1:2:926:C:O2'	12:O:124:ASP:O	2.31	0.45
1:2:1227:G:O2'	34:f:100:LEU:HD23	2.16	0.45
3:B:195:LYS:HD2	3:B:195:LYS:HA	1.75	0.45
5:E:159:THR:CG2	5:E:173:ILE:HB	2.47	0.45
21:D:20:GLU:CD	21:D:76:ARG:HH21	2.24	0.45
22:F:83:ARG:HG2	22:F:84:PHE:CD2	2.51	0.45
23:K:69:THR:O	23:K:73:VAL:HG23	2.17	0.45
30:U:55:PRO:HA	30:U:91:ILE:HG13	1.99	0.45
35:g:22:THR:OG1	35:g:70:GLN:O	2.31	0.45
39:j:111:ILE:HD11	39:j:177:LEU:HD11	1.99	0.45
40:k:191:PHE:HE1	40:k:215:LEU:HD11	1.82	0.45
1:2:9:U:N3	1:2:12:U:OP2	2.36	0.44
1:2:445:A:H5''	5:E:57:ASN:HD22	1.81	0.44
1:2:445:A:H2'	1:2:446:U:C6	2.51	0.44
1:2:760:A:C6	1:2:789:U:O4	2.70	0.44
5:E:175:PHE:CE1	5:E:198:ARG:HD2	2.45	0.44
6:G:103:GLY:H	6:G:106:LEU:HD23	1.82	0.44
21:D:7:LYS:CG	30:U:27:THR:HG21	2.47	0.44
22:F:52:ASP:OD1	22:F:52:ASP:O	2.35	0.44
33:d:21:CYS:SG	33:d:23:ILE:HB	2.57	0.44
35:g:24:LEU:HD22	35:g:34:LEU:HD11	1.98	0.44
36:i:51:CYS:SG	36:i:55:ASN:HB2	2.57	0.44
40:k:236:ILE:HG23	40:k:241:LEU:HB2	2.00	0.44
40:k:310:MET:N	40:k:310:MET:SD	2.90	0.44
40:k:441:LEU:O	40:k:510:ARG:HD2	2.16	0.44
7:H:43:PHE:CE1	7:H:60:VAL:HB	2.52	0.44
7:H:109:THR:OG1	7:H:110:GLN:N	2.51	0.44
28:S:25:ASN:HB2	31:Z:40:VAL:HG11	1.99	0.44
35:g:43:LEU:HD12	35:g:62:TYR:HD2	1.82	0.44
35:g:243:ALA:O	35:g:244:LYS:HG2	2.17	0.44
40:k:140:LEU:HB2	40:k:319:ARG:NH2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:829:U:H2'	1:2:830:U:O4'	2.18	0.44
1:2:1554:A:H1'	1:2:1558:U:OP2	2.17	0.44
1:2:1585:A:H2'	1:2:1586:G:H8	1.83	0.44
1:2:1794:C:O2	17:a:92:ARG:HB3	2.18	0.44
5:E:45:ILE:HA	5:E:61:VAL:HG11	1.99	0.44
5:E:122:LYS:HG2	5:E:123:LEU:N	2.32	0.44
6:G:145:PHE:HB3	6:G:147:LEU:HD13	1.99	0.44
7:H:101:LYS:HE3	7:H:112:ARG:HH12	1.81	0.44
8:I:196:ARG:O	8:I:199:ALA:HB3	2.17	0.44
9:J:123:HIS:CE1	19:e:37:ARG:HB2	2.53	0.44
16:Y:108:ARG:HG2	16:Y:111:ARG:HH22	1.82	0.44
20:h:17:ARG:HH11	20:h:21:ARG:HD3	1.81	0.44
21:D:13:ALA:HA	21:D:16:VAL:HG12	2.00	0.44
26:Q:35:PRO:HG2	26:Q:38:LEU:HD23	2.00	0.44
28:S:140:THR:HA	28:S:143:ARG:HH21	1.81	0.44
28:S:144:ARG:HD3	28:S:145:ARG:N	2.32	0.44
1:2:194:G:H2'	1:2:195:G:H5'	2.00	0.44
1:2:324:G:OP1	10:L:132:SER:OG	2.34	0.44
1:2:329:G:C6	1:2:330:A:C6	3.06	0.44
1:2:594:G:H2'	1:2:595:C:C6	2.53	0.44
1:2:677:G:H2'	1:2:678:G:C8	2.52	0.44
1:2:1050:G:H3'	1:2:1051:U:H4'	2.00	0.44
1:2:1293:G:H1	1:2:1302:U:H3	1.66	0.44
1:2:1373:U:H2'	1:2:1374:C:H6	1.81	0.44
1:2:1485:A:H2'	1:2:1486:G:C8	2.52	0.44
1:2:1648:U:H2'	1:2:1649:A:H8	1.80	0.44
5:E:72:VAL:HB	5:E:77:ARG:HG3	1.98	0.44
7:H:31:SER:HA	7:H:35:LYS:HG3	1.98	0.44
11:N:49:GLN:O	11:N:52:VAL:HG12	2.18	0.44
12:O:50:ALA:C	12:O:52:ARG:H	2.26	0.44
16:Y:15:ASN:HB3	16:Y:20:ARG:HG3	1.99	0.44
21:D:96:LEU:HD12	21:D:190:LYS:HG2	1.98	0.44
26:Q:23:LYS:HB2	26:Q:64:ASP:OD1	2.18	0.44
26:Q:94:GLN:HB2	26:Q:102:LYS:HD3	2.00	0.44
29:T:42:GLY:HA2	29:T:84:LYS:HB2	1.99	0.44
29:T:53:TRP:HH2	29:T:100:ILE:HD13	1.82	0.44
1:2:35:U:H2'	1:2:36:C:H6	1.83	0.44
1:2:158:U:O2'	6:G:87:ARG:NE	2.46	0.44
1:2:583:C:C2	1:2:584:A:C8	3.06	0.44
1:2:646:G:C6	1:2:688:G:C6	3.06	0.44
1:2:650:G:O6	1:2:684:A:N6	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:975:G:N2	1:2:1023:U:OP2	2.50	0.44
1:2:1025:A:N7	1:2:1770:C:O2'	2.43	0.44
1:2:1077:C:H2'	1:2:1078:U:H6	1.81	0.44
1:2:1564:U:H2'	1:2:1565:U:C6	2.53	0.44
1:2:1771:C:H2'	1:2:1772:G:C8	2.52	0.44
2:A:50:VAL:HG23	27:R:109:LEU:HD21	1.99	0.44
2:A:101:ARG:NH2	2:A:103:THR:HA	2.33	0.44
3:B:57:ALA:O	3:B:61:LEU:HD22	2.18	0.44
17:a:79:ILE:HD13	17:a:84:VAL:HG13	1.99	0.44
32:c:34:GLU:OE1	32:c:34:GLU:N	2.46	0.44
36:i:59:ALA:HB1	36:i:91:VAL:HG23	2.00	0.44
1:2:873:C:H2'	1:2:874:G:C8	2.53	0.44
1:2:901:G:H2'	1:2:902:U:C6	2.53	0.44
1:2:1243:A:H2'	1:2:1243:A:N3	2.31	0.44
4:C:178:PRO:HG3	9:J:57:ARG:HD3	1.99	0.44
10:L:14:GLN:CG	10:L:54:ILE:HG21	2.47	0.44
27:R:14:LYS:HB3	27:R:14:LYS:HE2	1.70	0.44
29:T:124:ILE:HD12	29:T:124:ILE:HA	1.84	0.44
35:g:47:ARG:O	35:g:57:VAL:N	2.48	0.44
40:k:410:ASP:OD1	40:k:410:ASP:N	2.49	0.44
1:2:433:G:N2	1:2:435:A:H3'	2.32	0.44
1:2:625:U:H2'	1:2:626:C:H6	1.83	0.44
1:2:698:U:H5'	7:H:106:SER:HA	1.99	0.44
1:2:1251:C:O4'	34:f:131:ALA:HB2	2.18	0.44
1:2:1366:G:C2	1:2:1367:G:C8	3.06	0.44
2:A:198:MET:CE	27:R:89:SER:HA	2.48	0.44
3:B:143:THR:HB	3:B:205:PHE:HE2	1.82	0.44
8:I:104:ILE:HG22	8:I:106:ALA:H	1.82	0.44
14:W:34:ILE:O	14:W:38:LEU:HG	2.17	0.44
15:X:141:GLU:N	15:X:141:GLU:OE1	2.51	0.44
17:a:11:ASN:O	17:a:11:ASN:ND2	2.51	0.44
21:D:162:GLN:OE1	21:D:163:PRO:HD2	2.17	0.44
28:S:52:VAL:HG11	28:S:69:ILE:HD11	1.98	0.44
1:2:30:G:H2'	1:2:31:C:C6	2.53	0.44
1:2:108:A:H2'	1:2:109:G:H8	1.81	0.44
1:2:305:U:OP1	10:L:105:LYS:HG3	2.17	0.44
1:2:958:U:O2	1:2:958:U:H2'	2.17	0.44
1:2:984:G:C4	1:2:985:G:C8	3.05	0.44
1:2:1488:A:H2'	1:2:1488:A:OP2	2.18	0.44
3:B:224:ASP:OD2	3:B:227:SER:HB3	2.17	0.44
7:H:118:LEU:HG	7:H:122:HIS:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:40:THR:OG1	8:I:59:ARG:HD3	2.17	0.44
17:a:73:TYR:CE2	17:a:83:ILE:HG13	2.52	0.44
22:F:38:ALA:O	22:F:40:GLN:N	2.47	0.44
36:i:62:ARG:HB3	36:i:91:VAL:O	2.18	0.44
39:j:212:SER:HB2	39:j:217:GLN:HA	2.00	0.44
1:2:812:U:O2'	1:2:813:A:H4'	2.18	0.44
1:2:930:C:OP1	3:B:116:LYS:NZ	2.51	0.44
1:2:1622:C:H2'	1:2:1623:C:C6	2.52	0.44
6:G:105:ASP:OD1	6:G:105:ASP:N	2.46	0.44
7:H:60:VAL:HG22	7:H:92:PHE:HA	2.00	0.44
9:J:49:LEU:O	9:J:53:ARG:HB2	2.17	0.44
12:O:20:PHE:HB3	12:O:27:PHE:HB2	2.00	0.44
24:M:110:SER:O	24:M:111:VAL:HG23	2.18	0.44
27:R:116:LYS:HG3	27:R:117:LEU:H	1.82	0.44
35:g:149:THR:OG1	35:g:180:ASP:OD1	2.32	0.44
1:2:152:G:C6	1:2:161:A:C6	3.06	0.43
1:2:216:A:H2'	1:2:217:A:C8	2.52	0.43
1:2:364:G:H5'	1:2:758:U:O2	2.18	0.43
1:2:387:G:OP2	1:2:422:G:O2'	2.32	0.43
1:2:514:A:C2	1:2:515:G:H1'	2.52	0.43
1:2:555:A:H4'	19:e:56:MET:HG3	1.99	0.43
1:2:720:G:N1	1:2:722:G:O6	2.45	0.43
1:2:995:U:H2'	1:2:996:G:H8	1.83	0.43
1:2:1040:G:OP1	2:A:31:VAL:HA	2.18	0.43
1:2:1227:G:H5'	24:M:38:LEU:HD22	1.99	0.43
1:2:1239:U:H2'	1:2:1241:A:OP2	2.17	0.43
1:2:1424:C:O2'	1:2:1426:2MG:H8	2.00	0.43
5:E:233:ARG:HD2	5:E:233:ARG:HA	1.90	0.43
6:G:159:ARG:HH21	6:G:170:THR:HG21	1.83	0.43
7:H:91:ILE:HD12	7:H:172:VAL:HG21	1.99	0.43
23:K:35:ILE:HG23	23:K:37:THR:H	1.82	0.43
1:2:304:C:H2'	1:2:305:U:C6	2.53	0.43
1:2:337:C:H5''	8:I:10:LYS:HG3	2.00	0.43
1:2:1226:A:O2'	24:M:108:GLY:O	2.28	0.43
1:2:1613:C:OP2	32:c:47:PRO:HB3	2.18	0.43
1:2:1794:C:C2	17:a:5:ARG:HG2	2.54	0.43
2:A:66:ALA:HB2	13:V:37:ALA:HB2	2.00	0.43
3:B:39:GLU:N	3:B:74:GLN:OE1	2.41	0.43
4:C:123:ALA:HB3	4:C:129:ALA:HB2	2.00	0.43
12:O:52:ARG:NH2	22:F:158:ARG:HH11	2.16	0.43
21:D:61:GLU:O	21:D:64:ARG:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:D:127:MET:HE2	21:D:154:ASP:CG	2.43	0.43
28:S:116:LEU:O	28:S:124:GLY:HA3	2.18	0.43
31:Z:80:LEU:CD2	31:Z:101:TYR:HE2	2.30	0.43
35:g:117:ASP:HB3	35:g:119:ASN:O	2.18	0.43
35:g:269:ILE:HG22	35:g:279:ASP:O	2.18	0.43
36:i:20:ASP:HB3	36:i:24:ARG:HD2	2.00	0.43
36:i:33:GLN:HB3	36:i:78:LEU:HD11	2.00	0.43
1:2:195:G:O2'	1:2:196:A:H8	2.02	0.43
1:2:235:A:H2'	1:2:236:C:O4'	2.18	0.43
1:2:254:U:C2	1:2:255:A:C8	3.07	0.43
1:2:406:A:H1'	1:2:1669:A:H2	1.82	0.43
1:2:808:G:H5''	10:L:148:LYS:HD2	2.00	0.43
1:2:811:A:H62	1:2:857:G:H2'	1.83	0.43
2:A:55:GLU:OE1	13:V:80:LYS:N	2.37	0.43
8:I:191:ALA:O	8:I:194:LEU:HD12	2.18	0.43
9:J:3:ARG:NH2	9:J:6:ARG:HH12	2.16	0.43
24:M:54:VAL:HG22	24:M:112:VAL:HB	2.00	0.43
25:P:81:ARG:NH2	25:P:120:SER:O	2.52	0.43
26:Q:39:VAL:HG12	26:Q:45:ARG:HG3	2.00	0.43
38:1:3:C:HO2'	39:j:185:ARG:HH12	1.63	0.43
38:1:64:RIA:H2A	38:1:64:RIA:N3	2.33	0.43
40:k:145:ALA:HB1	40:k:163:SER:HB2	1.98	0.43
1:2:760:A:C2	1:2:789:U:C5	3.06	0.43
1:2:1175:G:O2'	1:2:1194:C:O2'	2.25	0.43
1:2:1331:C:H2'	21:D:162:GLN:HE22	1.83	0.43
1:2:1519:G:H2'	1:2:1521:G:N2	2.33	0.43
1:2:1545:A:O2'	28:S:89:GLN:O	2.36	0.43
1:2:1617:C:H2'	1:2:1618:C:H6	1.84	0.43
15:X:69:ARG:HB3	15:X:86:PHE:CE2	2.52	0.43
32:c:42:ARG:HA	32:c:63:ALA:HB2	2.01	0.43
35:g:151:TRP:HE3	35:g:179:MET:HE1	1.83	0.43
40:k:157:GLU:N	40:k:158:PRO:HD2	2.33	0.43
1:2:176:U:H3'	1:2:177:U:H2'	2.00	0.43
1:2:206:U:O2	8:I:179:ARG:NH2	2.49	0.43
1:2:336:G:O2'	8:I:10:LYS:NZ	2.51	0.43
1:2:819:U:H2'	1:2:820:U:H4'	2.00	0.43
1:2:916:U:O2	12:O:41:ARG:HD2	2.18	0.43
1:2:1276:G:O3'	21:D:183:GLY:HA3	2.18	0.43
1:2:1584:A:OP1	26:Q:134:ALA:N	2.52	0.43
1:2:1601:U:H2'	1:2:1602:U:C6	2.54	0.43
2:A:35:PRO:C	2:A:37:VAL:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:176:ASP:OD1	5:E:176:ASP:C	2.61	0.43
16:Y:84:LYS:HG3	16:Y:85:PHE:CD1	2.53	0.43
19:e:29:GLN:OE1	19:e:30:PRO:HD2	2.19	0.43
22:F:135:VAL:HG22	22:F:200:LEU:HD13	1.99	0.43
24:M:25:LEU:HD12	24:M:91:TRP:CZ3	2.54	0.43
28:S:127:HIS:CD2	28:S:133:VAL:HG21	2.53	0.43
30:U:102:ARG:NH1	30:U:102:ARG:HB3	2.33	0.43
35:g:214:ASP:OD1	35:g:215:GLY:N	2.50	0.43
1:2:119:A:H2'	1:2:120:PSU:O4'	2.18	0.43
5:E:254:ARG:HD3	5:E:254:ARG:HA	1.89	0.43
6:G:121:ILE:HG22	6:G:122:GLU:H	1.84	0.43
11:N:25:TRP:CB	18:b:82:LYS:HD2	2.49	0.43
16:Y:91:LEU:HD13	16:Y:96:LEU:HB2	1.99	0.43
16:Y:113:ASN:O	16:Y:117:LYS:HG2	2.17	0.43
25:P:96:VAL:HG21	25:P:116:LEU:HB3	2.01	0.43
34:f:118:ARG:HG2	34:f:118:ARG:NH1	2.34	0.43
40:k:132:LEU:HB3	40:k:136:ILE:O	2.19	0.43
1:2:223:C:H2'	1:2:224:A:H8	1.83	0.43
1:2:1353:G:H1'	1:2:1370:G:N2	2.34	0.43
1:2:1562:U:H2'	1:2:1563:C:H6	1.83	0.43
3:B:125:VAL:HG22	3:B:127:VAL:HG13	2.01	0.43
10:L:99:ARG:HE	14:W:79:PHE:HE1	1.65	0.43
22:F:102:ASN:HB2	22:F:105:ASN:OD1	2.18	0.43
23:K:3:ILE:HG12	23:K:41:PHE:HB2	2.01	0.43
24:M:34:LEU:HB3	24:M:36:ARG:HG3	2.01	0.43
26:Q:46:PHE:O	26:Q:50:GLU:HG3	2.18	0.43
38:1:14:A:H2'	38:1:15:G:C4	2.53	0.43
39:j:111:ILE:HG23	39:j:172:TYR:HD2	1.84	0.43
40:k:197:HIS:CD2	40:k:198:ASP:N	2.87	0.43
1:2:116:U:H2'	1:2:117:U:C6	2.53	0.43
1:2:152:G:N7	16:Y:128:LYS:NZ	2.51	0.43
1:2:220:A:H2'	1:2:221:A:H8	1.83	0.43
1:2:473:A:H5'	9:J:144:PRO:HD2	2.00	0.43
1:2:761:G:N2	1:2:762:A:N7	2.67	0.43
1:2:1061:A:H2'	1:2:1062:U:O4'	2.18	0.43
1:2:1106:G:O2'	1:2:1107:G:H5'	2.19	0.43
1:2:1206:C:O2'	1:2:1207:A:OP2	2.36	0.43
1:2:1469:A:C8	1:2:1538:G:H1'	2.54	0.43
1:2:1568:A:H2'	1:2:1569:C:O4'	2.18	0.43
1:2:1750:U:O4	1:2:1751:A:N6	2.52	0.43
2:A:101:ARG:NH2	2:A:104:PRO:HD2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:101:ARG:HH21	2:A:104:PRO:HD2	1.84	0.43
4:C:126:VAL:HB	37:3:39:U:C5	2.54	0.43
5:E:71:LYS:HB3	5:E:91:THR:HB	2.01	0.43
10:L:125:VAL:HG22	10:L:137:PHE:HB3	2.00	0.43
18:b:14:SER:HA	18:b:17:ARG:HB2	2.00	0.43
22:F:41:GLU:OE1	22:F:41:GLU:O	2.37	0.43
25:P:118:GLU:O	28:S:122:HIS:N	2.52	0.43
31:Z:90:LYS:HA	31:Z:91:PRO:HD3	1.85	0.43
40:k:344:ASN:OD1	40:k:344:ASN:N	2.52	0.43
1:2:597:U:O4	1:2:598:A:N6	2.52	0.43
1:2:621:A:O2'	1:2:1031:G:H5'	2.18	0.43
1:2:985:G:H2'	1:2:985:G:N3	2.33	0.43
1:2:1485:A:H2'	1:2:1486:G:H8	1.84	0.43
1:2:1607:U:H2'	1:2:1608:G:O4'	2.18	0.43
1:2:1791:G:H4'	1:2:1792:A:OP1	2.18	0.43
2:A:37:VAL:HG21	2:A:46:ASN:HD22	1.83	0.43
2:A:92:HIS:ND1	2:A:202:TYR:OH	2.49	0.43
5:E:125:LYS:HB2	5:E:226:PHE:CD2	2.54	0.43
8:I:191:ALA:O	8:I:192:PHE:C	2.60	0.43
9:J:118:LEU:HD23	9:J:118:LEU:H	1.84	0.43
12:O:43:THR:O	12:O:46:MET:HB2	2.18	0.43
14:W:69:LEU:HD11	14:W:72:CYS:SG	2.58	0.43
22:F:63:TYR:CD2	22:F:166:PRO:HB2	2.54	0.43
22:F:186:PHE:CD2	22:F:187:ARG:HG2	2.54	0.43
26:Q:28:LEU:HB3	26:Q:64:ASP:HB2	2.01	0.43
26:Q:63:ILE:HD12	26:Q:92:TYR:CE2	2.52	0.43
26:Q:99:GLU:OE2	35:g:61:SER:N	2.51	0.43
29:T:117:SER:OG	29:T:120:GLY:O	2.36	0.43
29:T:127:ASN:HA	29:T:130:ARG:NH1	2.34	0.43
30:U:33:GLN:CD	30:U:33:GLN:N	2.76	0.43
30:U:70:THR:O	33:d:40:ARG:NH1	2.47	0.43
31:Z:70:LYS:C	31:Z:71:LEU:HD12	2.44	0.43
35:g:23:SER:OG	35:g:71:ASP:HA	2.18	0.43
1:2:186:G:H2'	8:I:139:ASN:HD22	1.83	0.43
1:2:1069:C:H2'	1:2:1070:U:C6	2.54	0.43
1:2:1105:U:H2'	1:2:1106:G:H8	1.84	0.43
1:2:1147:C:H2'	1:2:1148:G:H8	1.82	0.43
1:2:1165:A:H2'	1:2:1166:G:O4'	2.18	0.43
1:2:1373:U:H2'	1:2:1374:C:C6	2.54	0.43
1:2:1544:G:OP1	28:S:127:HIS:NE2	2.49	0.43
6:G:7:TYR:HD1	6:G:10:ASN:H	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:64:ASN:O	8:I:181:ASP:HA	2.19	0.43
8:I:196:ARG:O	8:I:200:LYS:HG2	2.18	0.43
10:L:46:LYS:HB3	10:L:46:LYS:HE3	1.74	0.43
15:X:107:PHE:CE1	15:X:123:LYS:HG3	2.54	0.43
26:Q:39:VAL:HG13	26:Q:41:PRO:HD2	2.00	0.43
35:g:304:ASP:OD1	35:g:305:GLY:N	2.52	0.43
38:l:56:C:H5	39:j:114:TYR:HD1	1.67	0.43
39:j:192:CYS:SG	39:j:255:ILE:HD12	2.59	0.43
40:k:318:ILE:O	40:k:413:VAL:HA	2.19	0.43
40:k:403:ASP:HB2	40:k:406:LEU:HB2	2.01	0.43
1:2:159:C:O3'	6:G:95:LYS:NZ	2.41	0.42
1:2:565:C:O2	19:e:13:LYS:NZ	2.39	0.42
1:2:608:U:C4	15:X:26:GLU:HG3	2.54	0.42
1:2:953:G:C4	1:2:954:A:C8	3.07	0.42
1:2:1113:G:O2'	1:2:1129:G:O6	2.30	0.42
1:2:1124:A:H4'	20:h:15:ARG:HH22	1.84	0.42
1:2:1143:U:H2'	1:2:1144:U:H6	1.82	0.42
1:2:1329:G:H2'	1:2:1330:A:O4'	2.19	0.42
1:2:1379:U:H1'	1:2:1514:A:N6	2.33	0.42
1:2:1436:G:H2'	1:2:1437:C:C6	2.54	0.42
1:2:1794:C:H6	17:a:7:SER:HB3	1.83	0.42
2:A:33:GLN:NE2	13:V:64:GLU:OE1	2.49	0.42
4:C:219:ALA:O	4:C:223:ILE:HG22	2.19	0.42
8:I:111:GLN:OE1	8:I:111:GLN:N	2.45	0.42
12:O:29:HIS:CE1	12:O:38:THR:HB	2.54	0.42
16:Y:104:SER:OG	16:Y:107:GLN:HG2	2.19	0.42
36:i:82:ARG:HD2	36:i:84:PHE:CZ	2.54	0.42
39:j:174:SER:O	39:j:178:THR:OG1	2.37	0.42
40:k:228:GLN:H	40:k:228:GLN:CD	2.26	0.42
40:k:431:GLU:HG3	40:k:484:ARG:CZ	2.49	0.42
1:2:277:U:H4'	1:2:278:G:O5'	2.17	0.42
1:2:399:A:H4'	1:2:400:A:H5''	2.00	0.42
1:2:789:U:C5	1:2:790:A:C8	3.06	0.42
1:2:884:G:H2'	1:2:885:U:N1	2.34	0.42
1:2:885:U:H2'	1:2:886:A:H8	1.84	0.42
1:2:902:U:H2'	1:2:904:A:OP2	2.19	0.42
1:2:1247:C:OP2	34:f:93:HIS:ND1	2.38	0.42
7:H:167:GLU:O	7:H:170:GLN:HB2	2.20	0.42
11:N:40:TYR:HB3	11:N:50:ILE:HG12	2.01	0.42
17:a:41:ILE:HG12	17:a:68:TYR:HD2	1.82	0.42
22:F:65:GLN:NE2	22:F:67:SER:OG	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Q:26:LYS:HE2	26:Q:26:LYS:HB2	1.91	0.42
30:U:25:ASN:HA	30:U:90:TYR:HA	2.01	0.42
36:i:29:LYS:HB3	36:i:35:TYR:CZ	2.54	0.42
40:k:359:ILE:HB	40:k:371:LYS:HB2	2.01	0.42
1:2:210:U:H5'	10:L:20:PHE:CD2	2.54	0.42
1:2:788:A:N1	1:2:789:U:H1'	2.33	0.42
1:2:884:G:H2'	1:2:885:U:C6	2.54	0.42
1:2:1210:A:H2'	1:2:1211:G:O4'	2.19	0.42
1:2:1366:G:O5'	29:T:7:ARG:NH2	2.51	0.42
1:2:1565:U:H2'	1:2:1566:C:H1'	2.01	0.42
1:2:1681:U:H2'	1:2:1682:U:O4'	2.18	0.42
3:B:149:GLN:HG2	3:B:151:LYS:O	2.20	0.42
4:C:86:MET:HE1	4:C:191:LYS:HE2	2.00	0.42
6:G:32:ILE:HD11	6:G:63:MET:HE2	2.00	0.42
9:J:121:SER:HB3	9:J:124:HIS:HB2	2.00	0.42
22:F:151:VAL:HG21	32:c:66:LEU:HD22	2.01	0.42
24:M:56:VAL:HG13	24:M:59:VAL:HG13	2.01	0.42
25:P:85:ILE:HD11	25:P:116:LEU:HD23	1.99	0.42
28:S:76:PRO:HB3	28:S:81:ILE:HD12	2.01	0.42
29:T:29:GLU:OE2	29:T:29:GLU:N	2.52	0.42
35:g:153:THR:OG1	35:g:178:GLY:HA2	2.18	0.42
35:g:171:ARG:NE	35:g:187:SER:HB2	2.27	0.42
39:j:173:ILE:HG13	39:j:177:LEU:HD13	2.01	0.42
1:2:66:U:OP1	6:G:136:LYS:NZ	2.50	0.42
1:2:130:C:N4	1:2:178:A:OP2	2.47	0.42
1:2:208:U:H2'	1:2:209:A:C8	2.54	0.42
1:2:818:G:C4	1:2:852:G:N2	2.88	0.42
1:2:1130:A:H2'	1:2:1131:A:O4'	2.19	0.42
1:2:1286:A:H4'	1:2:1287:G:H5'	2.02	0.42
1:2:1511:G:O2'	1:2:1513:A:N3	2.39	0.42
1:2:1530:U:H2'	1:2:1531:C:O4'	2.20	0.42
4:C:135:ILE:HD13	4:C:135:ILE:HA	1.90	0.42
8:I:85:PRO:O	10:L:11:ARG:NH1	2.52	0.42
9:J:134:ILE:HD12	9:J:134:ILE:N	2.34	0.42
9:J:169:PRO:HB2	9:J:173:ALA:HB3	2.00	0.42
17:a:23:CYS:SG	17:a:74:CYS:HB3	2.60	0.42
21:D:158:ILE:HD12	21:D:163:PRO:HB2	2.01	0.42
29:T:35:ASP:O	29:T:35:ASP:OD1	2.36	0.42
35:g:19:GLY:HA3	35:g:39:ARG:HB2	2.02	0.42
35:g:154:LYS:HG3	35:g:208:VAL:HG23	2.01	0.42
36:i:61:ILE:HD13	36:i:61:ILE:HA	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:35:U:H2'	1:2:36:C:C6	2.55	0.42
1:2:68:A:N6	6:G:132:ARG:O	2.49	0.42
1:2:513:G:C2	1:2:514:A:C8	3.08	0.42
1:2:601:U:H2'	1:2:602:U:C6	2.55	0.42
1:2:1201:A:H3'	1:2:1201:A:N3	2.35	0.42
1:2:1290:G:C2	1:2:1291:G:C8	3.07	0.42
1:2:1559:U:H2'	1:2:1560:G:C8	2.54	0.42
1:2:1716:A:H2'	1:2:1717:A:C8	2.55	0.42
4:C:58:ILE:HD12	4:C:61:ILE:HD12	2.01	0.42
5:E:36:HIS:CG	5:E:85:GLY:HA3	2.54	0.42
12:O:42:VAL:HG23	12:O:46:MET:HG3	2.02	0.42
14:W:6:VAL:HG21	14:W:29:PRO:HB2	2.01	0.42
15:X:107:PHE:HB2	15:X:121:ARG:C	2.45	0.42
23:K:10:LYS:HA	23:K:13:GLN:HE21	1.85	0.42
28:S:28:VAL:HG23	28:S:56:LYS:O	2.19	0.42
28:S:30:TYR:HA	28:S:33:THR:OG1	2.19	0.42
30:U:68:ARG:HH21	30:U:77:LYS:HG3	1.84	0.42
35:g:157:VAL:HG12	35:g:174:PHE:HB3	2.02	0.42
39:j:97:LYS:O	39:j:100:GLU:HG3	2.20	0.42
39:j:202:LYS:O	39:j:206:LYS:HG2	2.18	0.42
40:k:317:VAL:O	40:k:414:GLY:N	2.52	0.42
1:2:169:U:OP1	1:2:266:U:O2'	2.30	0.42
1:2:195:G:O6	8:I:142:ARG:NH1	2.46	0.42
1:2:205:A:H1'	1:2:261:U:N3	2.35	0.42
1:2:254:U:H2'	1:2:255:A:C8	2.54	0.42
1:2:470:A:H1'	9:J:8:TYR:HB2	2.02	0.42
1:2:511:A:H2'	1:2:512:U:C6	2.55	0.42
1:2:1100:G:H5''	14:W:76:SER:HB3	2.02	0.42
1:2:1374:C:H2'	1:2:1375:U:C6	2.54	0.42
1:2:1386:A:C6	1:2:1409:A:N7	2.88	0.42
1:2:1481:A:N3	1:2:1605:G:O2'	2.39	0.42
1:2:1493:C:O2'	1:2:1517:U:O2	2.23	0.42
1:2:1517:U:H2'	1:2:1518:U:C5	2.54	0.42
1:2:1770:C:OP2	20:h:2:ARG:NH1	2.50	0.42
1:2:1789:A:O2'	1:2:1791:G:H8	2.03	0.42
3:B:66:VAL:HG23	12:O:33:LEU:HB3	2.01	0.42
3:B:71:ALA:HB3	12:O:114:ARG:NH2	2.35	0.42
3:B:198:GLU:OE1	3:B:198:GLU:C	2.63	0.42
9:J:40:ARG:HA	9:J:43:TYR:CD2	2.55	0.42
15:X:103:LEU:HB3	15:X:126:LYS:HB2	2.01	0.42
35:g:171:ARG:HH11	35:g:189:ASN:CG	2.25	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:262:ALA:HB1	35:g:296:ALA:HB3	2.00	0.42
39:j:7:ARG:HD2	39:j:7:ARG:O	2.20	0.42
1:2:82:U:H2'	1:2:83:G:O4'	2.18	0.42
1:2:391:G:H5''	1:2:1727:C:O2'	2.19	0.42
1:2:564:C:H2'	36:i:64:LYS:HZ3	1.84	0.42
1:2:636:C:OP1	14:W:32:LYS:N	2.53	0.42
1:2:664:U:H2'	1:2:665:A:C8	2.55	0.42
1:2:1218:A:O2'	23:K:48:SER:HA	2.20	0.42
1:2:1337:C:H1'	1:2:1408:A:C5	2.54	0.42
1:2:1472:G:C2	1:2:1473:A:C5	3.08	0.42
1:2:1676:A:H2'	1:2:1677:G:O4'	2.20	0.42
2:A:18:LEU:HA	2:A:23:HIS:CD2	2.55	0.42
12:O:91:SER:HB2	12:O:93:THR:HG22	2.02	0.42
23:K:38:LYS:HB2	23:K:38:LYS:HE3	1.91	0.42
31:Z:55:PRO:C	31:Z:57:TYR:H	2.27	0.42
35:g:119:ASN:ND2	35:g:121:SER:OG	2.53	0.42
36:i:37:GLN:NE2	36:i:115:ILE:HG12	2.34	0.42
39:j:173:ILE:HG13	39:j:177:LEU:HD22	2.02	0.42
40:k:245:ILE:HD11	40:k:302:ILE:HD11	2.02	0.42
1:2:72:A:H4'	1:2:73:U:O5'	2.19	0.42
1:2:98:U:H2'	1:2:99:C:C6	2.55	0.42
1:2:385:G:OP1	8:I:23:LYS:HG2	2.19	0.42
1:2:779:A:O2'	1:2:780:A:O4'	2.38	0.42
1:2:871:G:H2'	1:2:872:U:O4'	2.20	0.42
1:2:1412:U:H5''	27:R:3:ARG:NH2	2.34	0.42
1:2:1514:A:O2'	1:2:1515:U:H5'	2.19	0.42
1:2:1689:A:N6	1:2:1708:U:O2'	2.53	0.42
1:2:1711:G:N3	1:2:1711:G:H2'	2.34	0.42
2:A:38:TYR:OH	27:R:108:GLU:HB2	2.20	0.42
6:G:159:ARG:HG2	6:G:172:ALA:HB2	2.01	0.42
13:V:5:LYS:HB2	13:V:7:GLN:OE1	2.20	0.42
17:a:58:VAL:HG23	17:a:59:TYR:CD2	2.55	0.42
25:P:18:LYS:HZ2	28:S:90:LYS:HB3	1.84	0.42
32:c:10:ALA:HB1	32:c:30:VAL:HB	2.02	0.42
1:2:27:U:H2'	1:2:28:A:H8	1.85	0.42
1:2:40:A:H3'	1:2:41:A:H8	1.85	0.42
1:2:403:G:H2'	1:2:404:C:H6	1.84	0.42
1:2:488:C:H2'	1:2:489:C:C5	2.55	0.42
1:2:606:G:H5'	1:2:612:G:N2	2.34	0.42
1:2:609:G:O2'	1:2:612:G:O2'	2.31	0.42
1:2:1194:C:OP1	30:U:77:LYS:NZ	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1447:U:H2'	1:2:1448:U:C6	2.53	0.42
1:2:1477:A:C2	1:2:1478:G:C8	3.07	0.42
1:2:1481:A:H2'	1:2:1482:G:C8	2.55	0.42
2:A:180:GLU:OE1	2:A:191:ARG:NH2	2.53	0.42
5:E:123:LEU:HD12	5:E:161:LYS:HA	2.02	0.42
9:J:28:LEU:HD12	9:J:28:LEU:HA	1.90	0.42
12:O:51:ASP:OD1	12:O:51:ASP:O	2.38	0.42
14:W:46:TYR:O	14:W:69:LEU:HB2	2.20	0.42
22:F:128:ASP:O	22:F:129:GLN:C	2.63	0.42
26:Q:13:LYS:HG2	26:Q:76:SER:HA	2.02	0.42
27:R:89:SER:OG	27:R:92:ASP:OD1	2.35	0.42
31:Z:55:PRO:O	31:Z:56:THR:OG1	2.32	0.42
40:k:108:HIS:HB3	40:k:111:HIS:CE1	2.55	0.42
1:2:278:G:C6	1:2:280:G:C6	3.08	0.42
1:2:565:C:OP1	36:i:62:ARG:NH1	2.53	0.42
1:2:692:C:H2'	1:2:693:U:C6	2.54	0.42
1:2:894:G:H4'	12:O:37:GLU:OE2	2.19	0.42
1:2:1076:C:C2	1:2:1077:C:C5	3.07	0.42
1:2:1450:U:H2'	1:2:1451:G:C8	2.54	0.42
1:2:1550:U:H2'	1:2:1551:G:O4'	2.20	0.42
2:A:139:VAL:HG13	2:A:141:ILE:HG13	2.01	0.42
3:B:190:PRO:C	3:B:191:GLU:OE1	2.63	0.42
12:O:99:GLN:NE2	17:a:44:ILE:O	2.37	0.42
21:D:219:GLU:HB2	21:D:220:PRO:HD3	2.01	0.42
24:M:124:ARG:HE	24:M:124:ARG:HB3	1.57	0.42
39:j:235:LEU:HD23	39:j:235:LEU:HA	1.94	0.42
40:k:151:GLN:HE22	40:k:182:ARG:H	1.68	0.42
1:2:16:G:H2'	1:2:17:C:C6	2.55	0.41
1:2:70:C:C4	1:2:71:A:C2	3.08	0.41
1:2:635:A:N1	1:2:860:U:C4	2.88	0.41
1:2:958:U:C6	11:N:61:THR:HB	2.55	0.41
1:2:1279:C:O2'	30:U:70:THR:HG22	2.20	0.41
1:2:1380:A:O4'	30:U:57:ARG:HB3	2.20	0.41
2:A:6:THR:O	2:A:191:ARG:NH1	2.53	0.41
2:A:11:SER:HA	27:R:115:LEU:HD23	2.01	0.41
2:A:81:TYR:CD1	2:A:167:LYS:HB2	2.55	0.41
3:B:142:PHE:O	3:B:208:GLN:N	2.53	0.41
8:I:64:ASN:OD1	8:I:65:PHE:N	2.53	0.41
8:I:116:HIS:CE1	8:I:147:ARG:HH12	2.38	0.41
11:N:93:LYS:O	11:N:96:VAL:HG12	2.20	0.41
17:a:85:ARG:HH11	17:a:85:ARG:HG3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:k:227:PRO:HB2	40:k:442:GLY:HA2	2.02	0.41
1:2:47:A:N1	1:2:385:G:H1'	2.35	0.41
1:2:274:C:H2'	1:2:275:C:O4'	2.20	0.41
1:2:471:U:H5''	9:J:11:THR:HG22	2.01	0.41
1:2:1639:C:H2'	1:2:1640:G:H8	1.84	0.41
1:2:1660:G:H2'	1:2:1661:G:C8	2.53	0.41
2:A:15:GLN:NE2	27:R:93:LEU:HD11	2.35	0.41
3:B:143:THR:HB	3:B:205:PHE:CE2	2.54	0.41
6:G:152:ASP:C	6:G:154:ARG:H	2.27	0.41
15:X:57:ILE:HA	36:i:85:GLN:HE21	1.84	0.41
18:b:23:THR:HG22	18:b:24:LEU:H	1.84	0.41
24:M:28:SER:OG	24:M:114:VAL:HG13	2.19	0.41
24:M:109:ALA:C	24:M:111:VAL:H	2.28	0.41
29:T:19:ALA:HB2	29:T:56:LYS:HA	2.03	0.41
35:g:176:SER:OG	35:g:186:TRP:NE1	2.40	0.41
1:2:76:A:H2	1:2:80:A:H2'	1.85	0.41
1:2:296:U:H2'	1:2:297:C:C6	2.56	0.41
1:2:301:U:OP1	8:I:22:ARG:NH2	2.53	0.41
1:2:415:A:H5'	1:2:416:A:C8	2.55	0.41
1:2:894:G:H22	1:2:916:U:H3	1.68	0.41
1:2:899:A:H1'	1:2:914:A:H2	1.85	0.41
1:2:1036:C:H1'	14:W:16:ASN:HD22	1.85	0.41
1:2:1295:A:H2'	1:2:1296:G:O4'	2.20	0.41
1:2:1470:C:H4'	1:2:1471:U:O5'	2.20	0.41
2:A:207:PRO:O	2:A:210:ILE:HG22	2.19	0.41
7:H:61:PHE:HB3	7:H:95:GLU:HG2	2.01	0.41
12:O:29:HIS:CD2	12:O:41:ARG:HG3	2.56	0.41
15:X:59:ILE:N	15:X:59:ILE:HD12	2.35	0.41
23:K:9:LYS:O	23:K:13:GLN:HG3	2.21	0.41
24:M:79:LEU:O	24:M:80:ILE:HD13	2.20	0.41
30:U:28:SER:OG	30:U:29:THR:N	2.54	0.41
36:i:28:TYR:N	36:i:28:TYR:CD1	2.88	0.41
1:2:793:U:H5'	1:2:794:U:O5'	2.21	0.41
1:2:866:G:H21	11:N:87:ASP:HB3	1.86	0.41
1:2:1240:G:H2'	1:2:1241:A:C8	2.56	0.41
1:2:1323:G:H5'	2:A:113:ARG:HH22	1.86	0.41
1:2:1556:U:OP1	28:S:122:HIS:ND1	2.40	0.41
1:2:1679:A:C8	6:G:66:GLY:HA3	2.55	0.41
1:2:1798:A:N6	37:3:19:A:HO2'	2.17	0.41
3:B:5:LYS:C	3:B:7:LYS:H	2.29	0.41
5:E:107:GLY:O	5:E:189:LEU:HD23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:62:PRO:HG2	6:G:83:CYS:SG	2.60	0.41
7:H:67:LEU:HD13	7:H:67:LEU:HA	1.79	0.41
8:I:6:ASP:OD1	8:I:8:ARG:N	2.48	0.41
17:a:10:ARG:O	17:a:33:ASP:HB2	2.20	0.41
21:D:169:GLU:HB3	21:D:190:LYS:NZ	2.31	0.41
28:S:14:ILE:HD12	28:S:14:ILE:HA	1.84	0.41
1:2:444:A:C8	1:2:445:A:C8	3.08	0.41
1:2:1059:U:C6	1:2:1060:U:H1'	2.54	0.41
1:2:1240:G:C8	25:P:79:HIS:HB2	2.56	0.41
1:2:1323:G:H4'	2:A:113:ARG:HH12	1.84	0.41
1:2:1350:G:H2'	1:2:1351:U:H6	1.85	0.41
1:2:1475:G:OP1	29:T:43:ASN:HB3	2.21	0.41
1:2:1551:G:N2	1:2:1553:A:H3'	2.36	0.41
2:A:52:LYS:HZ2	13:V:82:VAL:HA	1.85	0.41
2:A:195:TRP:CH2	2:A:197:ILE:HD11	2.56	0.41
7:H:4:PRO:HA	7:H:7:LYS:HE3	2.02	0.41
7:H:147:ASN:OD1	7:H:147:ASN:N	2.52	0.41
16:Y:6:THR:HG23	16:Y:28:LEU:HB2	2.03	0.41
28:S:35:ILE:HG23	28:S:38:VAL:HB	2.03	0.41
38:1:46:7MG:O2'	38:1:48:5MC:OP1	2.38	0.41
40:k:108:HIS:O	40:k:111:HIS:HB2	2.21	0.41
40:k:414:GLY:CA	40:k:468:SER:HB2	2.50	0.41
1:2:371:G:OP1	14:W:88:LYS:NZ	2.53	0.41
1:2:390:A:HO2'	1:2:1728:A:HO2'	1.63	0.41
1:2:846:A:O2'	1:2:847:C:O4'	2.29	0.41
1:2:1315:G:H2'	1:2:1316:C:C6	2.56	0.41
1:2:1436:G:H2'	1:2:1437:C:H6	1.85	0.41
2:A:184:LEU:HD12	13:V:45:ALA:HB2	2.02	0.41
5:E:122:LYS:NZ	5:E:143:ASP:OD2	2.45	0.41
8:I:3:ILE:O	8:I:30:GLY:N	2.54	0.41
12:O:17:ALA:HA	12:O:30:VAL:HG23	2.03	0.41
19:e:56:MET:H	19:e:56:MET:HG2	1.55	0.41
21:D:32:GLU:O	21:D:53:THR:OG1	2.37	0.41
23:K:24:LYS:HE2	23:K:63:TYR:HE1	1.85	0.41
29:T:73:VAL:HG11	29:T:102:ARG:HG3	2.02	0.41
31:Z:75:LEU:HA	31:Z:78:VAL:HB	2.02	0.41
39:j:21:MET:SD	39:j:102:TYR:HB2	2.60	0.41
40:k:319:ARG:HD2	45:k:603:MET:HE1	2.02	0.41
1:2:219:A:N7	1:2:831:U:H1'	2.36	0.41
1:2:532:U:H2'	1:2:533:A:H5''	2.03	0.41
1:2:563:G:N1	1:2:579:A:OP2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:565:C:H2'	1:2:566:A:O4'	2.21	0.41
1:2:1201:A:O2'	1:2:1205:U:N3	2.40	0.41
1:2:1583:U:H2'	1:2:1584:A:H8	1.85	0.41
4:C:230:LEU:HD13	13:V:23:ILE:HG23	2.02	0.41
8:I:36:THR:HA	8:I:58:LEU:HA	2.03	0.41
8:I:186:GLU:O	8:I:189:GLU:HB2	2.20	0.41
12:O:40:ALA:HB1	12:O:67:VAL:HG12	2.02	0.41
13:V:85:TYR:CD1	18:b:6:ASP:HB2	2.55	0.41
17:a:61:GLU:HA	17:a:61:GLU:OE2	2.21	0.41
23:K:16:PHE:CZ	23:K:77:ARG:HG3	2.56	0.41
27:R:20:TYR:O	27:R:24:LEU:HG	2.21	0.41
32:c:13:ILE:HD12	32:c:13:ILE:HA	1.87	0.41
33:d:47:ALA:HB1	33:d:52:PHE:HB2	2.03	0.41
35:g:308:LEU:O	35:g:319:VAL:HA	2.21	0.41
36:i:101:ARG:H	36:i:101:ARG:HG2	1.68	0.41
39:j:13:TYR:HB3	39:j:78:LYS:HE2	2.03	0.41
1:2:15:U:H2'	1:2:16:G:O4'	2.20	0.41
1:2:182:U:H2'	1:2:183:C:C6	2.55	0.41
1:2:188:C:H2'	1:2:189:C:C6	2.56	0.41
1:2:589:C:N4	1:2:590:A:H62	2.19	0.41
1:2:803:A:C5	14:W:107:SER:HA	2.56	0.41
1:2:1381:G:O5'	30:U:89:ARG:NH2	2.53	0.41
1:2:1388:U:H5'	27:R:3:ARG:HD3	2.02	0.41
1:2:1388:U:H5''	27:R:3:ARG:HH11	1.85	0.41
1:2:1577:U:H2'	1:2:1578:C:C6	2.55	0.41
1:2:1682:U:C2	1:2:1715:G:O6	2.74	0.41
4:C:212:LEU:HD12	4:C:212:LEU:HA	1.77	0.41
7:H:63:PRO:HB2	7:H:65:PRO:HD2	2.01	0.41
8:I:107:THR:N	8:I:108:PRO:HD2	2.36	0.41
9:J:45:ILE:CG2	9:J:104:PHE:HB2	2.51	0.41
9:J:80:LEU:HD23	9:J:80:LEU:HA	1.76	0.41
10:L:122:ILE:HG12	10:L:144:SER:HB3	2.03	0.41
28:S:64:GLU:OE1	28:S:65:GLU:N	2.53	0.41
30:U:24:ILE:N	30:U:91:ILE:O	2.34	0.41
39:j:247:ALA:HA	39:j:250:LYS:HE3	2.03	0.41
40:k:79:PRO:HG2	40:k:82:PRO:HB3	2.02	0.41
40:k:238:ILE:HG12	40:k:514:TRP:HB3	2.03	0.41
1:2:17:C:H4'	1:2:1108:G:C8	2.56	0.41
1:2:62:A:O2'	1:2:267:C:O2'	2.39	0.41
1:2:90:C:O2'	1:2:450:A:H5''	2.21	0.41
1:2:253:A:H2'	1:2:254:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:303:U:C2	1:2:304:C:C5	3.09	0.41
1:2:325:G:H2'	1:2:326:U:C6	2.56	0.41
1:2:431:G:H2'	1:2:432:C:C6	2.55	0.41
1:2:508:G:H2'	1:2:509:G:H8	1.80	0.41
1:2:996:G:C6	1:2:997:A:N7	2.89	0.41
1:2:997:A:C5	1:2:998:PSU:C2	3.09	0.41
1:2:1049:G:O6	1:2:1068:A:N6	2.54	0.41
1:2:1191:C:OP1	1:2:1193:A:H5'	2.20	0.41
1:2:1371:A:H2'	1:2:1372:C:C6	2.56	0.41
1:2:1551:G:H22	1:2:1554:A:P	2.44	0.41
1:2:1594:C:OP1	33:d:16:LYS:HD2	2.21	0.41
1:2:1606:U:H2'	1:2:1607:U:C6	2.55	0.41
2:A:22:VAL:HG13	2:A:162:CYS:HB2	2.02	0.41
3:B:3:VAL:HG12	39:j:89:ARG:HH21	1.86	0.41
5:E:72:VAL:N	5:E:75:LYS:O	2.52	0.41
5:E:179:LYS:HA	5:E:231:PRO:HD3	2.03	0.41
7:H:46:ILE:H	7:H:46:ILE:HD12	1.85	0.41
10:L:54:ILE:CG2	10:L:55:ASP:H	2.33	0.41
12:O:117:ASP:OD1	12:O:119:THR:HG22	2.20	0.41
13:V:16:LYS:HA	13:V:23:ILE:HA	2.02	0.41
15:X:9:LEU:HD23	15:X:9:LEU:HA	1.86	0.41
15:X:33:LEU:HD13	15:X:33:LEU:HA	1.90	0.41
15:X:126:LYS:HA	15:X:131:SER:HA	2.03	0.41
20:h:17:ARG:NH1	20:h:21:ARG:HD3	2.36	0.41
21:D:105:MET:CE	21:D:184:ILE:HD13	2.47	0.41
21:D:132:LYS:HE2	21:D:132:LYS:HB2	1.80	0.41
21:D:135:GLU:HG2	21:D:153:ALA:HB2	2.03	0.41
22:F:27:LEU:HB3	26:Q:27:GLY:O	2.21	0.41
24:M:49:GLU:O	24:M:115:LYS:HG2	2.20	0.41
27:R:20:TYR:CD2	27:R:38:ILE:HD12	2.55	0.41
28:S:101:LEU:HA	28:S:101:LEU:HD13	1.80	0.41
29:T:61:VAL:HG13	29:T:76:LEU:HD11	2.02	0.41
33:d:23:ILE:HD13	33:d:23:ILE:HA	1.82	0.41
35:g:308:LEU:HD12	35:g:309:PHE:N	2.36	0.41
38:1:16:H2U:H4'	38:1:16:H2U:OP1	2.20	0.41
39:j:166:LEU:HD23	39:j:166:LEU:HA	1.88	0.41
40:k:92:ALA:HA	40:k:95:ILE:HG22	2.02	0.41
40:k:129:LYS:C	40:k:131:GLU:H	2.29	0.41
40:k:142:TYR:CD1	40:k:395:LEU:HD23	2.56	0.41
40:k:239:MET:HE2	40:k:239:MET:HB2	1.88	0.41
1:2:168:A:C4	1:2:170:A:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:406:A:H1'	1:2:1669:A:C2	2.56	0.41
1:2:406:A:H2'	1:2:407:C:C6	2.56	0.41
1:2:749:U:H2'	1:2:750:U:C6	2.56	0.41
1:2:860:U:P	11:N:64:LYS:HZ1	2.44	0.41
1:2:1408:A:O2'	1:2:1409:A:C8	2.72	0.41
1:2:1450:U:H2'	1:2:1451:G:H8	1.86	0.41
1:2:1475:G:C6	1:2:1529:G:C6	3.09	0.41
1:2:1527:C:H2'	1:2:1528:C:C6	2.56	0.41
2:A:56:LYS:HD2	2:A:56:LYS:HA	1.72	0.41
3:B:3:VAL:O	3:B:4:GLY:C	2.63	0.41
5:E:181:VAL:HG23	5:E:227:VAL:HA	2.03	0.41
5:E:185:GLY:HA3	5:E:224:ASN:OD1	2.21	0.41
6:G:44:GLU:HG2	6:G:45:PHE:HD1	1.86	0.41
11:N:4:MET:HE2	11:N:4:MET:HB3	1.73	0.41
15:X:86:PHE:CD1	15:X:86:PHE:C	2.99	0.41
22:F:40:GLN:N	22:F:40:GLN:OE1	2.54	0.41
29:T:34:VAL:O	29:T:35:ASP:HB3	2.20	0.41
29:T:86:ARG:NH1	29:T:89:ARG:HE	2.19	0.41
30:U:97:ALA:HB1	30:U:101:LYS:HZ1	1.86	0.41
35:g:258:TRP:O	35:g:259:LEU:HD23	2.21	0.41
39:j:18:ASP:OD1	39:j:18:ASP:N	2.51	0.41
40:k:146:LYS:HG2	40:k:188:HIS:CD2	2.55	0.41
1:2:330:A:H2'	1:2:331:U:C6	2.57	0.40
1:2:331:U:OP1	8:I:31:ARG:NH1	2.54	0.40
1:2:611:U:OP2	15:X:5:LYS:NZ	2.44	0.40
1:2:700:C:O2'	1:2:701:U:P	2.79	0.40
1:2:793:U:H4'	1:2:794:U:OP2	2.21	0.40
1:2:806:A:H2'	1:2:807:U:H6	1.86	0.40
1:2:1011:U:C2	1:2:1012:A:C8	3.10	0.40
1:2:1077:C:C2	1:2:1078:U:C5	3.09	0.40
1:2:1133:C:H2'	1:2:1134:U:C6	2.56	0.40
1:2:1142:A:H2'	1:2:1143:U:H6	1.86	0.40
1:2:1343:A:H2'	1:2:1344:A:C8	2.56	0.40
1:2:1551:G:O2'	1:2:1553:A:N7	2.49	0.40
1:2:1606:U:O3'	26:Q:73:GLY:HA3	2.21	0.40
1:2:1689:A:N6	1:2:1709:C:C2	2.89	0.40
1:2:1713:G:H2'	1:2:1714:C:C6	2.57	0.40
1:2:1716:A:H2'	1:2:1717:A:H8	1.85	0.40
4:C:44:THR:HG23	4:C:47:GLY:H	1.86	0.40
5:E:241:GLY:O	5:E:244:ILE:HG12	2.22	0.40
7:H:58:LEU:HD23	7:H:88:ARG:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:107:THR:O	8:I:110:ARG:N	2.55	0.40
8:I:185:LEU:HD12	8:I:189:GLU:HB3	2.03	0.40
22:F:101:MET:HE3	22:F:101:MET:HB2	1.81	0.40
22:F:123:ILE:HG23	22:F:201:ILE:HD11	2.02	0.40
22:F:177:LEU:HD22	22:F:200:LEU:HD23	2.03	0.40
23:K:71:GLU:H	23:K:71:GLU:CD	2.19	0.40
29:T:75:LYS:HE3	29:T:75:LYS:HB3	1.73	0.40
35:g:201:GLY:HA3	35:g:230:TRP:HH2	1.86	0.40
39:j:20:VAL:HG21	39:j:73:VAL:HG23	2.02	0.40
39:j:119:PHE:CE2	39:j:165:VAL:HA	2.57	0.40
40:k:136:ILE:HD12	40:k:200:LEU:HD11	2.04	0.40
1:2:57:G:C4	1:2:91:G:N2	2.89	0.40
1:2:79:C:OP1	6:G:172:ALA:HB3	2.21	0.40
1:2:185:C:O2	1:2:185:C:H2'	2.21	0.40
1:2:477:A:H2	1:2:509:G:H22	1.69	0.40
1:2:569:A:N1	15:X:115:GLY:HA3	2.37	0.40
1:2:860:U:OP2	11:N:64:LYS:NZ	2.55	0.40
1:2:1141:A:H2'	1:2:1142:A:O4'	2.21	0.40
1:2:1413:U:OP1	27:R:45:ARG:NH2	2.53	0.40
5:E:35:PRO:HB2	5:E:36:HIS:CD2	2.55	0.40
5:E:88:ASP:HA	5:E:122:LYS:HE3	2.02	0.40
7:H:14:THR:O	7:H:18:LEU:HG	2.21	0.40
7:H:86:GLN:H	7:H:88:ARG:NH2	2.20	0.40
8:I:160:GLN:HB2	8:I:165:ARG:O	2.21	0.40
12:O:72:LYS:HE2	12:O:72:LYS:HB2	1.90	0.40
17:a:23:CYS:CB	17:a:28:ARG:H	2.34	0.40
18:b:24:LEU:HD23	18:b:24:LEU:HA	1.94	0.40
21:D:209:ILE:O	27:R:20:TYR:OH	2.39	0.40
22:F:53:VAL:HG12	22:F:66:ILE:HD12	2.03	0.40
22:F:82:LYS:HB2	22:F:85:ARG:HG3	2.03	0.40
22:F:128:ASP:CG	22:F:129:GLN:H	2.29	0.40
30:U:63:LEU:HD13	33:d:34:TYR:CZ	2.56	0.40
39:j:7:ARG:H	39:j:40:ASP:HB3	1.86	0.40
1:2:518:C:C4	1:2:533:A:C8	3.09	0.40
1:2:520:A:H2'	1:2:521:U:H6	1.85	0.40
1:2:531:U:H4'	16:Y:66:GLY:HA2	2.03	0.40
1:2:574:C:H41	15:X:65:ASN:CG	2.27	0.40
1:2:586:C:H2'	1:2:587:U:C6	2.56	0.40
1:2:599:U:H2'	1:2:600:A:H8	1.86	0.40
1:2:636:C:OP1	14:W:32:LYS:HG3	2.21	0.40
1:2:659:G:N3	1:2:659:G:H2'	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:867:G:H1	1:2:959:U:H3	1.68	0.40
1:2:1293:G:C6	1:2:1294:G:N7	2.90	0.40
1:2:1679:A:O3'	6:G:31:ARG:NH1	2.46	0.40
1:2:1679:A:H2'	6:G:65:GLN:NE2	2.36	0.40
1:2:1739:U:H2'	1:2:1740:U:C6	2.56	0.40
2:A:108:THR:HG23	2:A:135:GLU:OE1	2.22	0.40
3:B:121:ILE:HD12	3:B:207:LEU:HD21	2.04	0.40
5:E:120:SER:O	5:E:164:LEU:HB3	2.20	0.40
5:E:147:ILE:HG21	5:E:169:ILE:HG12	2.04	0.40
6:G:50:PHE:HD2	6:G:111:LEU:HD13	1.86	0.40
10:L:58:CYS:HB3	10:L:62:GLY:N	2.35	0.40
22:F:51:GLU:O	22:F:52:ASP:HB3	2.22	0.40
29:T:113:VAL:HG23	29:T:114:VAL:HG23	2.02	0.40
35:g:223:LYS:HD2	35:g:246:GLU:OE1	2.20	0.40
35:g:238:PHE:CD2	35:g:239:MET:HE3	2.56	0.40
39:j:193:PHE:O	40:k:359:ILE:HD11	2.22	0.40
1:2:57:G:C2	1:2:91:G:C2	3.09	0.40
1:2:645:U:H2'	1:2:646:G:H8	1.87	0.40
1:2:1238:U:H2'	1:2:1239:U:C6	2.57	0.40
1:2:1279:C:H2'	1:2:1280:G:C8	2.55	0.40
3:B:203:ASP:OD1	3:B:204:ILE:N	2.54	0.40
4:C:121:LYS:HG2	4:C:132:ALA:CB	2.51	0.40
12:O:81:ILE:HD11	12:O:112:ILE:HD12	2.03	0.40
15:X:93:LEU:HB3	19:e:11:ALA:HB1	2.04	0.40
17:a:20:PRO:HA	17:a:31:PRO:HA	2.03	0.40
20:h:16:LYS:HB3	20:h:16:LYS:HE2	1.83	0.40
21:D:80:LYS:O	21:D:83:THR:OG1	2.36	0.40
26:Q:104:GLU:HA	26:Q:104:GLU:OE2	2.21	0.40
27:R:3:ARG:H	27:R:3:ARG:HG2	1.75	0.40
38:1:21:A:O2'	38:1:22:G:H5''	2.22	0.40
39:j:166:LEU:O	39:j:170:LYS:HG3	2.21	0.40
40:k:106:ILE:HG12	40:k:216:LEU:HA	2.04	0.40
40:k:246:ILE:O	40:k:280:ILE:HA	2.21	0.40
1:2:53:G:H2'	1:2:54:C:H6	1.85	0.40
1:2:212:A:H2'	1:2:213:G:O4'	2.21	0.40
1:2:327:A:C4	1:2:328:G:C8	3.09	0.40
1:2:372:G:N2	1:2:603:A:OP1	2.52	0.40
1:2:545:C:H2'	1:2:546:U:C6	2.56	0.40
1:2:751:G:H2'	1:2:752:A:H8	1.83	0.40
1:2:1181:U:H4'	25:P:124:THR:OG1	2.20	0.40
1:2:1249:U:H5'	1:2:1250:U:OP2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1268:U:H5''	1:2:1430:U:OP1	2.22	0.40
5:E:45:ILE:HB	5:E:80:THR:HG22	2.02	0.40
9:J:110:GLN:NE2	9:J:126:ARG:HB2	2.36	0.40
13:V:3:ASN:OD1	13:V:3:ASN:C	2.65	0.40
22:F:42:ILE:HG23	22:F:71:TYR:CE1	2.56	0.40
22:F:226:ASN:HD22	22:F:226:ASN:HA	1.65	0.40
23:K:54:PHE:O	23:K:69:THR:HG22	2.20	0.40
38:1:11:C:H2'	38:1:12:G:H8	1.86	0.40
39:j:24:VAL:HG21	39:j:63:ILE:HG23	2.03	0.40
39:j:134:LEU:HD12	39:j:134:LEU:HA	1.81	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	217/254 (85%)	194 (89%)	23 (11%)	0	100	100
3	B	221/255 (87%)	202 (91%)	17 (8%)	2 (1%)	14	46
4	C	218/259 (84%)	208 (95%)	10 (5%)	0	100	100
5	E	258/261 (99%)	240 (93%)	18 (7%)	0	100	100
6	G	228/236 (97%)	220 (96%)	8 (4%)	0	100	100
7	H	182/190 (96%)	168 (92%)	13 (7%)	1 (0%)	24	57
8	I	184/201 (92%)	164 (89%)	20 (11%)	0	100	100
9	J	180/188 (96%)	173 (96%)	7 (4%)	0	100	100
10	L	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
11	N	149/151 (99%)	145 (97%)	4 (3%)	0	100	100
12	O	127/137 (93%)	115 (91%)	12 (9%)	0	100	100
13	V	85/87 (98%)	78 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	W	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
15	X	142/145 (98%)	133 (94%)	9 (6%)	0	100	100
16	Y	132/135 (98%)	124 (94%)	8 (6%)	0	100	100
17	a	100/119 (84%)	81 (81%)	19 (19%)	0	100	100
18	b	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
19	e	58/63 (92%)	52 (90%)	6 (10%)	0	100	100
20	h	23/25 (92%)	23 (100%)	0	0	100	100
21	D	225/237 (95%)	216 (96%)	9 (4%)	0	100	100
22	F	204/227 (90%)	184 (90%)	20 (10%)	0	100	100
23	K	94/106 (89%)	86 (92%)	8 (8%)	0	100	100
24	M	113/134 (84%)	99 (88%)	14 (12%)	0	100	100
25	P	115/142 (81%)	104 (90%)	11 (10%)	0	100	100
26	Q	139/143 (97%)	122 (88%)	15 (11%)	2 (1%)	9	38
27	R	128/136 (94%)	117 (91%)	11 (9%)	0	100	100
28	S	143/146 (98%)	130 (91%)	13 (9%)	0	100	100
29	T	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
30	U	104/117 (89%)	92 (88%)	12 (12%)	0	100	100
31	Z	76/108 (70%)	69 (91%)	7 (9%)	0	100	100
32	c	62/67 (92%)	57 (92%)	5 (8%)	0	100	100
33	d	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
34	f	72/150 (48%)	58 (81%)	14 (19%)	0	100	100
35	g	314/326 (96%)	291 (93%)	23 (7%)	0	100	100
36	i	108/153 (71%)	99 (92%)	9 (8%)	0	100	100
39	j	263/304 (86%)	244 (93%)	19 (7%)	0	100	100
40	k	468/527 (89%)	438 (94%)	30 (6%)	0	100	100
41	l	21/285 (7%)	21 (100%)	0	0	100	100
All	All	5706/6582 (87%)	5266 (92%)	435 (8%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	H	64	VAL
26	Q	41	PRO

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Mol	Chain	Res	Type
26	Q	42	GLU
3	B	221	PRO
3	B	4	GLY

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%)	178 (99%)	2 (1%)	65	75
3	B	202/228 (89%)	200 (99%)	2 (1%)	68	76
4	C	177/203 (87%)	177 (100%)	0	100	100
5	E	223/224 (100%)	221 (99%)	2 (1%)	70	76
6	G	192/200 (96%)	192 (100%)	0	100	100
7	H	164/170 (96%)	162 (99%)	2 (1%)	63	74
8	I	147/159 (92%)	147 (100%)	0	100	100
9	J	153/158 (97%)	153 (100%)	0	100	100
10	L	136/137 (99%)	134 (98%)	2 (2%)	57	72
11	N	128/128 (100%)	127 (99%)	1 (1%)	73	77
12	O	97/104 (93%)	97 (100%)	0	100	100
13	V	73/73 (100%)	72 (99%)	1 (1%)	59	72
14	W	110/111 (99%)	110 (100%)	0	100	100
15	X	119/120 (99%)	117 (98%)	2 (2%)	53	70
16	Y	108/109 (99%)	107 (99%)	1 (1%)	70	76
17	a	83/100 (83%)	81 (98%)	2 (2%)	43	65
18	b	71/72 (99%)	70 (99%)	1 (1%)	59	72
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%)	188 (100%)	0	100	100
22	F	174/194 (90%)	174 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	K	88/96 (92%)	88 (100%)	0	100	100
24	M	93/109 (85%)	93 (100%)	0	100	100
25	P	99/119 (83%)	99 (100%)	0	100	100
26	Q	117/119 (98%)	115 (98%)	2 (2%)	53	70
27	R	116/124 (94%)	116 (100%)	0	100	100
28	S	127/129 (98%)	126 (99%)	1 (1%)	73	77
29	T	117/118 (99%)	117 (100%)	0	100	100
30	U	96/107 (90%)	95 (99%)	1 (1%)	68	76
31	Z	60/88 (68%)	60 (100%)	0	100	100
32	c	55/59 (93%)	54 (98%)	1 (2%)	51	70
33	d	47/48 (98%)	47 (100%)	0	100	100
34	f	60/133 (45%)	60 (100%)	0	100	100
35	g	264/272 (97%)	264 (100%)	0	100	100
36	i	90/130 (69%)	90 (100%)	0	100	100
39	j	239/274 (87%)	238 (100%)	1 (0%)	84	81
40	k	393/449 (88%)	393 (100%)	0	100	100
41	l	22/246 (9%)	22 (100%)	0	100	100
All	All	4882/5595 (87%)	4858 (100%)	24 (0%)	78	81

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	111	ILE
2	A	158	VAL
3	B	6	ASN
3	B	89	ASP
5	E	87	MET
5	E	159	THR
7	H	66	SER
7	H	67	LEU
10	L	10	GLU
10	L	84	ILE
11	N	105	ASN
13	V	12	TYR
15	X	63	GLN
15	X	87	VAL

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Mol	Chain	Res	Type
16	Y	100	VAL
17	a	36	ILE
17	a	69	ASN
18	b	55	THR
26	Q	40	GLN
26	Q	76	SER
28	S	26	ILE
30	U	113	ASP
32	c	40	ILE
39	j	68	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	23	HIS
2	A	32	HIS
2	A	164	ASN
3	B	40	ASN
3	B	163	GLN
3	B	208	GLN
3	B	209	ASN
3	B	211	HIS
3	B	232	HIS
4	C	115	HIS
6	G	13	GLN
6	G	139	ASN
6	G	197	ASN
8	I	160	GLN
8	I	176	GLN
11	N	58	HIS
13	V	29	HIS
15	X	18	HIS
16	Y	22	GLN
18	b	42	ASN
19	e	46	ASN
19	e	51	ASN
21	D	101	GLN
21	D	159	HIS
22	F	65	GLN
22	F	202	ASN
23	K	58	GLN
24	M	51	GLN

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Mol	Chain	Res	Type
24	M	116	ASN
29	T	17	ASN
33	d	37	ASN
33	d	48	ASN
34	f	132	ASN
34	f	133	HIS
35	g	321	GLN
36	i	17	ASN
36	i	33	GLN
39	j	5	HIS
39	j	68	ASN
40	k	98	GLN
40	k	108	HIS
40	k	249	ASN
40	k	344	ASN
40	k	465	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1797/1798 (99%)	522 (29%)	30 (1%)
37	3	25/49 (51%)	15 (60%)	0
38	1	72/75 (96%)	29 (40%)	2 (2%)
All	All	1894/1922 (98%)	566 (29%)	32 (1%)

All (566) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	25	C
1	2	26	A
1	2	27	U
1	2	34	G
1	2	43	A
1	2	47	A
1	2	57	G
1	2	58	U
1	2	59	C
1	2	60	U
1	2	67	A

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Mol	Chain	Res	Type
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	80	A
1	2	81	G
1	2	104	A
1	2	114	C
1	2	115	G
1	2	121	U
1	2	127	G
1	2	129	U
1	2	130	C
1	2	132	U
1	2	133	U
1	2	135	A
1	2	136	C
1	2	137	U
1	2	140	A
1	2	146	A
1	2	152	G
1	2	155	A
1	2	160	U
1	2	161	A
1	2	167	A
1	2	169	U
1	2	173	U
1	2	176	U
1	2	177	U
1	2	178	A
1	2	184	U
1	2	185	C
1	2	187	A
1	2	191	U
1	2	192	U
1	2	194	G
1	2	195	G

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Mol	Chain	Res	Type
1	2	216	A
1	2	217	A
1	2	218	A
1	2	220	A
1	2	221	A
1	2	223	C
1	2	225	A
1	2	226	U
1	2	227	G
1	2	230	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	260	U
1	2	264	A
1	2	271	U
1	2	275	C
1	2	276	U
1	2	278	G
1	2	280	G
1	2	289	G
1	2	298	A
1	2	300	A
1	2	301	U
1	2	307	C
1	2	313	C
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	349	U

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Mol	Chain	Res	Type
1	2	359	A
1	2	360	C
1	2	382	G
1	2	390	A
1	2	398	A
1	2	399	A
1	2	400	A
1	2	401	C
1	2	404	C
1	2	411	A
1	2	415	A
1	2	416	A
1	2	422	G
1	2	423	C
1	2	424	A
1	2	425	G
1	2	436	A
1	2	438	U
1	2	439	U
1	2	440	A
1	2	443	C
1	2	445	A
1	2	447	C
1	2	454	C
1	2	459	A
1	2	463	A
1	2	467	A
1	2	474	A
1	2	476	A
1	2	482	A
1	2	483	C
1	2	487	G
1	2	488	C
1	2	489	C
1	2	490	C
1	2	491	A
1	2	493	U
1	2	494	C
1	2	495	G
1	2	496	G
1	2	499	C
1	2	501	U

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Mol	Chain	Res	Type
1	2	502	G
1	2	504	A
1	2	505	A
1	2	506	U
1	2	507	U
1	2	513	G
1	2	514	A
1	2	516	U
1	2	519	A
1	2	527	U
1	2	533	A
1	2	537	A
1	2	540	A
1	2	541	A
1	2	543	A
1	2	554	A
1	2	558	C
1	2	563	G
1	2	564	C
1	2	565	C
1	2	567	G
1	2	577	U
1	2	578	A
1	2	584	A
1	2	593	A
1	2	594	G
1	2	597	U
1	2	605	A
1	2	610	U
1	2	618	A
1	2	619	A
1	2	621	A
1	2	622	A
1	2	623	G
1	2	634	A
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

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Mol	Chain	Res	Type
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
1	2	695	U
1	2	696	C
1	2	697	C
1	2	701	U
1	2	702	G
1	2	704	C
1	2	707	A
1	2	709	C
1	2	710	U
1	2	711	G
1	2	712	U
1	2	714	C
1	2	717	C
1	2	718	U
1	2	721	U
1	2	722	G
1	2	727	C
1	2	729	G
1	2	730	G
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	736	C
1	2	738	G
1	2	739	G
1	2	741	C

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Mol	Chain	Res	Type
1	2	742	U
1	2	743	U
1	2	755	A
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
1	2	781	A
1	2	782	G
1	2	783	C
1	2	786	G
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	817	C
1	2	819	U
1	2	820	U
1	2	822	G
1	2	826	C
1	2	828	A
1	2	829	U
1	2	830	U
1	2	832	U
1	2	836	G
1	2	837	G
1	2	839	U
1	2	840	U
1	2	862	A
1	2	863	U
1	2	864	A
1	2	875	G
1	2	876	G
1	2	895	U

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Mol	Chain	Res	Type
1	2	897	A
1	2	903	G
1	2	912	G
1	2	913	G
1	2	915	U
1	2	916	U
1	2	917	U
1	2	918	A
1	2	919	U
1	2	920	U
1	2	932	A
1	2	934	U
1	2	941	G
1	2	944	U
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	985	G
1	2	986	G
1	2	987	A
1	2	991	A
1	2	995	U
1	2	998	PSU
1	2	1003	U
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

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Mol	Chain	Res	Type
1	2	1050	G
1	2	1051	U
1	2	1052	G
1	2	1055	U
1	2	1056	U
1	2	1057	U
1	2	1058	C
1	2	1059	U
1	2	1060	U
1	2	1061	A
1	2	1075	A
1	2	1081	C
1	2	1082	G
1	2	1085	A
1	2	1086	A
1	2	1091	A
1	2	1095	C
1	2	1096	U
1	2	1099	G
1	2	1108	G
1	2	1112	A
1	2	1113	G
1	2	1137	A
1	2	1149	G
1	2	1150	A
1	2	1155	C
1	2	1157	C
1	2	1158	C
1	2	1163	G
1	2	1166	G
1	2	1184	U
1	2	1185	U
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
1	2	1216	A
1	2	1217	G

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Mol	Chain	Res	Type
1	2	1224	U
1	2	1228	G
1	2	1230	U
1	2	1236	G
1	2	1237	A
1	2	1240	G
1	2	1241	A
1	2	1243	A
1	2	1244	G
1	2	1245	C
1	2	1246	U
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	1258	U
1	2	1259	U
1	2	1260	G
1	2	1268	U
1	2	1269	G
1	2	1272	G
1	2	1275	U
1	2	1283	C
1	2	1284	U
1	2	1296	G
1	2	1298	G
1	2	1306	U
1	2	1311	A
1	2	1313	U
1	2	1315	G
1	2	1317	G
1	2	1320	A
1	2	1321	A
1	2	1324	A
1	2	1332	C
1	2	1336	A
1	2	1337	C
1	2	1338	C
1	2	1339	U
1	2	1343	A

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Mol	Chain	Res	Type
1	2	1344	A
1	2	1345	A
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	1366	G
1	2	1370	G
1	2	1380	A
1	2	1386	A
1	2	1388	U
1	2	1389	A
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	1425	A
1	2	1426	2MG
1	2	1429	C
1	2	1431	G
1	2	1434	A
1	2	1442	A
1	2	1443	G
1	2	1444	A
1	2	1457	C
1	2	1458	A
1	2	1464	G
1	2	1469	A
1	2	1471	U
1	2	1476	G
1	2	1480	C
1	2	1484	G
1	2	1488	A

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Mol	Chain	Res	Type
1	2	1489	C
1	2	1490	A
1	2	1491	A
1	2	1494	U
1	2	1499	C
1	2	1509	G
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	1535	C
1	2	1538	G
1	2	1540	G
1	2	1552	U
1	2	1553	A
1	2	1555	U
1	2	1557	A
1	2	1558	U
1	2	1565	U
1	2	1566	C
1	2	1571	A
1	2	1572	G
1	2	1573	7MG
1	2	1581	A
1	2	1588	G
1	2	1594	C
1	2	1595	A
1	2	1599	G
1	2	1614	G
1	2	1617	C
1	2	1620	G
1	2	1632	C
1	2	1633	A
1	2	1646	A
1	2	1654	U
1	2	1655	U
1	2	1656	G
1	2	1662	C
1	2	1678	G
1	2	1679	A

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Mol	Chain	Res	Type
1	2	1682	U
1	2	1685	U
1	2	1687	A
1	2	1688	G
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	1701	C
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
1	2	1724	G
1	2	1725	G
1	2	1728	A
1	2	1729	A
1	2	1734	G
1	2	1742	A
1	2	1743	G
1	2	1748	A
1	2	1753	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	1778	G
1	2	1780	MA6
1	2	1787	G
1	2	1790	G
1	2	1791	G
1	2	1792	A

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Mol	Chain	Res	Type
1	2	1793	U
1	2	1794	C
1	2	1796	U
1	2	1797	U
1	2	1798	A
37	3	16	U
37	3	18	U
37	3	19	A
37	3	20	A
37	3	21	C
37	3	22	U
37	3	24	U
37	3	25	A
37	3	26	A
37	3	32	U
37	3	33	C
37	3	35	C
37	3	37	U
37	3	38	C
37	3	40	C
38	1	4	G
38	1	5	C
38	1	8	U
38	1	9	1MG
38	1	10	2MG
38	1	14	A
38	1	15	G
38	1	16	H2U
38	1	19	G
38	1	20	A
38	1	21	A
38	1	22	G
38	1	23	C
38	1	43	G
38	1	44	A
38	1	46	7MG
38	1	47	H2U
38	1	48	5MC
38	1	49	5MC
38	1	50	U
38	1	59	A
38	1	60	A

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Mol	Chain	Res	Type
38	1	61	C
38	1	64	RIA
38	1	69	C
38	1	71	C
38	1	74	C
38	1	75	C
38	1	76	A

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	26	A
1	2	66	U
1	2	74	U
1	2	78	A
1	2	216	A
1	2	217	A
1	2	239	C
1	2	277	U
1	2	279	U
1	2	423	C
1	2	513	G
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	793	U
1	2	828	A
1	2	1198	G
1	2	1206	C
1	2	1343	A
1	2	1430	U
1	2	1470	C
1	2	1513	A
1	2	1552	U
1	2	1571	A
1	2	1613	C
1	2	1765	G
38	1	43	G

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Mol	Chain	Res	Type
38	1	74	C

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

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
38	M2G	1	26	38	24,27,28	2.72	8 (33%)	33,40,43	1.74	7 (21%)
1	2MG	2	1570	1	23,26,27	2.95	8 (34%)	33,38,41	2.16	10 (30%)
1	5MC	2	1637	1	19,22,23	3.90	8 (42%)	26,32,35	0.98	2 (7%)
38	2MG	1	10	38	23,26,27	2.92	8 (34%)	33,38,41	2.22	10 (30%)
38	5MC	1	48	38	19,22,23	3.85	8 (42%)	26,32,35	1.09	2 (7%)
1	5MC	2	1006	1	19,22,23	3.83	8 (42%)	26,32,35	1.12	3 (11%)
1	PSU	2	1289	1	18,21,22	4.50	7 (38%)	21,30,33	1.86	5 (23%)
1	7MG	2	1573	1,38	23,26,27	3.64	11 (47%)	27,39,42	2.21	9 (33%)
1	MA6	2	1780	1	23,26,27	1.38	4 (17%)	33,38,41	3.33	12 (36%)
38	H2U	1	16	38	18,21,22	3.15	4 (22%)	19,30,33	1.49	4 (21%)
1	PSU	2	120	1	18,21,22	4.49	7 (38%)	21,30,33	1.97	5 (23%)
38	1MG	1	9	38	23,26,27	3.33	7 (30%)	33,39,42	2.32	8 (24%)
38	5MC	1	49	38	19,22,23	3.95	8 (42%)	26,32,35	1.17	4 (15%)
1	2MG	2	1426	1,42	23,26,27	2.92	8 (34%)	33,38,41	2.15	10 (30%)
1	PSU	2	465	1	18,21,22	4.46	7 (38%)	21,30,33	1.96	5 (23%)
38	H2U	1	47	38	18,21,22	3.20	4 (22%)	19,30,33	1.43	3 (15%)
38	7MG	1	46	38	23,26,27	3.65	11 (47%)	27,39,42	2.21	9 (33%)
1	PSU	2	766	1	18,21,22	4.49	8 (44%)	21,30,33	2.00	6 (28%)
38	1MA	1	58	38	21,25,26	3.14	6 (28%)	30,37,40	2.45	8 (26%)
1	B8N	2	1190	1	25,29,30	3.36	6 (24%)	28,42,45	1.99	7 (25%)
1	PSU	2	998	1	18,21,22	4.45	7 (38%)	21,30,33	2.03	6 (28%)
38	RIA	1	64	38	35,38,39	0.38	0	50,57,60	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	T6A	1	37	38	31,34,35	1.81	7 (22%)	43,49,52	2.24	14 (32%)

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

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

All (160) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1289	PSU	C6-C5	11.92	1.48	1.35
1	2	120	PSU	C6-C5	11.87	1.48	1.35
1	2	766	PSU	C6-C5	11.85	1.48	1.35
1	2	465	PSU	C6-C5	11.73	1.48	1.35
1	2	998	PSU	C6-C5	11.69	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	47	H2U	C2-N1	10.12	1.49	1.35
1	2	1289	PSU	C2-N1	10.06	1.49	1.36
1	2	465	PSU	C2-N1	10.02	1.49	1.36
1	2	120	PSU	C2-N1	10.02	1.49	1.36
1	2	998	PSU	C2-N1	9.99	1.49	1.36
1	2	766	PSU	C2-N1	9.93	1.49	1.36
38	1	16	H2U	C2-N1	9.86	1.49	1.35
38	1	58	1MA	C2-N3	9.68	1.48	1.30
38	1	49	5MC	C6-C5	9.35	1.49	1.34
1	2	1637	5MC	C6-C5	9.35	1.49	1.34
38	1	48	5MC	C6-C5	9.28	1.49	1.34
38	1	9	1MG	C2-N2	9.19	1.50	1.34
1	2	1006	5MC	C6-C5	8.94	1.49	1.34
38	1	46	7MG	C8-N9	8.86	1.51	1.45
1	2	1573	7MG	C8-N9	8.67	1.51	1.45
1	2	1190	B8N	C6-N1	8.45	1.57	1.36
1	2	1570	2MG	C2-N3	7.87	1.47	1.32
1	2	998	PSU	C2-N3	7.85	1.50	1.37
1	2	766	PSU	C2-N3	7.82	1.50	1.37
1	2	120	PSU	C2-N3	7.77	1.50	1.37
1	2	1289	PSU	C2-N3	7.75	1.50	1.37
1	2	1426	2MG	C2-N3	7.70	1.46	1.32
38	1	10	2MG	C2-N3	7.70	1.46	1.32
1	2	1190	B8N	C4-C5	7.65	1.64	1.47
1	2	465	PSU	C2-N3	7.64	1.50	1.37
1	2	1190	B8N	C4-N3	-7.46	1.27	1.40
38	1	58	1MA	C4-N3	7.15	1.50	1.35
38	1	46	7MG	C5-N7	7.14	1.44	1.35
38	1	9	1MG	C2-N3	7.04	1.44	1.33
1	2	1573	7MG	C5-N7	7.03	1.44	1.35
38	1	49	5MC	C5-C4	6.89	1.49	1.44
38	1	48	5MC	C4-N3	6.88	1.45	1.34
1	2	1006	5MC	C4-N3	6.88	1.45	1.34
38	1	26	M2G	C4-N3	6.86	1.50	1.34
1	2	1637	5MC	C5-C4	6.82	1.49	1.44
1	2	1570	2MG	C4-N3	6.81	1.49	1.34
38	1	49	5MC	C4-N3	6.81	1.45	1.34
38	1	26	M2G	C2-N2	6.80	1.47	1.35
38	1	10	2MG	C4-N3	6.75	1.49	1.34
1	2	1426	2MG	C4-N3	6.73	1.49	1.34
1	2	1637	5MC	C4-N3	6.72	1.44	1.34
38	1	47	H2U	C2-N3	6.57	1.49	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	1	9	1MG	C4-N3	6.56	1.49	1.34
38	1	16	H2U	C2-N3	6.52	1.49	1.38
1	2	1006	5MC	C5-C4	6.50	1.49	1.44
1	2	1006	5MC	C2-N3	6.33	1.48	1.36
38	1	48	5MC	C5-C4	6.32	1.48	1.44
1	2	1637	5MC	C2-N3	6.31	1.48	1.36
38	1	49	5MC	C2-N3	6.28	1.48	1.36
38	1	48	5MC	C2-N3	6.26	1.48	1.36
38	1	26	M2G	C2-N3	6.17	1.47	1.32
1	2	1573	7MG	C2-N3	5.96	1.47	1.33
38	1	46	7MG	C2-N3	5.92	1.47	1.33
1	2	1570	2MG	C2-N2	5.89	1.45	1.33
38	1	10	2MG	C2-N2	5.87	1.45	1.33
1	2	1573	7MG	C4-N3	5.86	1.47	1.34
1	2	1426	2MG	C2-N2	5.83	1.45	1.33
38	1	46	7MG	C4-N3	5.82	1.47	1.34
1	2	1190	B8N	C2-N1	5.80	1.56	1.39
38	1	9	1MG	C2-N1	5.52	1.47	1.37
1	2	1289	PSU	C6-N1	5.46	1.45	1.36
1	2	1573	7MG	C4-N9	5.45	1.44	1.37
1	2	120	PSU	C6-N1	5.39	1.45	1.36
1	2	465	PSU	C6-N1	5.32	1.45	1.36
38	1	37	T6A	C10-N11	5.27	1.50	1.35
1	2	766	PSU	C6-N1	5.26	1.44	1.36
1	2	998	PSU	C6-N1	5.24	1.44	1.36
1	2	1190	B8N	C6-C5	5.19	1.42	1.35
38	1	46	7MG	C4-N9	5.19	1.44	1.37
38	1	37	T6A	C10-N6	5.17	1.48	1.37
38	1	16	H2U	C4-N3	5.09	1.46	1.37
1	2	1573	7MG	C2-N2	5.05	1.46	1.34
38	1	47	H2U	C4-N3	5.02	1.46	1.37
1	2	1570	2MG	C2-N1	5.01	1.44	1.36
38	1	46	7MG	C2-N2	5.00	1.45	1.34
38	1	10	2MG	C2-N1	4.95	1.44	1.36
1	2	1426	2MG	C2-N1	4.92	1.44	1.36
38	1	58	1MA	C2-N1	4.91	1.45	1.35
38	1	49	5MC	C6-N1	4.81	1.46	1.38
38	1	49	5MC	C2-N1	4.79	1.50	1.40
1	2	1637	5MC	C6-N1	4.73	1.46	1.38
38	1	48	5MC	C6-N1	4.71	1.46	1.38
1	2	1006	5MC	C6-N1	4.52	1.45	1.38
1	2	1006	5MC	C4-N4	4.49	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1637	5MC	C4-N4	4.46	1.45	1.34
1	2	1006	5MC	C2-N1	4.46	1.49	1.40
38	1	49	5MC	C4-N4	4.45	1.45	1.34
38	1	48	5MC	C2-N1	4.45	1.49	1.40
1	2	1637	5MC	C2-N1	4.29	1.49	1.40
38	1	48	5MC	C4-N4	4.28	1.45	1.34
1	2	1190	B8N	C1'-C5	-4.26	1.40	1.50
38	1	58	1MA	C5-C6	4.10	1.54	1.43
38	1	46	7MG	C2-N1	3.95	1.47	1.37
1	2	1780	MA6	C6-N6	3.93	1.47	1.36
1	2	465	PSU	C4-N3	3.91	1.46	1.38
1	2	1289	PSU	C4-N3	3.90	1.46	1.38
1	2	1573	7MG	C2-N1	3.89	1.47	1.37
1	2	766	PSU	C4-N3	3.88	1.46	1.38
1	2	120	PSU	C4-N3	3.86	1.46	1.38
1	2	998	PSU	C4-N3	3.85	1.46	1.38
38	1	9	1MG	O6-C6	-3.71	1.15	1.23
38	1	26	M2G	C2-N1	3.68	1.45	1.36
1	2	1573	7MG	C5-C6	3.68	1.52	1.43
38	1	46	7MG	C5-C6	3.66	1.52	1.43
38	1	9	1MG	C5-C6	3.47	1.54	1.45
1	2	1573	7MG	C6-N1	3.31	1.45	1.38
38	1	46	7MG	C6-N1	3.29	1.45	1.38
38	1	9	1MG	C5-N7	-3.21	1.32	1.39
38	1	58	1MA	C5-N7	-3.04	1.33	1.39
1	2	1426	2MG	C5-N7	-2.94	1.33	1.39
1	2	1570	2MG	C5-N7	-2.92	1.33	1.39
38	1	10	2MG	C5-N7	-2.84	1.33	1.39
1	2	1780	MA6	C5-C4	-2.81	1.34	1.39
38	1	26	M2G	C6-N1	2.77	1.44	1.38
1	2	1637	5MC	O2-C2	-2.76	1.18	1.23
38	1	26	M2G	C5-N7	-2.75	1.33	1.39
1	2	1006	5MC	O2-C2	-2.73	1.18	1.23
38	1	48	5MC	O2-C2	-2.71	1.18	1.23
38	1	49	5MC	O2-C2	-2.70	1.18	1.23
38	1	26	M2G	C5-C6	2.59	1.54	1.44
38	1	37	T6A	C5-N7	-2.56	1.34	1.39
38	1	47	H2U	O2-C2	-2.55	1.18	1.23
38	1	10	2MG	C5-C6	2.55	1.53	1.44
38	1	46	7MG	O6-C6	-2.54	1.18	1.23
38	1	16	H2U	O2-C2	-2.53	1.18	1.23
1	2	1426	2MG	C5-C6	2.50	1.53	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1570	2MG	C5-C6	2.50	1.53	1.44
1	2	1426	2MG	O6-C6	-2.49	1.18	1.23
1	2	465	PSU	O4-C4	-2.48	1.18	1.23
1	2	1570	2MG	C6-N1	2.46	1.43	1.38
1	2	1573	7MG	O6-C6	-2.45	1.18	1.23
38	1	10	2MG	O6-C6	-2.45	1.18	1.23
1	2	766	PSU	O4-C4	-2.43	1.19	1.23
38	1	37	T6A	ODA-C13	2.43	1.29	1.22
1	2	998	PSU	O4-C4	-2.42	1.19	1.23
1	2	120	PSU	O4-C4	-2.42	1.19	1.23
38	1	10	2MG	C6-N1	2.42	1.43	1.38
1	2	1289	PSU	O4-C4	-2.40	1.19	1.23
1	2	1426	2MG	C6-N1	2.38	1.43	1.38
1	2	1570	2MG	O6-C6	-2.35	1.19	1.23
38	1	26	M2G	O6-C6	-2.33	1.19	1.23
38	1	37	T6A	C2-N1	2.31	1.38	1.33
1	2	1780	MA6	C5-N7	-2.29	1.34	1.39
38	1	37	T6A	C6-N6	2.26	1.44	1.39
38	1	58	1MA	CM1-N1	-2.20	1.42	1.46
1	2	766	PSU	O2-C2	-2.15	1.18	1.23
1	2	766	PSU	O4'-C1'	-2.14	1.40	1.43
1	2	998	PSU	O2-C2	-2.11	1.18	1.23
1	2	1573	7MG	C5-C4	2.09	1.44	1.37
1	2	465	PSU	O2-C2	-2.08	1.18	1.23
1	2	120	PSU	O2-C2	-2.07	1.19	1.23
38	1	46	7MG	C5-C4	2.07	1.44	1.37
1	2	1780	MA6	C8-N9	-2.07	1.34	1.37
38	1	37	T6A	C5-C4	-2.05	1.35	1.39
1	2	1289	PSU	O2-C2	-2.01	1.19	1.23

All (149) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1780	MA6	N1-C6-N6	-12.34	101.82	116.86
1	2	1780	MA6	C5-C6-N6	8.20	138.32	125.33
38	1	58	1MA	C1'-N9-C8	-6.90	107.14	126.73
38	1	10	2MG	C2-N3-C4	6.72	120.41	112.00
38	1	9	1MG	C1'-N9-C4	-6.71	106.66	126.49
1	2	1426	2MG	C2-N3-C4	6.52	120.16	112.00
1	2	1570	2MG	C2-N3-C4	6.46	120.08	112.00
38	1	9	1MG	C1'-N9-C8	6.28	144.56	126.73
38	1	58	1MA	C1'-N9-C4	5.96	144.10	126.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	37	T6A	N3-C2-N1	-5.71	119.94	128.58
1	2	1780	MA6	N1-C2-N3	-5.67	120.00	128.58
38	1	10	2MG	C5-C4-N3	-5.49	119.65	128.39
1	2	1570	2MG	C5-C4-N3	-5.45	119.71	128.39
1	2	1426	2MG	C5-C4-N3	-5.43	119.74	128.39
38	1	26	M2G	C5-C4-N3	-5.33	119.91	128.39
1	2	1190	B8N	C5-C4-N3	5.14	125.48	116.15
38	1	9	1MG	C5-C4-N3	-5.12	120.24	128.39
38	1	46	7MG	C5-C6-N1	5.10	119.92	110.94
38	1	58	1MA	N1-C2-N3	-5.10	119.93	126.00
38	1	37	T6A	C12-N11-C10	5.07	130.41	121.99
38	1	58	1MA	C5-C4-N3	-4.98	119.93	127.27
1	2	1573	7MG	C5-C6-N1	4.98	119.71	110.94
38	1	37	T6A	C5-C4-N3	-4.90	119.97	126.72
1	2	120	PSU	C4-N3-C2	-4.78	119.78	126.37
38	1	46	7MG	C2-N3-C4	4.75	120.49	112.30
1	2	1573	7MG	C2-N3-C4	4.74	120.47	112.30
1	2	1780	MA6	C5-C4-N3	-4.73	120.21	126.72
1	2	465	PSU	C4-N3-C2	-4.73	119.86	126.37
1	2	998	PSU	C4-N3-C2	-4.71	119.89	126.37
1	2	1289	PSU	C4-N3-C2	-4.63	119.99	126.37
1	2	766	PSU	C4-N3-C2	-4.61	120.02	126.37
1	2	766	PSU	N1-C2-N3	4.44	119.86	115.17
1	2	465	PSU	N1-C2-N3	4.43	119.84	115.17
1	2	998	PSU	N1-C2-N3	4.43	119.84	115.17
1	2	1190	B8N	C1'-C5-C4	4.39	124.27	117.61
1	2	120	PSU	N1-C2-N3	4.36	119.77	115.17
1	2	1190	B8N	C4-N3-C2	-4.36	120.25	125.62
1	2	1780	MA6	N9-C8-N7	-4.36	107.76	113.94
1	2	1573	7MG	C5-C4-N3	-4.35	119.96	128.13
38	1	26	M2G	C2-N3-C4	4.27	120.41	112.51
38	1	37	T6A	N6-C10-N11	4.26	119.63	113.77
38	1	37	T6A	C4-C5-C6	4.23	120.29	116.78
38	1	46	7MG	C5-C4-N3	-4.21	120.23	128.13
38	1	10	2MG	C2-N1-C6	-4.14	119.55	124.55
38	1	37	T6A	N9-C8-N7	-4.13	108.08	113.94
1	2	1570	2MG	C2-N1-C6	-4.04	119.67	124.55
1	2	1289	PSU	N1-C2-N3	4.04	119.42	115.17
1	2	1426	2MG	C2-N1-C6	-4.01	119.71	124.55
38	1	58	1MA	C2-N3-C4	3.93	120.23	112.53
38	1	46	7MG	C4-C5-N7	3.78	109.84	105.38
1	2	1573	7MG	C4-C5-N7	3.78	109.84	105.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1780	MA6	C4-C5-C6	3.76	119.80	115.91
38	1	48	5MC	C5-C6-N1	-3.64	119.36	123.31
38	1	9	1MG	C2-N3-C4	3.59	120.05	111.98
1	2	1570	2MG	N9-C4-N3	3.48	132.92	125.95
38	1	37	T6A	O10-C10-N6	-3.43	117.54	123.64
1	2	1780	MA6	C2-N1-C6	3.41	120.16	111.83
1	2	766	PSU	C6-N1-C2	-3.39	119.55	122.69
1	2	998	PSU	C6-N1-C2	-3.39	119.55	122.69
38	1	16	H2U	N3-C2-N1	3.36	120.03	116.65
38	1	47	H2U	N3-C2-N1	3.35	120.01	116.65
1	2	1190	B8N	N3-C2-N1	3.34	120.80	116.72
1	2	1780	MA6	C2-N3-C4	3.33	119.97	111.83
38	1	10	2MG	N9-C4-N3	3.33	132.61	125.95
38	1	37	T6A	C2-N3-C4	3.33	119.96	111.83
38	1	10	2MG	N1-C2-N2	3.32	119.95	116.56
1	2	998	PSU	C6-C5-C4	3.31	120.41	118.17
38	1	9	1MG	N9-C8-N7	-3.27	107.33	113.40
1	2	1426	2MG	N9-C4-N3	3.27	132.50	125.95
38	1	9	1MG	N9-C4-N3	3.23	132.42	125.95
38	1	26	M2G	N9-C4-N3	3.23	132.42	125.95
1	2	1006	5MC	C5-C6-N1	-3.23	119.81	123.31
1	2	1573	7MG	C5-C4-N9	3.21	110.45	106.33
38	1	58	1MA	N9-C8-N7	-3.20	107.47	113.40
38	1	46	7MG	C5-C4-N9	3.19	110.42	106.33
1	2	465	PSU	C6-N1-C2	-3.18	119.74	122.69
1	2	766	PSU	C6-C5-C4	3.17	120.31	118.17
1	2	120	PSU	C6-N1-C2	-3.11	119.80	122.69
1	2	120	PSU	C6-C5-C4	3.09	120.26	118.17
38	1	47	H2U	C5-C6-N1	3.06	120.77	111.52
1	2	465	PSU	C6-C5-C4	3.05	120.23	118.17
38	1	16	H2U	C5-C4-N3	2.97	119.85	116.69
38	1	37	T6A	C5-N7-C8	2.93	108.05	103.45
1	2	1289	PSU	C6-N1-C2	-2.92	119.98	122.69
1	2	1780	MA6	C5-N7-C8	2.90	108.01	103.45
38	1	46	7MG	O6-C6-C5	-2.90	120.51	127.62
38	1	16	H2U	C5-C6-N1	2.89	120.27	111.52
1	2	1780	MA6	N3-C4-N9	2.88	132.06	127.17
38	1	26	M2G	N9-C8-N7	-2.87	108.08	113.40
1	2	1190	B8N	O4-C4-N3	-2.86	115.34	119.99
1	2	1570	2MG	N9-C8-N7	-2.83	108.15	113.40
38	1	37	T6A	N3-C4-N9	2.83	131.98	127.17
38	1	9	1MG	C5-C6-N1	2.83	120.25	115.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1573	7MG	N9-C4-N3	2.82	129.59	125.46
1	2	998	PSU	O2-C2-N1	-2.81	119.89	122.79
1	2	1570	2MG	N1-C2-N2	2.81	119.43	116.56
1	2	1426	2MG	N1-C2-N2	2.80	119.42	116.56
38	1	47	H2U	C5-C4-N3	2.80	119.67	116.69
38	1	10	2MG	N9-C8-N7	-2.80	108.22	113.40
38	1	46	7MG	C2-N1-C6	-2.79	120.05	125.11
1	2	1573	7MG	C2-N1-C6	-2.77	120.08	125.11
1	2	1573	7MG	O6-C6-C5	-2.75	120.88	127.62
38	1	26	M2G	O6-C6-C5	-2.74	119.29	126.53
38	1	26	M2G	C5-C6-N1	2.67	120.06	113.25
1	2	766	PSU	O2-C2-N1	-2.67	120.04	122.79
38	1	10	2MG	C5-C6-N1	2.67	120.04	113.25
38	1	46	7MG	N9-C4-N3	2.65	129.34	125.46
1	2	465	PSU	O2-C2-N1	-2.63	120.08	122.79
1	2	1426	2MG	N9-C8-N7	-2.61	108.55	113.40
38	1	58	1MA	N9-C4-N3	2.59	132.80	126.90
1	2	1570	2MG	C5-C6-N1	2.57	119.80	113.25
1	2	1637	5MC	C5-C6-N1	-2.57	120.52	123.31
1	2	1426	2MG	C5-C6-N1	2.57	119.79	113.25
1	2	1570	2MG	O6-C6-C5	-2.57	119.76	126.53
38	1	49	5MC	O2-C2-N3	-2.56	118.30	122.33
1	2	1780	MA6	C4-N9-C8	2.55	108.42	105.74
1	2	120	PSU	O2-C2-N1	-2.53	120.18	122.79
38	1	16	H2U	O2-C2-N1	-2.53	120.06	123.10
38	1	10	2MG	O6-C6-C5	-2.49	119.97	126.53
1	2	1573	7MG	N9-C8-N7	2.48	106.89	103.37
1	2	1426	2MG	O6-C6-C5	-2.43	120.11	126.53
1	2	1289	PSU	C6-C5-C4	2.38	119.78	118.17
38	1	37	T6A	C4-C5-N7	-2.35	107.90	110.58
38	1	46	7MG	N9-C8-N7	2.32	106.66	103.37
1	2	1289	PSU	O2-C2-N1	-2.28	120.43	122.79
1	2	1426	2MG	CM2-N2-C2	-2.28	118.75	123.65
38	1	58	1MA	C8-N7-C5	2.28	108.32	104.26
38	1	9	1MG	C8-N7-C5	2.27	108.31	104.26
1	2	1190	B8N	C31-N3-C4	2.26	120.38	117.18
1	2	1006	5MC	CM5-C5-C6	-2.24	119.82	122.85
38	1	49	5MC	C5-C6-N1	-2.22	120.90	123.31
1	2	998	PSU	O4'-C1'-C2'	2.20	108.19	105.15
1	2	1780	MA6	C4-C5-N7	-2.19	108.08	110.58
38	1	48	5MC	C5-C4-N4	-2.18	118.32	121.39
1	2	1637	5MC	C5-C4-N3	-2.16	119.54	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	1	10	2MG	N1-C2-N3	-2.15	120.06	123.68
1	2	766	PSU	O4'-C1'-C2'	2.14	108.11	105.15
38	1	49	5MC	C5-C4-N3	-2.12	119.58	121.75
1	2	1426	2MG	N1-C2-N3	-2.11	120.13	123.68
1	2	1570	2MG	C8-N7-C5	2.11	108.01	104.26
1	2	1190	B8N	O4'-C1'-C2'	2.10	108.06	105.15
1	2	1570	2MG	N1-C2-N3	-2.10	120.15	123.68
1	2	1006	5MC	C5-C4-N3	-2.09	119.61	121.75
38	1	37	T6A	N6-C6-N1	2.09	122.96	117.54
38	1	10	2MG	C8-N7-C5	2.09	107.99	104.26
38	1	37	T6A	C4-N9-C8	2.08	107.92	105.74
38	1	26	M2G	C8-N7-C5	2.06	107.94	104.26
38	1	49	5MC	C1'-N1-C2	2.06	122.99	118.44
38	1	37	T6A	C5-C4-N9	2.06	108.05	105.81

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	998	PSU	O4'-C4'-C5'-O5'
1	2	1780	MA6	O4'-C4'-C5'-O5'
38	1	9	1MG	O4'-C4'-C5'-O5'
38	1	16	H2U	C4'-C5'-O5'-P
38	1	37	T6A	C14-C12-N11-C10
38	1	47	H2U	C4'-C5'-O5'-P
38	1	47	H2U	C3'-C4'-C5'-O5'
38	1	48	5MC	C4'-C5'-O5'-P
38	1	48	5MC	O4'-C4'-C5'-O5'
38	1	48	5MC	C3'-C4'-C5'-O5'
38	1	49	5MC	O4'-C4'-C5'-O5'
38	1	64	RIA	C4A-C5A-O5A-P
1	2	1190	B8N	O4'-C4'-C5'-O5'
1	2	1573	7MG	C3'-C4'-C5'-O5'
38	1	9	1MG	C3'-C4'-C5'-O5'
38	1	49	5MC	C3'-C4'-C5'-O5'
1	2	1573	7MG	O4'-C4'-C5'-O5'
38	1	47	H2U	O4'-C4'-C5'-O5'
38	1	64	RIA	O4'-C4A-C5A-O5A
1	2	1780	MA6	C3'-C4'-C5'-O5'
1	2	998	PSU	C3'-C4'-C5'-O5'
38	1	64	RIA	C3A-C4A-C5A-O5A
1	2	1190	B8N	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	2	1190	B8N	N34-C33-C34-O36
38	1	16	H2U	C2'-C1'-N1-C6
1	2	1190	B8N	C31-C32-C33-N34
38	1	64	RIA	C4'-C5'-O5'-P'
38	1	46	7MG	C4'-C5'-O5'-P
1	2	766	PSU	C3'-C4'-C5'-O5'
1	2	1190	B8N	N34-C33-C34-O35
38	1	10	2MG	O4'-C4'-C5'-O5'
38	1	47	H2U	C2'-C1'-N1-C6
1	2	998	PSU	C4'-C5'-O5'-P
1	2	1780	MA6	C4'-C5'-O5'-P
38	1	16	H2U	O4'-C1'-N1-C2
38	1	16	H2U	C3'-C4'-C5'-O5'
38	1	49	5MC	C2'-C1'-N1-C6
38	1	64	RIA	C2A-C1A-N9-C8
38	1	16	H2U	C2'-C1'-N1-C2
38	1	64	RIA	C2A-C1A-N9-C4
38	1	49	5MC	C2'-C1'-N1-C2

There are no ring outliers.

14 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	1637	5MC	1	0
38	1	48	5MC	1	0
1	2	1006	5MC	1	0
1	2	1289	PSU	1	0
1	2	1573	7MG	1	0
38	1	16	H2U	1	0
1	2	120	PSU	1	0
38	1	49	5MC	1	0
1	2	1426	2MG	1	0
38	1	47	H2U	2	0
38	1	46	7MG	1	0
1	2	998	PSU	1	0
38	1	64	RIA	3	0
38	1	37	T6A	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 121 ligands modelled in this entry, 119 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
44	GCP	k	601	-	32,34,34	3.19	12 (37%)	49,54,54	1.71	11 (22%)
45	MET	k	603	-	6,7,8	0.48	0	2,7,9	0.22	0

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
44	GCP	k	601	-	-	2/19/38/38	0/3/3/3
45	MET	k	603	-	-	0/5/6/8	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	k	601	GCP	O4'-C1'	8.72	1.62	1.42
44	k	601	GCP	C2'-C1'	-7.10	1.31	1.53
44	k	601	GCP	O4'-C4'	-6.33	1.30	1.45
44	k	601	GCP	PB-O3A	6.23	1.65	1.58
44	k	601	GCP	PA-O3A	5.45	1.65	1.59
44	k	601	GCP	C2-N2	4.86	1.45	1.34
44	k	601	GCP	C6-N1	-3.24	1.32	1.38
44	k	601	GCP	O2'-C2'	2.82	1.49	1.43
44	k	601	GCP	O3'-C3'	-2.75	1.36	1.43
44	k	601	GCP	O6-C6	-2.48	1.18	1.23
44	k	601	GCP	C5-N7	-2.34	1.34	1.39
44	k	601	GCP	PB-O2B	-2.01	1.51	1.56

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	k	601	GCP	C5-C4-N3	-5.35	119.88	128.39
44	k	601	GCP	C2-N3-C4	4.51	120.06	112.30
44	k	601	GCP	N9-C4-N3	3.07	132.09	125.95
44	k	601	GCP	N9-C8-N7	-2.95	107.93	113.40
44	k	601	GCP	C4'-O4'-C1'	-2.92	103.01	109.47
44	k	601	GCP	C2-N1-C6	-2.85	119.93	125.11
44	k	601	GCP	C5-C6-N1	2.66	120.02	113.25
44	k	601	GCP	PB-O3A-PA	-2.58	123.97	132.37
44	k	601	GCP	O6-C6-C5	-2.46	120.04	126.53
44	k	601	GCP	C8-N7-C5	2.21	108.20	104.26
44	k	601	GCP	C3'-C2'-C1'	2.11	105.45	101.46

There are no chirality outliers.

All (2) torsion outliers are listed below:

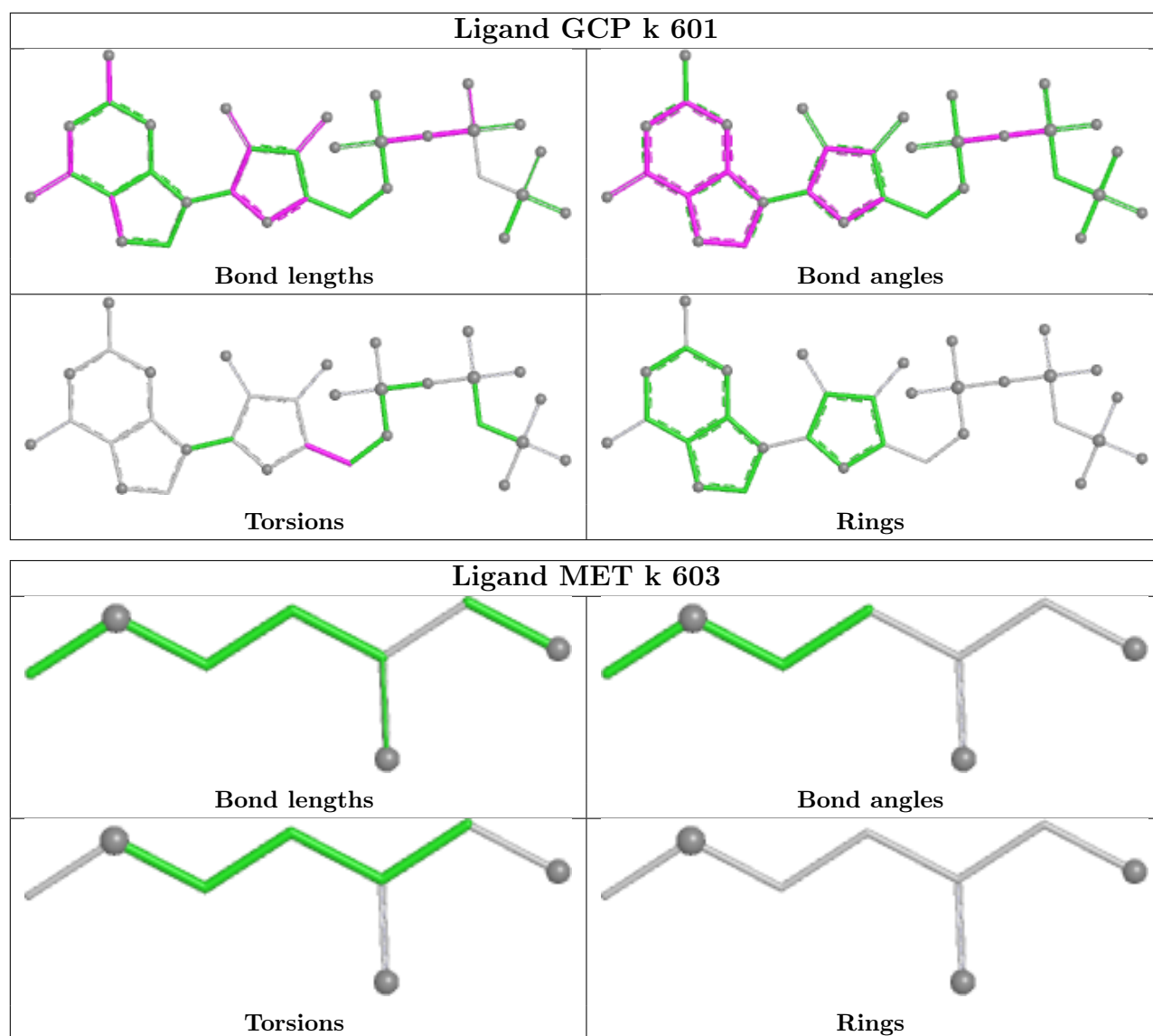
Mol	Chain	Res	Type	Atoms
44	k	601	GCP	O4'-C4'-C5'-O5'
44	k	601	GCP	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	k	601	GCP	3	0
45	k	603	MET	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

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	9.21
1	1	16:H2U	O3'	18:G	P	3.56
1	1	63:G	O3'	64:RIA	P	3.47

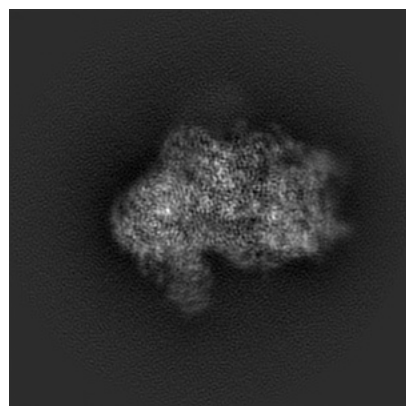
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19801. These allow visual inspection of the internal detail of the map and identification of artifacts.

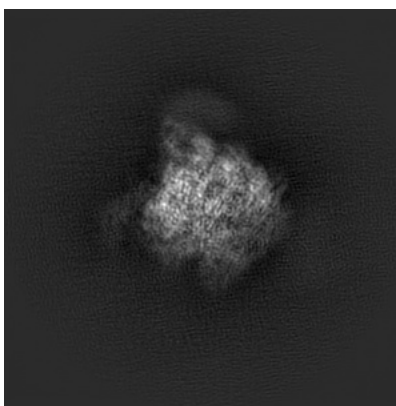
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

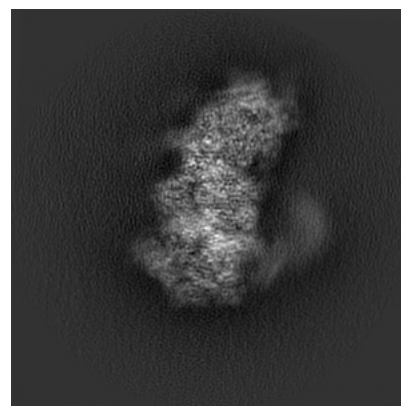
6.1.1 Primary map



X

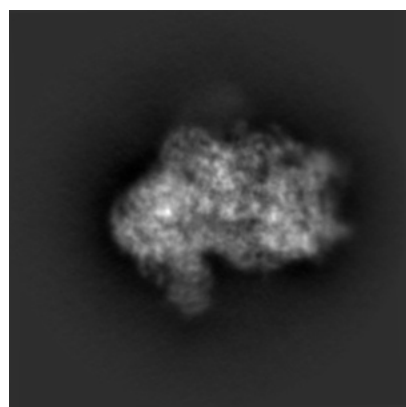


Y

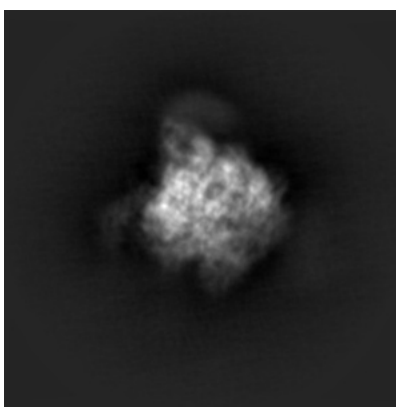


Z

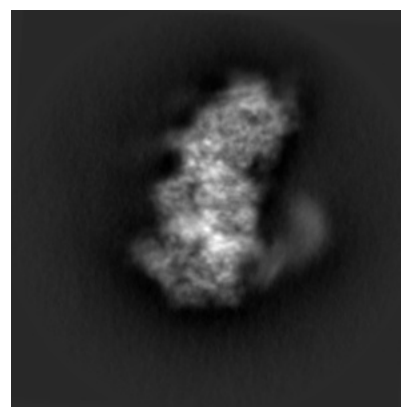
6.1.2 Raw map



X



Y

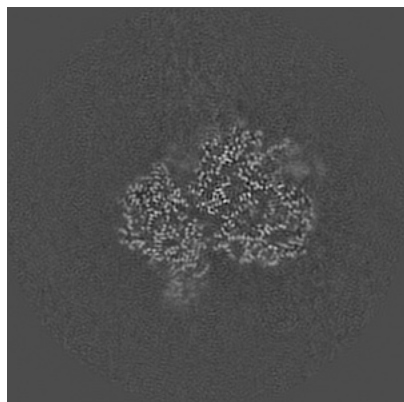


Z

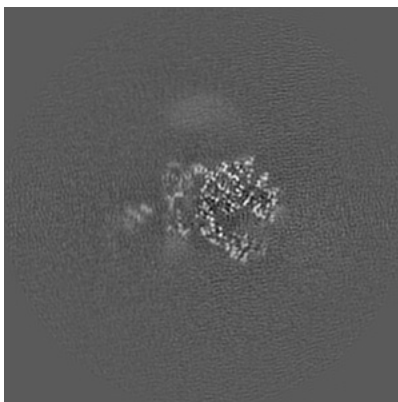
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

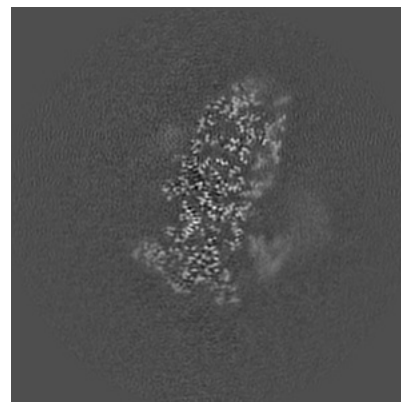
6.2.1 Primary map



X Index: 150

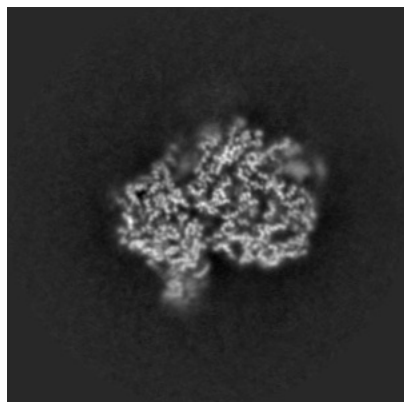


Y Index: 150

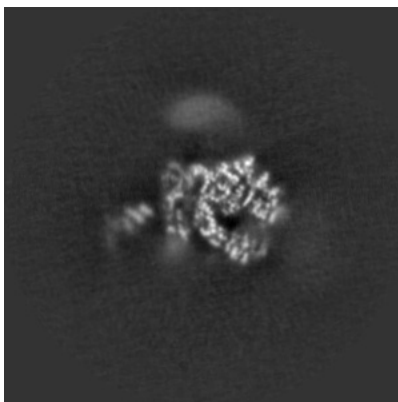


Z Index: 150

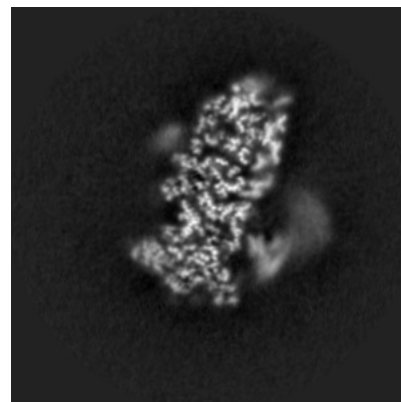
6.2.2 Raw map



X Index: 150



Y Index: 150

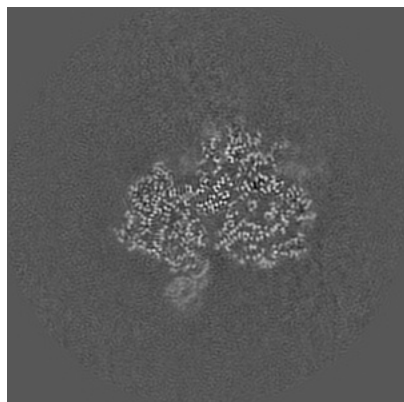


Z Index: 150

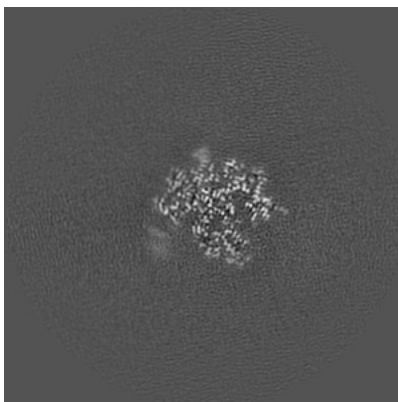
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

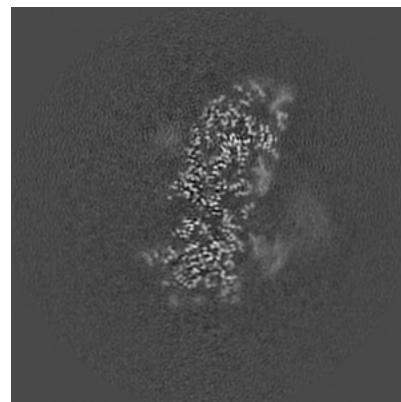
6.3.1 Primary map



X Index: 148

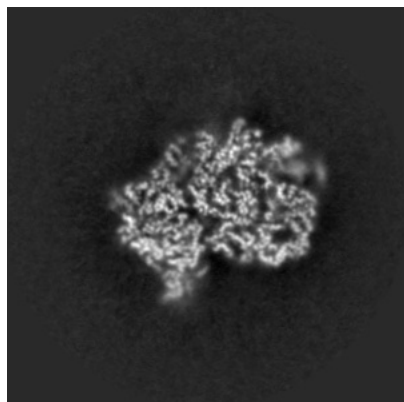


Y Index: 166

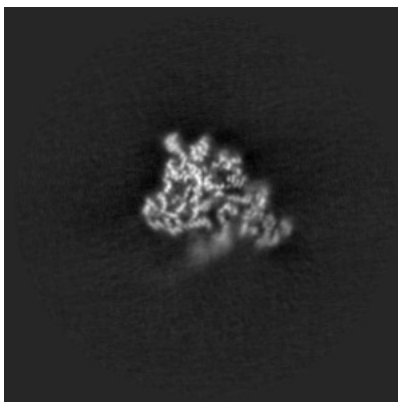


Z Index: 146

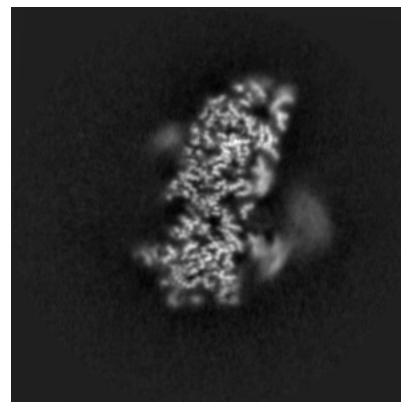
6.3.2 Raw map



X Index: 152



Y Index: 198

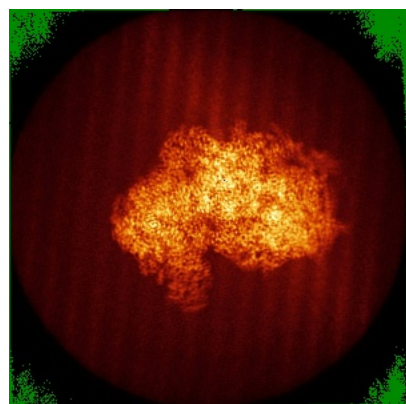


Z Index: 146

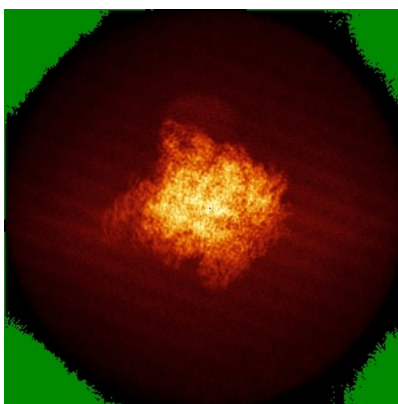
The images above show the largest variance slices of the map in three orthogonal directions.

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

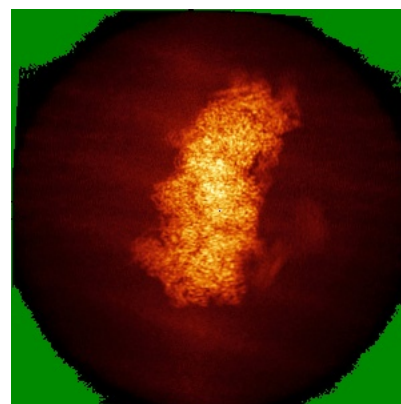
6.4.1 Primary map



X

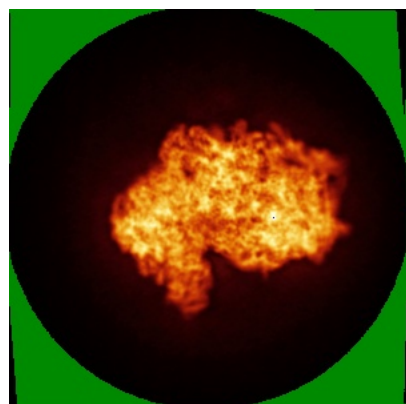


Y

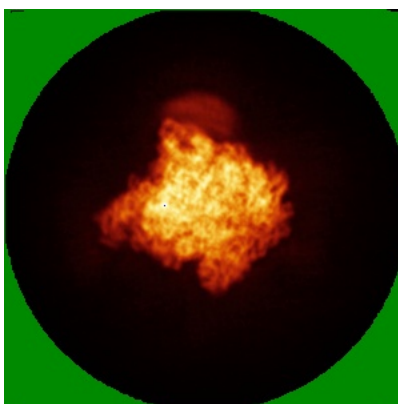


Z

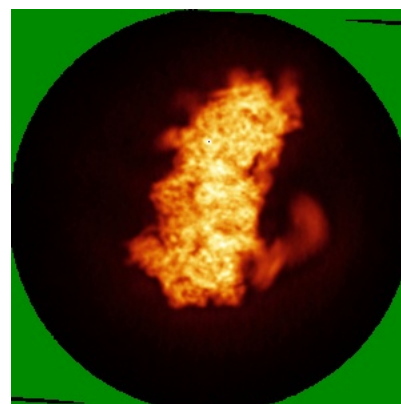
6.4.2 Raw map



X



Y

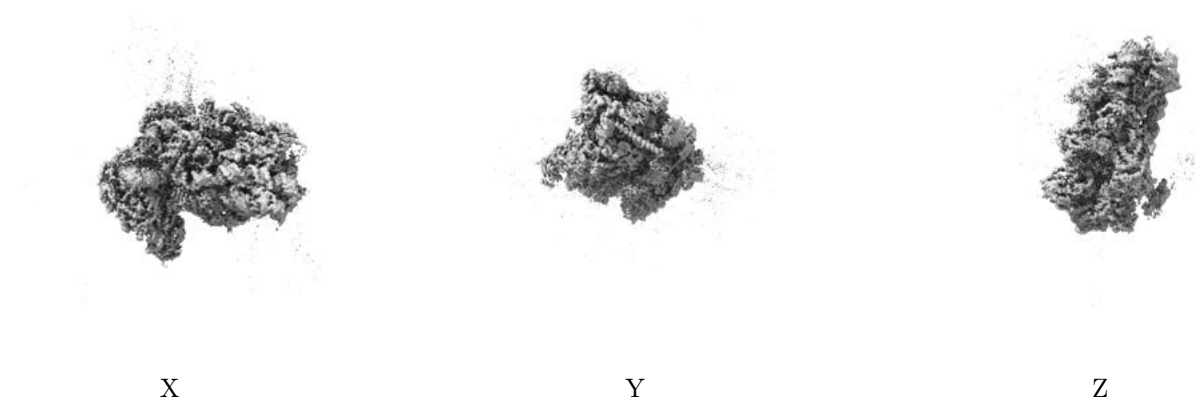


Z

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.

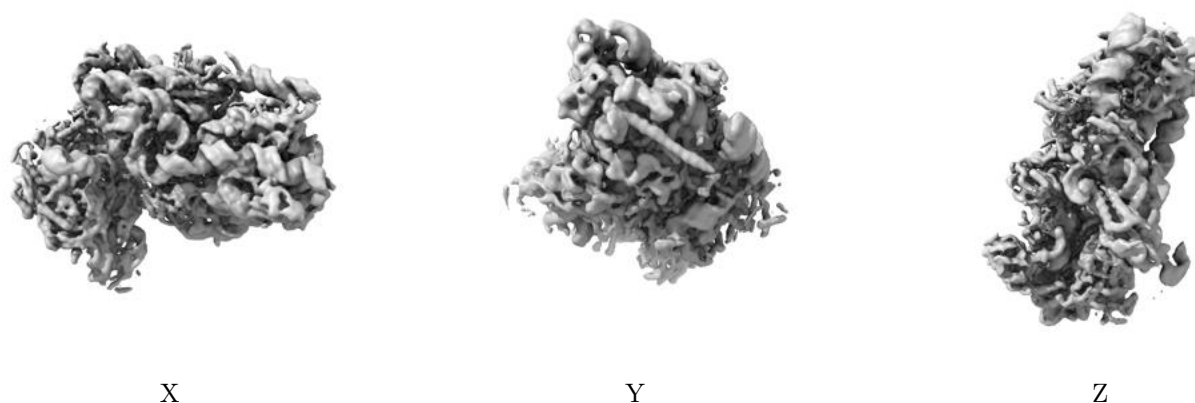
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

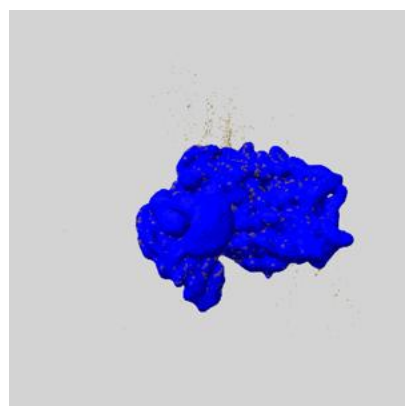
6.6 Mask visualisation [i](#)

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

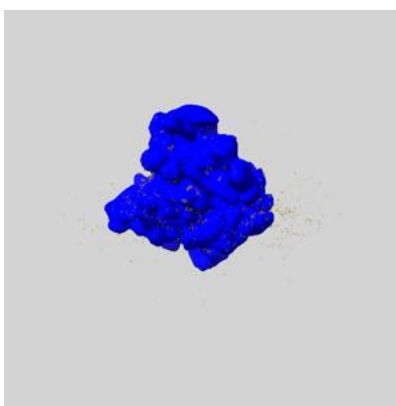
A mask typically either:

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

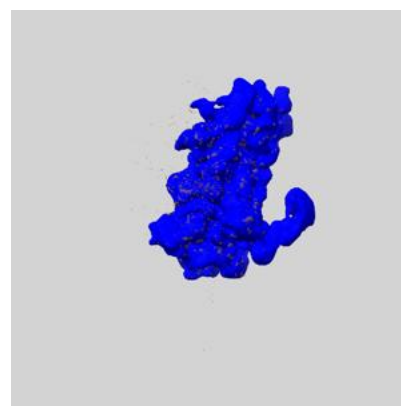
6.6.1 emd_19801_msk_1.map [i](#)



X



Y

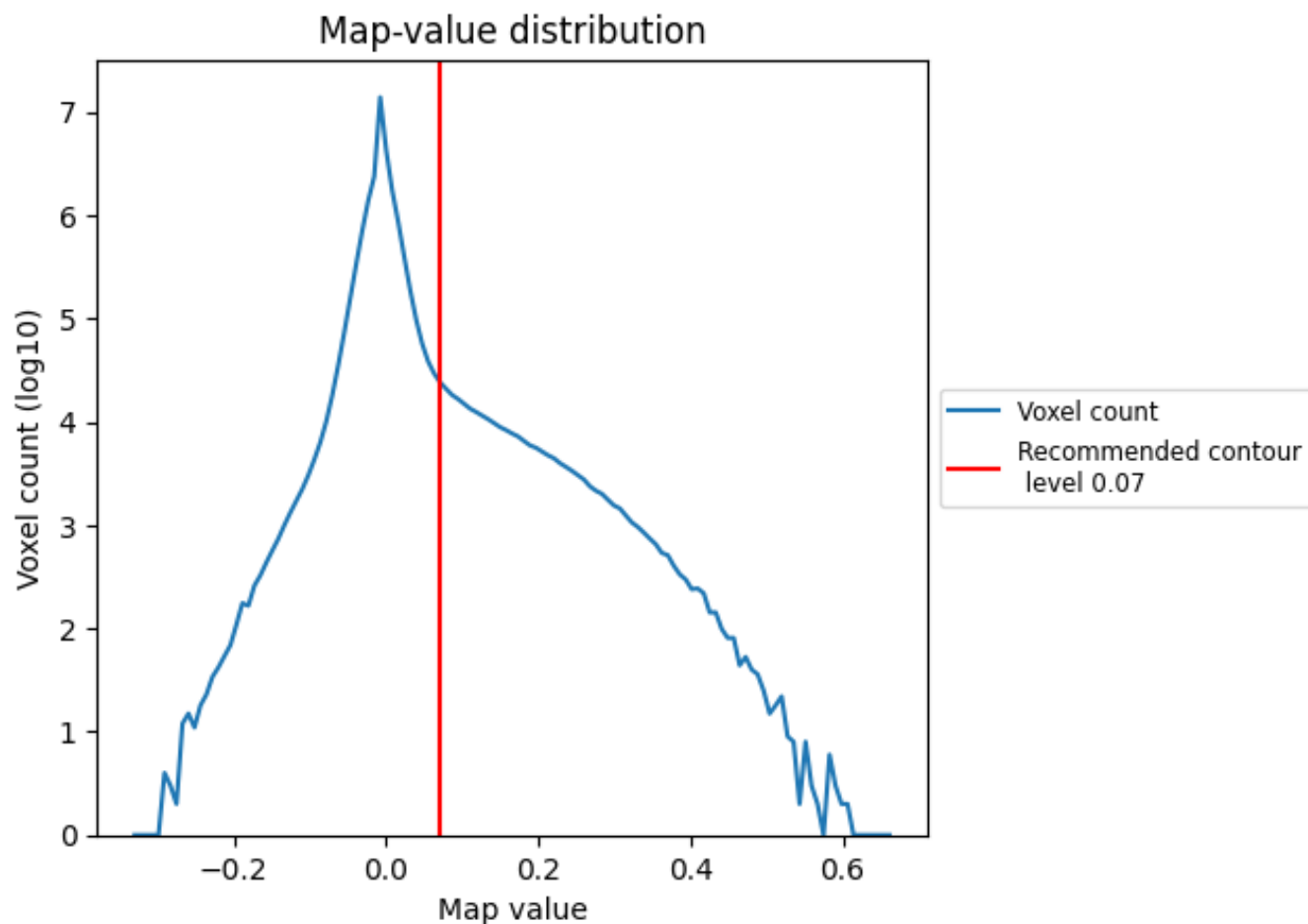


Z

7 Map analysis [i](#)

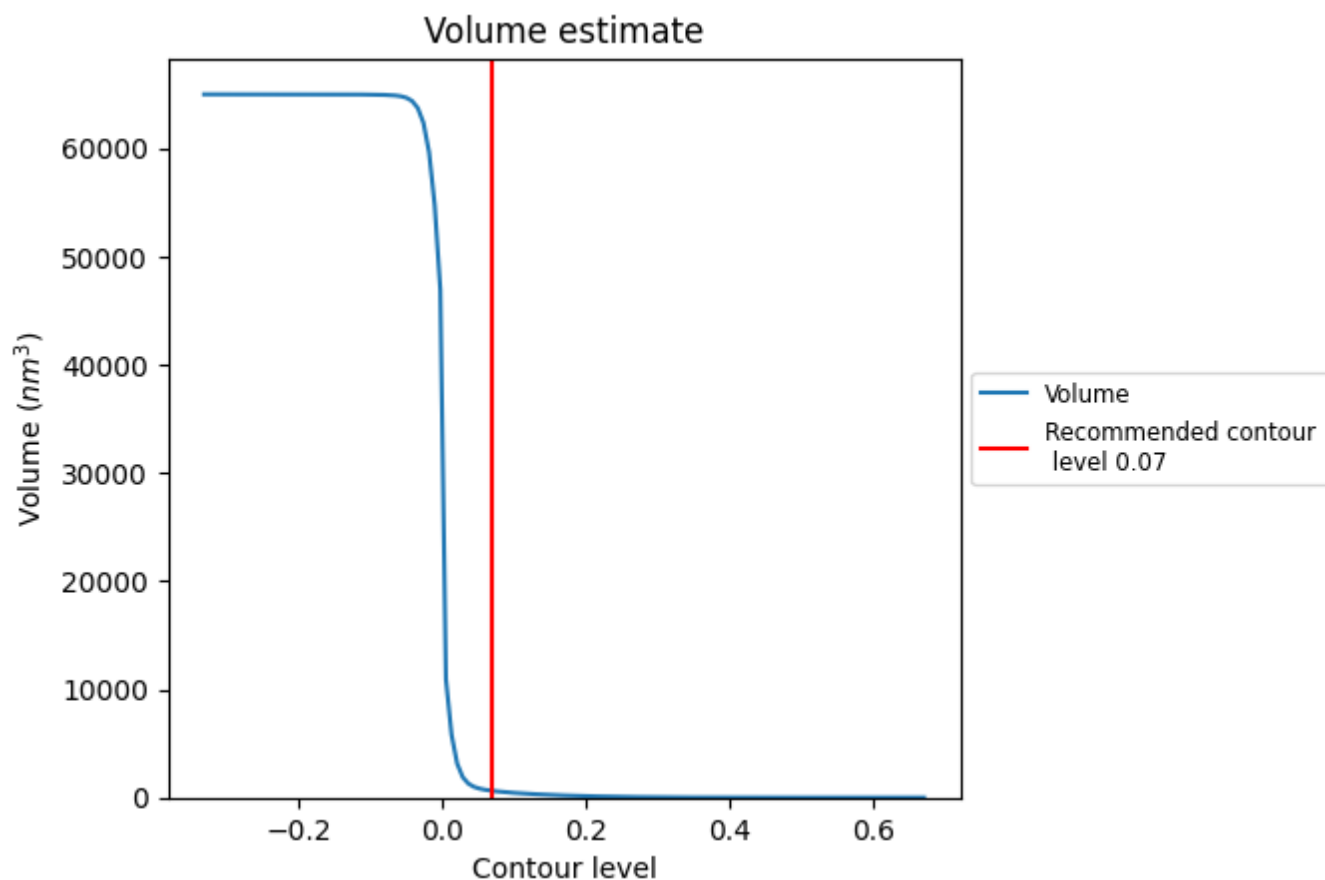
This section contains the results of statistical analysis of the map.

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.

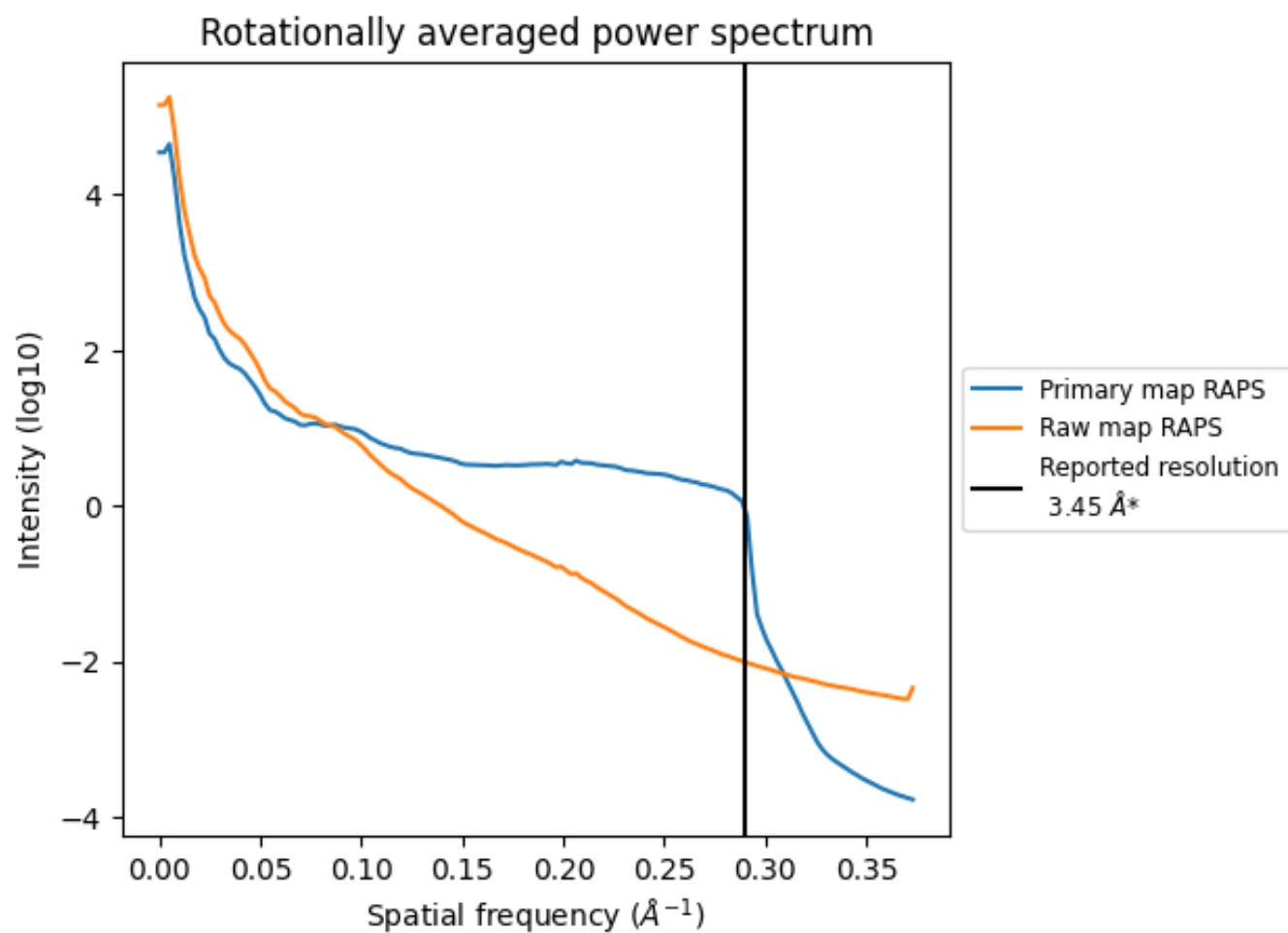
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 623 nm³; this corresponds to an approximate mass of 563 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 ⓘ

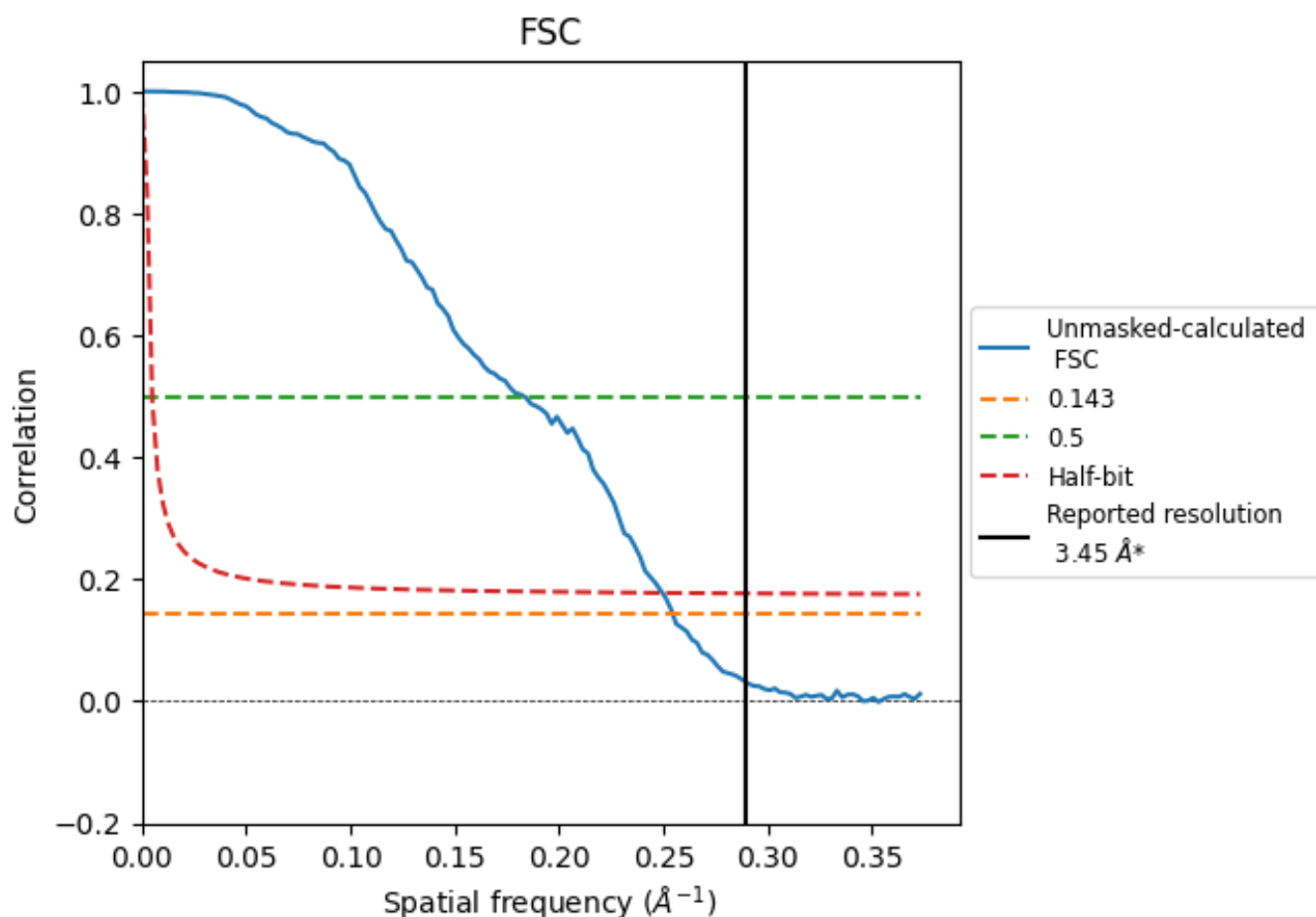


*Reported resolution corresponds to spatial frequency of 0.290 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.290 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

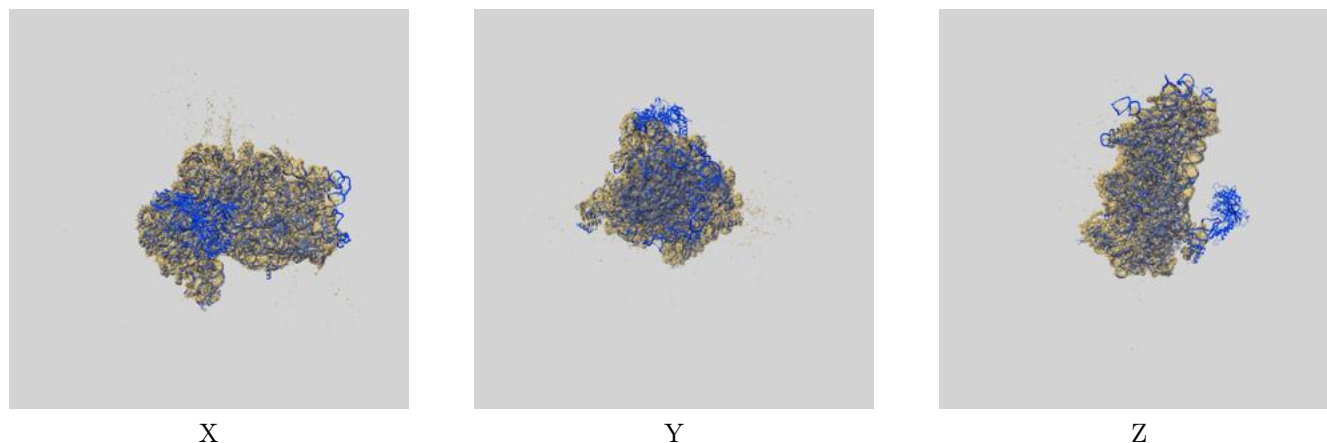
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.45	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.93	5.46	4.01

*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 3.93 differs from the reported value 3.45 by more than 10 %

9 Map-model fit [i](#)

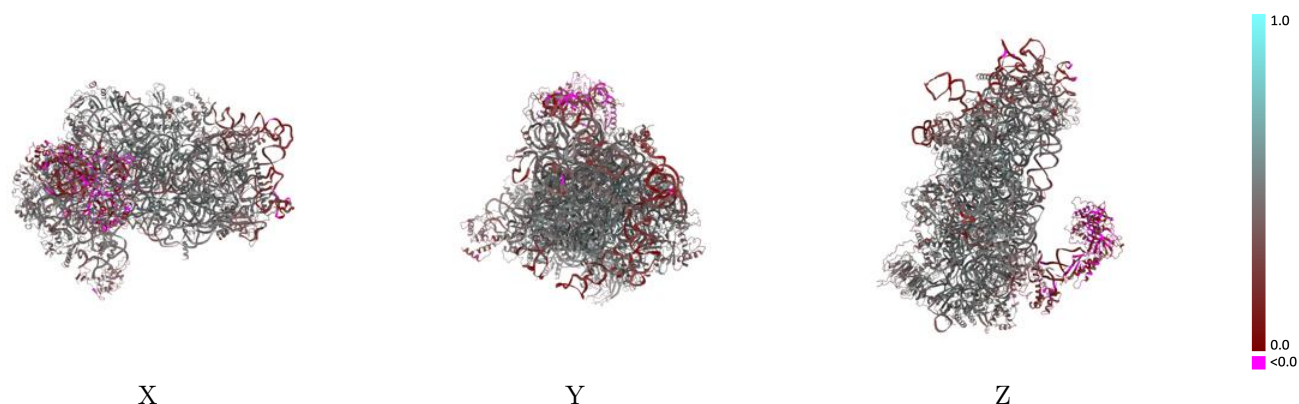
This section contains information regarding the fit between EMDB map EMD-19801 and PDB model 8S8D. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



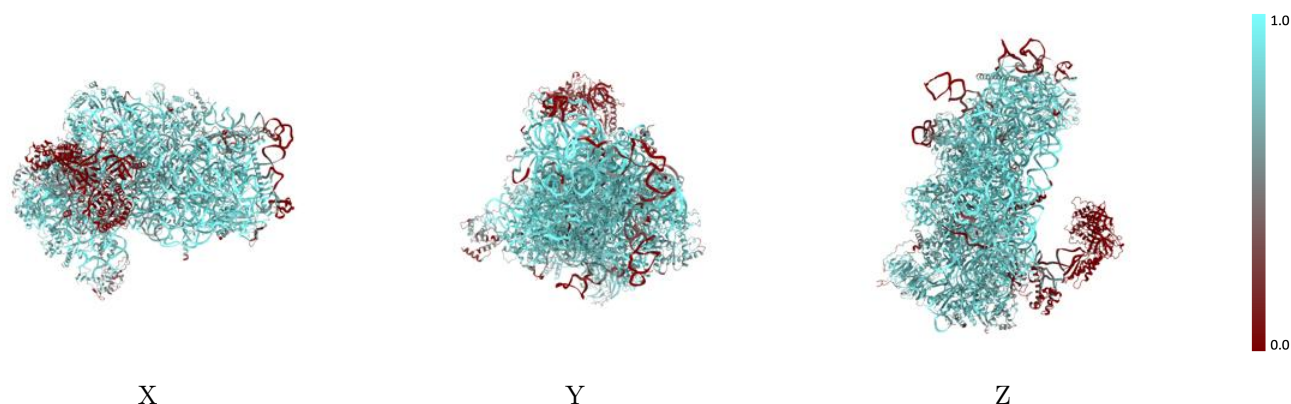
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



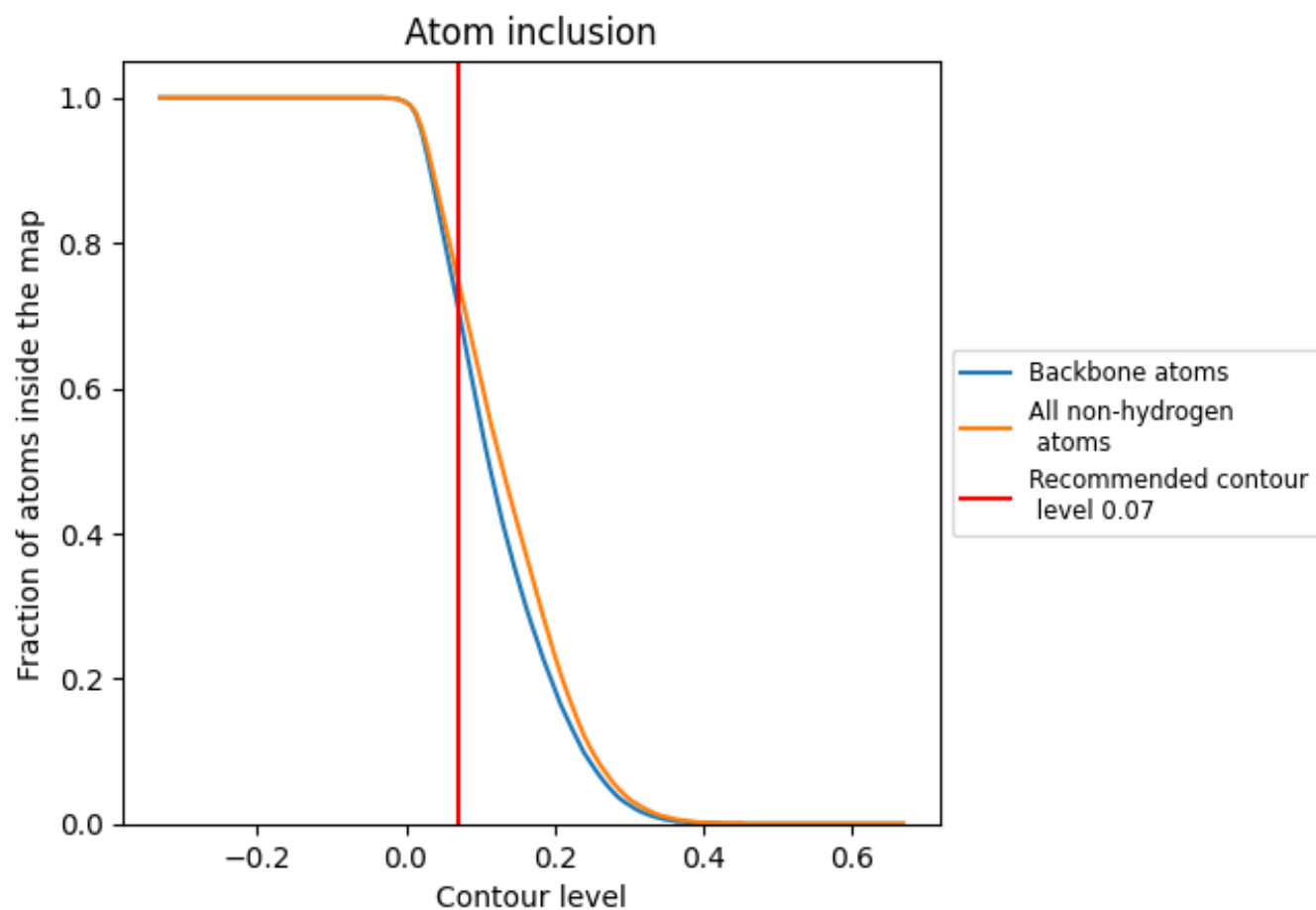
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 75% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7500	 0.4150
1	 0.5430	 0.2450
2	 0.8700	 0.4250
3	 0.3020	 0.3440
A	 0.8340	 0.4730
B	 0.7880	 0.4590
C	 0.8600	 0.5090
D	 0.7720	 0.4600
E	 0.8590	 0.4940
F	 0.7730	 0.4670
G	 0.7690	 0.4110
H	 0.6970	 0.4230
I	 0.7660	 0.4360
J	 0.8470	 0.4890
K	 0.7640	 0.4310
L	 0.7570	 0.4730
M	 0.3670	 0.2750
N	 0.8450	 0.4840
O	 0.8270	 0.4680
P	 0.8070	 0.4460
Q	 0.8550	 0.4730
R	 0.7290	 0.4400
S	 0.7880	 0.4350
T	 0.8590	 0.4700
U	 0.6980	 0.4350
V	 0.8790	 0.4880
W	 0.8560	 0.5080
X	 0.8090	 0.5000
Y	 0.8400	 0.4710
Z	 0.5660	 0.3660
a	 0.8400	 0.5000
b	 0.8240	 0.4840
c	 0.7520	 0.4890
d	 0.8690	 0.5090
e	 0.6860	 0.4520



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.5010	 0.3390
g	 0.7650	 0.4310
h	 0.1790	 0.4090
i	 0.3800	 0.4070
j	 0.0630	 0.1960
k	 0.0010	 0.1080
l	 0.0050	 0.0760