



Full wwPDB EM Validation Report ⓘ

Aug 3, 2026 – 10:46 AM EDT

PDB ID : 9OGY / pdb_00009ogy
EMDB ID : EMD-70479
Title : Megrivirus E 3' internal ribosome entry site (IRES) RNA core region bound to rabbit ribosome
Authors : Sherlock, M.E.; Kieft, J.S.
Deposited on : 2025-05-02
Resolution : 3.28 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:

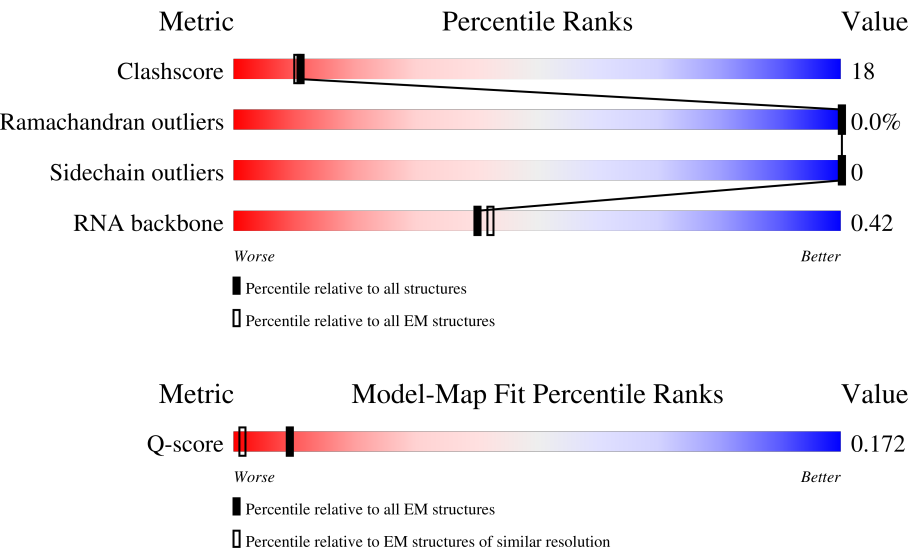
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.28 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	14492 (2.78 - 3.78)

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	1870	16% 31% 46% 13% 10%
2	A	270	28% 10% 19% 10% 60%
3	B	295	9% 36% 37% 26%

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Mol	Chain	Length	Quality of chain
4	C	264	
5	D	221	
6	E	281	
7	F	263	
8	G	204	
9	H	249	
10	I	432	
11	J	208	
12	K	194	
13	L	149	
14	M	158	
15	N	132	
16	O	151	
17	P	168	
18	Q	145	
19	R	172	
20	S	135	
21	T	152	
22	U	145	
23	V	119	
24	W	83	
25	X	130	
26	Y	143	
27	Z	131	
28	a	124	

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Mol	Chain	Length	Quality of chain
29	b	101	
30	c	84	
31	d	69	
32	e	56	
33	f	133	
34	g	188	
35	h	317	
36	n	25	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 77254 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	1680	Total	C	N	O	P	0	0
			35864	16009	6439	11737	1679		

- Molecule 2 is a RNA chain called Megrivirus E 3' IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	107	Total	C	N	O	P	0	0
			2280	1018	404	752	106		

- Molecule 3 is a protein called uS2 (SA).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 6 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 7 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	25	GLY	SER	conflict	UNP G1TK17
F	51	ARG	LYS	conflict	UNP G1TK17
F	78	THR	ALA	conflict	UNP G1TK17
F	156	VAL	MET	conflict	UNP G1TK17

- Molecule 8 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 9 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 10 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 11 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 12 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 13 is a protein called S10_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 14 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	151	Total	C	N	O	S	0	0
			1233	785	231	211	6		

- Molecule 15 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 16 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 17 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 18 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 19 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 20 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 21 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 22 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 23 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 24 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	3	ASN	SER	conflict	UNP G1TM82
W	4	ASP	ASN	conflict	UNP G1TM82
W	33	GLN	PRO	conflict	UNP G1TM82
W	50	PHE	SER	conflict	UNP G1TM82
W	75	ALA	SER	conflict	UNP G1TM82
W	76	ASP	HIS	conflict	UNP G1TM82
W	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 25 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 26 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 27 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 28 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	77	Total	C	N	O	S	0	0
			614	393	114	106	1		

- Molecule 29 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	28	ARG	CYS	conflict	UNP G1TFE8

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Chain	Residue	Modelled	Actual	Comment	Reference
b	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 30 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 31 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	67	Total	C	N	O	S	0	0
			530	321	108	99	2		

- Molecule 32 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 33 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 34 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 35 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 36 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

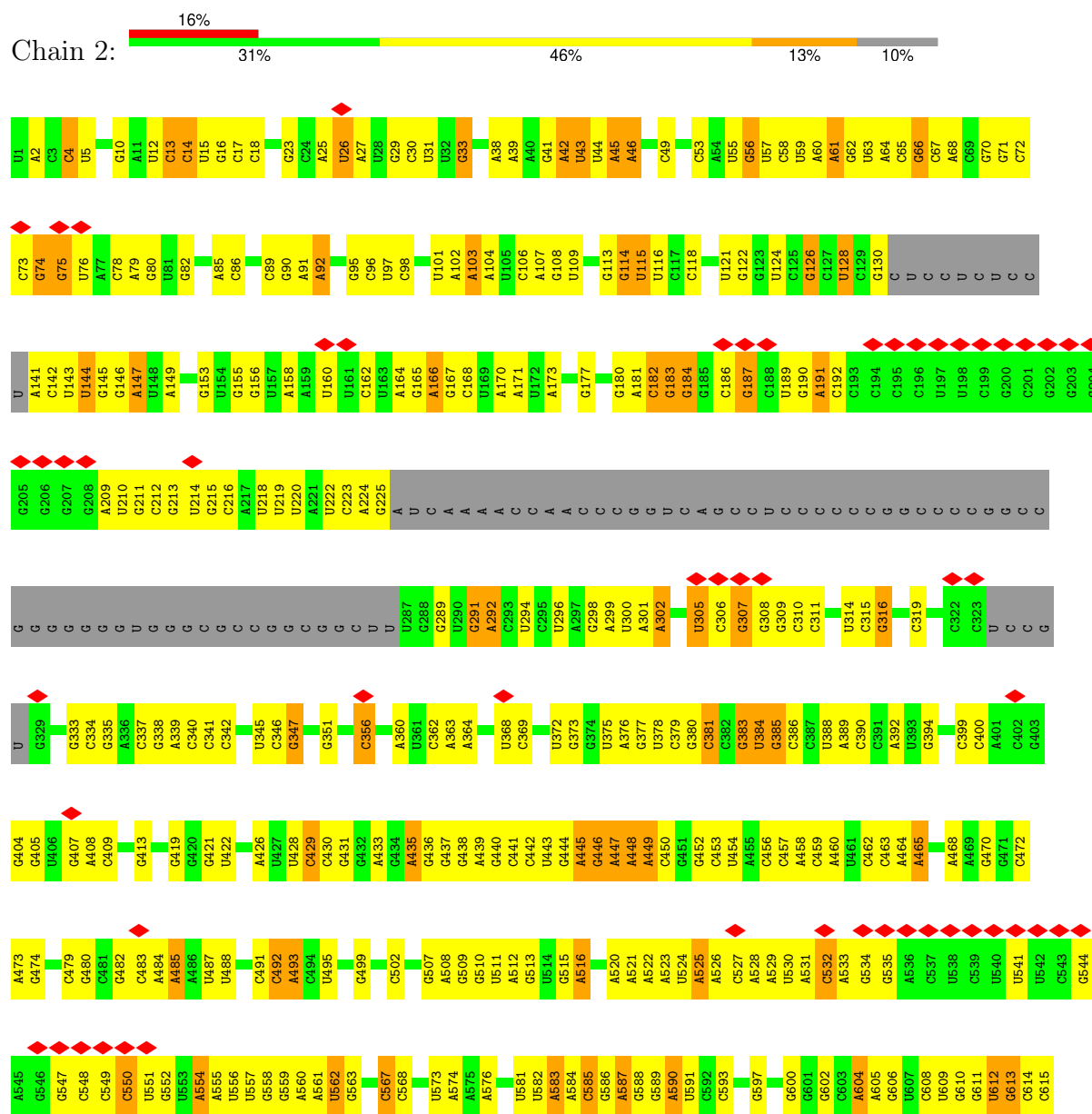
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	b	1	Total	Zn	0
			1	1	
37	g	1	Total	Zn	0
			1	1	

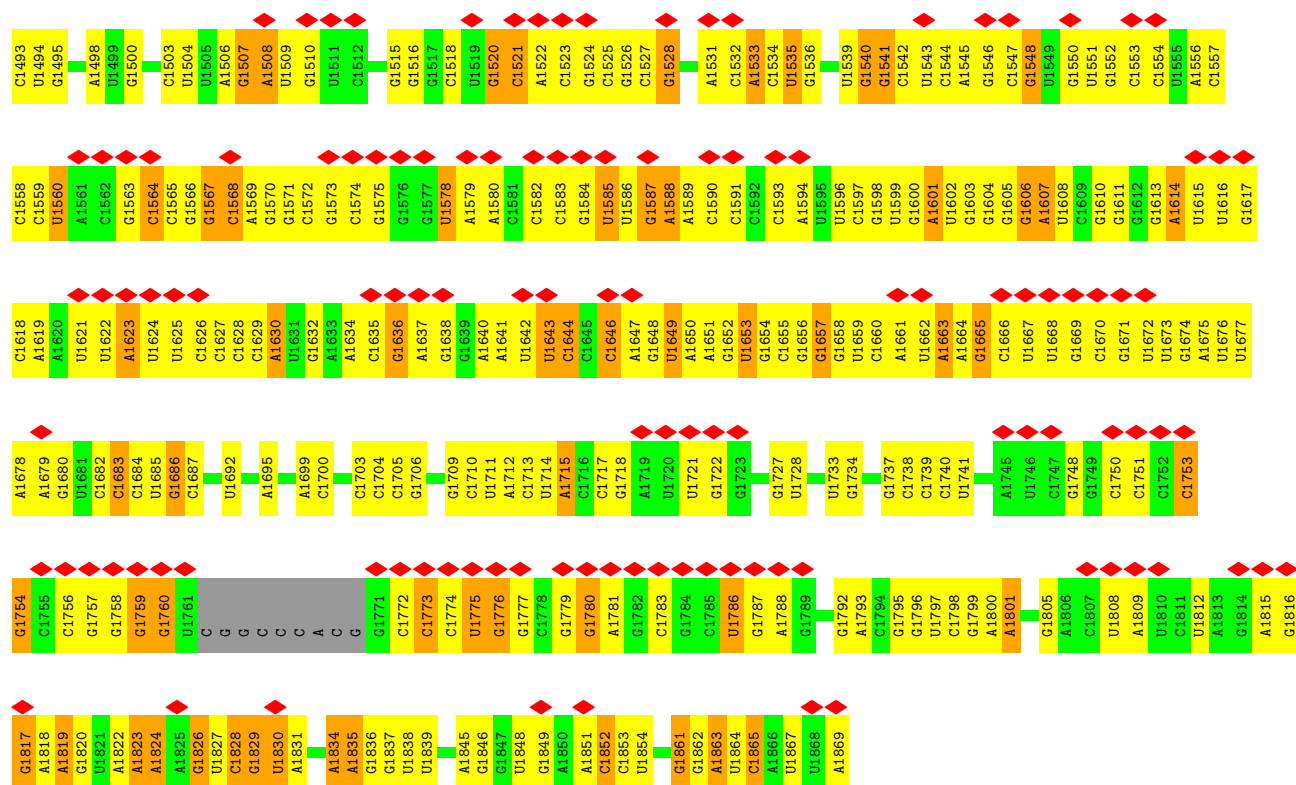
3 Residue-property plots

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

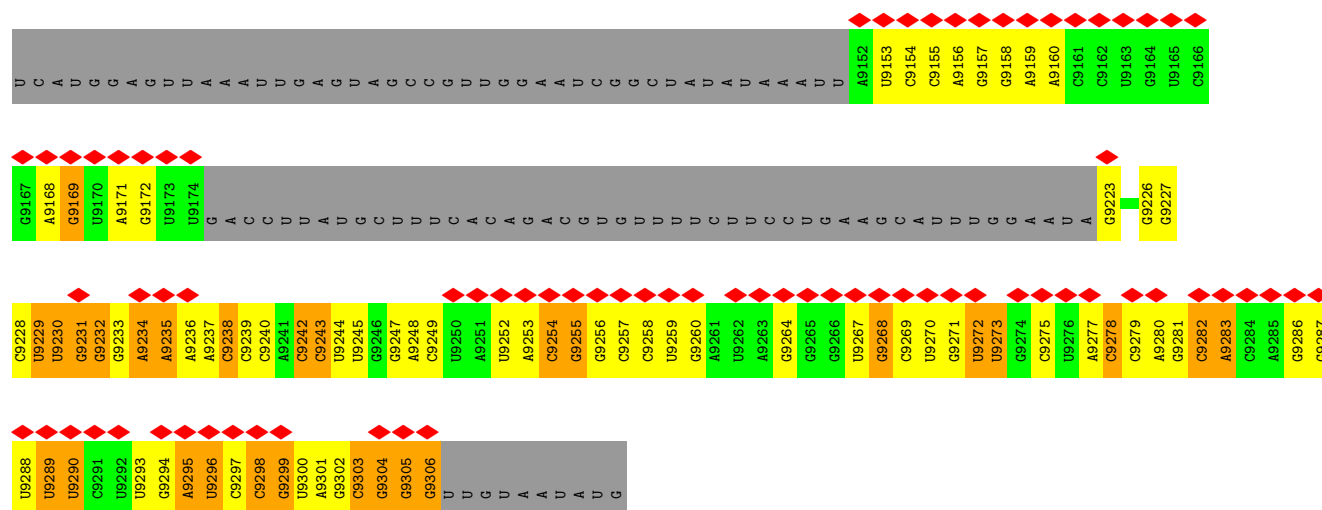
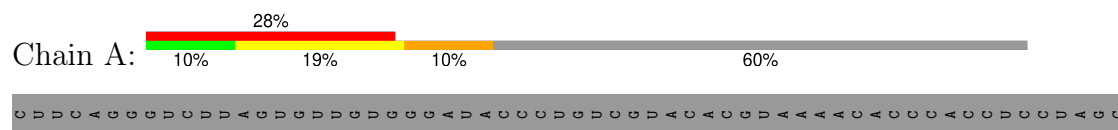
• Molecule 1: 18S ribosomal RNA







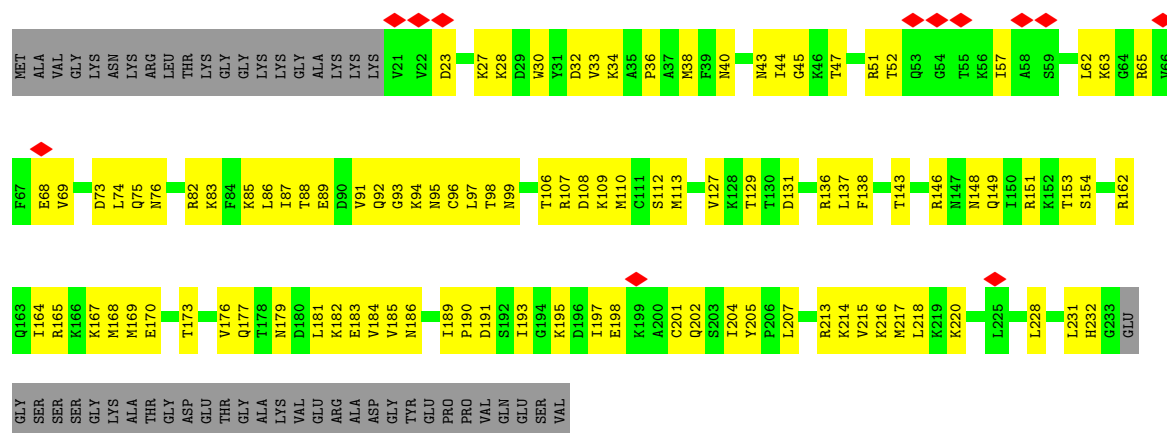
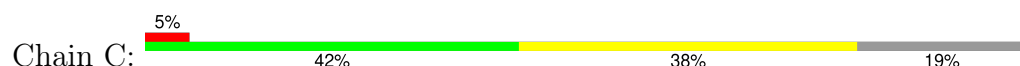
• Molecule 2: Megrivirus E 3' IRES RNA



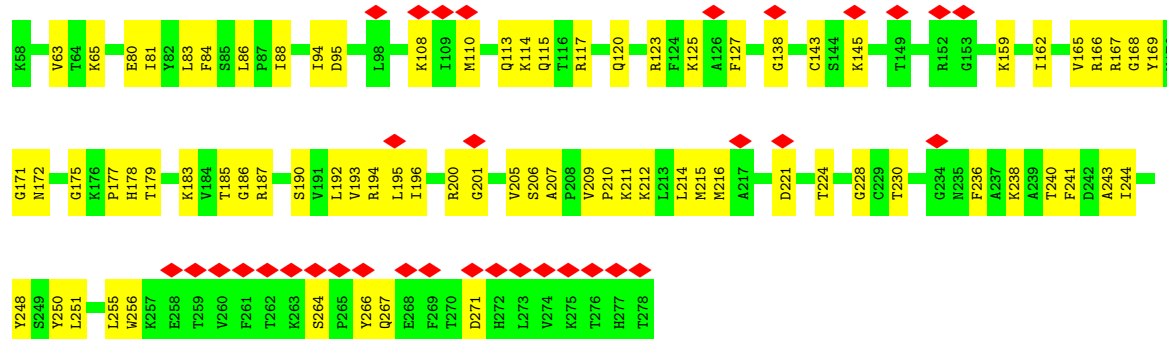
• Molecule 3: uS2 (SA)



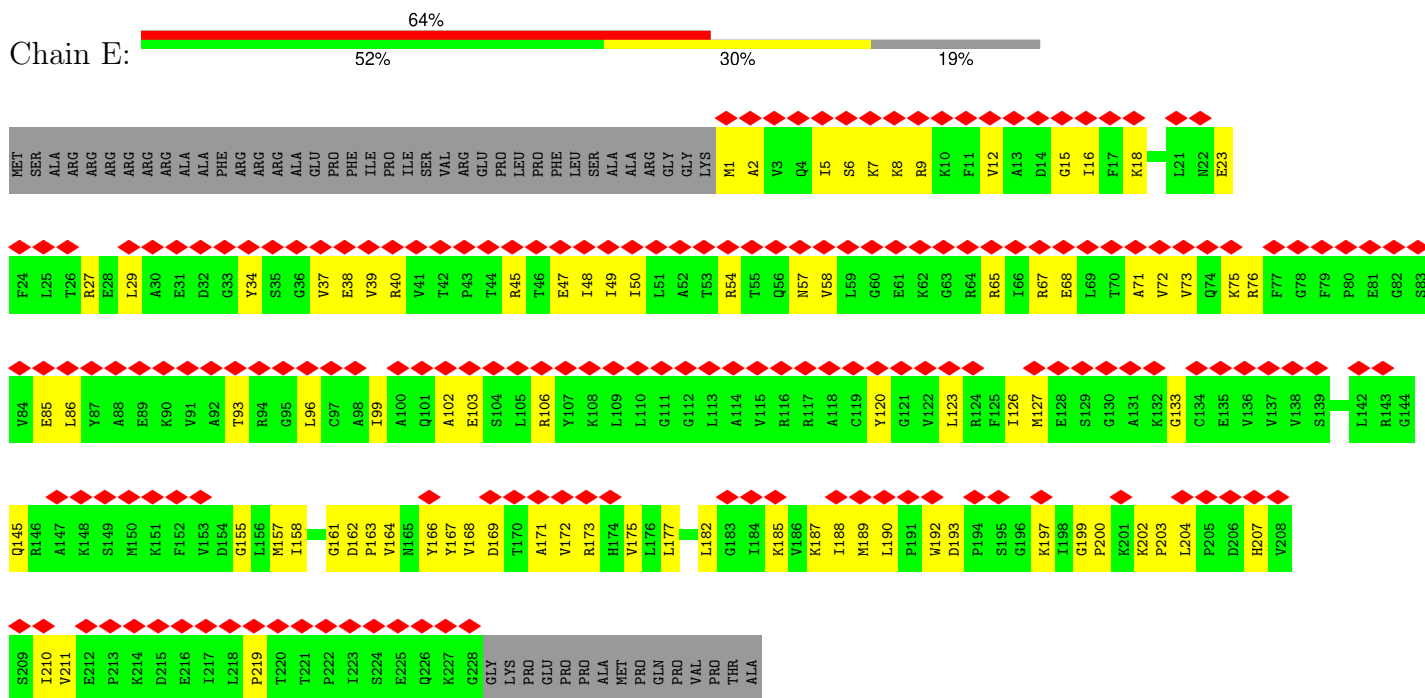
- Molecule 4: 40S ribosomal protein S3a



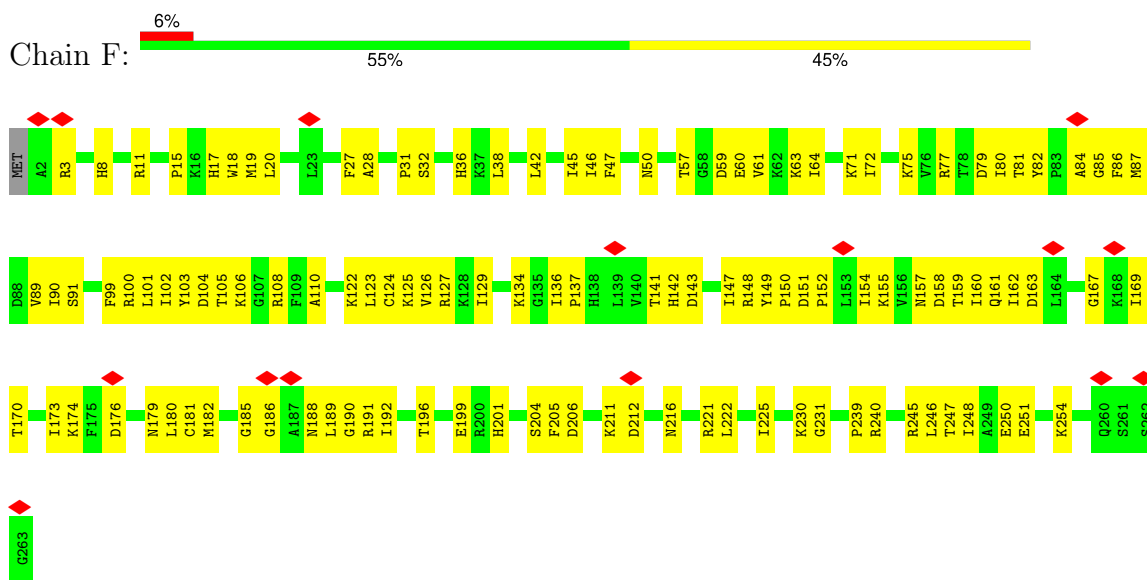
- Molecule 5: 40S ribosomal protein S2



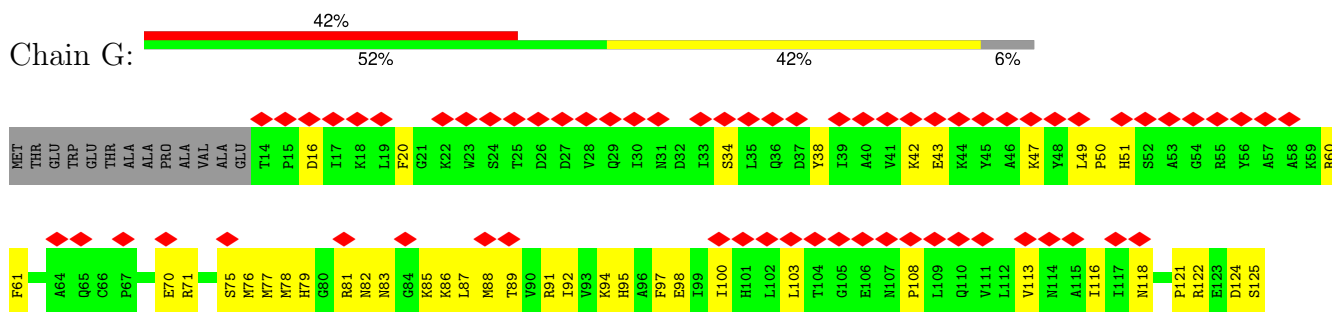
- Molecule 6: Ribosomal protein S3

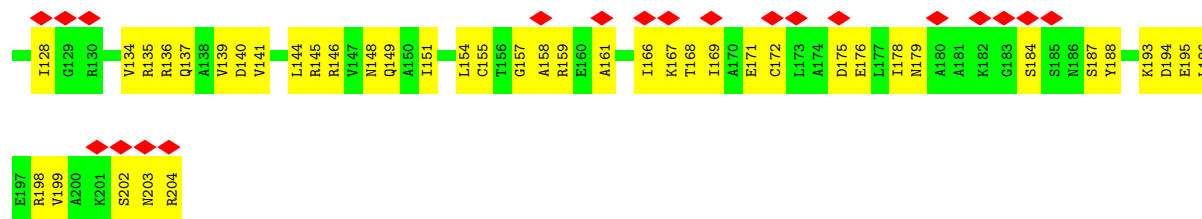


- Molecule 7: 40S ribosomal protein S4

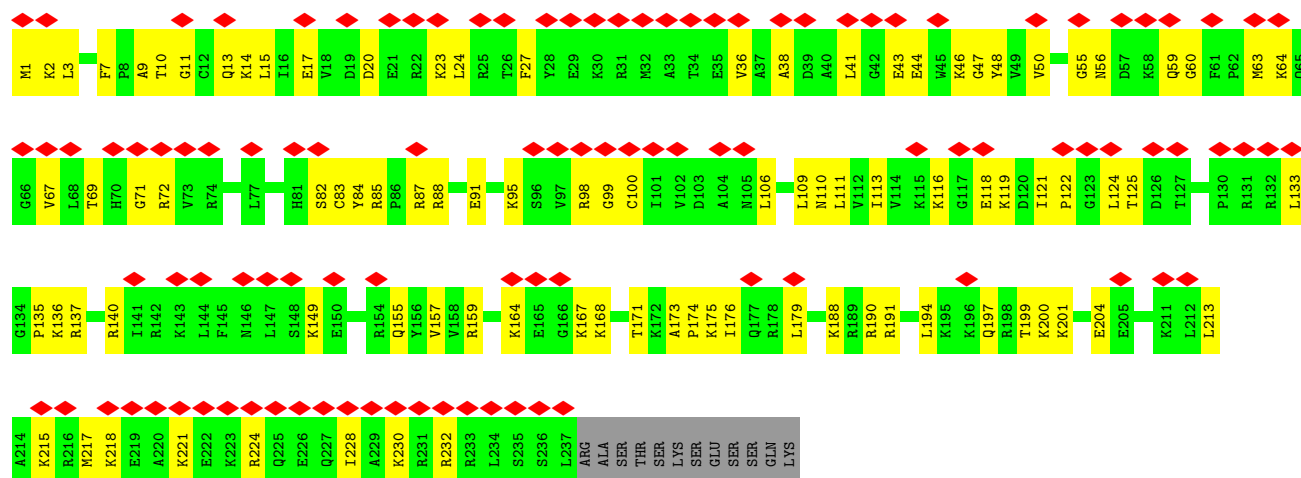
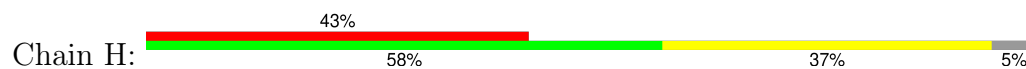


- Molecule 8: Ribosomal protein S5

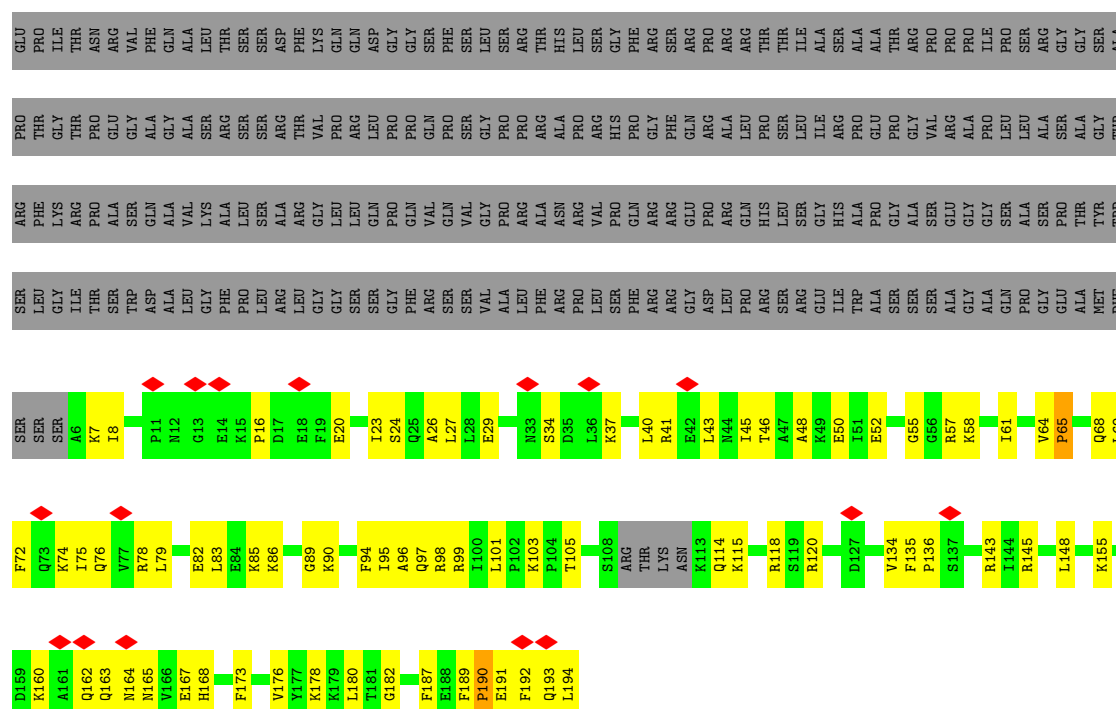




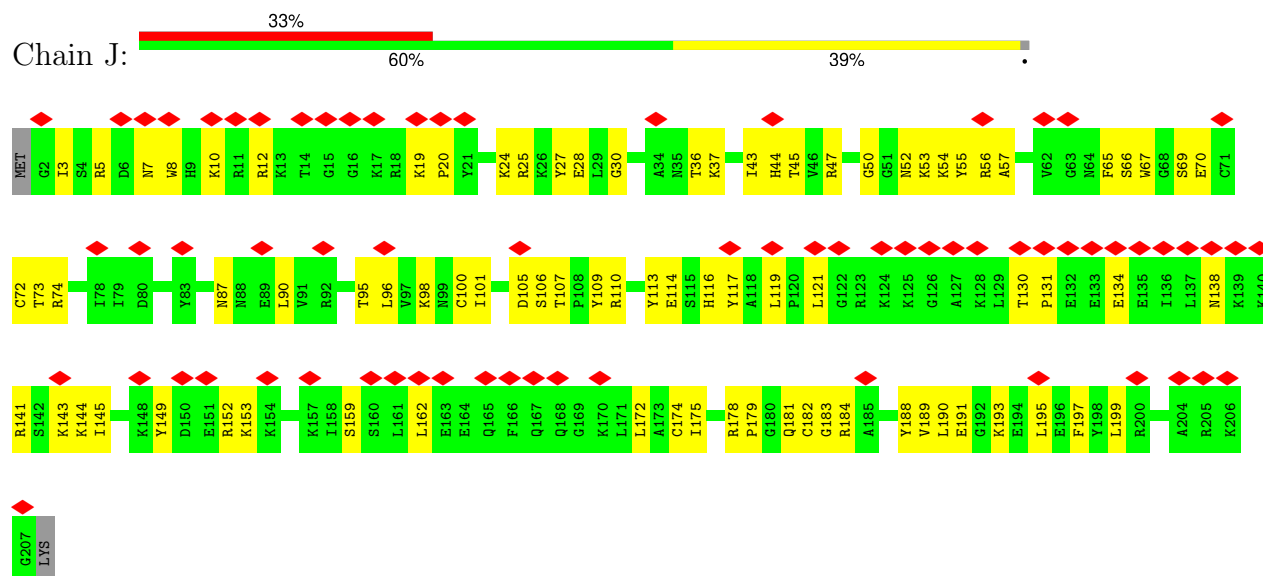
• Molecule 9: 40S ribosomal protein S6



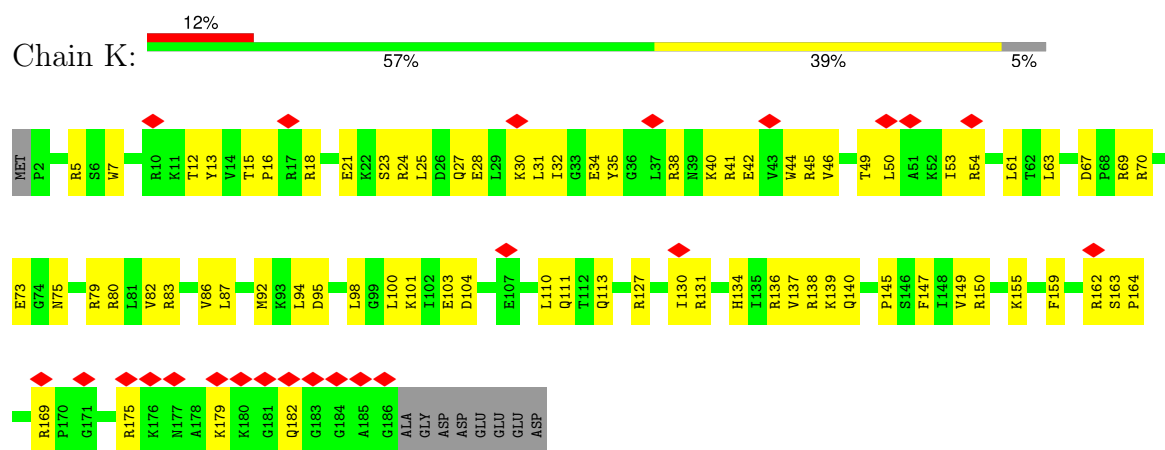
• Molecule 10: eS7



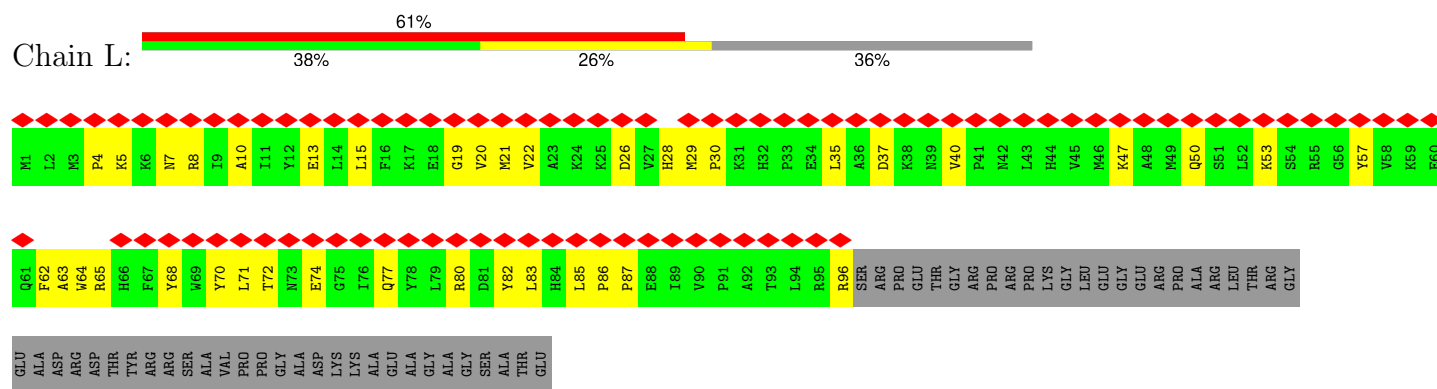
- Molecule 11: 40S ribosomal protein S8



- Molecule 12: Ribosomal protein S9 (Predicted)

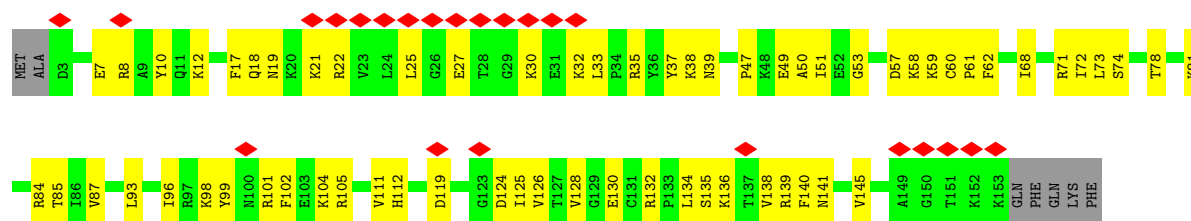


- Molecule 13: S10 plectin domain-containing protein

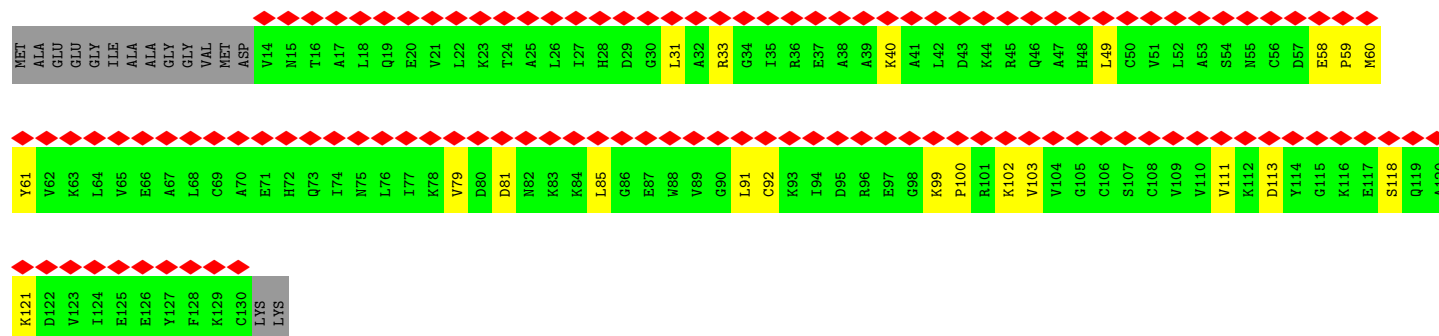
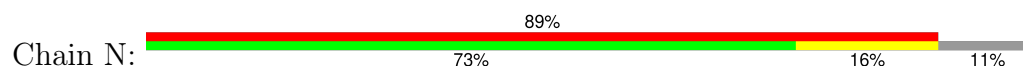


- Molecule 14: Ribosomal protein S11

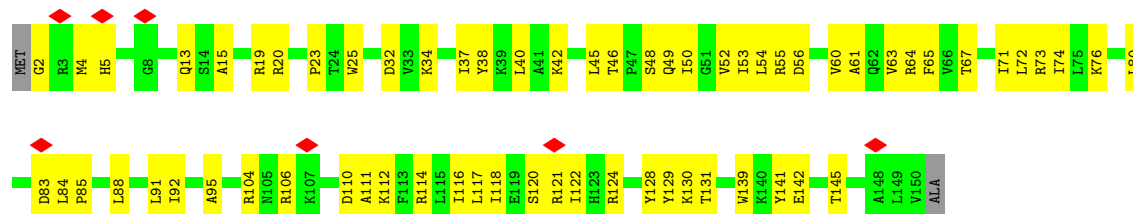




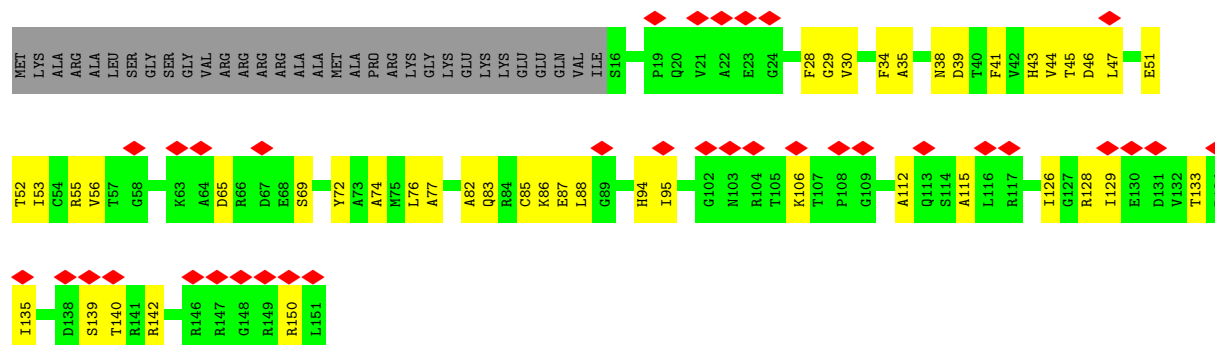
• Molecule 15: 40S ribosomal protein S12



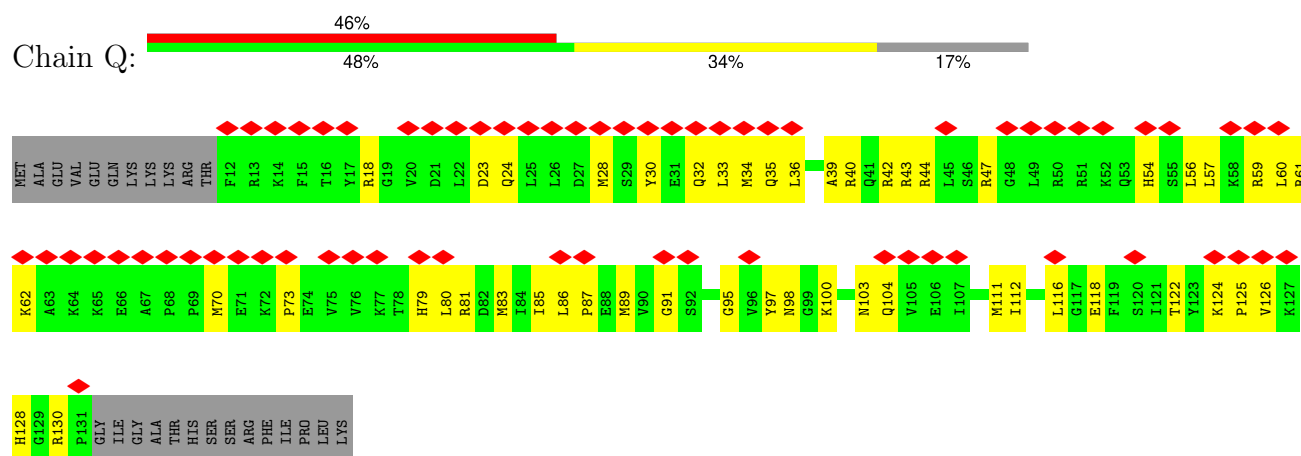
• Molecule 16: Ribosomal protein S13



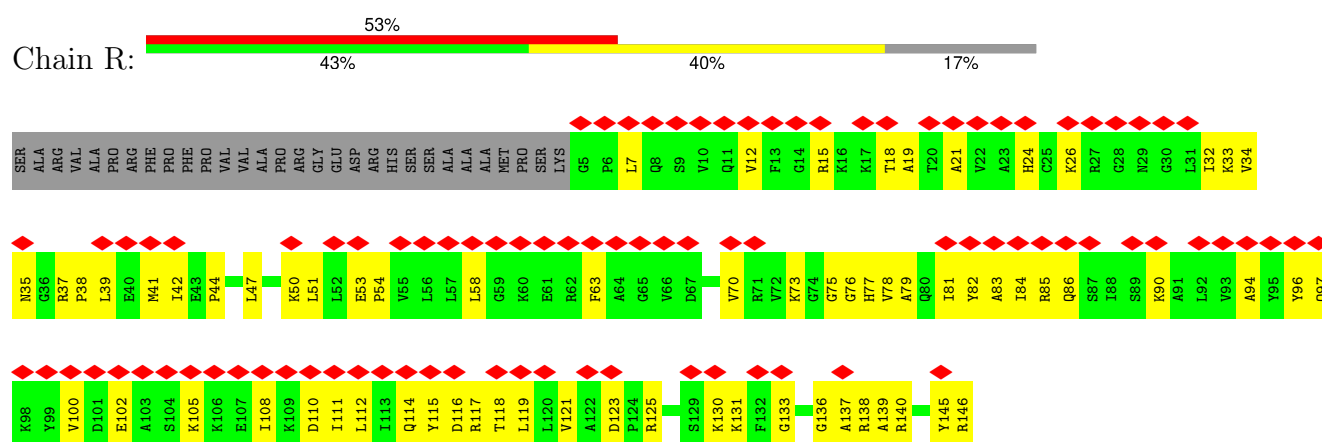
• Molecule 17: Ribosomal protein S14



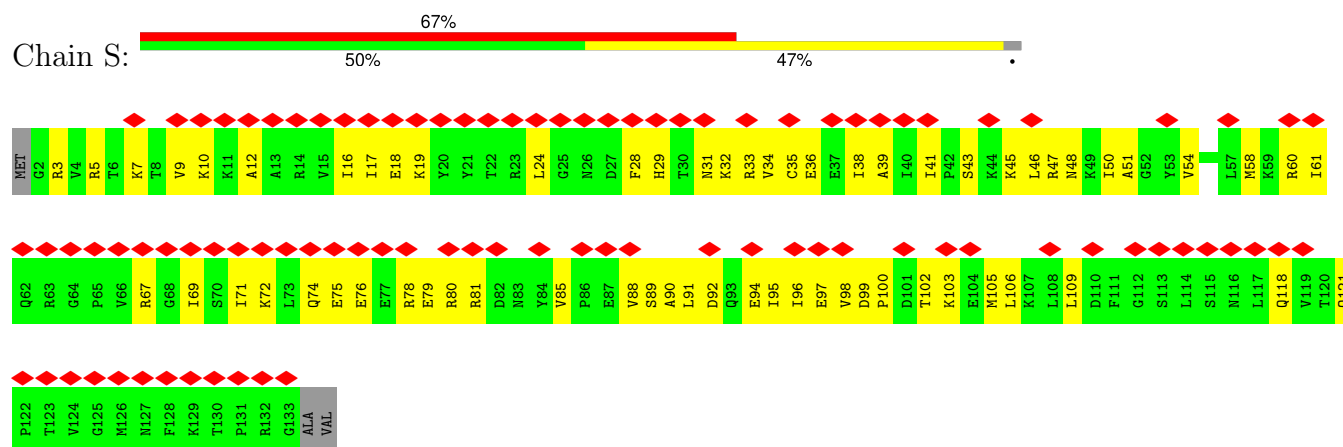
• Molecule 18: uS19



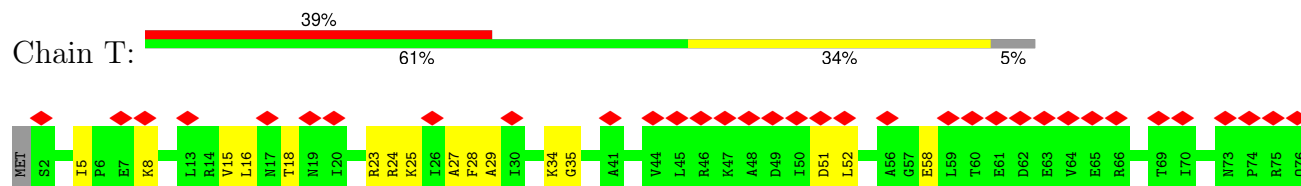
- Molecule 19: Ribosomal protein S16

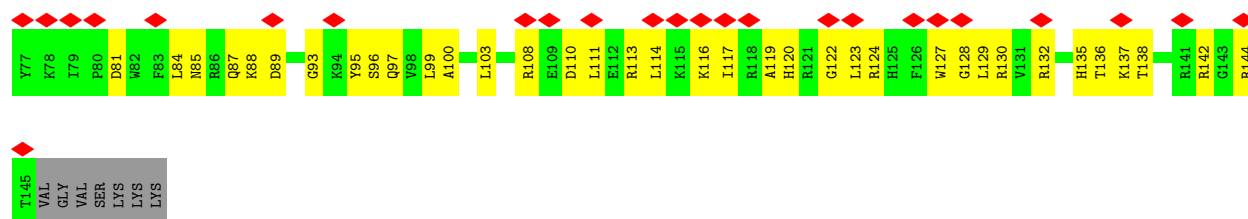


- Molecule 20: eS17

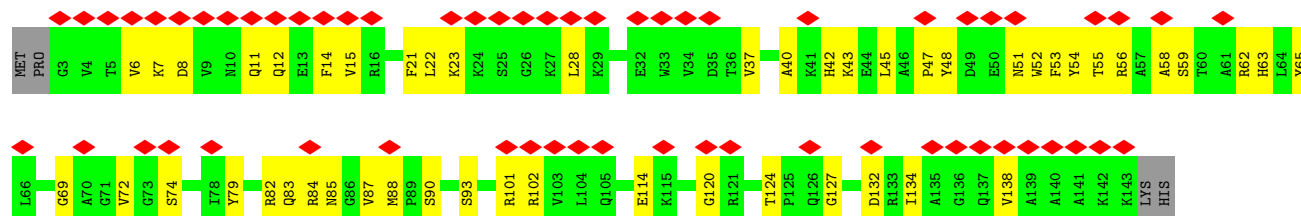
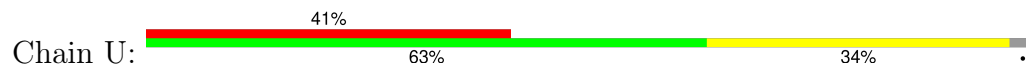


- Molecule 21: uS13

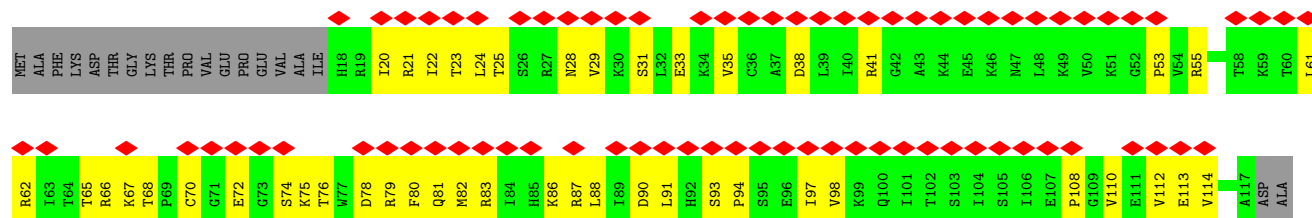




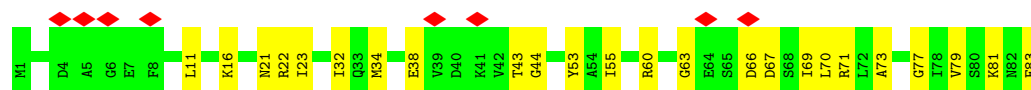
• Molecule 22: eS19



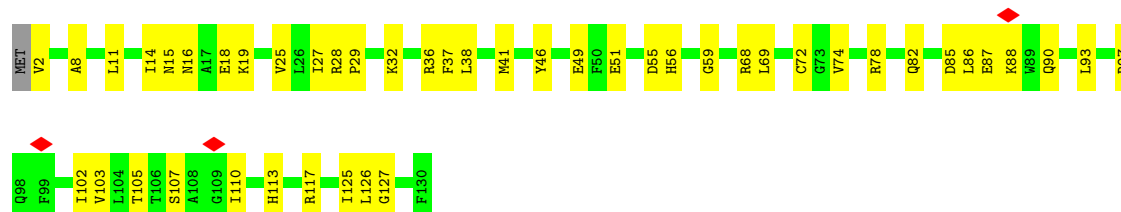
• Molecule 23: uS10



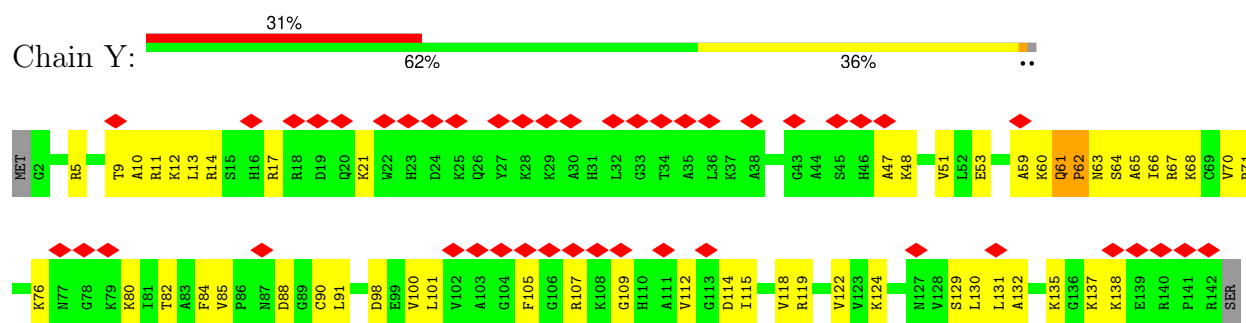
• Molecule 24: 40S ribosomal protein S21



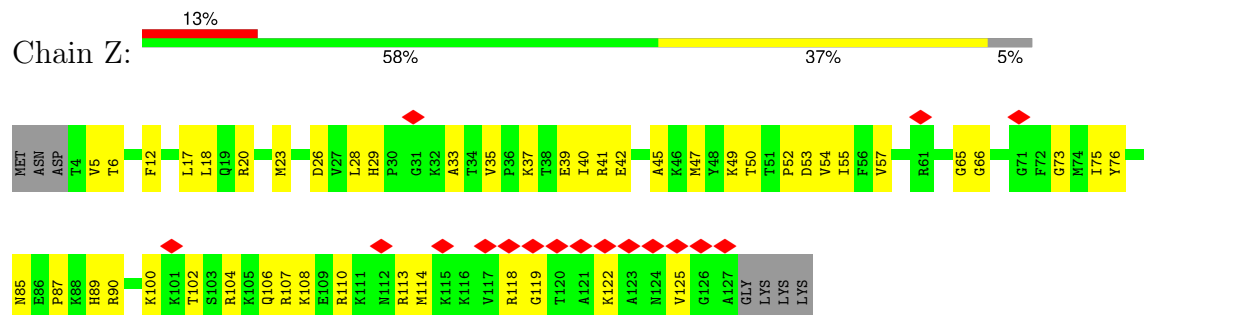
• Molecule 25: Ribosomal protein S15a



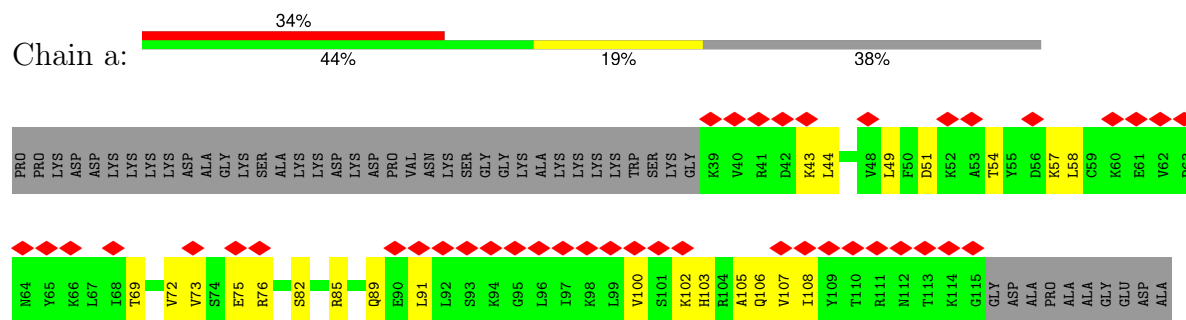
• Molecule 26: uS12



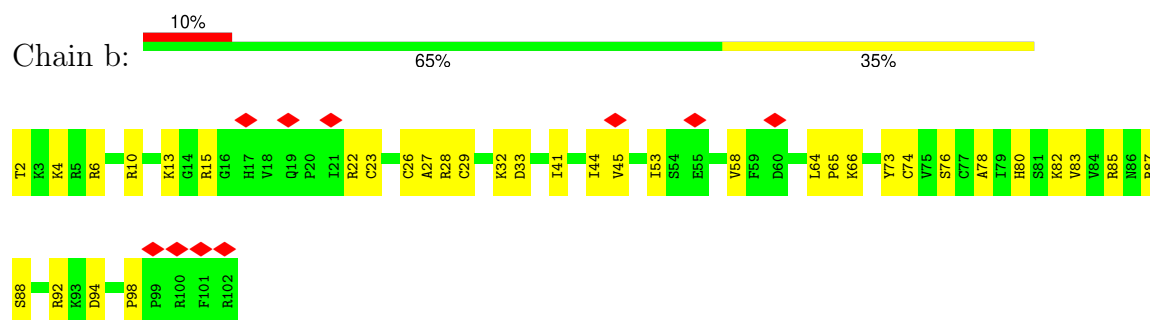
- Molecule 27: eS24



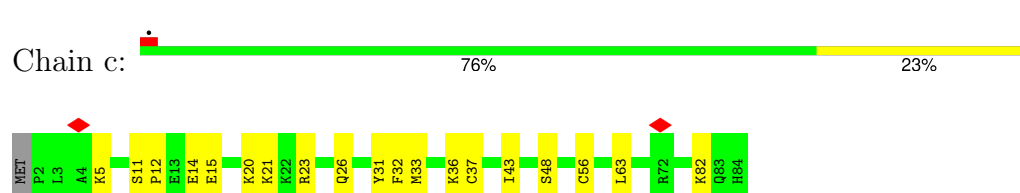
- Molecule 28: eS25



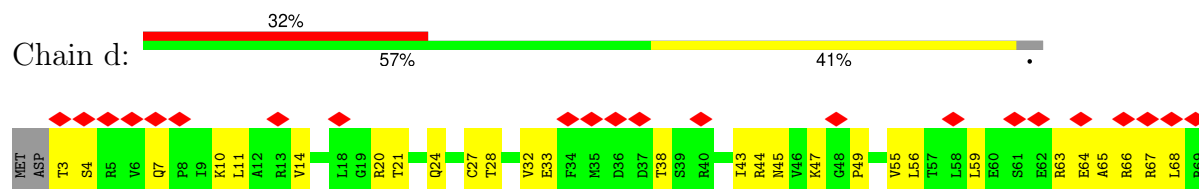
- Molecule 29: eS26



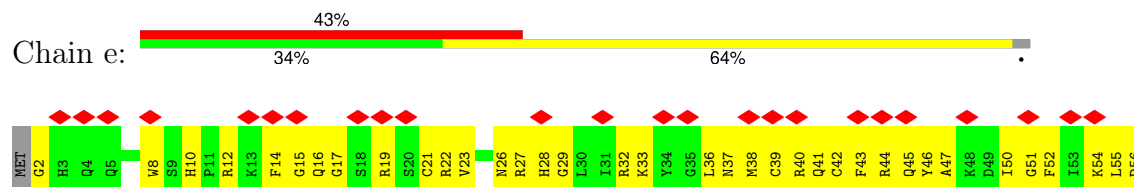
- Molecule 30: 40S ribosomal protein S27



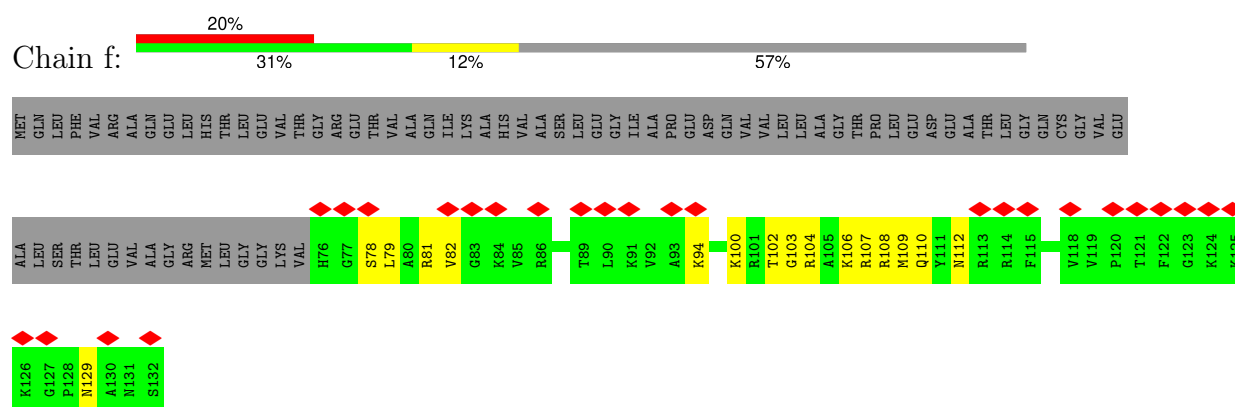
- Molecule 31: Ribosomal protein S28



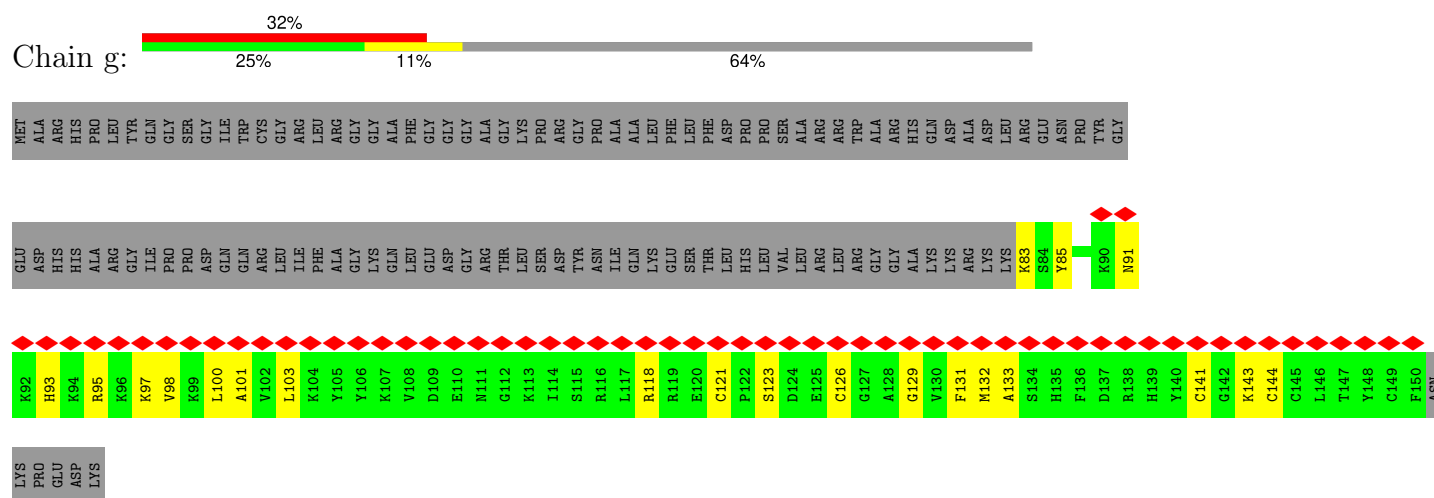
- Molecule 32: eS29



- Molecule 33: 40S ribosomal protein S30



- Molecule 34: eS31



- Molecule 35: RACK1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64736	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	2.249	Depositor
Minimum map value	-1.355	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.072	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	422.656, 422.656, 422.656	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8255, 0.8255, 0.8255	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
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	0.18	0/40102	0.30	0/62495
2	A	0.13	0/2547	0.31	0/3967
3	B	0.20	0/1747	0.39	0/2374
4	C	0.29	0/1756	0.40	0/2350
5	D	0.23	0/1753	0.44	0/2369
6	E	0.13	0/1796	0.36	0/2417
7	F	0.14	0/2118	0.36	0/2849
8	G	0.16	0/1531	0.44	0/2059
9	H	0.11	0/1946	0.30	0/2590
10	I	0.26	0/1510	0.58	4/2022 (0.2%)
11	J	0.12	0/1715	0.34	0/2287
12	K	0.14	0/1550	0.35	0/2069
13	L	0.11	0/834	0.31	0/1125
14	M	0.16	0/1254	0.37	0/1677
15	N	0.09	0/918	0.25	0/1233
16	O	0.27	0/1226	0.44	0/1649
17	P	0.23	0/1029	0.42	0/1380
18	Q	0.13	0/1017	0.35	0/1358
19	R	0.18	0/1146	0.41	0/1534
20	S	0.14	0/1082	0.36	0/1452
21	T	0.16	0/1208	0.40	0/1618
22	U	0.17	0/1115	0.39	0/1493
23	V	0.13	0/805	0.35	0/1081
24	W	0.21	0/643	0.48	0/860
25	X	0.31	0/1051	0.46	0/1406
26	Y	0.17	0/1116	0.41	0/1490
27	Z	0.13	0/1028	0.36	0/1366
28	a	0.13	0/620	0.38	0/831
29	b	0.23	0/828	0.42	0/1109
30	c	0.27	0/665	0.44	0/891
31	d	0.17	0/532	0.42	0/712
32	e	0.15	0/470	0.38	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.10	0/462	0.28	0/607
34	g	0.08	0/567	0.26	0/753
35	h	0.10	0/2493	0.32	0/3394
36	n	0.16	0/240	0.47	0/305
All	All	0.18	0/82420	0.34	4/119795 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
26	Y	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	I	190	PRO	CA-N-CD	-9.71	98.40	112.00
10	I	190	PRO	N-CD-CG	-5.90	94.34	103.20
10	I	65	PRO	CA-C-N	5.42	124.67	120.33
10	I	65	PRO	C-N-CA	5.42	124.67	120.33

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	Y	61	GLN	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35864	0	18113	1053	0
2	A	2280	0	1153	64	0
3	B	1710	0	1708	103	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	1729	0	1803	73	0
5	D	1716	0	1806	71	0
6	E	1768	0	1866	76	0
7	F	2076	0	2177	99	0
8	G	1509	0	1563	84	0
9	H	1923	0	2089	81	0
10	I	1488	0	1582	63	0
11	J	1686	0	1772	72	0
12	K	1525	0	1640	64	0
13	L	810	0	836	30	0
14	M	1233	0	1310	64	0
15	N	908	0	939	14	0
16	O	1202	0	1289	60	0
17	P	1016	0	1039	36	0
18	Q	997	0	1045	50	0
19	R	1128	0	1195	58	0
20	S	1068	0	1121	60	0
21	T	1190	0	1249	55	0
22	U	1097	0	1130	50	0
23	V	795	0	862	40	0
24	W	636	0	637	25	0
25	X	1034	0	1080	43	0
26	Y	1098	0	1167	53	0
27	Z	1011	0	1083	39	0
28	a	614	0	678	23	0
29	b	814	0	863	32	0
30	c	651	0	672	14	0
31	d	530	0	561	30	0
32	e	459	0	452	38	0
33	f	457	0	502	23	0
34	g	555	0	563	16	0
35	h	2436	0	2393	97	0
36	n	239	0	289	13	0
37	b	1	0	0	0	0
37	g	1	0	0	0	0
All	All	77254	0	60227	2459	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

All (2459) 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)
1:2:1472:C:N4	1:2:1476:A:H62	1.37	1.20
1:2:1472:C:H42	1:2:1476:A:N6	1.41	1.18
1:2:1276:A:H62	1:2:1321:G:H21	1.05	0.98
22:U:85:ASN:HB3	22:U:88:MET:HB2	1.46	0.98
1:2:1452:A:H61	1:2:1473:G:H21	1.10	0.97
1:2:955:A:H62	1:2:971:G:H21	1.10	0.96
1:2:1452:A:H61	1:2:1473:G:N2	1.65	0.95
1:2:1332:A:H62	1:2:1493:C:H42	1.03	0.94
1:2:1452:A:N6	1:2:1473:G:H21	1.66	0.93
19:R:44:PRO:HG2	19:R:47:LEU:HB2	1.51	0.91
10:I:65:PRO:HG2	10:I:68:GLN:HE22	1.35	0.91
1:2:1033:G:H1	1:2:1080:A:HO2'	1.17	0.88
1:2:1652:G:H1	1:2:1672:U:H3	1.15	0.88
5:D:113:GLN:HB3	5:D:120:GLN:HE21	1.37	0.88
8:G:77:MET:SD	8:G:82:ASN:ND2	2.49	0.86
7:F:71:LYS:HB2	7:F:91:SER:HB2	1.58	0.86
24:W:66:ASP:OD1	24:W:67:ASP:N	2.09	0.85
1:2:1332:A:H62	1:2:1493:C:N4	1.75	0.85
3:B:57:LYS:NZ	3:B:160:ALA:O	2.11	0.84
1:2:114:G:H5'	14:M:132:ARG:HD3	1.60	0.83
8:G:49:LEU:HD22	19:R:50:LYS:HD3	1.61	0.83
8:G:78:MET:HG3	8:G:79:HIS:H	1.42	0.83
18:Q:111:MET:HA	21:T:117:ILE:HD11	1.60	0.83
1:2:919:A:OP2	16:O:64:ARG:NH2	2.12	0.83
1:2:1144:A:H5'	1:2:1355:C:H41	1.44	0.83
19:R:97:GLN:HB3	19:R:105:LYS:HE3	1.62	0.81
1:2:955:A:H62	1:2:971:G:N2	1.77	0.81
12:K:32:ILE:HD11	12:K:40:LYS:HB3	1.63	0.81
1:2:1649:U:H2'	1:2:1650:A:H8	1.44	0.81
26:Y:101:LEU:HB3	26:Y:124:LYS:HB2	1.61	0.81
1:2:1224:G:N2	1:2:1642:U:O2	2.14	0.80
6:E:47:GLU:HG2	6:E:85:GLU:H	1.47	0.80
1:2:146:G:H1	1:2:173:A:H61	1.30	0.80
3:B:57:LYS:NZ	3:B:162:PRO:HD3	1.96	0.80
8:G:76:MET:O	8:G:159:ARG:NH2	2.15	0.80
12:K:18:ARG:O	12:K:24:ARG:NH2	2.15	0.79
8:G:166:ILE:HD11	28:a:75:GLU:HB3	1.65	0.79
22:U:72:VAL:HG21	22:U:101:ARG:HE	1.47	0.79
1:2:1024:A:OP2	16:O:124:ARG:NH2	2.15	0.79
1:2:1598:G:O6	28:a:85:ARG:NH1	2.16	0.79
1:2:225:G:N2	1:2:296:U:O4	2.14	0.79
1:2:1356:G:OP1	5:D:238:LYS:NZ	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:22:ARG:NH2	25:X:18:GLU:O	2.16	0.78
1:2:1276:A:H62	1:2:1321:G:N2	1.82	0.78
1:2:1656:G:H1	1:2:1668:U:H3	0.81	0.78
3:B:156:TYR:HB3	24:W:60:ARG:HH21	1.48	0.78
3:B:57:LYS:HZ1	3:B:162:PRO:HD3	1.47	0.78
1:2:116:U:O2	1:2:347:G:N2	2.11	0.78
1:2:39:A:H62	1:2:515:G:H21	1.32	0.77
1:2:1579:A:O2'	1:2:1582:C:N4	2.17	0.77
9:H:59:GLN:OE1	9:H:72:ARG:NH2	2.17	0.77
1:2:446:G:OP1	11:J:50:GLY:N	2.14	0.77
1:2:1183:A:H5'	36:n:11:ARG:HE	1.48	0.77
35:h:87:LEU:HB3	35:h:101:PHE:HB2	1.67	0.77
1:2:1657:G:H1	1:2:1667:U:H3	1.33	0.77
6:E:133:GLY:HA3	6:E:155:GLY:HA3	1.65	0.77
1:2:1116:C:N4	2:A:9238:C:O2'	2.18	0.76
24:W:16:LYS:NZ	24:W:21:ASN:O	2.17	0.76
26:Y:60:LYS:HG3	26:Y:61:GLN:H	1.48	0.76
1:2:55:U:O2	1:2:90:G:N2	2.19	0.75
6:E:192:TRP:HA	6:E:200:PRO:HD2	1.68	0.75
23:V:79:ARG:O	32:e:54:LYS:NZ	2.16	0.75
3:B:191:ARG:HH12	24:W:44:GLY:HA3	1.52	0.75
1:2:1453:C:OP1	20:S:48:ASN:ND2	2.20	0.75
1:2:1616:U:OP2	18:Q:43:ARG:NH2	2.20	0.75
6:E:1:MET:SD	6:E:2:ALA:N	2.59	0.75
33:f:100:LYS:HG2	33:f:102:THR:H	1.51	0.75
1:2:1564:C:OP2	22:U:101:ARG:NH1	2.18	0.75
1:2:1402:A:H3'	1:2:1405:A:H62	1.50	0.75
1:2:1488:C:H3'	1:2:1489:A:H4'	1.67	0.75
1:2:1324:G:H1	1:2:1504:U:H3	0.82	0.74
25:X:15:ASN:ND2	25:X:72:CYS:O	2.20	0.74
29:b:22:ARG:NH1	29:b:29:CYS:SG	2.60	0.74
1:2:621:C:OP1	26:Y:107:ARG:NH1	2.20	0.74
18:Q:57:LEU:HG	18:Q:83:MET:HE1	1.69	0.74
1:2:1479:G:H5''	19:R:138:ARG:HH12	1.52	0.74
23:V:21:ARG:HD3	23:V:88:LEU:HD13	1.68	0.74
1:2:1656:G:H2'	1:2:1657:G:H8	1.53	0.74
26:Y:71:ARG:HD2	26:Y:80:LYS:HB3	1.68	0.74
1:2:116:U:H3	1:2:347:G:H1	0.77	0.73
14:M:104:LYS:O	26:Y:11:ARG:NH2	2.21	0.73
1:2:1405:A:H2	1:2:1443:C:H42	1.34	0.73
1:2:1138:C:OP1	3:B:155:ARG:NH2	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:49:LEU:HB3	15:N:111:VAL:HB	1.70	0.73
1:2:1406:G:OP1	1:2:1428:G:N2	2.22	0.73
1:2:874:G:N3	10:I:114:GLN:NE2	2.35	0.73
1:2:1394:G:H1	1:2:1451:G:H1	1.37	0.73
1:2:1550:G:O2'	1:2:1558:C:O2	2.07	0.72
1:2:1851:A:OP1	36:n:9:ARG:NH2	2.21	0.72
27:Z:100:LYS:HG2	27:Z:102:THR:HG22	1.70	0.72
1:2:464:A:H3'	1:2:465:A:H8	1.54	0.72
1:2:1112:U:H3	1:2:1113:A:H62	1.37	0.72
1:2:1424:G:H2'	1:2:1425:G:H8	1.53	0.72
1:2:445:A:H5''	11:J:47:ARG:HH22	1.54	0.72
1:2:981:A:H2'	1:2:982:G:C8	2.25	0.72
1:2:1330:G:N2	1:2:1334:G:OP2	2.22	0.72
1:2:1718:G:H21	1:2:1815:A:H62	1.36	0.72
3:B:191:ARG:NH1	24:W:43:THR:O	2.22	0.72
1:2:1848:U:O4	36:n:12:ARG:NH1	2.22	0.72
4:C:129:THR:OG1	4:C:131:ASP:O	2.07	0.72
12:K:136:ARG:NH1	12:K:159:PHE:O	2.22	0.72
20:S:33:ARG:NH1	35:h:107:ASP:OD2	2.23	0.72
7:F:63:LYS:HD3	27:Z:85:ASN:HB2	1.69	0.72
7:F:15:PRO:HG2	7:F:18:TRP:HE1	1.55	0.72
25:X:103:VAL:HG23	25:X:126:LEU:HB2	1.72	0.72
1:2:1332:A:N6	1:2:1493:C:H42	1.83	0.72
1:2:955:A:N6	1:2:971:G:H21	1.86	0.72
10:I:74:LYS:O	10:I:78:ARG:NH1	2.23	0.72
35:h:120:ILE:HB	35:h:132:TRP:HB2	1.72	0.72
1:2:1657:G:O6	1:2:1667:U:O4	2.07	0.71
4:C:63:LYS:O	4:C:88:THR:OG1	2.07	0.71
8:G:204:ARG:HH21	31:d:63:ARG:HD3	1.54	0.71
1:2:15:U:O2'	1:2:669:A:N6	2.24	0.71
1:2:1199:A:OP1	29:b:2:THR:N	2.23	0.71
16:O:4:MET:HE1	16:O:121:ARG:HG3	1.73	0.71
1:2:1661:A:OP2	32:e:32:ARG:NH1	2.23	0.71
4:C:191:ASP:HB3	4:C:195:LYS:HE3	1.72	0.71
7:F:176:ASP:OD1	7:F:179:ASN:ND2	2.24	0.71
16:O:46:THR:H	16:O:49:GLN:HE21	1.36	0.71
18:Q:18:ARG:HH21	21:T:88:LYS:HB3	1.56	0.71
1:2:1643:U:H2'	1:2:1644:C:C5	2.26	0.71
6:E:37:VAL:HG12	6:E:50:ILE:HG22	1.72	0.71
1:2:162:C:O2'	9:H:95:LYS:NZ	2.23	0.71
5:D:113:GLN:HB3	5:D:120:GLN:NE2	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:482:G:O2'	1:2:484:A:N7	2.24	0.70
1:2:1099:G:H22	1:2:1133:A:H2	1.39	0.70
7:F:60:GLU:OE2	27:Z:20:ARG:NH2	2.24	0.70
16:O:91:LEU:HB3	16:O:122:ILE:HG22	1.74	0.70
1:2:1050:A:OP1	1:2:1846:G:N2	2.24	0.70
1:2:1532:C:H3'	1:2:1637:A:H62	1.56	0.70
10:I:65:PRO:HG2	10:I:68:GLN:NE2	2.07	0.70
20:S:33:ARG:HA	20:S:36:GLU:HG2	1.74	0.70
33:f:78:SER:O	33:f:81:ARG:NH1	2.24	0.70
33:f:100:LYS:HG3	33:f:106:LYS:HD2	1.72	0.70
5:D:95:ASP:OD1	5:D:159:LYS:NZ	2.24	0.70
19:R:34:VAL:HG12	19:R:70:VAL:HB	1.74	0.70
29:b:74:CYS:SG	29:b:76:SER:OG	2.49	0.70
1:2:678:U:H3	1:2:1027:A:H62	1.40	0.69
1:2:292:A:O2'	14:M:39:ASN:O	2.10	0.69
8:G:125:SER:O	31:d:47:LYS:NZ	2.22	0.69
10:I:58:LYS:HE2	10:I:90:LYS:HD2	1.74	0.69
22:U:124:THR:HG23	22:U:127:GLY:H	1.57	0.69
28:a:43:LYS:NZ	28:a:44:LEU:O	2.26	0.69
1:2:1253:A:OP2	1:2:1526:G:N2	2.26	0.69
3:B:184:ARG:HD3	3:B:191:ARG:HD3	1.74	0.69
6:E:102:ALA:HB2	6:E:171:ALA:HB1	1.74	0.69
1:2:109:U:O2	14:M:71:ARG:NH2	2.25	0.69
1:2:681:U:H4'	26:Y:9:THR:HG22	1.73	0.69
1:2:1601:A:O2'	1:2:1635:C:N4	2.24	0.69
2:A:9229:U:O2'	2:A:9232:G:N7	2.21	0.69
1:2:1455:A:H61	1:2:1471:C:H42	1.41	0.69
1:2:1091:C:HO2'	25:X:2:VAL:N	1.91	0.69
5:D:194:ARG:HE	5:D:196:ILE:HD11	1.57	0.69
8:G:204:ARG:NH2	31:d:64:GLU:O	2.26	0.69
10:I:83:LEU:HD13	10:I:86:LYS:HD3	1.73	0.69
13:L:65:ARG:NH1	32:e:21:CYS:O	2.26	0.69
1:2:1618:C:OP2	18:Q:47:ARG:NH2	2.26	0.69
2:A:9169:G:O6	2:A:9252:U:O2	2.11	0.69
26:Y:132:ALA:HB1	26:Y:138:LYS:HB2	1.75	0.69
35:h:286:CYS:HA	35:h:302:TYR:HA	1.74	0.69
1:2:101:U:OP1	11:J:19:LYS:NZ	2.26	0.68
1:2:1481:G:OP2	1:2:1482:C:N4	2.27	0.68
1:2:12:U:H2'	1:2:13:C:C6	2.28	0.68
8:G:91:ARG:HH22	28:a:105:ALA:HB2	1.57	0.68
1:2:212:C:H2'	1:2:213:G:C8	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1479:G:O3'	19:R:131:LYS:NZ	2.25	0.68
1:2:615:C:O2'	33:f:81:ARG:NH2	2.27	0.68
26:Y:132:ALA:HA	26:Y:135:LYS:HE2	1.74	0.68
9:H:69:THR:HG22	9:H:71:GLY:H	1.58	0.68
16:O:37:ILE:HD13	16:O:74:ILE:HD11	1.74	0.68
23:V:22:ILE:HG22	23:V:114:VAL:HG12	1.76	0.68
3:B:33:GLN:NE2	24:W:63:GLY:O	2.26	0.68
1:2:953:C:O2	17:P:55:ARG:NH1	2.24	0.68
8:G:95:HIS:HB3	28:a:106:GLN:HE22	1.59	0.68
11:J:73:THR:O	11:J:74:ARG:NH1	2.27	0.68
1:2:1098:C:H2'	1:2:1099:G:C8	2.29	0.68
3:B:49:ILE:HD13	3:B:162:PRO:HB2	1.76	0.67
10:I:190:PRO:HD2	10:I:190:PRO:O	1.93	0.67
1:2:1864:U:OP2	29:b:4:LYS:NZ	2.24	0.67
3:B:173:LEU:HG	3:B:177:MET:HE3	1.76	0.67
32:e:12:ARG:NH2	32:e:14:PHE:O	2.26	0.67
7:F:31:PRO:HA	7:F:81:THR:HB	1.75	0.67
17:P:106:LYS:HE2	17:P:135:ILE:HD12	1.77	0.67
14:M:59:LYS:HD2	14:M:134:LEU:HD23	1.76	0.67
10:I:158:LEU:HD11	10:I:187:PHE:HD2	1.58	0.67
16:O:5:HIS:HB3	16:O:117:LEU:HD13	1.77	0.67
10:I:178:LYS:HD2	10:I:182:GLY:HA2	1.76	0.67
24:W:79:VAL:O	24:W:81:LYS:NZ	2.27	0.67
1:2:1506:A:H4'	1:2:1507:G:H2'	1.76	0.67
1:2:952:G:O2'	17:P:51:GLU:OE2	2.13	0.67
1:2:1189:A:H2'	1:2:1190:A:H8	1.60	0.67
1:2:1394:G:OP1	19:R:15:ARG:NH1	2.27	0.67
9:H:2:LYS:HZ3	9:H:17:GLU:HB2	1.58	0.67
1:2:1324:G:O6	1:2:1504:U:O4	2.13	0.67
1:2:1344:A:H4'	1:2:1345:G:H5'	1.77	0.67
33:f:108:ARG:HD2	33:f:112:ASN:HD22	1.60	0.67
1:2:65:C:H41	9:H:136:LYS:HB2	1.59	0.67
1:2:399:C:N3	14:M:104:LYS:NZ	2.34	0.67
2:A:9260:G:O2'	2:A:9264:G:N1	2.27	0.67
1:2:619:A:N1	26:Y:114:ASP:N	2.43	0.66
8:G:140:ASP:HB2	31:d:44:ARG:HH21	1.61	0.66
3:B:2:SER:OG	3:B:3:GLY:N	2.26	0.66
6:E:6:SER:HB2	6:E:9:ARG:HD3	1.76	0.66
1:2:1656:G:O6	1:2:1668:U:O4	2.13	0.66
3:B:68:ILE:HD11	3:B:121:LEU:HD13	1.76	0.66
12:K:63:LEU:HD23	12:K:70:ARG:HB2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:65:PHE:O	11:J:109:TYR:OH	2.12	0.66
9:H:197:GLN:HA	9:H:200:LYS:HG2	1.76	0.66
16:O:49:GLN:HA	16:O:52:VAL:HG12	1.77	0.66
1:2:804:U:O2	1:2:860:G:N2	2.25	0.66
1:2:1816:G:N2	1:2:1817:G:H22	1.94	0.66
14:M:84:ARG:HG2	14:M:112:HIS:CE1	2.31	0.66
23:V:61:LEU:HB2	23:V:82:MET:HE2	1.76	0.66
27:Z:54:VAL:HB	27:Z:76:TYR:HB2	1.76	0.66
3:B:50:ASN:HB3	3:B:53:ARG:HD3	1.77	0.66
10:I:61:ILE:HD11	10:I:176:VAL:HG23	1.77	0.66
11:J:66:SER:H	11:J:188:TYR:HA	1.60	0.66
16:O:130:LYS:NZ	16:O:139:TRP:O	2.21	0.66
8:G:118:ASN:O	8:G:193:LYS:NZ	2.26	0.66
25:X:78:ARG:HE	25:X:126:LEU:HD23	1.59	0.66
1:2:1040:G:H2'	1:2:1041:G:C8	2.31	0.66
1:2:1663:A:H4'	1:2:1664:A:H5'	1.78	0.66
12:K:83:ARG:HH12	12:K:150:ARG:HD2	1.60	0.66
24:W:32:ILE:HD12	24:W:55:ILE:HB	1.77	0.66
1:2:1507:G:HO2'	34:g:83:LYS:N	1.94	0.66
3:B:2:SER:O	3:B:63:ARG:NH2	2.29	0.66
3:B:81:ASN:HA	3:B:84:GLN:HE21	1.61	0.66
8:G:175:ASP:O	8:G:179:ASN:ND2	2.29	0.66
23:V:94:PRO:HD2	23:V:97:ILE:HD13	1.77	0.66
1:2:1155:U:OP1	5:D:185:THR:OG1	2.14	0.65
1:2:1355:C:HO2'	5:D:238:LYS:HZ3	1.44	0.65
1:2:1656:G:H2'	1:2:1657:G:C8	2.30	0.65
6:E:67:ARG:HH22	13:L:96:ARG:HD3	1.61	0.65
30:c:36:LYS:NZ	30:c:37:CYS:O	2.27	0.65
1:2:522:A:H5''	12:K:145:PRO:HD2	1.78	0.65
1:2:215:G:N2	1:2:311:C:O2	2.24	0.65
14:M:22:ARG:HB2	14:M:25:LEU:HG	1.78	0.65
17:P:34:PHE:HB3	17:P:41:PHE:HB2	1.78	0.65
27:Z:55:ILE:HG12	27:Z:75:ILE:HG22	1.78	0.65
1:2:934:G:H5'	1:2:994:C:H1'	1.78	0.65
1:2:1202:U:O2'	5:D:114:LYS:NZ	2.17	0.65
1:2:1541:G:H5'	22:U:59:SER:HB3	1.78	0.65
1:2:1660:C:O2	32:e:32:ARG:NH2	2.28	0.65
8:G:144:LEU:HD23	31:d:49:PRO:HG2	1.79	0.65
1:2:45:A:H4'	1:2:46:A:H5'	1.79	0.65
1:2:300:U:H2'	1:2:301:A:H8	1.62	0.65
28:a:73:VAL:HA	28:a:76:ARG:HG2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:83:LYS:N	34:g:85:TYR:HH	1.94	0.65
35:h:90:TRP:HD1	35:h:92:LEU:HD23	1.61	0.65
1:2:1450:G:H2'	1:2:1451:G:C8	2.31	0.65
2:A:9303:C:O2'	2:A:9304:G:O5'	2.12	0.65
1:2:1355:C:O2'	5:D:238:LYS:NZ	2.24	0.65
2:A:9157:G:H2'	2:A:9158:G:C8	2.31	0.65
3:B:71:PRO:HG3	3:B:186:ARG:HH22	1.62	0.65
1:2:1455:A:H2'	1:2:1456:G:H8	1.60	0.65
10:I:7:LYS:NZ	10:I:40:LEU:O	2.30	0.65
22:U:85:ASN:CB	22:U:88:MET:HB2	2.26	0.65
26:Y:61:GLN:O	26:Y:63:ASN:N	2.30	0.65
31:d:67:ARG:HG3	31:d:68:LEU:HD23	1.79	0.65
1:2:70:G:OP2	9:H:167:LYS:NZ	2.29	0.64
1:2:1624:U:H3	18:Q:40:ARG:HH22	1.45	0.64
23:V:66:ARG:NH2	23:V:74:SER:O	2.30	0.64
1:2:641:A:OP2	33:f:107:ARG:NH1	2.30	0.64
3:B:124:VAL:HG12	3:B:126:ASP:H	1.62	0.64
1:2:440:G:OP1	1:2:1798:C:O2'	2.13	0.64
1:2:946:U:H2'	1:2:947:G:H8	1.61	0.64
1:2:1566:G:O2'	1:2:1568:C:N4	2.21	0.64
21:T:5:ILE:HB	28:a:49:LEU:HB2	1.79	0.64
21:T:129:LEU:HD21	21:T:144:ARG:HH22	1.63	0.64
1:2:874:G:H2'	1:2:875:A:H8	1.62	0.64
1:2:973:C:N3	17:P:55:ARG:NH2	2.44	0.64
1:2:1007:C:H2'	1:2:1008:A:C8	2.33	0.64
1:2:1192:U:OP1	26:Y:119:ARG:NH2	2.31	0.64
6:E:75:LYS:HE3	13:L:21:MET:HA	1.80	0.64
11:J:65:PHE:O	11:J:73:THR:OG1	2.16	0.64
29:b:22:ARG:NH2	29:b:27:ALA:O	2.30	0.64
1:2:980:A:H2'	1:2:981:A:H8	1.62	0.64
1:2:1464:C:H3'	1:2:1465:A:H8	1.62	0.64
12:K:21:GLU:OE2	12:K:25:LEU:N	2.23	0.64
23:V:66:ARG:NH1	23:V:76:THR:O	2.30	0.64
1:2:980:A:H2'	1:2:981:A:C8	2.32	0.64
1:2:1255:G:O3'	32:e:40:ARG:NH2	2.31	0.64
18:Q:87:PRO:HG3	18:Q:112:ILE:HG21	1.78	0.64
1:2:1228:A:H2'	1:2:1229:G:H8	1.63	0.64
3:B:169:HIS:CD2	3:B:203:PHE:HE2	2.15	0.64
35:h:79:LEU:HG	35:h:87:LEU:HD11	1.80	0.64
5:D:210:PRO:HB3	5:D:240:THR:HG21	1.79	0.64
1:2:1092:G:OP1	16:O:2:GLY:N	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1376:A:OP1	20:S:67:ARG:NH2	2.31	0.64
2:A:9259:U:H2'	2:A:9260:G:H2'	1.80	0.63
14:M:99:TYR:HE2	26:Y:14:ARG:HG2	1.63	0.63
1:2:1834:A:H2	1:2:1837:G:H1	1.45	0.63
9:H:20:ASP:HB2	9:H:23:LYS:HE2	1.80	0.63
1:2:1658:G:OP2	1:2:1660:C:N4	2.30	0.63
2:A:9256:G:O6	2:A:9267:U:O2	2.17	0.63
17:P:30:VAL:HG12	17:P:94:HIS:HB2	1.78	0.63
1:2:372:U:OP1	14:M:136:LYS:NZ	2.24	0.63
1:2:637:U:O2	33:f:129:ASN:ND2	2.26	0.63
1:2:1668:U:O3'	23:V:79:ARG:NH2	2.32	0.63
23:V:82:MET:N	23:V:82:MET:SD	2.72	0.63
25:X:37:PHE:CE1	25:X:103:VAL:HG21	2.33	0.63
28:a:58:LEU:HD21	28:a:91:LEU:HD11	1.80	0.63
1:2:582:U:H1'	27:Z:33:ALA:HB2	1.80	0.63
16:O:40:LEU:HD21	16:O:53:ILE:HD11	1.80	0.63
22:U:82:ARG:NH2	22:U:90:SER:OG	2.31	0.63
1:2:39:A:H62	1:2:515:G:N2	1.96	0.63
1:2:1010:G:H2'	1:2:1011:A:H8	1.63	0.63
32:e:16:GLN:OE1	32:e:19:ARG:NH2	2.32	0.63
1:2:156:G:N2	9:H:60:GLY:O	2.29	0.63
5:D:178:HIS:HB3	5:D:200:ARG:HH11	1.64	0.63
18:Q:61:ARG:NH2	18:Q:89:MET:SD	2.72	0.63
28:a:54:THR:HA	28:a:57:LYS:HE2	1.81	0.63
1:2:625:G:O6	26:Y:64:SER:N	2.30	0.63
1:2:1539:U:H4'	22:U:47:PRO:HA	1.81	0.63
8:G:136:ARG:O	8:G:203:ASN:ND2	2.32	0.63
22:U:51:ASN:HB2	22:U:54:TYR:CD2	2.34	0.63
9:H:2:LYS:HE3	9:H:15:LEU:HD23	1.81	0.62
18:Q:95:GLY:HA2	18:Q:103:ASN:O	1.98	0.62
1:2:821:G:N7	12:K:138:ARG:NH2	2.41	0.62
1:2:1275:G:O4'	1:2:1506:A:N6	2.32	0.62
5:D:201:GLY:N	5:D:221:ASP:OD2	2.32	0.62
6:E:75:LYS:HE2	13:L:22:VAL:HG13	1.80	0.62
8:G:47:LYS:NZ	8:G:70:GLU:OE2	2.30	0.62
9:H:106:LEU:HD13	9:H:109:LEU:HD21	1.80	0.62
19:R:140:ARG:HH22	23:V:75:LYS:HG3	1.65	0.62
1:2:1706:G:H1	1:2:1829:G:N2	1.97	0.62
3:B:87:VAL:O	3:B:90:PHE:HB3	1.99	0.62
3:B:180:ARG:HG3	3:B:195:TRP:HE1	1.64	0.62
4:C:91:VAL:HG22	4:C:96:CYS:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1677:U:O4	1:2:1678:A:N6	2.33	0.62
5:D:183:LYS:HD3	5:D:194:ARG:NH2	2.14	0.62
10:I:69:LEU:HD22	10:I:96:ALA:HB2	1.81	0.62
19:R:21:ALA:HB2	19:R:83:ALA:HB1	1.81	0.62
21:T:99:LEU:O	21:T:103:LEU:N	2.28	0.62
31:d:20:ARG:HG2	31:d:28:THR:HG23	1.81	0.62
1:2:492:C:O5'	27:Z:104:ARG:NH1	2.32	0.62
1:2:846:G:OP2	7:F:108:ARG:NH1	2.33	0.62
1:2:1331:C:O5'	1:2:1489:A:O2'	2.17	0.62
1:2:1636:G:N2	1:2:1636:G:OP2	2.33	0.62
5:D:81:ILE:HG23	5:D:86:LEU:HB2	1.80	0.62
19:R:115:TYR:HD2	19:R:119:LEU:HD11	1.64	0.62
1:2:582:U:H2'	1:2:583:A:H5''	1.80	0.62
1:2:583:A:H3'	1:2:584:A:H8	1.64	0.62
1:2:1256:G:C2	32:e:29:GLY:HA2	2.35	0.62
1:2:1351:G:O2'	1:2:1378:A:N1	2.26	0.62
1:2:1867:U:H3	29:b:98:PRO:HD2	1.65	0.62
1:2:14:C:H5'	5:D:190:SER:HB3	1.81	0.62
1:2:223:C:H2'	1:2:224:A:C8	2.35	0.62
1:2:600:G:OP2	1:2:630:U:O2'	2.18	0.62
1:2:864:A:H2'	1:2:865:A:H8	1.62	0.62
1:2:1301:A:OP2	32:e:2:GLY:N	2.33	0.62
1:2:379:C:O2	11:J:5:ARG:NE	2.32	0.62
1:2:1377:U:H5''	3:B:102:ARG:HH22	1.63	0.62
1:2:146:G:HO2'	1:2:147:A:H8	1.46	0.62
4:C:149:GLN:HE21	4:C:151:ARG:HB3	1.64	0.62
7:F:122:LYS:NZ	7:F:143:ASP:OD2	2.33	0.62
15:N:92:CYS:HB3	15:N:103:VAL:HG22	1.82	0.62
16:O:25:TRP:CD1	30:c:82:LYS:HZ2	2.18	0.62
1:2:1623:A:N7	21:T:132:ARG:NH1	2.47	0.62
1:2:1737:G:H2'	1:2:1738:C:C6	2.35	0.62
5:D:195:LEU:HD13	5:D:224:THR:HG22	1.81	0.62
13:L:19:GLY:HA3	13:L:71:LEU:HD22	1.82	0.62
1:2:585:C:OP2	12:K:175:ARG:NH1	2.34	0.61
1:2:1010:G:H2'	1:2:1011:A:C8	2.34	0.61
1:2:1626:C:H2'	1:2:1627:C:H6	1.65	0.61
8:G:198:ARG:O	8:G:202:SER:OG	2.14	0.61
1:2:334:C:OP2	9:H:190:ARG:NH2	2.33	0.61
7:F:59:ASP:OD1	7:F:60:GLU:N	2.33	0.61
23:V:68:THR:OG1	23:V:70:CYS:O	2.16	0.61
24:W:16:LYS:HA	24:W:23:ILE:HA	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:57:U:H1'	1:2:499:G:H1'	1.82	0.61
1:2:115:U:O2'	1:2:381:C:O2	2.12	0.61
1:2:300:U:H2'	1:2:301:A:C8	2.35	0.61
1:2:1450:G:H2'	1:2:1451:G:H8	1.66	0.61
2:A:9236:A:H2'	2:A:9237:A:C8	2.36	0.61
1:2:126:G:H8	9:H:199:THR:HG21	1.65	0.61
1:2:1112:U:O2	1:2:1121:G:O6	2.19	0.61
3:B:22:GLY:O	3:B:164:ASN:ND2	2.33	0.61
14:M:101:ARG:HH21	26:Y:5:ARG:HG3	1.64	0.61
5:D:248:TYR:O	5:D:250:TYR:N	2.33	0.61
1:2:1217:A:O2'	1:2:1684:C:O2	2.18	0.61
1:2:1374:C:O2'	1:2:1464:C:O2	2.16	0.61
16:O:104:ARG:HE	16:O:106:ARG:HH22	1.49	0.61
18:Q:34:MET:HB2	18:Q:42:ARG:HB2	1.83	0.61
19:R:19:ALA:HA	19:R:73:LYS:O	2.00	0.61
6:E:15:GLY:HA2	6:E:18:LYS:HE3	1.80	0.61
16:O:55:ARG:NH1	16:O:56:ASP:OD1	2.32	0.61
35:h:11:LEU:HB2	35:h:307:VAL:HB	1.83	0.61
1:2:805:U:N3	1:2:859:G:O6	2.34	0.61
1:2:1189:A:H2'	1:2:1190:A:C8	2.35	0.61
1:2:1220:A:O2'	8:G:145:ARG:NH2	2.32	0.61
1:2:1284:A:H5'	1:2:1285:G:H2'	1.82	0.61
1:2:1635:C:H3'	1:2:1636:G:H21	1.66	0.61
5:D:166:ARG:HH12	5:D:255:LEU:HD11	1.66	0.61
9:H:135:PRO:HB3	9:H:140:ARG:HB3	1.83	0.61
1:2:655:A:H4'	1:2:656:G:H3'	1.83	0.60
1:2:1587:G:N1	22:U:74:SER:OG	2.34	0.60
9:H:1:MET:HE1	9:H:109:LEU:HD23	1.83	0.60
20:S:17:ILE:HD13	20:S:24:LEU:HD11	1.82	0.60
1:2:987:A:OP1	29:b:32:LYS:NZ	2.23	0.60
1:2:1139:C:N4	1:2:1148:A:C6	2.69	0.60
4:C:36:PRO:HA	4:C:232:HIS:CE1	2.37	0.60
6:E:123:LEU:O	6:E:127:MET:HG2	2.02	0.60
7:F:191:ARG:HG2	7:F:245:ARG:HB2	1.83	0.60
14:M:93:LEU:HB3	14:M:102:PHE:HD2	1.66	0.60
24:W:16:LYS:HG2	24:W:23:ILE:HG22	1.83	0.60
1:2:91:A:OP2	1:2:446:G:N1	2.23	0.60
1:2:1204:G:O2'	1:2:1700:C:OP2	2.19	0.60
26:Y:131:LEU:HD23	26:Y:135:LYS:HD3	1.83	0.60
1:2:1144:A:H2'	1:2:1145:A:C8	2.36	0.60
1:2:1276:A:N6	1:2:1321:G:H21	1.89	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1649:U:H2'	1:2:1650:A:C8	2.33	0.60
1:2:1863:A:OP2	29:b:4:LYS:NZ	2.33	0.60
4:C:82:ARG:NH1	4:C:189:ILE:O	2.35	0.60
19:R:12:VAL:HG11	19:R:90:LYS:HB3	1.83	0.60
25:X:28:ARG:HB3	25:X:29:PRO:HD3	1.83	0.60
30:c:21:LYS:HZ1	30:c:26:GLN:HE22	1.47	0.60
35:h:93:THR:HG23	35:h:94:THR:HG23	1.81	0.60
1:2:1464:C:H3'	1:2:1465:A:C8	2.36	0.60
7:F:127:ARG:NH1	7:F:141:THR:O	2.35	0.60
35:h:18:VAL:HA	35:h:35:SER:HA	1.82	0.60
35:h:188:HIS:HE1	35:h:224:GLY:HA3	1.66	0.60
1:2:380:G:OP2	11:J:181:GLN:NE2	2.26	0.60
28:a:85:ARG:HG2	28:a:89:GLN:HE22	1.67	0.60
36:n:1:MET:HE1	36:n:9:ARG:HE	1.65	0.60
1:2:298:G:H2'	1:2:299:A:H8	1.67	0.60
1:2:993:G:OP2	1:2:1132:C:O2'	2.17	0.60
3:B:54:THR:HG22	3:B:162:PRO:HG2	1.84	0.60
8:G:169:ILE:HA	8:G:172:CYS:HB2	1.83	0.60
1:2:552:G:H5''	33:f:108:ARG:HH22	1.67	0.60
1:2:809:A:H2	1:2:855:G:H1	1.49	0.60
1:2:1657:G:O3'	32:e:33:LYS:NZ	2.26	0.60
3:B:85:ARG:NH1	3:B:201:LEU:O	2.34	0.60
6:E:7:LYS:NZ	23:V:113:GLU:OE2	2.32	0.60
3:B:52:LYS:H	20:S:109:LEU:HD21	1.67	0.60
5:D:209:VAL:HG23	5:D:210:PRO:HD3	1.83	0.60
24:W:32:ILE:HD11	24:W:60:ARG:HD2	1.82	0.60
31:d:7:GLN:NE2	31:d:59:LEU:O	2.34	0.60
11:J:182:CYS:O	11:J:184:ARG:NH1	2.35	0.59
28:a:100:VAL:HB	28:a:108:ILE:HG23	1.82	0.59
35:h:42:MET:HE3	35:h:59:LEU:HD21	1.84	0.59
1:2:874:G:O2'	1:2:875:A:OP1	2.20	0.59
1:2:913:A:OP1	10:I:99:ARG:NH2	2.35	0.59
1:2:1480:A:O2'	32:e:56:ASP:O	2.20	0.59
1:2:1535:U:OP2	8:G:168:THR:OG1	2.15	0.59
3:B:109:THR:N	3:B:136:GLU:OE2	2.33	0.59
11:J:110:ARG:NH1	11:J:114:GLU:OE2	2.36	0.59
12:K:130:ILE:HD13	12:K:145:PRO:HA	1.84	0.59
1:2:31:U:O2'	1:2:643:A:N1	2.28	0.59
1:2:144:U:H2'	1:2:145:G:H8	1.66	0.59
1:2:360:A:N6	1:2:400:C:O2	2.35	0.59
1:2:1337:C:H2'	1:2:1338:G:H8	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:118:SER:HB2	15:N:121:LYS:HB2	1.84	0.59
17:P:126:ILE:HD11	29:b:53:ILE:HG23	1.84	0.59
19:R:76:GLY:O	19:R:77:HIS:ND1	2.35	0.59
22:U:6:VAL:HG11	22:U:65:TYR:HE2	1.68	0.59
1:2:1183:A:H4'	36:n:11:ARG:HH21	1.65	0.59
1:2:146:G:H1	1:2:173:A:N6	1.98	0.59
1:2:422:U:OP1	14:M:98:LYS:NZ	2.36	0.59
1:2:876:C:H2'	1:2:877:C:C6	2.37	0.59
1:2:483:C:OP1	26:Y:76:LYS:NZ	2.35	0.59
1:2:929:G:N2	1:2:1013:U:O2	2.35	0.59
1:2:1309:C:H41	34:g:133:ALA:HB2	1.68	0.59
1:2:1672:U:H2'	1:2:1673:U:C6	2.38	0.59
5:D:193:VAL:HG11	5:D:240:THR:HG22	1.84	0.59
12:K:63:LEU:O	12:K:70:ARG:NH1	2.36	0.59
1:2:394:G:H5'	14:M:81:LYS:HB3	1.84	0.59
1:2:1525:C:N4	1:2:1526:G:O6	2.36	0.59
1:2:1709:G:H2'	1:2:1710:C:C6	2.38	0.59
5:D:138:GLY:HA3	5:D:162:ILE:HG22	1.84	0.59
5:D:206:SER:HB3	5:D:210:PRO:HG2	1.84	0.59
11:J:25:ARG:N	11:J:28:GLU:OE2	2.33	0.59
30:c:15:GLU:O	30:c:23:ARG:NE	2.34	0.59
35:h:155:ARG:HE	35:h:156:PHE:H	1.50	0.59
1:2:25:A:HO2'	1:2:26:U:H6	1.50	0.59
1:2:439:A:OP1	11:J:24:LYS:NZ	2.33	0.59
1:2:1144:A:H2'	1:2:1145:A:H8	1.68	0.59
1:2:1178:U:H2'	1:2:1179:G:H8	1.68	0.59
16:O:63:VAL:HG11	16:O:71:ILE:HG23	1.84	0.59
23:V:24:LEU:HD12	23:V:110:VAL:HG12	1.85	0.59
1:2:1322:G:H2'	1:2:1323:U:C6	2.38	0.58
1:2:1401:A:H2'	1:2:1402:A:H8	1.68	0.58
18:Q:30:TYR:HA	18:Q:33:LEU:HB2	1.85	0.58
1:2:1119:A:N7	2:A:9231:G:N1	2.51	0.58
1:2:1237:C:H2'	1:2:1238:U:O4'	2.03	0.58
1:2:1275:G:N2	1:2:1506:A:OP2	2.36	0.58
6:E:72:VAL:HA	6:E:75:LYS:HZ3	1.67	0.58
10:I:46:THR:HG23	10:I:65:PRO:HD3	1.84	0.58
29:b:73:TYR:HE2	29:b:83:VAL:HG21	1.68	0.58
32:e:21:CYS:SG	32:e:22:ARG:N	2.77	0.58
35:h:7:LEU:HD11	35:h:308:ARG:HE	1.68	0.58
1:2:935:G:H2'	1:2:936:G:H8	1.67	0.58
15:N:40:LYS:HG3	34:g:129:GLY:HA3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:29:G:OP1	26:Y:124:LYS:NZ	2.35	0.58
1:2:1015:U:OP2	30:c:20:LYS:NZ	2.33	0.58
1:2:1045:U:H2'	1:2:1046:U:H6	1.68	0.58
1:2:1264:C:O2	1:2:1266:C:N4	2.35	0.58
1:2:1672:U:OP1	19:R:18:THR:OG1	2.13	0.58
2:A:9155:C:H2'	2:A:9156:A:H8	1.69	0.58
7:F:185:GLY:H	7:F:189:LEU:HD13	1.68	0.58
8:G:187:SER:OG	8:G:188:TYR:N	2.37	0.58
22:U:59:SER:O	22:U:63:HIS:ND1	2.34	0.58
1:2:583:A:OP1	12:K:162:ARG:NH2	2.36	0.58
16:O:122:ILE:HD11	16:O:141:TYR:CE2	2.39	0.58
17:P:35:ALA:HB2	17:P:112:ALA:HB2	1.85	0.58
1:2:457:C:H2'	1:2:458:A:H8	1.68	0.58
1:2:654:A:OP2	1:2:655:A:O2'	2.21	0.58
1:2:1652:G:O2'	8:G:85:LYS:NZ	2.35	0.58
8:G:124:ASP:HB3	8:G:196:LEU:HD21	1.85	0.58
35:h:200:VAL:HG22	35:h:207:CYS:HB3	1.84	0.58
1:2:46:A:N7	1:2:97:U:O2'	2.35	0.58
1:2:525:A:H61	1:2:590:A:H5'	1.67	0.58
1:2:751:G:N2	1:2:792:C:N3	2.50	0.58
1:2:830:A:OP2	1:2:846:G:N2	2.36	0.58
1:2:1101:U:H2'	1:2:1102:G:C8	2.37	0.58
8:G:157:GLY:O	8:G:161:ALA:HB2	2.03	0.58
12:K:16:PRO:HD2	12:K:44:TRP:CZ2	2.38	0.58
5:D:186:GLY:HA3	5:D:243:ALA:HB2	1.86	0.58
31:d:7:GLN:OE1	31:d:10:LYS:NZ	2.31	0.58
1:2:1223:A:H5'	8:G:78:MET:HE3	1.86	0.58
1:2:1565:C:H2'	1:2:1566:G:C8	2.39	0.58
1:2:1641:A:O2'	19:R:146:ARG:NH2	2.36	0.58
11:J:98:LYS:HB3	11:J:178:ARG:HA	1.85	0.58
1:2:1643:U:H2'	1:2:1644:C:H5	1.68	0.58
2:A:9157:G:H2'	2:A:9158:G:H8	1.68	0.58
6:E:106:ARG:HG3	6:E:175:VAL:HG12	1.85	0.58
16:O:71:ILE:HA	16:O:74:ILE:HG12	1.84	0.58
1:2:1297:U:H2'	1:2:1298:G:H2'	1.86	0.57
3:B:89:LYS:O	3:B:93:ALA:N	2.33	0.57
16:O:38:TYR:O	16:O:42:LYS:HG2	2.04	0.57
1:2:482:G:H5''	26:Y:76:LYS:HE3	1.86	0.57
1:2:508:A:C5	1:2:509:G:H1'	2.38	0.57
1:2:531:A:H3'	1:2:532:C:H5''	1.85	0.57
1:2:1045:U:H2'	1:2:1046:U:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1714:U:H2'	1:2:1715:A:C8	2.39	0.57
4:C:52:THR:HG22	4:C:57:ILE:HA	1.86	0.57
4:C:89:GLU:HG3	4:C:228:LEU:HD22	1.87	0.57
5:D:110:MET:HE3	5:D:127:PHE:HE2	1.69	0.57
1:2:1224:G:C2	1:2:1642:U:O2	2.57	0.57
1:2:1588:A:H2'	1:2:1589:A:O4'	2.03	0.57
1:2:1808:U:H2'	1:2:1809:A:C8	2.39	0.57
3:B:42:LYS:HG3	3:B:43:SER:O	2.04	0.57
8:G:34:SER:HB3	31:d:11:LEU:HD11	1.85	0.57
23:V:83:ARG:HH11	32:e:55:LEU:HD13	1.68	0.57
1:2:492:C:H6	27:Z:104:ARG:HH12	1.52	0.57
1:2:525:A:O5'	1:2:590:A:N6	2.29	0.57
1:2:946:U:H2'	1:2:947:G:C8	2.40	0.57
1:2:1606:G:H4'	1:2:1607:A:H8	1.70	0.57
10:I:75:ILE:HD13	10:I:78:ARG:HH11	1.69	0.57
27:Z:57:VAL:HG12	27:Z:73:GLY:HA2	1.86	0.57
1:2:373:G:H4'	14:M:85:THR:HG21	1.86	0.57
1:2:530:U:H3	1:2:554:A:H61	1.51	0.57
1:2:1670:C:H2'	1:2:1671:G:H8	1.69	0.57
1:2:1486:A:H2'	1:2:1487:A:H8	1.70	0.57
1:2:1818:A:O2'	36:n:17:ARG:NH1	2.38	0.57
2:A:9271:G:H2'	2:A:9299:G:H8	1.69	0.57
3:B:41:ARG:HE	3:B:45:GLY:HA2	1.69	0.57
3:B:169:HIS:HD2	3:B:203:PHE:HE2	1.53	0.57
7:F:201:HIS:HD2	7:F:206:ASP:HA	1.70	0.57
11:J:110:ARG:HA	11:J:121:LEU:HD23	1.85	0.57
16:O:83:ASP:OD1	16:O:84:LEU:N	2.38	0.57
1:2:943:U:O2'	17:P:135:ILE:O	2.20	0.57
1:2:1475:G:N2	1:2:1475:G:OP2	2.34	0.57
1:2:1605:G:O6	1:2:1632:G:O2'	2.19	0.57
8:G:168:THR:HG21	28:a:106:GLN:HB3	1.85	0.57
11:J:149:TYR:O	11:J:153:LYS:HG2	2.05	0.57
1:2:70:G:N2	1:2:71:G:O6	2.38	0.57
1:2:624:C:N4	26:Y:63:ASN:OD1	2.37	0.57
1:2:1337:C:H2'	1:2:1338:G:C8	2.40	0.57
7:F:102:ILE:HD12	7:F:239:PRO:HD3	1.86	0.57
13:L:20:VAL:HG12	13:L:70:TYR:HA	1.87	0.57
1:2:436:G:O6	1:2:458:A:N6	2.37	0.57
1:2:815:U:O4	1:2:816:A:N6	2.37	0.57
1:2:1672:U:H2'	1:2:1673:U:H6	1.69	0.57
16:O:45:LEU:HB3	16:O:49:GLN:HG3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1224:G:H2'	1:2:1225:U:C6	2.40	0.57
1:2:1232:U:OP2	21:T:135:HIS:ND1	2.38	0.57
1:2:1608:U:H4'	21:T:130:ARG:HH11	1.69	0.57
3:B:85:ARG:HA	3:B:88:LEU:HD12	1.87	0.57
7:F:104:ASP:HB3	7:F:110:ALA:HB2	1.86	0.57
21:T:114:LEU:HB3	21:T:122:GLY:HA3	1.86	0.57
35:h:5:MET:HE1	35:h:270:LEU:HD22	1.87	0.57
1:2:479:C:H2'	1:2:480:G:H8	1.70	0.56
1:2:948:C:H2'	1:2:949:G:H8	1.70	0.56
1:2:1133:A:C2	1:2:1134:G:C8	2.93	0.56
1:2:1358:U:OP2	5:D:123:ARG:NH2	2.38	0.56
1:2:1779:G:H2'	1:2:1780:G:O4'	2.04	0.56
5:D:256:TRP:NE1	25:X:68:ARG:HB2	2.19	0.56
11:J:116:HIS:O	11:J:152:ARG:NH1	2.32	0.56
11:J:174:CYS:SG	11:J:175:ILE:N	2.78	0.56
21:T:113:ARG:HE	21:T:114:LEU:HD22	1.70	0.56
1:2:516:A:N1	1:2:643:A:O2'	2.38	0.56
1:2:1154:U:H6	5:D:194:ARG:HD2	1.70	0.56
3:B:26:GLY:HA2	3:B:164:ASN:HB3	1.86	0.56
3:B:91:ALA:O	3:B:95:GLY:N	2.38	0.56
12:K:103:GLU:H	12:K:103:GLU:CD	2.13	0.56
26:Y:61:GLN:HB3	26:Y:62:PRO:HD3	1.87	0.56
26:Y:67:ARG:HG3	26:Y:115:ILE:HG22	1.87	0.56
35:h:158:PRO:HG2	35:h:202:PRO:HA	1.85	0.56
1:2:85:A:H5'	27:Z:119:GLY:HA2	1.87	0.56
1:2:647:U:H2'	1:2:648:A:H8	1.70	0.56
1:2:849:A:H2'	1:2:850:C:C6	2.41	0.56
1:2:1222:G:O3'	8:G:78:MET:HE2	2.04	0.56
1:2:1243:U:OP1	1:2:1518:C:O2'	2.23	0.56
4:C:181:LEU:HA	4:C:184:VAL:HG12	1.87	0.56
8:G:134:VAL:HG23	8:G:135:ARG:H	1.70	0.56
13:L:4:PRO:HD2	13:L:7:ASN:HD21	1.69	0.56
14:M:49:GLU:O	14:M:53:GLY:N	2.38	0.56
17:P:39:ASP:N	17:P:69:SER:HB3	2.20	0.56
19:R:123:ASP:OD1	19:R:125:ARG:NH1	2.38	0.56
20:S:97:GLU:OE1	20:S:118:GLN:NE2	2.37	0.56
26:Y:91:LEU:HD13	33:f:82:VAL:HG11	1.86	0.56
35:h:91:ASP:N	35:h:96:THR:O	2.28	0.56
1:2:155:G:N1	1:2:156:G:O6	2.39	0.56
1:2:852:G:OP2	1:2:854:A:N6	2.38	0.56
1:2:1169:G:H21	1:2:1191:C:N4	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:181:GLU:O	3:B:185:MET:HE3	2.05	0.56
4:C:62:LEU:HD12	4:C:65:ARG:NE	2.21	0.56
22:U:28:LEU:HD12	22:U:53:PHE:HE2	1.70	0.56
22:U:40:ALA:HB2	22:U:79:TYR:CE2	2.40	0.56
35:h:236:ILE:HG12	35:h:252:THR:HG22	1.87	0.56
1:2:1625:U:H2'	1:2:1626:C:H6	1.71	0.56
3:B:120:ARG:HH12	5:D:267:GLN:HG3	1.71	0.56
7:F:251:GLU:HA	7:F:254:LYS:HG2	1.87	0.56
27:Z:47:MET:O	27:Z:49:LYS:NZ	2.39	0.56
27:Z:122:LYS:HA	27:Z:125:VAL:HG12	1.87	0.56
1:2:64:A:H61	1:2:82:G:H3'	1.70	0.56
1:2:552:G:H5'	33:f:108:ARG:HH12	1.70	0.56
1:2:864:A:H2'	1:2:865:A:C8	2.39	0.56
1:2:1550:G:H1'	1:2:1559:C:H1'	1.87	0.56
4:C:146:ARG:HB2	4:C:149:GLN:HB2	1.87	0.56
10:I:148:LEU:HD12	25:X:49:GLU:OE1	2.05	0.56
12:K:86:VAL:HG13	12:K:87:LEU:HD12	1.87	0.56
14:M:99:TYR:CE2	26:Y:14:ARG:HG2	2.40	0.56
19:R:118:THR:HA	19:R:121:VAL:HG12	1.86	0.56
33:f:79:LEU:HA	33:f:81:ARG:HH11	1.69	0.56
1:2:33:G:H1	1:2:522:A:H2	1.53	0.56
1:2:687:C:N3	10:I:118:ARG:NH2	2.53	0.56
1:2:1297:U:O2	1:2:1298:G:N2	2.28	0.56
2:A:9306:G:N7	31:d:67:ARG:NH2	2.54	0.56
8:G:128:ILE:HG13	8:G:137:GLN:HG2	1.88	0.56
14:M:78:THR:HB	14:M:87:VAL:HG13	1.87	0.56
17:P:43:HIS:HD2	17:P:55:ARG:HB3	1.70	0.56
9:H:84:TYR:OH	9:H:91:GLU:OE2	2.24	0.56
26:Y:17:ARG:HD3	26:Y:21:LYS:HG3	1.88	0.56
1:2:380:G:N1	1:2:383:G:OP2	2.33	0.56
1:2:1461:G:C6	1:2:1463:U:H1'	2.40	0.56
1:2:1515:G:H2'	1:2:1516:G:H8	1.71	0.56
1:2:568:C:H42	1:2:582:U:H3	1.52	0.56
9:H:121:ILE:HD12	9:H:122:PRO:HD2	1.87	0.56
18:Q:28:MET:HE2	18:Q:33:LEU:HG	1.88	0.56
32:e:21:CYS:SG	32:e:39:CYS:N	2.79	0.56
1:2:1213:C:H2'	1:2:1214:A:C8	2.41	0.55
1:2:1668:U:O2'	23:V:79:ARG:NH1	2.36	0.55
1:2:1678:A:O2'	1:2:1679:A:O4'	2.22	0.55
2:A:9239:C:H2'	2:A:9240:C:C6	2.41	0.55
3:B:81:ASN:OD1	3:B:82:THR:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:197:VAL:HG23	3:B:198:MET:H	1.71	0.55
5:D:169:TYR:OH	5:D:175:GLY:O	2.25	0.55
8:G:94:LYS:O	8:G:98:GLU:HG2	2.05	0.55
1:2:809:A:H2	1:2:855:G:N1	2.04	0.55
1:2:1094:C:O2	25:X:16:ASN:ND2	2.40	0.55
1:2:1651:A:O2'	8:G:83:ASN:HB2	2.07	0.55
4:C:47:THR:OG1	17:P:46:ASP:OD2	2.18	0.55
13:L:5:LYS:HD3	13:L:8:ARG:HH12	1.71	0.55
32:e:47:ALA:HA	32:e:50:ILE:HB	1.88	0.55
1:2:89:C:N4	1:2:90:G:O6	2.39	0.55
1:2:535:G:N1	1:2:550:C:O2	2.40	0.55
1:2:1722:G:H1	1:2:1812:U:H3	1.52	0.55
2:A:9257:C:H2'	2:A:9258:C:C6	2.41	0.55
2:A:9293:U:OP1	2:A:9296:U:O2'	2.23	0.55
19:R:75:GLY:HA3	19:R:79:ALA:HB3	1.87	0.55
1:2:647:U:H2'	1:2:648:A:C8	2.42	0.55
1:2:809:A:H2'	1:2:810:A:O4'	2.07	0.55
1:2:1239:U:O2	1:2:1241:A:H3'	2.07	0.55
4:C:107:ARG:NH1	17:P:133:THR:O	2.31	0.55
7:F:124:CYS:HB3	7:F:141:THR:HB	1.88	0.55
19:R:116:ASP:HB3	19:R:119:LEU:HG	1.87	0.55
26:Y:85:VAL:HG11	26:Y:91:LEU:HD11	1.88	0.55
35:h:155:ARG:HG2	35:h:200:VAL:H	1.71	0.55
1:2:309:G:H2'	1:2:310:C:C6	2.42	0.55
1:2:667:U:H5''	1:2:1087:A:C5	2.41	0.55
1:2:1044:G:H5'	1:2:1045:U:OP1	2.07	0.55
1:2:1182:A:C5	1:2:1183:A:H1'	2.42	0.55
1:2:1474:A:H5''	19:R:121:VAL:HG23	1.87	0.55
1:2:1709:G:C6	1:2:1826:G:O6	2.59	0.55
1:2:1822:A:H2'	1:2:1823:A:C4	2.41	0.55
35:h:226:HIS:NE2	35:h:229:THR:OG1	2.38	0.55
1:2:1260:A:H61	1:2:1617:G:H21	1.54	0.55
6:E:157:MET:HE3	6:E:158:ILE:H	1.71	0.55
22:U:83:GLN:HB2	22:U:93:SER:HB3	1.89	0.55
1:2:183:G:O2'	1:2:184:G:O5'	2.24	0.55
1:2:860:G:O2'	1:2:861:A:O4'	2.23	0.55
1:2:1430:C:H2'	1:2:1431:G:C8	2.42	0.55
1:2:1665:G:C2	22:U:88:MET:HE1	2.42	0.55
2:A:9158:G:H1	2:A:9290:U:H3	1.55	0.55
6:E:177:LEU:HD12	6:E:182:LEU:HD13	1.88	0.55
14:M:7:GLU:HG2	14:M:8:ARG:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:5:ARG:HD2	20:S:10:LYS:HG3	1.88	0.55
1:2:156:G:H21	9:H:60:GLY:C	2.15	0.55
1:2:1446:A:H1'	1:2:1447:G:C8	2.42	0.55
1:2:1676:U:H4'	8:G:71:ARG:HH12	1.72	0.55
1:2:1854:U:OP1	17:P:150:ARG:NH2	2.38	0.55
8:G:78:MET:HG3	8:G:79:HIS:N	2.19	0.55
20:S:71:ILE:HD12	20:S:74:GLN:HA	1.89	0.55
26:Y:124:LYS:HD2	26:Y:129:SER:HA	1.88	0.55
36:n:16:LYS:HA	36:n:19:LYS:HZ2	1.70	0.55
1:2:107:A:H2'	1:2:108:G:H8	1.72	0.55
1:2:1387:G:C2	1:2:1388:A:H1'	2.42	0.55
6:E:23:GLU:OE2	6:E:27:ARG:NH1	2.40	0.55
35:h:40:ILE:HD11	35:h:66:VAL:HG21	1.89	0.55
35:h:256:ILE:HB	35:h:270:LEU:HB3	1.88	0.55
16:O:110:ASP:OD1	16:O:111:ALA:N	2.40	0.55
1:2:121:U:H2'	1:2:122:G:H8	1.72	0.54
1:2:527:C:H2'	1:2:528:A:H8	1.72	0.54
10:I:34:SER:O	10:I:37:LYS:NZ	2.40	0.54
24:W:32:ILE:HG22	24:W:34:MET:H	1.71	0.54
33:f:108:ARG:O	33:f:112:ASN:ND2	2.40	0.54
35:h:212:LYS:HD2	35:h:235:ILE:HG12	1.88	0.54
1:2:1005:G:OP2	4:C:162:ARG:NH1	2.40	0.54
7:F:45:ILE:HA	7:F:61:VAL:HG21	1.88	0.54
7:F:72:ILE:N	7:F:75:LYS:O	2.19	0.54
9:H:188:LYS:O	9:H:191:ARG:HG2	2.08	0.54
14:M:112:HIS:HB2	14:M:138:VAL:HG11	1.88	0.54
18:Q:54:HIS:HB3	18:Q:57:LEU:HB2	1.89	0.54
25:X:11:LEU:HD11	25:X:37:PHE:HE2	1.72	0.54
1:2:1478:U:H2'	1:2:1479:G:H8	1.72	0.54
1:2:1515:G:H2'	1:2:1516:G:C8	2.42	0.54
1:2:1710:C:H42	1:2:1824:A:H61	1.55	0.54
4:C:182:LYS:O	4:C:186:ASN:ND2	2.39	0.54
13:L:80:ARG:HH11	13:L:87:PRO:HA	1.72	0.54
1:2:29:G:H2'	1:2:30:C:C6	2.43	0.54
1:2:1835:A:N1	29:b:80:HIS:ND1	2.55	0.54
19:R:96:TYR:HB3	19:R:105:LYS:HB3	1.88	0.54
19:R:140:ARG:HH12	23:V:75:LYS:HB2	1.73	0.54
21:T:24:ARG:NH2	21:T:28:PHE:O	2.41	0.54
22:U:11:GLN:HA	22:U:14:PHE:HB3	1.89	0.54
1:2:1139:C:C4	1:2:1148:A:C6	2.95	0.54
1:2:1454:A:H2	1:2:1455:A:H62	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:25:THR:HG22	23:V:86:LYS:HG2	1.89	0.54
29:b:44:ILE:HD12	29:b:65:PRO:HG2	1.90	0.54
1:2:677:G:H2'	1:2:678:U:C6	2.42	0.54
1:2:917:U:H1'	10:I:118:ARG:HD2	1.89	0.54
3:B:42:LYS:HE3	3:B:48:ILE:HD11	1.89	0.54
10:I:75:ILE:HG22	10:I:79:LEU:HD23	1.89	0.54
27:Z:6:THR:HG22	27:Z:28:LEU:HB3	1.89	0.54
1:2:60:A:H2'	1:2:61:A:C5	2.42	0.54
1:2:1593:C:OP1	28:a:103:HIS:NE2	2.35	0.54
1:2:1668:U:H2'	1:2:1669:G:H8	1.71	0.54
1:2:1717:C:H2'	1:2:1718:G:C8	2.43	0.54
6:E:219:PRO:HG2	35:h:190:GLY:HA2	1.89	0.54
8:G:71:ARG:CZ	8:G:151:ILE:HG21	2.38	0.54
21:T:25:LYS:O	21:T:29:ALA:N	2.38	0.54
35:h:19:THR:HA	35:h:287:THR:HG21	1.90	0.54
1:2:659:G:O2'	1:2:662:G:O2'	2.25	0.54
1:2:928:G:H2'	1:2:929:G:C8	2.43	0.54
1:2:1737:G:H2'	1:2:1738:C:H6	1.73	0.54
19:R:81:ILE:HA	19:R:84:ILE:HG12	1.88	0.54
20:S:46:LEU:O	20:S:50:ILE:HG23	2.08	0.54
23:V:21:ARG:HE	23:V:90:ASP:HB3	1.72	0.54
30:c:36:LYS:HB2	30:c:43:ILE:HG22	1.90	0.54
35:h:212:LYS:HA	35:h:235:ILE:HG23	1.89	0.54
1:2:118:C:H1'	1:2:445:A:C6	2.43	0.54
1:2:223:C:H2'	1:2:224:A:H8	1.73	0.54
1:2:1593:C:P	28:a:103:HIS:HE2	2.30	0.54
4:C:83:LYS:HE2	4:C:106:THR:HA	1.90	0.54
6:E:164:VAL:HG23	6:E:168:VAL:HG21	1.90	0.54
6:E:167:TYR:OH	6:E:203:PRO:O	2.26	0.54
14:M:57:ASP:OD1	14:M:58:LYS:N	2.40	0.54
23:V:66:ARG:HH11	23:V:67:LYS:H	1.55	0.54
30:c:31:TYR:O	30:c:48:SER:OG	2.19	0.54
35:h:99:ARG:NH2	35:h:135:LEU:O	2.37	0.54
1:2:442:C:H2'	1:2:443:U:C6	2.43	0.54
1:2:1277:C:H2'	1:2:1278:A:C8	2.43	0.54
1:2:1711:U:H2'	1:2:1712:A:C8	2.43	0.54
3:B:104:THR:O	3:B:107:THR:OG1	2.24	0.54
32:e:22:ARG:HB3	32:e:38:MET:HE1	1.90	0.54
1:2:215:G:H2'	1:2:216:C:C6	2.43	0.53
1:2:1397:U:O2'	35:h:60:ARG:NH1	2.41	0.53
1:2:1477:U:OP2	20:S:3:ARG:NH1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1532:C:H2'	1:2:1637:A:N7	2.23	0.53
1:2:1617:G:O6	18:Q:43:ARG:NH1	2.40	0.53
6:E:192:TRP:HD1	6:E:200:PRO:HG2	1.72	0.53
7:F:11:ARG:HA	7:F:28:ALA:HB2	1.89	0.53
12:K:31:LEU:O	12:K:35:TYR:HB2	2.08	0.53
18:Q:34:MET:SD	18:Q:35:GLN:N	2.81	0.53
1:2:659:G:HO2'	1:2:662:G:HO2'	1.56	0.53
1:2:1024:A:OP1	16:O:4:MET:HG3	2.09	0.53
1:2:1718:G:N2	1:2:1815:A:H62	2.05	0.53
6:E:38:GLU:HB2	6:E:49:ILE:HG23	1.90	0.53
6:E:157:MET:HE2	6:E:187:LYS:HE3	1.89	0.53
18:Q:85:ILE:HG12	18:Q:111:MET:SD	2.48	0.53
35:h:218:LEU:HB3	35:h:227:LEU:HD12	1.88	0.53
1:2:155:G:H4'	9:H:15:LEU:HD21	1.90	0.53
1:2:1133:A:H4'	29:b:13:LYS:HG3	1.91	0.53
2:A:9286:G:H2'	2:A:9287:G:H8	1.74	0.53
7:F:47:PHE:HE2	7:F:90:ILE:HG21	1.74	0.53
9:H:88:ARG:HB3	9:H:91:GLU:HG2	1.90	0.53
10:I:52:GLU:N	10:I:52:GLU:OE1	2.42	0.53
18:Q:33:LEU:HD23	18:Q:36:LEU:HD23	1.90	0.53
19:R:102:GLU:HA	19:R:105:LYS:HG2	1.90	0.53
29:b:82:LYS:HD3	29:b:85:ARG:HH21	1.74	0.53
1:2:1408:U:O4	1:2:1409:A:N6	2.41	0.53
2:A:9226:G:H2'	2:A:9227:G:C8	2.43	0.53
9:H:48:TYR:OH	9:H:116:LYS:NZ	2.38	0.53
22:U:83:GLN:NE2	22:U:85:ASN:OD1	2.37	0.53
23:V:91:LEU:HD13	23:V:93:SER:HB2	1.89	0.53
24:W:73:ALA:O	24:W:77:GLY:N	2.40	0.53
1:2:1094:C:H1'	25:X:16:ASN:HD22	1.72	0.53
1:2:1547:C:N3	1:2:1669:G:N2	2.56	0.53
6:E:40:ARG:HD3	23:V:108:PRO:HB3	1.90	0.53
8:G:47:LYS:NZ	8:G:51:HIS:O	2.33	0.53
18:Q:18:ARG:HA	21:T:93:GLY:HA3	1.91	0.53
35:h:172:LYS:HA	35:h:195:LEU:HD23	1.90	0.53
35:h:256:ILE:HD12	35:h:270:LEU:HD23	1.91	0.53
1:2:219:U:H2'	1:2:220:U:H6	1.73	0.53
1:2:818:A:H2'	1:2:819:G:H8	1.74	0.53
1:2:1651:A:H2'	1:2:1652:G:H8	1.73	0.53
6:E:123:LEU:HA	6:E:126:ILE:HG22	1.91	0.53
7:F:137:PRO:HB2	7:F:150:PRO:HD2	1.91	0.53
13:L:57:TYR:O	13:L:72:THR:OG1	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:74:ALA:HB1	17:P:115:ALA:HB2	1.91	0.53
1:2:809:A:OP1	7:F:186:GLY:HA3	2.08	0.53
1:2:1322:G:H2'	1:2:1323:U:H6	1.72	0.53
4:C:136:ARG:HB2	4:C:218:LEU:HD11	1.91	0.53
27:Z:37:LYS:HA	27:Z:40:ILE:HD12	1.90	0.53
27:Z:45:ALA:HB1	27:Z:50:THR:O	2.08	0.53
1:2:346:C:H2'	1:2:347:G:O4'	2.08	0.53
7:F:127:ARG:NH1	7:F:142:HIS:HA	2.24	0.53
21:T:114:LEU:HA	21:T:117:ILE:HG22	1.91	0.53
35:h:88:ARG:HH12	35:h:90:TRP:HB2	1.73	0.53
1:2:65:C:H2'	9:H:133:LEU:HD22	1.90	0.53
1:2:86:C:OP1	27:Z:118:ARG:NH2	2.37	0.53
1:2:1759:G:O2'	1:2:1760:G:OP1	2.23	0.53
7:F:15:PRO:O	7:F:18:TRP:HD1	1.92	0.53
12:K:21:GLU:OE1	12:K:23:SER:N	2.41	0.53
24:W:67:ASP:O	24:W:71:ARG:HG2	2.09	0.53
25:X:102:ILE:HG22	25:X:113:HIS:ND1	2.24	0.53
35:h:106:LYS:HE3	35:h:126:ASP:HB3	1.90	0.53
35:h:147:HIS:HD2	35:h:151:VAL:HG22	1.74	0.53
1:2:464:A:H3'	1:2:465:A:C8	2.41	0.53
1:2:844:U:OP2	7:F:240:ARG:NH1	2.41	0.53
2:A:9271:G:H2'	2:A:9299:G:C8	2.44	0.53
6:E:161:GLY:O	6:E:164:VAL:HG12	2.09	0.53
6:E:202:LYS:HD2	6:E:203:PRO:HD2	1.91	0.53
35:h:220:ASP:HB2	35:h:227:LEU:HD21	1.89	0.53
1:2:39:A:P	12:K:7:TRP:HE1	2.32	0.52
1:2:612:U:O2'	1:2:613:G:OP1	2.27	0.52
1:2:1200:A:O2'	1:2:1357:A:N1	2.39	0.52
1:2:1541:G:H21	22:U:12:GLN:CD	2.17	0.52
1:2:1676:U:O3'	8:G:71:ARG:NH2	2.41	0.52
4:C:33:VAL:HA	4:C:96:CYS:HB3	1.91	0.52
14:M:85:THR:OG1	14:M:111:VAL:O	2.21	0.52
35:h:68:ASP:HB3	35:h:111:VAL:HG22	1.90	0.52
1:2:106:C:H2'	1:2:107:A:H8	1.74	0.52
1:2:379:C:H2'	1:2:380:G:C8	2.44	0.52
1:2:877:C:H2'	1:2:878:G:C8	2.44	0.52
1:2:913:A:C5	10:I:98:ARG:HG2	2.44	0.52
1:2:1406:G:H2'	1:2:1407:U:C6	2.44	0.52
1:2:1713:C:H2'	1:2:1714:U:C6	2.44	0.52
2:A:9229:U:H3'	2:A:9230:U:H2'	1.91	0.52
2:A:9288:U:H2'	2:A:9289:U:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:40:ASN:ND2	4:C:76:ASN:OD1	2.35	0.52
6:E:12:VAL:O	6:E:16:ILE:HG12	2.09	0.52
12:K:21:GLU:OE2	12:K:24:ARG:HG2	2.09	0.52
21:T:16:LEU:HD13	21:T:99:LEU:HD11	1.91	0.52
1:2:1516:G:H5''	18:Q:81:ARG:HH11	1.75	0.52
4:C:87:ILE:O	4:C:99:ASN:N	2.42	0.52
14:M:96:ILE:HD12	26:Y:10:ALA:HB1	1.91	0.52
35:h:17:TRP:HB2	35:h:303:THR:HA	1.90	0.52
35:h:44:LYS:N	35:h:54:ILE:O	2.43	0.52
1:2:305:U:H2'	1:2:308:G:H4'	1.90	0.52
1:2:310:C:H2'	1:2:311:C:C6	2.44	0.52
1:2:1258:A:C6	1:2:1659:U:H2'	2.44	0.52
3:B:137:ALA:HB1	3:B:142:LEU:HD22	1.89	0.52
8:G:122:ARG:NE	31:d:59:LEU:HB2	2.24	0.52
16:O:106:ARG:H	16:O:106:ARG:HD2	1.73	0.52
19:R:34:VAL:O	19:R:37:ARG:N	2.34	0.52
26:Y:115:ILE:HD12	26:Y:118:VAL:HB	1.91	0.52
27:Z:102:THR:HG23	27:Z:107:ARG:HD3	1.92	0.52
1:2:634:A:H2'	1:2:635:G:H8	1.74	0.52
1:2:1177:U:H2'	1:2:1178:U:C6	2.43	0.52
8:G:51:HIS:HE2	19:R:82:TYR:HE2	1.58	0.52
11:J:37:LYS:HE2	11:J:95:THR:HG22	1.91	0.52
16:O:142:GLU:O	16:O:145:THR:OG1	2.25	0.52
25:X:86:LEU:HD22	25:X:117:ARG:HH21	1.73	0.52
1:2:751:G:H1	1:2:792:C:N4	2.06	0.52
1:2:934:G:H22	1:2:1008:A:H2	1.58	0.52
1:2:969:U:O2	1:2:971:G:N1	2.42	0.52
1:2:1626:C:C2	1:2:1627:C:C5	2.98	0.52
19:R:105:LYS:HA	19:R:108:ILE:HG12	1.92	0.52
29:b:22:ARG:HA	29:b:28:ARG:O	2.10	0.52
1:2:1256:G:N1	32:e:29:GLY:HA2	2.25	0.52
1:2:1262:C:H2'	1:2:1263:U:O4'	2.09	0.52
5:D:80:GLU:OE1	5:D:80:GLU:N	2.31	0.52
5:D:168:GLY:N	5:D:179:THR:O	2.35	0.52
10:I:165:ASN:O	10:I:168:HIS:NE2	2.43	0.52
11:J:101:ILE:HG22	11:J:172:LEU:HD22	1.90	0.52
17:P:72:TYR:CE2	17:P:76:LEU:HD11	2.44	0.52
26:Y:68:LYS:HE3	33:f:82:VAL:HG12	1.91	0.52
1:2:942:G:H2'	1:2:943:U:C6	2.44	0.52
4:C:88:THR:HA	4:C:98:THR:HA	1.91	0.52
10:I:162:GLN:HG3	10:I:165:ASN:OD1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:43:HIS:CD2	17:P:55:ARG:HB3	2.45	0.52
19:R:7:LEU:HD21	19:R:26:LYS:HD3	1.92	0.52
26:Y:135:LYS:HE3	26:Y:137:LYS:HB2	1.91	0.52
1:2:29:G:H2'	1:2:30:C:H6	1.74	0.52
1:2:301:A:H1'	11:J:72:CYS:HA	1.90	0.52
1:2:338:G:H2'	1:2:339:A:H8	1.75	0.52
1:2:520:A:H2'	1:2:521:A:H8	1.75	0.52
1:2:807:G:H2'	1:2:808:A:C8	2.45	0.52
4:C:149:GLN:NE2	4:C:151:ARG:O	2.43	0.52
6:E:54:ARG:HB3	6:E:57:ASN:HB2	1.91	0.52
9:H:7:PHE:HE1	9:H:9:ALA:HB3	1.74	0.52
12:K:110:LEU:HD22	12:K:147:PHE:HD2	1.75	0.52
12:K:110:LEU:HD23	12:K:130:ILE:HD11	1.92	0.52
1:2:128:U:C4	1:2:215:G:N2	2.78	0.52
1:2:209:A:H2'	1:2:210:U:O4'	2.10	0.52
1:2:314:U:H2'	1:2:315:C:C6	2.44	0.52
1:2:1113:A:N6	1:2:1121:G:O6	2.43	0.52
1:2:1722:G:O6	1:2:1812:U:O4	2.28	0.52
2:A:9223:G:H1	2:A:9242:C:H5	1.57	0.52
15:N:58:GLU:HB2	15:N:61:TYR:HB2	1.92	0.52
22:U:40:ALA:HB3	22:U:43:LYS:HD3	1.91	0.52
35:h:191:HIS:NE2	35:h:215:GLN:O	2.43	0.52
1:2:91:A:H5''	1:2:92:A:H5''	1.91	0.51
1:2:897:U:H2'	1:2:898:U:O4'	2.10	0.51
31:d:21:THR:HG23	31:d:27:CYS:HB3	1.93	0.51
1:2:874:G:H2'	1:2:875:A:C8	2.44	0.51
4:C:45:GLY:HA3	17:P:47:LEU:HD12	1.91	0.51
19:R:133:GLY:O	19:R:140:ARG:NH1	2.43	0.51
20:S:75:GLU:O	20:S:79:GLU:N	2.41	0.51
34:g:100:LEU:HG	34:g:103:LEU:HD13	1.93	0.51
1:2:292:A:OP2	1:2:292:A:H8	1.93	0.51
1:2:375:U:H1'	14:M:7:GLU:OE2	2.11	0.51
1:2:1130:G:N2	1:2:1130:G:OP2	2.44	0.51
1:2:1161:U:P	26:Y:12:LYS:HZ3	2.34	0.51
1:2:1168:G:H2'	1:2:1169:G:O4'	2.09	0.51
1:2:1653:U:H3	1:2:1671:G:H1	1.55	0.51
19:R:39:LEU:HG	19:R:51:LEU:HD22	1.93	0.51
1:2:183:G:O2'	1:2:184:G:O4'	2.26	0.51
1:2:526:A:O2'	1:2:527:C:O4'	2.18	0.51
1:2:562:U:H2'	1:2:563:G:C8	2.45	0.51
3:B:41:ARG:HB2	3:B:47:TYR:CD1	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:178:HIS:HB3	5:D:200:ARG:NH1	2.26	0.51
1:2:920:A:C8	1:2:922:A:C8	2.98	0.51
1:2:1228:A:H2'	1:2:1229:G:C8	2.45	0.51
3:B:200:ASP:HA	3:B:203:PHE:CD1	2.45	0.51
8:G:71:ARG:NH1	8:G:75:SER:HB2	2.25	0.51
14:M:135:SER:OG	14:M:136:LYS:N	2.43	0.51
1:2:525:A:O2'	1:2:526:A:O4'	2.23	0.51
1:2:558:G:H2'	1:2:559:G:C8	2.46	0.51
3:B:118:GLU:HG3	5:D:65:LYS:HG3	1.92	0.51
21:T:23:ARG:H	21:T:23:ARG:HD2	1.76	0.51
25:X:18:GLU:OE1	25:X:69:LEU:HB3	2.10	0.51
1:2:645:C:H2'	1:2:646:G:H8	1.76	0.51
1:2:958:G:H2'	1:2:959:G:C8	2.45	0.51
1:2:1536:G:H4'	8:G:81:ARG:NH1	2.26	0.51
1:2:1706:G:H22	1:2:1829:G:N2	2.09	0.51
2:A:9158:G:H22	2:A:9290:U:H3	1.58	0.51
10:I:164:ASN:OD1	10:I:165:ASN:N	2.43	0.51
11:J:105:ASP:OD1	11:J:106:SER:N	2.43	0.51
11:J:143:LYS:HG3	11:J:144:LYS:HD3	1.93	0.51
28:a:54:THR:HA	28:a:57:LYS:HG2	1.92	0.51
35:h:32:LEU:HD13	35:h:71:ILE:HD11	1.90	0.51
35:h:109:LEU:HG	35:h:125:ARG:NH1	2.26	0.51
1:2:66:G:O6	1:2:82:G:O2'	2.24	0.51
1:2:309:G:OP2	11:J:55:TYR:OH	2.29	0.51
1:2:441:C:H4'	1:2:1738:C:H5'	1.92	0.51
1:2:445:A:O2'	1:2:446:G:OP1	2.27	0.51
1:2:1136:U:H2'	1:2:1137:U:C6	2.46	0.51
3:B:148:CYS:O	3:B:162:PRO:HA	2.10	0.51
23:V:78:ASP:OD2	32:e:44:ARG:NH1	2.43	0.51
36:n:2:ARG:HH21	36:n:4:LYS:HD3	1.75	0.51
1:2:307:G:N2	11:J:45:THR:O	2.44	0.51
1:2:436:G:H2'	1:2:437:G:C8	2.46	0.51
1:2:1486:A:H2'	1:2:1487:A:C8	2.45	0.51
2:A:9301:A:H2'	2:A:9302:G:C8	2.45	0.51
4:C:44:ILE:HD11	4:C:73:ASP:HB3	1.92	0.51
13:L:8:ARG:NH2	13:L:82:TYR:OH	2.43	0.51
1:2:107:A:H2'	1:2:108:G:C8	2.46	0.51
1:2:1273:C:O2	1:2:1274:G:O2'	2.26	0.51
21:T:108:ARG:HD3	21:T:111:LEU:HD22	1.93	0.51
29:b:73:TYR:CE2	29:b:83:VAL:HG21	2.45	0.51
1:2:10:G:O2'	5:D:120:GLN:NE2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:72:C:OP2	9:H:168:LYS:NZ	2.32	0.50
1:2:389:A:H2'	1:2:390:C:C6	2.46	0.50
1:2:870:A:O4'	1:2:915:G:N2	2.44	0.50
1:2:872:A:N7	1:2:874:G:C8	2.79	0.50
1:2:1258:A:N6	1:2:1659:U:H2'	2.26	0.50
4:C:109:LYS:O	4:C:112:SER:OG	2.23	0.50
6:E:203:PRO:HB2	6:E:207:HIS:CE1	2.46	0.50
6:E:204:LEU:O	6:E:207:HIS:ND1	2.45	0.50
8:G:100:ILE:HD13	8:G:178:ILE:HG12	1.92	0.50
8:G:136:ARG:HH11	8:G:199:VAL:HG21	1.76	0.50
14:M:119:ASP:OD1	14:M:119:ASP:N	2.42	0.50
21:T:114:LEU:HD12	21:T:119:ALA:HB3	1.93	0.50
22:U:83:GLN:O	22:U:90:SER:HA	2.11	0.50
1:2:121:U:H2'	1:2:122:G:C8	2.45	0.50
1:2:1236:G:H2'	1:2:1237:C:C6	2.46	0.50
1:2:1717:C:H2'	1:2:1718:G:H8	1.75	0.50
1:2:1776:G:H2'	1:2:1777:G:C8	2.46	0.50
4:C:62:LEU:HA	4:C:65:ARG:HE	1.76	0.50
4:C:62:LEU:O	4:C:65:ARG:HD2	2.12	0.50
5:D:205:VAL:O	5:D:224:THR:OG1	2.26	0.50
6:E:45:ARG:O	6:E:45:ARG:HD2	2.11	0.50
9:H:194:LEU:HD23	9:H:197:GLN:NE2	2.27	0.50
27:Z:110:ARG:HA	27:Z:113:ARG:NH1	2.26	0.50
34:g:118:ARG:HB3	34:g:132:MET:H	1.75	0.50
1:2:104:A:OP1	11:J:12:ARG:NE	2.44	0.50
1:2:865:A:H2'	1:2:866:U:C6	2.46	0.50
1:2:1135:C:H2'	1:2:1136:U:C6	2.46	0.50
1:2:1261:C:O2	32:e:10:HIS:NE2	2.45	0.50
1:2:1629:C:H2'	1:2:1630:A:C8	2.46	0.50
1:2:1659:U:H5	1:2:1660:C:C4	2.30	0.50
1:2:1703:C:H2'	1:2:1704:C:O4'	2.11	0.50
1:2:1709:G:O6	1:2:1824:A:N6	2.44	0.50
4:C:173:THR:HG22	4:C:177:GLN:OE1	2.12	0.50
5:D:251:LEU:HD23	25:X:68:ARG:HA	1.94	0.50
6:E:127:MET:HE1	6:E:133:GLY:HA2	1.91	0.50
19:R:41:MET:HE1	22:U:11:GLN:HG2	1.92	0.50
20:S:28:PHE:O	20:S:32:LYS:HB3	2.12	0.50
23:V:23:THR:HB	23:V:113:GLU:HG2	1.92	0.50
33:f:109:MET:HA	33:f:112:ASN:HD21	1.75	0.50
1:2:523:A:OP2	12:K:38:ARG:NE	2.44	0.50
1:2:946:U:C2	1:2:947:G:C8	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1508:A:C5	1:2:1510:G:O6	2.64	0.50
1:2:1618:C:H2'	1:2:1619:A:C8	2.46	0.50
1:2:1775:U:H2'	1:2:1776:G:N7	2.26	0.50
3:B:52:LYS:HB2	20:S:109:LEU:HD21	1.93	0.50
6:E:23:GLU:OE1	13:L:63:ALA:HB1	2.12	0.50
6:E:47:GLU:HG2	6:E:85:GLU:N	2.22	0.50
7:F:60:GLU:O	7:F:64:ILE:HG12	2.11	0.50
9:H:116:LYS:NZ	9:H:119:LYS:O	2.36	0.50
12:K:82:VAL:HG11	12:K:92:MET:HG3	1.93	0.50
13:L:47:LYS:O	13:L:50:GLN:HG3	2.11	0.50
14:M:22:ARG:H	14:M:25:LEU:HD11	1.77	0.50
25:X:82:GLN:H	25:X:85:ASP:HB3	1.76	0.50
35:h:18:VAL:HG21	35:h:301:GLY:HA3	1.93	0.50
1:2:491:C:O2'	1:2:493:A:N7	2.45	0.50
1:2:557:U:H2'	1:2:558:G:H8	1.77	0.50
1:2:1016:U:H5'	16:O:15:ALA:O	2.11	0.50
1:2:1398:G:H1	1:2:1448:A:H61	1.60	0.50
1:2:1626:C:H2'	1:2:1627:C:C6	2.44	0.50
1:2:1772:C:N3	1:2:1773:C:N4	2.59	0.50
2:A:9234:A:O3'	2:A:9235:A:H4'	2.11	0.50
10:I:82:GLU:HA	10:I:85:LYS:HG2	1.92	0.50
16:O:84:LEU:HD12	16:O:85:PRO:HD2	1.94	0.50
19:R:136:GLY:H	19:R:139:ALA:HB3	1.75	0.50
36:n:16:LYS:HA	36:n:19:LYS:HG2	1.94	0.50
1:2:146:G:N2	1:2:173:A:N1	2.53	0.50
1:2:634:A:H2'	1:2:635:G:C8	2.46	0.50
3:B:111:GLN:HE22	5:D:63:VAL:HG22	1.75	0.50
3:B:169:HIS:HA	3:B:203:PHE:CE2	2.47	0.50
4:C:191:ASP:O	4:C:195:LYS:HG2	2.11	0.50
6:E:172:VAL:HG13	6:E:185:LYS:HG2	1.94	0.50
10:I:192:PHE:HB2	30:c:12:PRO:HD3	1.94	0.50
14:M:74:SER:OG	14:M:126:VAL:O	2.23	0.50
34:g:118:ARG:HB2	34:g:131:PHE:HB3	1.92	0.50
35:h:79:LEU:HD23	35:h:111:VAL:HB	1.93	0.50
1:2:868:G:C8	10:I:115:LYS:HD3	2.46	0.50
1:2:1040:G:N1	1:2:1041:G:C6	2.79	0.50
1:2:1064:C:C2	1:2:1065:G:C8	3.00	0.50
1:2:1324:G:N2	1:2:1504:U:O2	2.32	0.50
3:B:13:GLU:O	3:B:17:LYS:HG2	2.11	0.50
8:G:204:ARG:NH2	31:d:63:ARG:HD3	2.26	0.50
1:2:457:C:H2'	1:2:458:A:C8	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1152:U:O3'	25:X:19:LYS:NZ	2.45	0.50
1:2:1468:C:H2'	1:2:1469:A:H8	1.75	0.50
1:2:1541:G:O6	1:2:1593:C:N4	2.45	0.50
1:2:1563:G:H2'	1:2:1564:C:C6	2.47	0.50
1:2:1629:C:H2'	1:2:1630:A:H8	1.77	0.50
7:F:123:LEU:HD21	7:F:159:THR:HB	1.94	0.50
9:H:55:GLY:N	9:H:63:MET:SD	2.85	0.50
1:2:385:G:O2'	11:J:10:LYS:NZ	2.45	0.50
1:2:609:U:H2'	1:2:610:G:H8	1.77	0.50
1:2:1651:A:H2'	1:2:1652:G:C8	2.47	0.50
1:2:1680:G:N2	31:d:24:GLN:O	2.38	0.50
1:2:1818:A:H8	1:2:1819:A:C8	2.30	0.50
3:B:36:GLN:O	3:B:53:ARG:NH1	2.44	0.50
11:J:28:GLU:OE1	11:J:28:GLU:N	2.44	0.50
12:K:136:ARG:HD2	12:K:139:LYS:HD3	1.94	0.50
25:X:102:ILE:HG13	25:X:125:ILE:HD11	1.93	0.50
32:e:16:GLN:HA	32:e:19:ARG:NH1	2.27	0.50
35:h:27:PHE:CD2	35:h:30:MET:HB3	2.47	0.50
1:2:17:C:H2'	1:2:18:C:H6	1.77	0.49
1:2:91:A:OP1	1:2:446:G:N2	2.42	0.49
1:2:145:G:H2'	1:2:146:G:C8	2.47	0.49
1:2:338:G:H2'	1:2:339:A:C8	2.47	0.49
1:2:429:C:H2'	1:2:430:C:H6	1.76	0.49
1:2:643:A:H4'	1:2:644:G:H5'	1.94	0.49
1:2:1040:G:H2'	1:2:1041:G:H8	1.75	0.49
1:2:1388:A:H61	6:E:161:GLY:HA3	1.77	0.49
4:C:201:CYS:HB2	4:C:207:LEU:HD21	1.92	0.49
7:F:141:THR:HG22	7:F:160:ILE:HD11	1.92	0.49
11:J:8:TRP:HZ3	11:J:20:PRO:HA	1.77	0.49
11:J:113:TYR:HD2	11:J:121:LEU:HD22	1.77	0.49
16:O:63:VAL:HG11	16:O:71:ILE:CG2	2.41	0.49
19:R:83:ALA:O	19:R:86:GLN:HG2	2.12	0.49
20:S:31:ASN:HA	20:S:34:VAL:HB	1.93	0.49
32:e:17:GLY:HA2	32:e:27:ARG:NE	2.27	0.49
1:2:291:G:H2'	1:2:292:A:C8	2.47	0.49
1:2:305:U:H3	11:J:184:ARG:NH1	2.10	0.49
1:2:957:A:C4	1:2:958:G:C8	3.00	0.49
1:2:1172:U:H5''	36:n:10:MET:SD	2.52	0.49
1:2:1224:G:N1	1:2:1642:U:N3	2.61	0.49
1:2:1465:A:H2'	1:2:1466:G:O4'	2.12	0.49
1:2:1827:U:H2'	1:2:1828:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:97:LEU:HD22	4:C:232:HIS:HD2	1.77	0.49
4:C:189:ILE:HB	4:C:190:PRO:HD3	1.94	0.49
5:D:248:TYR:OH	24:W:11:LEU:HD21	2.12	0.49
7:F:176:ASP:OD1	7:F:176:ASP:N	2.45	0.49
7:F:181:CYS:SG	7:F:225:ILE:HG23	2.52	0.49
12:K:42:GLU:O	12:K:45:ARG:HG2	2.13	0.49
12:K:137:VAL:O	12:K:140:GLN:HG3	2.12	0.49
16:O:118:ILE:O	16:O:122:ILE:HG23	2.11	0.49
1:2:407:G:OP1	1:2:407:G:N2	2.34	0.49
1:2:655:A:H1'	1:2:658:U:OP1	2.12	0.49
1:2:1438:A:H2'	1:2:1439:A:C8	2.46	0.49
1:2:1446:A:H1'	1:2:1447:G:H8	1.77	0.49
1:2:1521:C:H5''	21:T:136:THR:HB	1.93	0.49
1:2:1607:A:H2	21:T:142:ARG:HH22	1.58	0.49
11:J:36:THR:HG23	11:J:96:LEU:HB2	1.94	0.49
17:P:44:VAL:HG12	17:P:53:ILE:HD11	1.94	0.49
20:S:76:GLU:HA	20:S:79:GLU:HB3	1.94	0.49
1:2:109:U:OP1	1:2:810:A:O2'	2.23	0.49
1:2:141:A:OP2	9:H:149:LYS:NZ	2.46	0.49
1:2:639:C:OP1	33:f:110:GLN:HG2	2.12	0.49
1:2:1040:G:C6	1:2:1041:G:C6	2.99	0.49
1:2:1664:A:HO2'	1:2:1666:C:H5	1.59	0.49
7:F:248:ILE:HA	7:F:251:GLU:OE2	2.12	0.49
25:X:55:ASP:OD1	25:X:59:GLY:HA2	2.12	0.49
1:2:106:C:OP1	1:2:431:G:O2'	2.31	0.49
1:2:459:C:H2'	1:2:460:A:O4'	2.13	0.49
1:2:1013:U:OP1	1:2:1129:G:O2'	2.23	0.49
1:2:1317:C:H2'	1:2:1318:G:H8	1.78	0.49
26:Y:90:CYS:SG	26:Y:130:LEU:HD21	2.53	0.49
29:b:87:ARG:NH2	29:b:92:ARG:O	2.45	0.49
33:f:103:GLY:H	33:f:106:LYS:HD3	1.78	0.49
35:h:147:HIS:CD2	35:h:151:VAL:HG22	2.47	0.49
1:2:42:A:O2'	1:2:43:U:O4'	2.29	0.49
1:2:1139:C:C4	1:2:1148:A:N6	2.81	0.49
1:2:1321:G:H2'	1:2:1322:G:C8	2.47	0.49
1:2:1356:G:O3'	5:D:125:LYS:NZ	2.46	0.49
1:2:1578:U:O2	6:E:6:SER:OG	2.31	0.49
8:G:87:LEU:HD21	19:R:78:VAL:CG2	2.43	0.49
9:H:10:THR:HG21	9:H:125:THR:HA	1.94	0.49
11:J:101:ILE:HD12	11:J:190:LEU:HD11	1.93	0.49
31:d:3:THR:OG1	31:d:4:SER:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:114:SER:HA	35:h:156:PHE:CE2	2.47	0.49
35:h:258:ILE:HD11	35:h:268:ASP:HB3	1.95	0.49
1:2:960:U:OP2	17:P:38:ASN:ND2	2.45	0.49
1:2:1271:C:H4'	1:2:1303:C:H5''	1.95	0.49
1:2:1598:G:N7	28:a:82:SER:N	2.60	0.49
1:2:1737:G:H1	1:2:1797:U:H3	1.60	0.49
3:B:198:MET:HB3	3:B:201:LEU:HB2	1.95	0.49
8:G:42:LYS:O	8:G:43:GLU:HG3	2.12	0.49
12:K:75:ASN:O	12:K:79:ARG:HG2	2.12	0.49
20:S:24:LEU:HB2	20:S:31:ASN:HB3	1.93	0.49
22:U:14:PHE:HE2	22:U:62:ARG:HB3	1.77	0.49
23:V:20:ILE:HG21	23:V:98:VAL:HG21	1.95	0.49
31:d:45:ASN:ND2	31:d:66:ARG:O	2.45	0.49
35:h:30:MET:HE1	35:h:44:LYS:HD2	1.94	0.49
1:2:633:C:H2'	1:2:634:A:H8	1.77	0.49
1:2:1030:A:H2'	1:2:1031:A:C8	2.48	0.49
1:2:1296:U:O2	1:2:1303:C:N4	2.34	0.49
1:2:1667:U:H2'	1:2:1668:U:O4'	2.13	0.49
2:A:9153:U:H2'	2:A:9154:C:C6	2.48	0.49
11:J:145:ILE:H	11:J:145:ILE:HD12	1.77	0.49
12:K:13:TYR:HB2	12:K:44:TRP:HB3	1.94	0.49
18:Q:59:ARG:O	18:Q:62:LYS:HG2	2.13	0.49
19:R:111:ILE:O	19:R:114:GLN:HG3	2.13	0.49
35:h:79:LEU:HD21	35:h:87:LEU:HD21	1.94	0.49
1:2:1740:C:H2'	1:2:1741:U:C6	2.47	0.49
8:G:194:ASP:OD1	8:G:195:GLU:N	2.45	0.49
9:H:3:LEU:HD12	9:H:111:LEU:HD11	1.94	0.49
9:H:27:PHE:CE2	9:H:41:LEU:HD21	2.48	0.49
13:L:10:ALA:O	13:L:13:GLU:HG3	2.13	0.49
13:L:74:GLU:O	13:L:77:GLN:HG3	2.12	0.49
16:O:45:LEU:HB2	16:O:50:ILE:HD11	1.94	0.49
19:R:123:ASP:O	19:R:125:ARG:N	2.45	0.49
22:U:69:GLY:HA2	22:U:120:GLY:HA3	1.95	0.49
27:Z:5:VAL:HA	27:Z:28:LEU:O	2.13	0.49
1:2:298:G:H2'	1:2:299:A:C8	2.48	0.49
1:2:383:G:O2'	1:2:384:U:OP1	2.27	0.49
1:2:437:G:N2	1:2:1801:A:OP1	2.46	0.49
1:2:458:A:H2'	1:2:459:C:H6	1.78	0.49
1:2:604:A:H5'	1:2:605:A:OP2	2.13	0.49
1:2:993:G:O6	29:b:15:ARG:HG3	2.13	0.49
1:2:1112:U:H3	1:2:1113:A:N6	2.08	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1236:G:H2'	1:2:1237:C:H6	1.78	0.49
1:2:1597:C:OP2	28:a:85:ARG:NH2	2.36	0.49
1:2:1668:U:C2	1:2:1669:G:C8	3.01	0.49
1:2:1826:G:H8	1:2:1826:G:OP2	1.95	0.49
2:A:9238:C:H2'	2:A:9239:C:C6	2.47	0.49
6:E:45:ARG:O	6:E:47:GLU:N	2.46	0.49
20:S:12:ALA:HB3	20:S:50:ILE:HG21	1.94	0.49
1:2:90:G:H2'	1:2:91:A:O4'	2.13	0.48
1:2:116:U:O4	1:2:347:G:O6	2.31	0.48
1:2:789:G:H2'	1:2:790:C:C6	2.48	0.48
1:2:959:G:H1	17:P:65:ASP:HB2	1.78	0.48
1:2:1596:U:P	28:a:85:ARG:HH21	2.35	0.48
1:2:1608:U:O4	1:2:1632:G:N2	2.44	0.48
3:B:159:ILE:HD11	24:W:34:MET:HE1	1.95	0.48
8:G:20:PHE:CZ	8:G:50:PRO:HG3	2.49	0.48
18:Q:79:HIS:HA	18:Q:97:TYR:HB2	1.93	0.48
21:T:84:LEU:HD22	21:T:97:GLN:HG2	1.94	0.48
27:Z:39:GLU:HA	27:Z:42:GLU:HG3	1.94	0.48
1:2:430:C:C2	1:2:431:G:C8	3.01	0.48
1:2:433:A:OP1	11:J:25:ARG:NH2	2.47	0.48
1:2:482:G:N2	1:2:485:A:OP2	2.47	0.48
1:2:962:A:N1	1:2:1055:A:O2'	2.45	0.48
2:A:9278:C:H2'	2:A:9279:C:C6	2.47	0.48
3:B:7:VAL:HG13	3:B:8:LEU:HG	1.95	0.48
5:D:271:ASP:OD1	5:D:271:ASP:N	2.44	0.48
6:E:102:ALA:HB1	6:E:173:ARG:HD3	1.95	0.48
12:K:54:ARG:NH2	12:K:98:LEU:O	2.46	0.48
14:M:126:VAL:HG12	14:M:145:VAL:HG22	1.95	0.48
18:Q:56:LEU:O	18:Q:60:LEU:HD23	2.13	0.48
22:U:134:ILE:O	22:U:138:VAL:HG23	2.13	0.48
1:2:79:A:H2'	1:2:80:G:O4'	2.14	0.48
1:2:1134:G:C6	1:2:1135:C:N4	2.81	0.48
1:2:1666:C:H2'	1:2:1667:U:C6	2.47	0.48
2:A:9287:G:H2'	2:A:9288:U:C6	2.48	0.48
12:K:12:THR:HG22	12:K:45:ARG:HB2	1.94	0.48
23:V:38:ASP:HA	23:V:41:ARG:HG2	1.95	0.48
1:2:103:A:H5'	11:J:12:ARG:CZ	2.43	0.48
1:2:449:A:O3'	7:F:3:ARG:NH1	2.47	0.48
1:2:1400:U:H3	23:V:55:ARG:HH22	1.61	0.48
1:2:1532:C:H5''	1:2:1533:A:C8	2.48	0.48
3:B:191:ARG:NH2	24:W:44:GLY:O	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:179:ASN:HB2	4:C:183:GLU:HG3	1.96	0.48
7:F:196:THR:HG21	7:F:211:LYS:HG2	1.94	0.48
9:H:85:ARG:HG3	9:H:87:ARG:HH12	1.76	0.48
14:M:132:ARG:O	14:M:134:LEU:HD12	2.13	0.48
19:R:33:LYS:HG2	19:R:38:PRO:HA	1.94	0.48
32:e:43:PHE:HE1	32:e:52:PHE:HE2	1.60	0.48
35:h:166:VAL:HG12	35:h:176:VAL:HG12	1.95	0.48
1:2:445:A:H5''	11:J:47:ARG:NH2	2.27	0.48
1:2:448:A:H5''	11:J:24:LYS:O	2.13	0.48
1:2:520:A:H2'	1:2:521:A:C8	2.49	0.48
4:C:153:THR:OG1	4:C:154:SER:N	2.46	0.48
8:G:97:PHE:HD1	8:G:108:PRO:HB2	1.79	0.48
27:Z:102:THR:OG1	27:Z:106:GLN:OE1	2.19	0.48
35:h:88:ARG:NH1	35:h:90:TRP:HB2	2.29	0.48
35:h:124:SER:OG	35:h:125:ARG:N	2.46	0.48
1:2:1087:A:C5	1:2:1861:G:C6	3.01	0.48
1:2:1797:U:H2'	1:2:1798:C:C6	2.48	0.48
1:2:1834:A:H2	1:2:1837:G:N1	2.11	0.48
2:A:9279:C:H2'	2:A:9280:A:C8	2.49	0.48
3:B:197:VAL:HG23	3:B:198:MET:N	2.29	0.48
8:G:47:LYS:NZ	8:G:49:LEU:O	2.29	0.48
10:I:65:PRO:HA	10:I:97:GLN:HB3	1.96	0.48
10:I:163:GLN:O	10:I:167:GLU:HG2	2.14	0.48
14:M:72:ILE:HD12	14:M:128:VAL:O	2.14	0.48
23:V:53:PRO:HB2	23:V:87:ARG:HH21	1.78	0.48
28:a:51:ASP:OD1	28:a:54:THR:HG22	2.14	0.48
30:c:33:MET:HE2	30:c:48:SER:HA	1.94	0.48
32:e:17:GLY:HA2	32:e:27:ARG:HE	1.78	0.48
35:h:245:ARG:HH22	35:h:291:TRP:HH2	1.61	0.48
1:2:75:G:N2	9:H:155:GLN:OE1	2.46	0.48
1:2:219:U:H2'	1:2:220:U:C6	2.49	0.48
1:2:1453:C:O2	1:2:1453:C:H2'	2.13	0.48
3:B:53:ARG:O	3:B:57:LYS:HG2	2.14	0.48
3:B:174:MET:HA	3:B:177:MET:HG2	1.95	0.48
10:I:50:GLU:OE2	10:I:58:LYS:HE3	2.14	0.48
16:O:117:LEU:O	16:O:120:SER:OG	2.31	0.48
18:Q:70:MET:O	18:Q:70:MET:HG2	2.13	0.48
35:h:23:THR:HG21	35:h:291:TRP:O	2.14	0.48
1:2:170:A:H2'	1:2:171:A:C8	2.49	0.48
1:2:421:G:H5'	14:M:98:LYS:HG3	1.96	0.48
1:2:1030:A:H2'	1:2:1031:A:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1043:G:N2	1:2:1074:C:C4	2.82	0.48
1:2:1291:A:H2'	1:2:1292:C:C6	2.48	0.48
1:2:1590:C:H3'	1:2:1591:C:H6	1.77	0.48
1:2:1661:A:C8	32:e:14:PHE:HB2	2.48	0.48
2:A:9287:G:H2'	2:A:9288:U:H6	1.79	0.48
3:B:160:ALA:O	3:B:161:ILE:HD13	2.14	0.48
4:C:23:ASP:N	4:C:23:ASP:OD1	2.44	0.48
6:E:34:TYR:CE1	6:E:37:VAL:HG13	2.49	0.48
7:F:189:LEU:HD12	7:F:190:GLY:H	1.79	0.48
11:J:8:TRP:CZ3	11:J:20:PRO:HA	2.49	0.48
20:S:41:ILE:HG22	20:S:43:SER:H	1.77	0.48
1:2:380:G:OP1	11:J:56:ARG:NH2	2.45	0.48
1:2:439:A:H4'	1:2:1799:G:H4'	1.96	0.48
1:2:1017:U:O2'	16:O:48:SER:O	2.30	0.48
1:2:1617:G:H3'	18:Q:47:ARG:HH12	1.79	0.48
4:C:38:MET:SD	4:C:231:LEU:HD11	2.54	0.48
4:C:92:GLN:HG2	4:C:93:GLY:N	2.28	0.48
6:E:6:SER:H	6:E:9:ARG:NE	2.12	0.48
9:H:121:ILE:HG21	9:H:124:LEU:HB2	1.96	0.48
35:h:44:LYS:HB3	35:h:54:ILE:HG23	1.96	0.48
1:2:1223:A:H5'	8:G:78:MET:CE	2.43	0.48
1:2:1300:U:H2'	18:Q:59:ARG:HH12	1.79	0.48
3:B:99:ILE:HD11	3:B:117:ARG:NH1	2.29	0.48
4:C:108:ASP:N	4:C:108:ASP:OD1	2.44	0.48
4:C:167:LYS:HA	4:C:170:GLU:HG2	1.94	0.48
7:F:72:ILE:HG21	7:F:82:TYR:CE2	2.48	0.48
15:N:99:LYS:HG3	15:N:100:PRO:HD2	1.95	0.48
25:X:14:ILE:HD11	25:X:27:ILE:HD11	1.96	0.48
29:b:73:TYR:HB3	29:b:78:ALA:HB2	1.95	0.48
1:2:56:G:H2'	1:2:57:U:C6	2.49	0.47
1:2:91:A:P	1:2:446:G:H22	2.37	0.47
1:2:587:A:H1'	1:2:590:A:H1'	1.95	0.47
1:2:818:A:P	12:K:80:ARG:HH22	2.37	0.47
1:2:1203:U:O4	5:D:115:GLN:HB3	2.14	0.47
1:2:1617:G:N7	18:Q:43:ARG:NH1	2.58	0.47
2:A:9270:U:H2'	2:A:9271:G:C8	2.48	0.47
3:B:89:LYS:HE2	3:B:202:TYR:HA	1.96	0.47
3:B:108:PHE:HD2	3:B:136:GLU:HG3	1.79	0.47
4:C:86:LEU:HB3	4:C:98:THR:OG1	2.14	0.47
5:D:81:ILE:HG21	5:D:88:ILE:HD11	1.95	0.47
6:E:48:ILE:HG22	6:E:86:LEU:HG	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:100:ARG:HG3	7:F:102:ILE:HG23	1.96	0.47
12:K:38:ARG:HA	33:f:104:ARG:HD2	1.96	0.47
16:O:25:TRP:CG	30:c:82:LYS:HZ2	2.32	0.47
24:W:38:GLU:OE2	24:W:38:GLU:N	2.32	0.47
1:2:76:U:H4'	9:H:155:GLN:HE22	1.80	0.47
1:2:430:C:H2'	1:2:431:G:H8	1.78	0.47
1:2:584:A:OP1	12:K:169:ARG:NH1	2.45	0.47
1:2:1727:G:H2'	1:2:1728:U:C6	2.49	0.47
6:E:163:PRO:HA	6:E:166:TYR:CZ	2.49	0.47
14:M:47:PRO:HG2	14:M:50:ALA:HB2	1.96	0.47
16:O:34:LYS:HA	16:O:37:ILE:HG22	1.95	0.47
17:P:28:PHE:CZ	29:b:58:VAL:HG21	2.50	0.47
17:P:29:GLY:O	17:P:94:HIS:N	2.46	0.47
27:Z:87:PRO:HG2	27:Z:90:ARG:HE	1.78	0.47
1:2:1208:A:H4'	1:2:1835:A:N7	2.29	0.47
7:F:155:LYS:HG2	7:F:174:LYS:HE2	1.97	0.47
10:I:135:PHE:N	10:I:136:PRO:HD2	2.29	0.47
25:X:14:ILE:HD13	25:X:25:VAL:HG11	1.96	0.47
1:2:404:G:H2'	1:2:405:G:H8	1.79	0.47
1:2:522:A:H4'	12:K:131:ARG:CZ	2.44	0.47
1:2:562:U:H2'	1:2:563:G:H8	1.78	0.47
1:2:1078:C:C2	1:2:1079:C:C5	3.03	0.47
1:2:1332:A:C2	1:2:1500:G:H1'	2.49	0.47
1:2:1601:A:N6	1:2:1636:G:N3	2.58	0.47
22:U:15:VAL:HG23	22:U:58:ALA:HB3	1.97	0.47
26:Y:53:GLU:HG2	26:Y:71:ARG:HB3	1.96	0.47
27:Z:41:ARG:NH2	27:Z:52:PRO:O	2.47	0.47
1:2:555:A:N6	1:2:589:G:N3	2.59	0.47
1:2:1100:A:C2	1:2:1133:A:C2	3.02	0.47
1:2:1289:U:O4	1:2:1311:C:N4	2.48	0.47
1:2:1649:U:H3'	1:2:1674:G:H22	1.80	0.47
5:D:123:ARG:CZ	5:D:143:CYS:HB3	2.44	0.47
7:F:42:LEU:N	7:F:84:ALA:O	2.47	0.47
7:F:46:ILE:HD12	7:F:50:ASN:OD1	2.14	0.47
8:G:167:LYS:HB3	8:G:171:GLU:OE2	2.14	0.47
10:I:40:LEU:HD12	10:I:43:LEU:HB2	1.97	0.47
18:Q:30:TYR:HD1	18:Q:33:LEU:HD12	1.79	0.47
19:R:42:ILE:HD13	19:R:84:ILE:HD12	1.96	0.47
32:e:12:ARG:NH2	32:e:15:GLY:HA3	2.29	0.47
35:h:20:GLN:HG2	35:h:69:VAL:H	1.79	0.47
35:h:149:GLU:HG2	35:h:150:TRP:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:282:GLU:OE2	35:h:285:GLN:NE2	2.37	0.47
1:2:340:C:H2'	1:2:341:C:C6	2.49	0.47
1:2:1350:U:C2	1:2:1351:G:C8	3.02	0.47
2:A:9258:C:H2'	2:A:9259:U:C6	2.50	0.47
5:D:214:LEU:HD13	5:D:244:ILE:HD12	1.95	0.47
6:E:39:VAL:HG22	6:E:48:ILE:HD12	1.97	0.47
7:F:57:THR:OG1	7:F:59:ASP:OD1	2.31	0.47
7:F:189:LEU:HD12	7:F:190:GLY:N	2.29	0.47
20:S:32:LYS:HE2	20:S:47:ARG:HH22	1.79	0.47
28:a:69:THR:HG22	28:a:72:VAL:HG12	1.96	0.47
1:2:95:G:H1	1:2:435:A:H61	1.63	0.47
1:2:351:G:OP1	11:J:7:ASN:ND2	2.48	0.47
1:2:557:U:H2'	1:2:558:G:C8	2.50	0.47
1:2:633:C:H2'	1:2:634:A:C8	2.49	0.47
1:2:656:G:N2	1:2:663:C:H5''	2.30	0.47
1:2:801:U:H2'	1:2:802:A:H8	1.80	0.47
1:2:804:U:H2'	1:2:805:U:C6	2.49	0.47
1:2:818:A:H2'	1:2:819:G:C8	2.49	0.47
1:2:862:A:C8	25:X:107:SER:HA	2.50	0.47
1:2:1016:U:H6	16:O:61:ALA:HB1	1.80	0.47
1:2:1080:A:H5''	1:2:1184:G:O2'	2.14	0.47
1:2:1286:G:N2	1:2:1312:G:O2'	2.40	0.47
1:2:1410:C:H2'	1:2:1411:G:C8	2.49	0.47
1:2:1455:A:H2'	1:2:1456:G:C8	2.47	0.47
1:2:1650:A:N6	1:2:1674:G:O2'	2.48	0.47
2:A:9304:G:H4'	2:A:9305:G:OP1	2.15	0.47
3:B:173:LEU:HG	3:B:177:MET:CE	2.44	0.47
7:F:61:VAL:HG22	7:F:80:ILE:HD11	1.96	0.47
8:G:158:ALA:HA	8:G:161:ALA:HB3	1.95	0.47
9:H:221:LYS:HD3	9:H:224:ARG:HH21	1.79	0.47
11:J:44:HIS:O	11:J:56:ARG:N	2.45	0.47
11:J:197:PHE:CE2	14:M:10:TYR:HB2	2.49	0.47
17:P:72:TYR:O	17:P:76:LEU:HG	2.15	0.47
23:V:24:LEU:HD11	23:V:112:VAL:HG22	1.95	0.47
23:V:80:PHE:HB3	32:e:52:PHE:HB3	1.97	0.47
26:Y:84:PHE:HB2	26:Y:118:VAL:HG11	1.97	0.47
33:f:107:ARG:O	33:f:110:GLN:HG3	2.15	0.47
1:2:1310:U:H5''	1:2:1311:C:OP2	2.14	0.47
2:A:9299:G:H2'	2:A:9300:U:C6	2.49	0.47
3:B:34:MET:HE3	3:B:154:LEU:HD11	1.97	0.47
3:B:178:LEU:O	3:B:182:VAL:HG23	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:68:GLU:OE1	4:C:85:LYS:HG2	2.15	0.47
7:F:212:ASP:HB2	7:F:216:ASN:HB2	1.96	0.47
8:G:38:TYR:CE2	8:G:144:LEU:HB2	2.50	0.47
13:L:64:TRP:CE3	32:e:23:VAL:HG13	2.50	0.47
18:Q:23:ASP:OD1	18:Q:24:GLN:N	2.46	0.47
19:R:42:ILE:HB	19:R:51:LEU:HD11	1.97	0.47
3:B:121:LEU:HD21	3:B:145:ILE:HD13	1.97	0.47
7:F:125:LYS:HD2	7:F:159:THR:HG22	1.97	0.47
8:G:113:VAL:O	8:G:116:ILE:HG22	2.15	0.47
10:I:70:LYS:O	10:I:74:LYS:NZ	2.34	0.47
14:M:57:ASP:OD2	14:M:84:ARG:HD3	2.14	0.47
17:P:85:CYS:HA	17:P:88:LEU:HD12	1.96	0.47
20:S:54:VAL:O	20:S:58:MET:HG2	2.15	0.47
21:T:113:ARG:HG2	21:T:116:LYS:HZ3	1.79	0.47
25:X:8:ALA:HA	25:X:74:VAL:HG21	1.96	0.47
25:X:32:LYS:HD2	25:X:36:ARG:HH22	1.78	0.47
1:2:567:C:N4	1:2:568:C:H41	2.12	0.47
1:2:996:A:OP1	16:O:114:ARG:NH2	2.29	0.47
5:D:167:ARG:HB3	5:D:177:PRO:HB2	1.96	0.47
19:R:123:ASP:CG	19:R:125:ARG:HD3	2.39	0.47
20:S:61:ILE:HG21	20:S:69:ILE:HD11	1.96	0.47
21:T:87:GLN:HG3	21:T:95:TYR:CE1	2.50	0.47
22:U:23:LYS:HD3	22:U:54:TYR:CE2	2.49	0.47
23:V:29:VAL:O	23:V:33:GLU:HG2	2.15	0.47
26:Y:107:ARG:HD3	26:Y:112:VAL:HG22	1.97	0.47
35:h:45:LEU:HD22	35:h:52:TYR:CD2	2.49	0.47
1:2:581:U:H2'	1:2:582:U:C6	2.50	0.46
1:2:967:C:H2'	1:2:968:U:C6	2.50	0.46
1:2:1239:U:OP1	18:Q:124:LYS:NZ	2.39	0.46
1:2:1323:U:H2'	1:2:1324:G:C8	2.50	0.46
1:2:1798:C:H2'	1:2:1799:G:O4'	2.15	0.46
1:2:1865:C:H5''	29:b:87:ARG:HH21	1.79	0.46
3:B:184:ARG:HB3	3:B:191:ARG:HE	1.80	0.46
19:R:94:ALA:HA	19:R:97:GLN:HG2	1.96	0.46
24:W:11:LEU:HD23	24:W:11:LEU:H	1.79	0.46
35:h:59:LEU:HD22	35:h:90:TRP:CE2	2.50	0.46
1:2:381:C:H41	11:J:27:TYR:HB2	1.79	0.46
1:2:456:C:H2'	1:2:457:C:C6	2.50	0.46
2:A:9304:G:H2'	2:A:9306:G:N3	2.29	0.46
4:C:136:ARG:HG2	4:C:138:PHE:CE1	2.50	0.46
9:H:191:ARG:HA	9:H:194:LEU:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:145:ARG:NH2	25:X:51:GLU:OE1	2.48	0.46
12:K:79:ARG:HA	12:K:82:VAL:HG22	1.96	0.46
19:R:110:ASP:OD1	19:R:111:ILE:N	2.48	0.46
20:S:78:ARG:HA	20:S:81:ARG:HD3	1.97	0.46
21:T:34:LYS:HB3	21:T:100:ALA:CB	2.46	0.46
35:h:231:ASP:OD1	35:h:231:ASP:N	2.47	0.46
1:2:375:U:O4	1:2:376:A:N6	2.49	0.46
1:2:419:G:O2'	25:X:88:LYS:HD2	2.15	0.46
1:2:509:G:H2'	1:2:510:G:H8	1.80	0.46
1:2:636:C:OP2	33:f:94:LYS:NZ	2.48	0.46
1:2:1336:C:H2'	1:2:1337:C:C6	2.50	0.46
1:2:1727:G:H2'	1:2:1728:U:H6	1.80	0.46
5:D:210:PRO:HD3	5:D:236:PHE:HE2	1.79	0.46
7:F:15:PRO:CG	7:F:18:TRP:HE1	2.27	0.46
16:O:63:VAL:O	16:O:67:THR:HG22	2.16	0.46
1:2:1065:G:H2'	1:2:1066:U:C6	2.51	0.46
1:2:1605:G:C5	1:2:1606:G:N1	2.84	0.46
1:2:1658:G:H2'	1:2:1659:U:C6	2.50	0.46
2:A:9229:U:H5'	2:A:9230:U:H3'	1.96	0.46
4:C:87:ILE:C	4:C:98:THR:HG1	2.22	0.46
5:D:108:LYS:HD3	5:D:110:MET:HE2	1.97	0.46
6:E:157:MET:HE3	6:E:158:ILE:N	2.30	0.46
10:I:8:ILE:HD13	10:I:16:PRO:HB3	1.98	0.46
10:I:89:GLY:C	10:I:90:LYS:HD3	2.41	0.46
14:M:30:LYS:HA	14:M:32:LYS:HZ2	1.81	0.46
17:P:129:ILE:O	29:b:65:PRO:HG3	2.15	0.46
25:X:11:LEU:HD21	25:X:37:PHE:CE2	2.51	0.46
30:c:56:CYS:HB3	30:c:63:LEU:HD21	1.97	0.46
32:e:47:ALA:O	32:e:51:GLY:N	2.29	0.46
1:2:38:A:OP1	12:K:5:ARG:HG3	2.15	0.46
1:2:89:C:O2	1:2:499:G:H4'	2.15	0.46
1:2:870:A:H62	1:2:915:G:H2'	1.80	0.46
1:2:1076:G:C6	1:2:1077:A:N7	2.83	0.46
1:2:1237:C:H1'	18:Q:128:HIS:HE1	1.81	0.46
1:2:1240:A:C8	18:Q:100:LYS:HE2	2.50	0.46
1:2:1428:G:O2'	1:2:1585:U:O4	2.23	0.46
1:2:1792:G:H2'	1:2:1793:A:H8	1.81	0.46
4:C:217:MET:HG2	4:C:220:LYS:HE3	1.96	0.46
8:G:87:LEU:HD21	19:R:78:VAL:HG21	1.96	0.46
10:I:158:LEU:HD11	10:I:187:PHE:CD2	2.45	0.46
13:L:26:ASP:N	13:L:26:ASP:OD1	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:71:ILE:HG21	20:S:75:GLU:HG3	1.96	0.46
21:T:124:ARG:HE	21:T:127:TRP:HE3	1.62	0.46
23:V:67:LYS:HD3	23:V:78:ASP:HB3	1.98	0.46
31:d:33:GLU:OE1	31:d:38:THR:HA	2.15	0.46
1:2:17:C:H2'	1:2:18:C:C6	2.51	0.46
1:2:373:G:O6	1:2:392:A:N6	2.49	0.46
1:2:1659:U:O2	1:2:1664:A:N7	2.48	0.46
4:C:193:ILE:O	4:C:197:ILE:HG12	2.16	0.46
7:F:199:GLU:OE1	7:F:199:GLU:N	2.48	0.46
8:G:60:ARG:HG3	8:G:61:PHE:HD2	1.80	0.46
10:I:26:ALA:HB1	10:I:86:LYS:HZ1	1.80	0.46
11:J:57:ALA:HB2	11:J:183:GLY:HA2	1.98	0.46
14:M:72:ILE:O	14:M:73:LEU:HD23	2.15	0.46
14:M:136:LYS:O	14:M:139:ARG:NH1	2.48	0.46
17:P:83:GLN:O	17:P:87:GLU:HG2	2.15	0.46
35:h:203:ASP:OD1	35:h:204:GLY:N	2.49	0.46
1:2:74:G:O6	9:H:159:ARG:NH1	2.49	0.46
1:2:462:C:H2'	1:2:463:C:C6	2.51	0.46
1:2:604:A:H2'	1:2:639:C:O2'	2.16	0.46
1:2:1250:A:O2'	1:2:1251:A:OP1	2.30	0.46
5:D:165:VAL:HG11	5:D:244:ILE:HG12	1.98	0.46
6:E:29:LEU:HD21	6:E:58:VAL:HG23	1.97	0.46
7:F:151:ASP:OD1	7:F:152:PRO:HD2	2.16	0.46
7:F:247:THR:N	7:F:250:GLU:OE2	2.48	0.46
20:S:78:ARG:HD3	20:S:81:ARG:HD3	1.97	0.46
1:2:605:A:O2'	1:2:638:C:O2	2.33	0.46
1:2:1224:G:N1	1:2:1642:U:C2	2.83	0.46
1:2:1375:G:H5'	1:2:1464:C:O2	2.16	0.46
1:2:1468:C:H2'	1:2:1469:A:C8	2.50	0.46
1:2:1619:A:O3'	18:Q:44:ARG:NH1	2.48	0.46
1:2:1712:A:H2'	1:2:1713:C:C6	2.51	0.46
7:F:32:SER:N	7:F:81:THR:O	2.42	0.46
10:I:95:ILE:HD13	10:I:180:LEU:HD11	1.98	0.46
11:J:73:THR:HA	11:J:109:TYR:HE1	1.80	0.46
17:P:45:THR:HG22	17:P:52:THR:HA	1.98	0.46
1:2:1154:U:O3'	5:D:194:ARG:NH1	2.49	0.46
2:A:9305:G:C6	31:d:43:ILE:HG12	2.51	0.46
3:B:131:HIS:CE1	3:B:132:GLN:HG2	2.50	0.46
11:J:105:ASP:OD2	11:J:107:THR:OG1	2.34	0.46
20:S:100:PRO:O	20:S:103:LYS:HG2	2.15	0.46
1:2:1308:U:O2'	1:2:1309:C:H6	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1532:C:H3'	1:2:1637:A:N6	2.27	0.46
1:2:1599:U:H4'	1:2:1600:G:H5''	1.97	0.46
1:2:1603:G:C5	21:T:28:PHE:HD2	2.34	0.46
1:2:1625:U:H2'	1:2:1626:C:C6	2.51	0.46
1:2:1629:C:H1'	21:T:85:ASN:HA	1.97	0.46
3:B:33:GLN:HB2	3:B:154:LEU:HD13	1.98	0.46
5:D:205:VAL:O	5:D:206:SER:OG	2.34	0.46
6:E:162:ASP:N	6:E:163:PRO:HD2	2.31	0.46
7:F:136:ILE:HG13	7:F:149:TYR:CE1	2.51	0.46
7:F:147:ILE:HG21	7:F:169:ILE:HD11	1.97	0.46
10:I:41:ARG:HD3	10:I:41:ARG:HA	1.69	0.46
32:e:45:GLN:HG3	32:e:46:TYR:CD1	2.52	0.46
35:h:72:SER:HB2	35:h:117:ASN:CG	2.41	0.46
1:2:379:C:H2'	1:2:380:G:H8	1.81	0.45
1:2:1008:A:H2'	1:2:1009:A:H8	1.81	0.45
1:2:1033:G:N1	1:2:1080:A:O2'	2.20	0.45
2:A:9254:C:HO2'	2:A:9255:G:H8	1.63	0.45
3:B:89:LYS:HE3	3:B:201:LEU:O	2.16	0.45
6:E:73:VAL:HG12	6:E:76:ARG:CZ	2.46	0.45
8:G:204:ARG:HH12	31:d:66:ARG:HD3	1.79	0.45
11:J:98:LYS:HB2	11:J:98:LYS:HE2	1.80	0.45
12:K:30:LYS:HD3	12:K:34:GLU:OE1	2.16	0.45
14:M:38:LYS:NZ	14:M:61:PRO:O	2.36	0.45
20:S:60:ARG:HH22	20:S:67:ARG:HG2	1.81	0.45
26:Y:98:ASP:OD1	26:Y:98:ASP:N	2.47	0.45
35:h:240:CYS:HB3	35:h:291:TRP:HE1	1.80	0.45
1:2:651:U:H2'	1:2:652:U:C6	2.52	0.45
1:2:866:U:H2'	1:2:867:G:C8	2.51	0.45
1:2:1245:G:N2	23:V:72:GLU:OE2	2.49	0.45
1:2:1342:U:N3	1:2:1483:A:N7	2.43	0.45
1:2:1503:C:H2'	1:2:1504:U:C6	2.52	0.45
1:2:1550:G:H4'	1:2:1558:C:O2'	2.17	0.45
2:A:9303:C:H4'	2:A:9304:G:OP1	2.16	0.45
6:E:99:ILE:HG23	6:E:173:ARG:HH22	1.81	0.45
7:F:85:GLY:O	7:F:101:LEU:HD22	2.16	0.45
7:F:126:VAL:HG22	7:F:158:ASP:O	2.17	0.45
8:G:121:PRO:HD2	8:G:149:GLN:HG3	1.97	0.45
9:H:82:SER:OG	9:H:83:CYS:N	2.50	0.45
11:J:43:ILE:HG22	11:J:57:ALA:HA	1.97	0.45
21:T:15:VAL:HG22	21:T:16:LEU:HG	1.98	0.45
21:T:25:LYS:HG3	21:T:27:ALA:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Z:35:VAL:HG23	27:Z:40:ILE:HD11	1.98	0.45
32:e:16:GLN:NE2	32:e:19:ARG:HH12	2.13	0.45
1:2:460:A:H1'	1:2:470:G:N2	2.32	0.45
1:2:558:G:H2'	1:2:559:G:H8	1.81	0.45
1:2:1094:C:H1'	25:X:16:ASN:ND2	2.31	0.45
1:2:1657:G:O6	1:2:1667:U:C4	2.69	0.45
1:2:1671:G:H2'	1:2:1672:U:H6	1.81	0.45
2:A:9228:C:H2'	2:A:9229:U:H4'	1.98	0.45
7:F:206:ASP:HB2	7:F:222:LEU:HD22	1.99	0.45
8:G:78:MET:O	8:G:79:HIS:ND1	2.49	0.45
8:G:139:VAL:HA	31:d:63:ARG:NH2	2.31	0.45
10:I:160:LYS:HZ1	10:I:189:PHE:HA	1.80	0.45
14:M:57:ASP:HB3	14:M:60:CYS:SG	2.56	0.45
16:O:85:PRO:HG2	16:O:129:TYR:CD1	2.51	0.45
20:S:89:SER:C	20:S:91:LEU:H	2.25	0.45
20:S:98:VAL:HG13	20:S:102:THR:HG23	1.97	0.45
29:b:87:ARG:NH1	29:b:94:ASP:HB2	2.32	0.45
1:2:528:A:H2'	1:2:529:A:H8	1.82	0.45
1:2:602:G:N2	1:2:621:C:N3	2.65	0.45
1:2:683:G:N1	1:2:1022:U:OP2	2.46	0.45
1:2:1406:G:H2'	1:2:1407:U:H6	1.82	0.45
1:2:1455:A:H61	1:2:1471:C:N4	2.09	0.45
1:2:1738:C:H2'	1:2:1739:C:H6	1.82	0.45
2:A:9227:G:H2'	2:A:9228:C:C6	2.51	0.45
3:B:85:ARG:HG3	3:B:89:LYS:HZ1	1.82	0.45
4:C:214:LYS:NZ	4:C:216:LYS:HE2	2.32	0.45
6:E:73:VAL:HA	6:E:76:ARG:HG2	1.99	0.45
6:E:157:MET:SD	6:E:189:MET:HB2	2.56	0.45
7:F:90:ILE:HB	7:F:99:PHE:HB2	1.98	0.45
11:J:159:SER:HB3	11:J:162:LEU:HB2	1.97	0.45
18:Q:118:GLU:OE2	21:T:120:HIS:N	2.49	0.45
22:U:102:ARG:HD3	22:U:102:ARG:HA	1.83	0.45
35:h:62:HIS:CG	35:h:82:SER:HB2	2.52	0.45
1:2:60:A:O2'	1:2:316:G:O2'	2.27	0.45
1:2:92:A:H61	1:2:444:G:H1'	1.82	0.45
1:2:149:A:C8	1:2:170:A:N6	2.84	0.45
1:2:521:A:H2'	1:2:522:A:O4'	2.16	0.45
1:2:799:U:H3	1:2:867:G:H22	1.64	0.45
1:2:1115:U:H5''	1:2:1116:C:H5	1.80	0.45
1:2:1343:U:H3	1:2:1484:A:N6	2.15	0.45
1:2:1355:C:HO2'	5:D:238:LYS:NZ	2.12	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1472:C:N4	1:2:1476:A:N6	2.22	0.45
3:B:82:THR:HG22	3:B:171:VAL:HG11	1.99	0.45
3:B:122:LEU:HB3	3:B:142:LEU:HD21	1.97	0.45
6:E:103:GLU:CD	6:E:173:ARG:HH12	2.24	0.45
9:H:67:VAL:HG23	9:H:69:THR:H	1.81	0.45
10:I:43:LEU:HD12	10:I:72:PHE:CE1	2.51	0.45
12:K:86:VAL:HG23	12:K:104:ASP:HB3	1.97	0.45
20:S:9:VAL:O	20:S:50:ILE:HG22	2.15	0.45
21:T:128:GLY:O	21:T:130:ARG:NH2	2.50	0.45
22:U:52:TRP:HA	22:U:55:THR:HG22	1.98	0.45
1:2:991:G:C6	1:2:1134:G:H4'	2.51	0.45
1:2:1372:U:H2'	1:2:1373:C:C6	2.52	0.45
1:2:1460:C:H2'	1:2:1461:G:O4'	2.16	0.45
2:A:9256:G:H1'	2:A:9268:G:N2	2.32	0.45
2:A:9286:G:H2'	2:A:9287:G:C8	2.52	0.45
3:B:189:ILE:HG21	3:B:195:TRP:CD1	2.52	0.45
5:D:210:PRO:O	5:D:214:LEU:HD23	2.17	0.45
8:G:51:HIS:HB2	8:G:86:LYS:HE2	1.98	0.45
9:H:55:GLY:O	9:H:56:ASN:ND2	2.50	0.45
9:H:98:ARG:HD3	9:H:99:GLY:O	2.16	0.45
11:J:100:CYS:SG	11:J:175:ILE:HD13	2.56	0.45
12:K:50:LEU:HA	12:K:53:ILE:HG22	1.99	0.45
14:M:71:ARG:N	14:M:130:GLU:OE1	2.50	0.45
34:g:121:CYS:SG	34:g:123:SER:OG	2.70	0.45
1:2:63:U:O2'	1:2:170:A:N3	2.44	0.45
1:2:372:U:H2'	1:2:373:G:C8	2.52	0.45
1:2:1102:G:H2'	1:2:1103:C:C6	2.51	0.45
1:2:1481:G:H2'	1:2:1482:C:C2	2.52	0.45
1:2:1627:C:C2	1:2:1628:C:C5	3.05	0.45
1:2:1738:C:H2'	1:2:1739:C:C6	2.52	0.45
4:C:91:VAL:HG13	4:C:95:ASN:O	2.17	0.45
5:D:211:LYS:O	5:D:215:MET:HG2	2.16	0.45
7:F:185:GLY:N	7:F:189:LEU:HD13	2.31	0.45
9:H:27:PHE:HE2	9:H:41:LEU:HD21	1.82	0.45
9:H:44:GLU:HA	9:H:119:LYS:HD3	1.99	0.45
9:H:50:VAL:HG23	9:H:113:ILE:HD13	1.99	0.45
10:I:24:SER:O	10:I:27:LEU:HG	2.17	0.45
18:Q:85:ILE:HG23	18:Q:112:ILE:HA	1.98	0.45
35:h:101:PHE:CE1	35:h:136:GLY:HA2	2.51	0.45
1:2:1115:U:H5''	1:2:1116:C:C5	2.50	0.45
1:2:1409:A:N6	1:2:1438:A:H61	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1712:A:H2'	1:2:1713:C:H6	1.82	0.45
11:J:36:THR:HG21	11:J:179:PRO:HB2	1.99	0.45
13:L:35:LEU:HD23	13:L:40:VAL:HG11	1.98	0.45
19:R:38:PRO:HD3	22:U:8:ASP:OD1	2.16	0.45
23:V:28:ASN:HB3	23:V:31:SER:OG	2.17	0.45
25:X:102:ILE:HD12	25:X:127:GLY:O	2.16	0.45
29:b:41:ILE:HG22	29:b:66:LYS:HE3	1.97	0.45
1:2:71:G:C6	1:2:79:A:C8	3.05	0.45
1:2:164:A:O2'	1:2:165:G:O4'	2.19	0.45
1:2:186:C:H3'	1:2:187:G:H8	1.82	0.45
1:2:218:U:H2'	1:2:219:U:H6	1.82	0.45
1:2:373:G:C6	1:2:392:A:N6	2.85	0.45
1:2:507:G:OP1	27:Z:108:LYS:NZ	2.38	0.45
1:2:1533:A:H2	1:2:1536:G:N3	2.15	0.45
1:2:1608:U:H4'	21:T:130:ARG:NH1	2.31	0.45
1:2:1614:A:H2'	1:2:1615:U:C6	2.52	0.45
3:B:14:ASP:OD1	3:B:180:ARG:NH2	2.30	0.45
4:C:32:ASP:OD1	4:C:32:ASP:N	2.48	0.45
8:G:88:MET:SD	8:G:92:ILE:HD12	2.56	0.45
8:G:128:ILE:HD12	31:d:68:LEU:O	2.17	0.45
9:H:157:VAL:HG21	9:H:176:ILE:HD11	1.98	0.45
16:O:19:ARG:NH2	16:O:23:PRO:HB3	2.31	0.45
19:R:58:LEU:HB2	19:R:63:PHE:HE2	1.82	0.45
19:R:96:TYR:HA	19:R:100:VAL:HG22	1.97	0.45
27:Z:107:ARG:NH2	27:Z:110:ARG:HD3	2.32	0.45
1:2:4:C:H4'	5:D:207:ALA:HB2	1.98	0.45
1:2:309:G:H2'	1:2:310:C:H6	1.82	0.45
1:2:512:A:H2'	1:2:513:G:H8	1.82	0.45
1:2:637:U:H2'	1:2:638:C:C6	2.51	0.45
1:2:1025:U:O3'	1:2:1089:G:N2	2.49	0.45
1:2:1374:C:O4'	1:2:1465:A:O2'	2.32	0.45
1:2:1572:C:H2'	1:2:1573:G:C8	2.52	0.45
1:2:1624:U:H3	18:Q:40:ARG:NH2	2.13	0.45
1:2:1733:U:H2'	1:2:1734:G:O4'	2.17	0.45
4:C:110:MET:SD	4:C:213:ARG:HD2	2.57	0.45
10:I:55:GLY:HA3	10:I:57:ARG:HH22	1.82	0.45
16:O:91:LEU:HB3	16:O:122:ILE:CG2	2.45	0.45
19:R:130:LYS:HG3	19:R:137:ALA:HA	1.98	0.45
20:S:45:LYS:HE2	20:S:45:LYS:HB2	1.75	0.45
21:T:5:ILE:HB	28:a:49:LEU:CB	2.45	0.45
22:U:84:ARG:HA	22:U:90:SER:OG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Z:18:LEU:HD13	27:Z:20:ARG:CZ	2.47	0.45
27:Z:26:ASP:N	27:Z:26:ASP:OD1	2.50	0.45
35:h:109:LEU:HD13	35:h:152:SER:HA	1.99	0.45
35:h:113:PHE:HB3	35:h:117:ASN:HD22	1.82	0.45
1:2:1646:C:C4	1:2:1678:A:H2	2.35	0.44
2:A:9269:C:H2'	2:A:9270:U:C6	2.52	0.44
3:B:52:LYS:N	20:S:109:LEU:HD21	2.32	0.44
4:C:165:ARG:O	4:C:169:MET:HE3	2.17	0.44
7:F:105:THR:HG23	7:F:106:LYS:HG3	1.98	0.44
7:F:246:LEU:HD23	7:F:246:LEU:H	1.81	0.44
29:b:10:ARG:HB2	29:b:33:ASP:OD1	2.17	0.44
32:e:36:LEU:H	32:e:36:LEU:HD12	1.82	0.44
1:2:222:U:H2'	1:2:223:C:C6	2.52	0.44
1:2:291:G:N2	14:M:68:ILE:O	2.32	0.44
1:2:444:G:N2	1:2:446:G:H3'	2.33	0.44
1:2:666:U:O2'	1:2:1087:A:H2'	2.17	0.44
1:2:1147:C:OP1	29:b:6:ARG:NH1	2.49	0.44
7:F:20:LEU:HD23	7:F:20:LEU:H	1.81	0.44
7:F:85:GLY:C	7:F:101:LEU:HD22	2.43	0.44
10:I:143:ARG:HB2	10:I:155:LYS:HE3	1.98	0.44
12:K:69:ARG:NH2	12:K:73:GLU:OE2	2.50	0.44
26:Y:60:LYS:HG3	26:Y:61:GLN:N	2.24	0.44
1:2:75:G:H2'	1:2:76:U:H5''	1.98	0.44
1:2:181:A:O5'	1:2:182:C:H5''	2.17	0.44
1:2:458:A:H2'	1:2:459:C:C6	2.51	0.44
1:2:1539:U:O2'	22:U:48:TYR:N	2.36	0.44
1:2:1545:A:H2	1:2:1671:G:H1'	1.83	0.44
8:G:151:ILE:HD12	8:G:154:LEU:HD21	1.99	0.44
10:I:48:ALA:HA	10:I:61:ILE:O	2.17	0.44
11:J:67:TRP:HB3	11:J:70:GLU:OE2	2.18	0.44
11:J:134:GLU:O	11:J:138:ASN:ND2	2.50	0.44
16:O:128:TYR:HA	16:O:131:THR:HG22	2.00	0.44
23:V:81:GLN:HB3	23:V:83:ARG:NH2	2.32	0.44
34:g:121:CYS:HB3	34:g:126:CYS:SG	2.57	0.44
1:2:12:U:H2'	1:2:13:C:H6	1.77	0.44
1:2:617:G:H4'	26:Y:88:ASP:HB2	1.98	0.44
1:2:832:G:H2'	1:2:833:C:C6	2.52	0.44
1:2:875:A:H61	1:2:911:C:H42	1.65	0.44
1:2:1123:C:C2	1:2:1124:C:C5	3.06	0.44
1:2:1135:C:C4	1:2:1136:U:C4	3.05	0.44
1:2:1233:G:O6	21:T:138:THR:HG21	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:127:VAL:HG11	4:C:176:VAL:HB	2.00	0.44
5:D:186:GLY:CA	5:D:243:ALA:HB2	2.46	0.44
6:E:169:ASP:OD1	6:E:169:ASP:N	2.51	0.44
9:H:188:LYS:HG2	9:H:191:ARG:CZ	2.47	0.44
12:K:46:VAL:HA	12:K:49:THR:HG22	1.98	0.44
16:O:73:ARG:O	16:O:76:LYS:HG3	2.17	0.44
21:T:23:ARG:HD2	21:T:23:ARG:N	2.31	0.44
22:U:40:ALA:HB2	22:U:79:TYR:HE2	1.80	0.44
31:d:14:VAL:HG22	31:d:32:VAL:HG12	1.99	0.44
35:h:108:VAL:HA	35:h:124:SER:HA	2.00	0.44
1:2:26:U:H2'	1:2:27:A:C8	2.53	0.44
1:2:165:G:H8	9:H:110:ASN:ND2	2.16	0.44
1:2:388:U:H2'	1:2:389:A:C8	2.53	0.44
1:2:612:U:HO2'	1:2:613:G:P	2.41	0.44
1:2:625:G:H22	26:Y:65:ALA:HB2	1.82	0.44
1:2:1203:U:O2'	5:D:117:ARG:HB3	2.17	0.44
1:2:1394:G:N2	1:2:1451:G:H22	2.15	0.44
1:2:1449:G:H2'	1:2:1450:G:C8	2.52	0.44
3:B:39:TYR:CD2	20:S:105:MET:HB2	2.52	0.44
3:B:52:LYS:HB2	20:S:109:LEU:HD11	1.99	0.44
4:C:137:LEU:HD13	4:C:215:VAL:HG22	2.00	0.44
6:E:190:LEU:HD13	6:E:199:GLY:HA2	1.98	0.44
7:F:122:LYS:HD3	7:F:162:ILE:HD11	1.99	0.44
8:G:79:HIS:HB3	8:G:159:ARG:HD3	1.99	0.44
10:I:45:ILE:HG22	10:I:64:VAL:HG22	2.00	0.44
13:L:83:LEU:HB3	13:L:85:LEU:HD23	1.98	0.44
16:O:42:LYS:HD3	16:O:80:LEU:HD21	2.00	0.44
20:S:36:GLU:HB3	20:S:47:ARG:NE	2.33	0.44
20:S:80:ARG:HG3	20:S:81:ARG:HD2	1.99	0.44
25:X:105:THR:HG22	25:X:110:ILE:HD12	1.99	0.44
35:h:5:MET:HE2	35:h:310:TRP:CD2	2.53	0.44
1:2:115:U:H2'	1:2:116:U:H6	1.83	0.44
1:2:1242:U:O5'	1:2:1243:U:H5''	2.18	0.44
1:2:1258:A:H62	1:2:1660:C:H5'	1.83	0.44
1:2:1564:C:H2'	1:2:1565:C:C6	2.52	0.44
2:A:9158:G:H2'	2:A:9159:A:C8	2.52	0.44
3:B:89:LYS:HA	3:B:92:ALA:HB3	1.99	0.44
7:F:201:HIS:N	7:F:206:ASP:OD1	2.29	0.44
9:H:50:VAL:CG2	9:H:111:LEU:HB3	2.48	0.44
18:Q:56:LEU:HA	18:Q:59:ARG:HE	1.83	0.44
19:R:24:HIS:CE1	19:R:26:LYS:HE2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:94:GLU:HG2	20:S:95:ILE:N	2.32	0.44
1:2:668:A:H5'	1:2:669:A:OP2	2.17	0.44
1:2:808:A:C6	1:2:809:A:C2	3.06	0.44
1:2:1310:U:O2'	34:g:143:LYS:HG2	2.18	0.44
6:E:72:VAL:HA	6:E:75:LYS:NZ	2.33	0.44
9:H:43:GLU:O	9:H:46:LYS:HG2	2.18	0.44
10:I:134:VAL:HG12	10:I:173:PHE:CZ	2.53	0.44
13:L:22:VAL:HG12	13:L:68:TYR:HD1	1.83	0.44
14:M:27:GLU:O	14:M:30:LYS:NZ	2.44	0.44
14:M:134:LEU:HD21	14:M:141:ASN:HD21	1.83	0.44
15:N:59:PRO:HG2	15:N:60:MET:SD	2.58	0.44
25:X:93:LEU:HD23	25:X:93:LEU:HA	1.85	0.44
1:2:76:U:H4'	9:H:155:GLN:NE2	2.33	0.44
1:2:91:A:H2'	9:H:88:ARG:HH12	1.83	0.44
1:2:146:G:O6	9:H:137:ARG:NH2	2.51	0.44
1:2:155:G:H21	9:H:56:ASN:CG	2.21	0.44
1:2:337:C:H2'	1:2:338:G:C8	2.52	0.44
1:2:825:A:H2'	1:2:826:A:C8	2.53	0.44
1:2:1520:G:OP1	21:T:137:LYS:HB2	2.18	0.44
1:2:1607:A:OP1	22:U:87:VAL:HG21	2.17	0.44
1:2:1656:G:N2	1:2:1668:U:O2	2.30	0.44
9:H:13:GLN:O	9:H:14:LYS:HD2	2.18	0.44
16:O:104:ARG:HE	16:O:106:ARG:NH2	2.15	0.44
21:T:34:LYS:HB3	21:T:100:ALA:HB1	1.98	0.44
23:V:80:PHE:CD1	32:e:52:PHE:HB3	2.53	0.44
1:2:71:G:H2'	1:2:72:C:C6	2.53	0.44
1:2:298:G:OP1	7:F:134:LYS:HA	2.18	0.44
1:2:616:A:OP2	26:Y:66:ILE:N	2.50	0.44
1:2:751:G:H1	1:2:792:C:H42	1.65	0.44
1:2:1077:A:C6	1:2:1078:C:C5	3.06	0.44
1:2:1260:A:N6	1:2:1619:A:C5	2.85	0.44
1:2:1329:U:O2'	1:2:1332:A:OP1	2.28	0.44
1:2:1387:G:H3'	1:2:1388:A:H8	1.82	0.44
3:B:51:LEU:O	3:B:54:THR:OG1	2.23	0.44
4:C:185:VAL:O	4:C:189:ILE:HG12	2.16	0.44
5:D:228:GLY:O	5:D:230:THR:HG23	2.17	0.44
7:F:87:MET:HE2	7:F:123:LEU:H	1.83	0.44
9:H:38:ALA:HB1	9:H:41:LEU:HD12	2.00	0.44
14:M:130:GLU:HB3	14:M:140:PHE:CZ	2.53	0.44
16:O:19:ARG:HH21	16:O:23:PRO:HB3	1.83	0.44
16:O:122:ILE:HD11	16:O:141:TYR:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:15:VAL:O	21:T:18:THR:OG1	2.34	0.44
21:T:89:ASP:OD2	21:T:96:SER:OG	2.35	0.44
23:V:65:THR:HG21	32:e:43:PHE:CE2	2.53	0.44
1:2:155:G:H2'	1:2:156:G:C8	2.52	0.43
1:2:213:G:H2'	1:2:214:U:C6	2.53	0.43
1:2:445:A:HO2'	1:2:446:G:P	2.40	0.43
1:2:639:C:H2'	1:2:640:A:H8	1.83	0.43
1:2:808:A:O2'	7:F:221:ARG:NH1	2.51	0.43
1:2:915:G:OP1	10:I:120:ARG:NH1	2.40	0.43
1:2:1120:U:N3	1:2:1121:G:N7	2.65	0.43
1:2:1134:G:C4	1:2:1135:C:C5	3.06	0.43
1:2:1246:A:C8	1:2:1247:C:H5	2.36	0.43
1:2:1540:G:H5''	22:U:56:ARG:HH21	1.83	0.43
1:2:1560:U:O2'	1:2:1583:C:H1'	2.18	0.43
1:2:1787:G:H2'	1:2:1788:A:H8	1.83	0.43
3:B:41:ARG:NE	3:B:45:GLY:HA2	2.32	0.43
7:F:89:VAL:HG23	7:F:100:ARG:NH1	2.33	0.43
7:F:122:LYS:HE2	7:F:142:HIS:HE1	1.82	0.43
12:K:24:ARG:O	12:K:28:GLU:HG3	2.18	0.43
14:M:18:GLN:NE2	14:M:19:ASN:OD1	2.51	0.43
14:M:130:GLU:HB3	14:M:140:PHE:CE1	2.53	0.43
15:N:31:LEU:HD13	15:N:33:ARG:HG3	1.98	0.43
16:O:54:LEU:HB3	16:O:60:VAL:CG1	2.48	0.43
21:T:8:LYS:HG3	21:T:8:LYS:O	2.17	0.43
35:h:14:HIS:NE2	35:h:33:SER:OG	2.35	0.43
1:2:218:U:H2'	1:2:219:U:C6	2.53	0.43
1:2:299:A:H2'	1:2:300:U:H6	1.83	0.43
1:2:511:U:C2	1:2:512:A:C8	3.06	0.43
1:2:1100:A:N1	1:2:1133:A:N1	2.65	0.43
1:2:1175:G:C6	1:2:1176:G:C5	3.07	0.43
1:2:1668:U:H2'	1:2:1669:G:C8	2.53	0.43
2:A:9235:A:H1'	2:A:9236:A:C8	2.53	0.43
2:A:9271:G:H8	2:A:9271:G:O5'	2.01	0.43
2:A:9298:C:O2	31:d:38:THR:HG22	2.18	0.43
4:C:69:VAL:HG21	4:C:74:LEU:HD22	2.00	0.43
4:C:198:GLU:O	4:C:202:GLN:HG2	2.18	0.43
5:D:212:LYS:O	5:D:216:MET:HG2	2.18	0.43
9:H:7:PHE:O	9:H:11:GLY:N	2.51	0.43
13:L:15:LEU:HA	13:L:21:MET:HE1	1.99	0.43
13:L:29:MET:HE3	13:L:30:PRO:HD2	1.98	0.43
14:M:35:ARG:NH1	14:M:53:GLY:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:93:LEU:HD12	14:M:102:PHE:HB3	2.00	0.43
14:M:99:TYR:CZ	26:Y:13:LEU:HD22	2.52	0.43
18:Q:80:LEU:HB3	18:Q:83:MET:SD	2.57	0.43
20:S:99:ASP:HB3	20:S:102:THR:HG22	2.00	0.43
31:d:45:ASN:CG	31:d:65:ALA:HB1	2.44	0.43
1:2:166:A:C2	1:2:167:G:C5	3.06	0.43
1:2:821:G:C6	12:K:150:ARG:HD3	2.53	0.43
1:2:883:U:O4	1:2:904:A:N6	2.51	0.43
1:2:935:G:H2'	1:2:936:G:C8	2.50	0.43
1:2:1211:G:H2'	1:2:1212:G:O4'	2.18	0.43
1:2:1739:C:N3	1:2:1796:G:N1	2.67	0.43
3:B:212:LYS:HE2	3:B:212:LYS:HB3	1.81	0.43
8:G:146:ARG:HA	8:G:149:GLN:NE2	2.34	0.43
11:J:66:SER:O	11:J:189:VAL:HG22	2.18	0.43
16:O:95:ALA:HA	16:O:118:ILE:HD11	2.01	0.43
32:e:42:CYS:HA	32:e:45:GLN:HB3	1.99	0.43
35:h:116:ASP:OD1	35:h:116:ASP:N	2.42	0.43
35:h:152:SER:H	35:h:169:GLY:HA2	1.83	0.43
1:2:816:A:H2'	1:2:817:G:O4'	2.18	0.43
1:2:819:G:H2'	1:2:820:U:C6	2.53	0.43
1:2:1117:C:H2'	1:2:1118:C:C6	2.53	0.43
1:2:1734:G:H21	1:2:1800:A:H62	1.65	0.43
2:A:9223:G:O6	2:A:9243:C:N4	2.48	0.43
3:B:39:TYR:CE2	20:S:105:MET:HB2	2.54	0.43
4:C:109:LYS:HG3	4:C:113:MET:HE3	1.99	0.43
4:C:143:THR:HB	4:C:205:TYR:CE1	2.54	0.43
5:D:256:TRP:CE2	25:X:68:ARG:HD3	2.53	0.43
7:F:80:ILE:HG23	7:F:81:THR:HG23	2.00	0.43
8:G:139:VAL:HB	31:d:45:ASN:O	2.18	0.43
8:G:141:VAL:HG21	8:G:149:GLN:HE22	1.83	0.43
12:K:134:HIS:ND1	12:K:163:SER:HB2	2.34	0.43
35:h:247:TRP:CH2	35:h:267:VAL:HG11	2.53	0.43
1:2:453:C:C2	1:2:454:U:C5	3.07	0.43
1:2:919:A:H4'	1:2:920:A:C5'	2.48	0.43
1:2:1264:C:N4	1:2:1518:C:H41	2.17	0.43
1:2:1311:C:OP2	1:2:1311:C:H3'	2.18	0.43
1:2:1330:G:N2	1:2:1333:U:H3'	2.34	0.43
1:2:1503:C:H2'	1:2:1504:U:H6	1.84	0.43
1:2:1658:G:H2'	1:2:1659:U:H6	1.84	0.43
3:B:29:ASN:HB2	3:B:151:ASP:OD1	2.17	0.43
3:B:120:ARG:HH11	5:D:266:TYR:HB2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:182:VAL:O	3:B:186:ARG:HG3	2.18	0.43
6:E:34:TYR:HE1	6:E:37:VAL:HG13	1.82	0.43
7:F:155:LYS:N	7:F:158:ASP:OD2	2.49	0.43
11:J:172:LEU:HD23	11:J:172:LEU:HA	1.85	0.43
12:K:87:LEU:HD11	12:K:100:LEU:HD11	1.99	0.43
12:K:110:LEU:HD22	12:K:147:PHE:CD2	2.54	0.43
14:M:37:TYR:CE2	14:M:51:ILE:HG23	2.53	0.43
16:O:32:ASP:OD1	16:O:32:ASP:N	2.50	0.43
18:Q:104:GLN:H	18:Q:104:GLN:HG3	1.71	0.43
20:S:18:GLU:O	20:S:72:LYS:NZ	2.47	0.43
21:T:52:LEU:HD23	21:T:52:LEU:H	1.82	0.43
35:h:43:TRP:CZ3	35:h:55:PRO:HG3	2.54	0.43
1:2:53:C:O3'	27:Z:108:LYS:HD3	2.17	0.43
1:2:60:A:H2'	1:2:61:A:C4	2.53	0.43
1:2:894:G:H2'	1:2:894:G:N3	2.33	0.43
1:2:1124:C:C2	1:2:1125:C:C5	3.07	0.43
1:2:1142:G:N2	1:2:1146:C:N3	2.67	0.43
1:2:1342:U:H4'	1:2:1343:U:H5'	2.00	0.43
1:2:1706:G:H1	1:2:1829:G:H22	1.66	0.43
1:2:1772:C:H2'	1:2:1773:C:C5	2.53	0.43
2:A:9271:G:H3'	2:A:9272:U:H5'	1.99	0.43
2:A:9280:A:H2'	2:A:9281:G:C8	2.54	0.43
2:A:9282:C:O2'	2:A:9283:A:OP1	2.32	0.43
3:B:57:LYS:NZ	3:B:161:ILE:HA	2.33	0.43
10:I:20:GLU:O	10:I:23:ILE:HG22	2.18	0.43
10:I:26:ALA:O	10:I:29:GLU:HG3	2.18	0.43
11:J:67:TRP:NE1	11:J:191:GLU:OE1	2.51	0.43
16:O:20:ARG:HH12	25:X:56:HIS:CD2	2.37	0.43
17:P:142:ARG:NH1	29:b:26:CYS:O	2.43	0.43
19:R:54:PRO:O	19:R:58:LEU:HB2	2.19	0.43
20:S:16:ILE:HD11	20:S:38:ILE:HG21	2.00	0.43
20:S:76:GLU:HA	20:S:79:GLU:CB	2.49	0.43
22:U:21:PHE:CG	22:U:134:ILE:HD11	2.54	0.43
26:Y:48:LYS:HD3	26:Y:101:LEU:HD13	1.99	0.43
35:h:108:VAL:O	35:h:125:ARG:NH1	2.52	0.43
1:2:609:U:H2'	1:2:610:G:C8	2.52	0.43
1:2:827:A:H2'	1:2:828:G:O4'	2.19	0.43
1:2:1007:C:H2'	1:2:1008:A:H8	1.84	0.43
1:2:1374:C:C1'	1:2:1465:A:HO2'	2.31	0.43
1:2:1453:C:O4'	20:S:48:ASN:HB3	2.18	0.43
9:H:228:ILE:HG23	9:H:232:ARG:CZ	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:20:ARG:HA	16:O:65:PHE:CE2	2.54	0.43
20:S:74:GLN:HG2	20:S:79:GLU:OE1	2.19	0.43
21:T:28:PHE:HZ	22:U:45:LEU:HD13	1.84	0.43
21:T:113:ARG:HE	21:T:114:LEU:CD2	2.31	0.43
1:2:96:C:O2	1:2:473:A:O2'	2.36	0.43
1:2:610:G:H2'	1:2:611:G:H8	1.83	0.43
1:2:958:G:C6	1:2:959:G:C6	3.07	0.43
1:2:1200:A:H8	1:2:1200:A:O5'	2.01	0.43
1:2:1234:C:H41	21:T:137:LYS:HD3	1.84	0.43
1:2:1237:C:H1'	18:Q:128:HIS:CE1	2.54	0.43
1:2:1476:A:H4'	1:2:1477:U:OP2	2.18	0.43
6:E:210:ILE:HG12	20:S:39:ALA:HB2	2.00	0.43
8:G:124:ASP:N	8:G:124:ASP:OD1	2.52	0.43
9:H:7:PHE:CE1	9:H:9:ALA:HB3	2.53	0.43
14:M:124:ASP:OD1	14:M:125:ILE:N	2.51	0.43
15:N:79:VAL:HG21	15:N:85:LEU:HD12	2.00	0.43
18:Q:83:MET:HB2	18:Q:116:LEU:HD12	2.00	0.43
22:U:114:GLU:OE1	22:U:124:THR:N	2.51	0.43
34:g:98:VAL:HG23	34:g:101:ALA:HB2	1.99	0.43
35:h:214:GLY:HA3	35:h:233:GLY:O	2.19	0.43
1:2:78:C:H5'	9:H:173:ALA:HB3	2.00	0.43
1:2:155:G:C2	1:2:156:G:C6	3.07	0.43
1:2:222:U:H5''	14:M:17:PHE:CD2	2.54	0.43
1:2:528:A:H2'	1:2:529:A:C8	2.54	0.43
1:2:895:G:H2'	1:2:896:U:C6	2.54	0.43
1:2:1242:U:O2'	1:2:1518:C:H4'	2.19	0.43
1:2:1403:C:H4'	1:2:1404:U:H5''	2.00	0.43
1:2:1619:A:H4'	18:Q:44:ARG:CZ	2.48	0.43
1:2:1826:G:H8	1:2:1826:G:P	2.42	0.43
1:2:1845:A:OP2	36:n:11:ARG:NH1	2.52	0.43
3:B:156:TYR:CB	24:W:60:ARG:HH21	2.27	0.43
9:H:213:LEU:O	9:H:217:MET:HG2	2.19	0.43
10:I:101:LEU:HD13	10:I:120:ARG:HB3	2.01	0.43
13:L:86:PRO:HA	13:L:87:PRO:HD3	1.90	0.43
14:M:104:LYS:HE2	14:M:104:LYS:HB2	1.90	0.43
19:R:117:ARG:O	19:R:121:VAL:HG12	2.18	0.43
26:Y:47:ALA:O	26:Y:101:LEU:HD12	2.18	0.43
26:Y:105:PHE:CZ	26:Y:115:ILE:HD11	2.54	0.43
34:g:91:ASN:OD1	34:g:91:ASN:N	2.51	0.43
1:2:574:A:H4'	27:Z:89:HIS:HB3	2.00	0.43
1:2:805:U:C4	1:2:859:G:O6	2.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1272:C:H2'	1:2:1273:C:C6	2.54	0.43
1:2:1318:G:H2'	1:2:1319:U:C6	2.54	0.43
1:2:1548:G:H1	1:2:1584:G:H1	1.67	0.43
1:2:1630:A:H4'	21:T:35:GLY:C	2.44	0.43
1:2:1706:G:H22	1:2:1829:G:H21	1.66	0.43
1:2:1795:G:H2'	1:2:1796:G:C8	2.53	0.43
2:A:9273:U:H1'	2:A:9275:C:H41	1.83	0.43
4:C:27:LYS:HG2	4:C:51:ARG:HB2	2.01	0.43
6:E:193:ASP:N	6:E:193:ASP:OD1	2.52	0.43
7:F:125:LYS:HZ1	7:F:157:ASN:C	2.27	0.43
7:F:204:SER:OG	7:F:205:PHE:N	2.51	0.43
8:G:76:MET:HA	8:G:155:CYS:SG	2.58	0.43
9:H:201:LYS:O	9:H:204:GLU:HG2	2.18	0.43
10:I:71:SER:HA	10:I:74:LYS:HE2	2.01	0.43
11:J:117:TYR:HB3	11:J:119:LEU:HD23	2.01	0.43
12:K:16:PRO:HB2	12:K:24:ARG:NH2	2.34	0.43
13:L:37:ASP:N	13:L:37:ASP:OD1	2.52	0.43
18:Q:73:PRO:HG3	18:Q:91:GLY:O	2.19	0.43
29:b:53:ILE:HG21	29:b:64:LEU:HD11	2.01	0.43
31:d:67:ARG:HG3	31:d:68:LEU:H	1.84	0.43
1:2:167:G:H2'	1:2:168:C:C6	2.54	0.42
1:2:922:A:C6	1:2:923:G:C4	3.07	0.42
5:D:178:HIS:ND1	5:D:200:ARG:HD3	2.34	0.42
7:F:181:CYS:SG	7:F:182:MET:N	2.93	0.42
8:G:76:MET:HE1	8:G:158:ALA:CB	2.49	0.42
12:K:30:LYS:HA	12:K:30:LYS:HE2	1.99	0.42
15:N:113:ASP:OD1	15:N:113:ASP:N	2.49	0.42
16:O:45:LEU:HB2	16:O:50:ILE:CD1	2.49	0.42
26:Y:51:VAL:HG22	26:Y:70:VAL:HG11	2.01	0.42
1:2:379:C:C2	1:2:380:G:C8	3.07	0.42
1:2:956:G:O2'	1:2:972:A:N1	2.44	0.42
1:2:1226:G:H2'	1:2:1227:G:H5'	2.00	0.42
1:2:1546:G:H1	1:2:1655:C:H1'	1.84	0.42
1:2:1628:C:H2'	1:2:1629:C:H6	1.84	0.42
2:A:9158:G:H2'	2:A:9159:A:H8	1.84	0.42
3:B:24:HIS:CE1	3:B:25:LEU:HD22	2.54	0.42
3:B:122:LEU:CB	3:B:142:LEU:HD21	2.49	0.42
3:B:130:ASP:C	3:B:133:PRO:HD2	2.44	0.42
4:C:28:LYS:HE3	4:C:28:LYS:HB2	1.86	0.42
6:E:203:PRO:HB2	6:E:207:HIS:HE1	1.82	0.42
7:F:87:MET:HE3	7:F:100:ARG:NH2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:180:LEU:HD21	7:F:192:ILE:HD11	2.00	0.42
9:H:27:PHE:HE1	9:H:36:VAL:HG21	1.83	0.42
9:H:46:LYS:HE2	9:H:46:LYS:HA	2.00	0.42
12:K:101:LYS:HD3	12:K:101:LYS:HA	1.78	0.42
14:M:10:TYR:OH	14:M:12:LYS:HD3	2.19	0.42
16:O:19:ARG:O	16:O:19:ARG:HG3	2.18	0.42
20:S:28:PHE:HD2	20:S:29:HIS:CE1	2.37	0.42
25:X:103:VAL:HG22	25:X:127:GLY:O	2.19	0.42
36:n:7:LYS:HE3	36:n:11:ARG:HD2	2.01	0.42
1:2:74:G:N2	1:2:78:C:OP2	2.50	0.42
1:2:114:G:C2	1:2:383:G:C6	3.08	0.42
1:2:525:A:N6	1:2:590:A:H5'	2.35	0.42
1:2:743:U:H3	1:2:798:G:H2'	1.85	0.42
1:2:907:G:H8	1:2:907:G:O5'	2.02	0.42
1:2:1221:G:H2'	1:2:1222:G:C8	2.54	0.42
1:2:1426:U:H4'	22:U:7:LYS:HD3	2.01	0.42
1:2:1541:G:N2	22:U:12:GLN:OE1	2.52	0.42
1:2:1739:C:H2'	1:2:1740:C:C6	2.54	0.42
6:E:211:VAL:O	20:S:19:LYS:NZ	2.50	0.42
7:F:8:HIS:HB3	7:F:27:PHE:HE2	1.85	0.42
7:F:86:PHE:HE1	7:F:103:TYR:H	1.66	0.42
8:G:176:GLU:OE1	8:G:187:SER:OG	2.25	0.42
9:H:215:LYS:HG3	9:H:218:LYS:NZ	2.33	0.42
11:J:190:LEU:HB2	11:J:195:LEU:HD13	2.00	0.42
17:P:150:ARG:HD3	17:P:150:ARG:H	1.84	0.42
26:Y:60:LYS:CG	26:Y:61:GLN:H	2.27	0.42
35:h:40:ILE:HD12	35:h:88:ARG:HH21	1.84	0.42
1:2:864:A:N1	1:2:865:A:N6	2.68	0.42
1:2:1037:G:H4'	1:2:1845:A:H4'	2.02	0.42
1:2:1102:G:C2	1:2:1103:C:C4	3.07	0.42
1:2:1198:G:C6	1:2:1199:A:C6	3.07	0.42
1:2:1568:C:H2'	1:2:1569:A:C8	2.55	0.42
7:F:163:ASP:O	7:F:167:GLY:N	2.52	0.42
7:F:179:ASN:HA	7:F:231:GLY:HA2	2.01	0.42
7:F:196:THR:HG21	7:F:211:LYS:CG	2.50	0.42
14:M:81:LYS:HD3	14:M:81:LYS:HA	1.77	0.42
15:N:61:TYR:CE2	34:g:103:LEU:HD11	2.55	0.42
35:h:113:PHE:HB3	35:h:117:ASN:HA	2.01	0.42
35:h:119:GLN:CD	35:h:131:LEU:HB3	2.44	0.42
35:h:246:TYR:HE2	35:h:262:GLU:HB3	1.83	0.42
1:2:160:U:O2'	1:2:162:C:O5'	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:171:A:C8	1:2:173:A:N7	2.88	0.42
1:2:413:G:H5'	1:2:814:U:O2	2.19	0.42
1:2:1427:C:H2'	1:2:1429:G:C8	2.54	0.42
1:2:1468:C:H4'	8:G:60:ARG:NH1	2.34	0.42
3:B:24:HIS:CD2	20:S:102:THR:HG21	2.54	0.42
3:B:69:GLU:OE2	3:B:70:ASN:HB2	2.19	0.42
4:C:36:PRO:HA	4:C:232:HIS:HE1	1.83	0.42
5:D:241:PHE:O	5:D:244:ILE:HG22	2.19	0.42
6:E:67:ARG:HH22	13:L:96:ARG:HH11	1.67	0.42
7:F:79:ASP:HB3	7:F:82:TYR:HB2	2.01	0.42
18:Q:30:TYR:CE1	18:Q:86:LEU:HD21	2.54	0.42
21:T:81:ASP:HB2	21:T:95:TYR:CE2	2.55	0.42
24:W:53:TYR:CD2	24:W:69:ILE:HD11	2.54	0.42
1:2:17:C:H5'	1:2:1166:G:H5'	2.02	0.42
1:2:92:A:C6	1:2:447:A:C6	3.07	0.42
1:2:289:G:H5'	7:F:129:ILE:HD11	2.02	0.42
1:2:345:U:H2'	1:2:346:C:O4'	2.19	0.42
1:2:962:A:H2	1:2:1056:U:H5'	1.85	0.42
1:2:1109:C:H2'	1:2:1110:G:O4'	2.19	0.42
1:2:1218:C:H1'	1:2:1683:C:H42	1.84	0.42
1:2:1256:G:N1	1:2:1659:U:H5''	2.34	0.42
1:2:1317:C:H2'	1:2:1318:G:C8	2.55	0.42
1:2:1374:C:H2'	1:2:1375:G:O4'	2.20	0.42
1:2:1402:A:N6	1:2:1441:U:O2'	2.53	0.42
1:2:1567:G:H1'	22:U:37:VAL:HG12	2.02	0.42
1:2:1593:C:C2	1:2:1594:A:C8	3.08	0.42
1:2:1671:G:H2'	1:2:1672:U:C6	2.55	0.42
1:2:1677:U:C4	1:2:1678:A:N6	2.86	0.42
5:D:145:LYS:HA	5:D:145:LYS:HD3	1.85	0.42
6:E:93:THR:HB	6:E:96:LEU:HB2	2.01	0.42
33:f:94:LYS:HD2	33:f:94:LYS:HA	1.88	0.42
35:h:236:ILE:HG22	35:h:239:LEU:HD11	2.01	0.42
1:2:512:A:H2'	1:2:513:G:C8	2.55	0.42
1:2:524:U:H3	33:f:100:LYS:NZ	2.18	0.42
1:2:610:G:C4	1:2:611:G:C8	3.08	0.42
1:2:677:G:H2'	1:2:678:U:C5	2.54	0.42
1:2:1083:A:O2'	1:2:1084:A:OP1	2.37	0.42
1:2:1169:G:H21	1:2:1191:C:H42	1.67	0.42
1:2:1254:C:H2'	1:2:1255:G:C8	2.55	0.42
1:2:1302:G:H1'	1:2:1304:U:OP2	2.19	0.42
1:2:1481:G:H2'	1:2:1482:C:N1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1542:C:O5'	1:2:1542:C:H6	2.02	0.42
1:2:1558:C:H2'	1:2:1559:C:C6	2.55	0.42
3:B:19:LEU:HB3	20:S:96:ILE:HG21	2.02	0.42
4:C:164:ILE:O	4:C:168:MET:HG3	2.19	0.42
9:H:164:LYS:HE3	9:H:167:LYS:HD2	2.01	0.42
14:M:7:GLU:HG2	14:M:8:ARG:N	2.34	0.42
15:N:33:ARG:HD3	15:N:91:LEU:HD23	2.02	0.42
17:P:56:VAL:HG23	17:P:77:ALA:HB1	2.00	0.42
26:Y:71:ARG:NH1	26:Y:82:THR:OG1	2.53	0.42
35:h:89:LEU:HD13	35:h:99:ARG:HB2	2.01	0.42
1:2:42:A:C2	1:2:426:A:C6	3.08	0.42
1:2:307:G:N1	11:J:44:HIS:HD2	2.18	0.42
1:2:743:U:N3	1:2:798:G:N3	2.68	0.42
1:2:1123:C:H2'	1:2:1124:C:H6	1.85	0.42
1:2:1495:G:C2	32:e:41:GLN:HB3	2.55	0.42
1:2:1654:G:H2'	1:2:1655:C:C6	2.55	0.42
2:A:9295:A:H4'	2:A:9296:U:OP1	2.18	0.42
19:R:35:ASN:O	22:U:7:LYS:NZ	2.36	0.42
21:T:5:ILE:HD13	28:a:49:LEU:HD23	2.01	0.42
25:X:102:ILE:CG1	25:X:125:ILE:HD11	2.50	0.42
27:Z:23:MET:HE2	27:Z:23:MET:HB2	1.92	0.42
1:2:170:A:O2'	1:2:171:A:O4'	2.27	0.42
1:2:356:C:P	14:M:105:ARG:HH22	2.41	0.42
1:2:1015:U:O2'	1:2:1017:U:OP2	2.35	0.42
1:2:1319:U:H2'	1:2:1320:G:C8	2.55	0.42
1:2:1454:A:OP2	20:S:3:ARG:NH2	2.50	0.42
1:2:1508:A:N7	1:2:1510:G:O6	2.52	0.42
5:D:172:ASN:ND2	12:K:95:ASP:OD2	2.53	0.42
6:E:65:ARG:O	6:E:68:GLU:HG3	2.19	0.42
6:E:167:TYR:HH	6:E:203:PRO:C	2.27	0.42
8:G:198:ARG:HA	8:G:198:ARG:NE	2.35	0.42
10:I:75:ILE:HD13	10:I:78:ARG:NH1	2.34	0.42
12:K:63:LEU:HD21	12:K:67:ASP:OD2	2.20	0.42
12:K:179:LYS:O	12:K:182:GLN:HG3	2.20	0.42
16:O:46:THR:O	16:O:50:ILE:HG12	2.19	0.42
18:Q:98:ASN:O	18:Q:122:THR:HG23	2.20	0.42
19:R:140:ARG:HH22	23:V:75:LYS:CG	2.31	0.42
21:T:5:ILE:HD11	21:T:58:GLU:HB3	2.00	0.42
21:T:120:HIS:HA	21:T:123:LEU:HB2	2.01	0.42
22:U:22:LEU:HB3	22:U:28:LEU:HD21	2.02	0.42
27:Z:42:GLU:HA	27:Z:52:PRO:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:5:U:O2'	1:2:602:G:O3'	2.36	0.42
1:2:302:A:O5'	11:J:74:ARG:NH1	2.53	0.42
1:2:491:C:O2	1:2:493:A:N6	2.53	0.42
1:2:525:A:H2'	1:2:526:A:C8	2.55	0.42
1:2:929:G:H2'	1:2:930:C:O4'	2.19	0.42
1:2:1665:G:C4	22:U:88:MET:SD	3.13	0.42
1:2:1830:U:O2	1:2:1831:A:N6	2.32	0.42
2:A:9159:A:H2'	2:A:9160:A:H8	1.85	0.42
2:A:9169:G:O6	2:A:9252:U:C2	2.71	0.42
3:B:130:ASP:O	3:B:133:PRO:HD2	2.20	0.42
4:C:30:TRP:O	4:C:94:LYS:NZ	2.45	0.42
4:C:62:LEU:HA	4:C:65:ARG:NE	2.34	0.42
7:F:19:MET:HE2	7:F:19:MET:HB2	1.85	0.42
7:F:64:ILE:HG23	27:Z:17:LEU:HD21	2.02	0.42
7:F:188:ASN:HA	7:F:245:ARG:HH22	1.85	0.42
9:H:20:ASP:O	9:H:24:LEU:HD23	2.19	0.42
9:H:201:LYS:HA	9:H:204:GLU:OE2	2.20	0.42
10:I:75:ILE:HG22	10:I:75:ILE:O	2.19	0.42
20:S:92:ASP:OD1	20:S:92:ASP:N	2.50	0.42
20:S:106:LEU:HD23	20:S:106:LEU:HA	1.83	0.42
27:Z:110:ARG:O	27:Z:114:MET:HG2	2.19	0.42
29:b:23:CYS:SG	29:b:26:CYS:HB2	2.59	0.42
29:b:45:VAL:HG11	29:b:53:ILE:HD13	2.01	0.42
35:h:14:HIS:O	35:h:305:ASN:ND2	2.41	0.42
35:h:45:LEU:HD22	35:h:52:TYR:HD2	1.84	0.42
35:h:64:HIS:ND1	35:h:83:TRP:HB2	2.35	0.42
1:2:42:A:H2'	1:2:43:U:C2	2.55	0.41
1:2:581:U:H5''	27:Z:65:GLY:H	1.85	0.41
1:2:1034:A:N6	1:2:1082:A:C8	2.88	0.41
1:2:1101:U:H2'	1:2:1102:G:H8	1.80	0.41
1:2:1361:G:H1'	1:2:1379:A:N7	2.35	0.41
1:2:1394:G:N7	1:2:1395:C:C5	2.88	0.41
1:2:1402:A:H3'	1:2:1405:A:N6	2.27	0.41
1:2:1527:C:H2'	1:2:1528:G:C8	2.54	0.41
3:B:206:ASP:OD1	3:B:206:ASP:N	2.49	0.41
7:F:36:HIS:CE1	7:F:85:GLY:HA3	2.55	0.41
8:G:167:LYS:NZ	8:G:175:ASP:OD2	2.41	0.41
9:H:188:LYS:HG2	9:H:191:ARG:NH2	2.35	0.41
30:c:32:PHE:O	30:c:82:LYS:HG2	2.20	0.41
1:2:65:C:C6	9:H:174:PRO:HB3	2.54	0.41
1:2:1204:G:H3'	1:2:1204:G:OP2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1287:A:P	34:g:97:LYS:HE3	2.60	0.41
1:2:1320:G:H3'	1:2:1321:G:C8	2.56	0.41
1:2:1415:C:O2'	22:U:132:ASP:OD2	2.31	0.41
2:A:9288:U:H2'	2:A:9289:U:H6	1.84	0.41
8:G:103:LEU:HD13	8:G:178:ILE:HG13	2.02	0.41
8:G:151:ILE:HD12	8:G:154:LEU:HD11	2.01	0.41
10:I:193:GLN:C	10:I:194:LEU:HD12	2.44	0.41
12:K:61:LEU:HD21	12:K:94:LEU:HG	2.02	0.41
13:L:62:PHE:CZ	13:L:65:ARG:HA	2.54	0.41
16:O:112:LYS:O	16:O:116:ILE:HG12	2.20	0.41
20:S:121:GLN:OE1	20:S:121:GLN:N	2.51	0.41
1:2:78:C:O2'	9:H:175:LYS:HE3	2.20	0.41
1:2:124:U:H4'	7:F:148:ARG:HH12	1.86	0.41
1:2:460:A:H1'	1:2:470:G:H22	1.85	0.41
1:2:677:G:H8	1:2:677:G:O5'	2.03	0.41
1:2:943:U:H2'	1:2:944:A:O4'	2.21	0.41
1:2:1177:U:C2	1:2:1178:U:C5	3.09	0.41
1:2:1543:U:O2'	1:2:1544:C:H5'	2.21	0.41
1:2:1677:U:H5''	8:G:148:ASN:ND2	2.35	0.41
1:2:1722:G:N1	1:2:1812:U:N3	2.59	0.41
1:2:1786:U:H2'	1:2:1787:G:C8	2.55	0.41
3:B:190:SER:HB3	3:B:193:HIS:NE2	2.36	0.41
9:H:116:LYS:HD3	9:H:125:THR:HG21	2.02	0.41
11:J:195:LEU:O	11:J:199:LEU:HG	2.20	0.41
12:K:155:LYS:HB3	12:K:155:LYS:HE2	1.84	0.41
16:O:13:GLN:N	16:O:13:GLN:OE1	2.53	0.41
19:R:53:GLU:HB2	19:R:85:ARG:HH21	1.85	0.41
21:T:34:LYS:HE3	21:T:103:LEU:HD22	2.02	0.41
35:h:247:TRP:CZ3	35:h:258:ILE:HD12	2.55	0.41
1:2:39:A:H5'	12:K:7:TRP:NE1	2.34	0.41
1:2:146:G:O2'	1:2:147:A:H8	2.00	0.41
1:2:299:A:H2'	1:2:300:U:C6	2.55	0.41
1:2:822:U:H3	1:2:826:A:H62	1.68	0.41
1:2:919:A:H4'	1:2:920:A:O5'	2.20	0.41
1:2:1121:G:O2'	4:C:204:ILE:O	2.38	0.41
1:2:1332:A:O2'	6:E:145:GLN:O	2.38	0.41
2:A:9299:G:C2	2:A:9300:U:C4	3.08	0.41
3:B:121:LEU:HD23	3:B:122:LEU:N	2.35	0.41
7:F:104:ASP:OD1	7:F:108:ARG:HG2	2.20	0.41
16:O:72:LEU:HD12	16:O:72:LEU:HA	1.80	0.41
21:T:87:GLN:HG3	21:T:95:TYR:CD1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:123:LEU:HB3	21:T:127:TRP:CZ3	2.55	0.41
23:V:35:VAL:HG21	23:V:110:VAL:HB	2.02	0.41
24:W:70:LEU:HD11	24:W:83:PHE:CZ	2.55	0.41
25:X:87:GLU:HA	25:X:90:GLN:HG2	2.02	0.41
31:d:67:ARG:HG3	31:d:68:LEU:N	2.35	0.41
32:e:26:ASN:HB3	32:e:28:HIS:CD2	2.55	0.41
33:f:79:LEU:HA	33:f:81:ARG:NH1	2.35	0.41
35:h:240:CYS:O	35:h:248:LEU:HD12	2.21	0.41
1:2:587:A:C4	1:2:590:A:H8	2.39	0.41
1:2:597:G:N1	1:2:640:A:N6	2.68	0.41
1:2:1374:C:H2'	1:2:1375:G:C8	2.55	0.41
1:2:1520:G:H21	18:Q:126:VAL:HG11	1.84	0.41
1:2:1753:C:H5''	1:2:1754:G:OP1	2.20	0.41
1:2:1787:G:H2'	1:2:1788:A:C8	2.56	0.41
3:B:78:SER:O	3:B:100:ALA:HA	2.20	0.41
5:D:120:GLN:OE1	5:D:120:GLN:HA	2.20	0.41
6:E:193:ASP:OD2	6:E:197:LYS:N	2.53	0.41
7:F:75:LYS:HD3	7:F:77:ARG:NH2	2.35	0.41
10:I:103:LYS:O	10:I:105:THR:N	2.53	0.41
11:J:193:LYS:NZ	14:M:33:LEU:HD21	2.35	0.41
18:Q:28:MET:HB2	18:Q:32:GLN:HE21	1.85	0.41
19:R:58:LEU:HD11	19:R:112:LEU:HD11	2.02	0.41
27:Z:41:ARG:NH2	27:Z:53:ASP:HA	2.36	0.41
35:h:3:GLU:HG3	35:h:312:VAL:HG13	2.02	0.41
1:2:59:U:H2'	1:2:61:A:OP2	2.20	0.41
1:2:346:C:OP1	7:F:38:LEU:N	2.39	0.41
1:2:429:C:H2'	1:2:430:C:C6	2.55	0.41
1:2:441:C:H2'	1:2:442:C:C6	2.55	0.41
1:2:1019:C:H2'	1:2:1020:A:O4'	2.19	0.41
1:2:1134:G:H2'	1:2:1135:C:H6	1.86	0.41
1:2:1214:A:O2'	1:2:1216:C:OP2	2.33	0.41
1:2:1374:C:OP2	20:S:7:LYS:NZ	2.52	0.41
7:F:15:PRO:HG2	7:F:17:HIS:HE1	1.85	0.41
11:J:130:THR:OG1	11:J:131:PRO:HD3	2.21	0.41
13:L:80:ARG:NH1	13:L:87:PRO:HA	2.36	0.41
18:Q:56:LEU:O	18:Q:59:ARG:HG2	2.21	0.41
20:S:51:ALA:HA	20:S:54:VAL:HG12	2.02	0.41
25:X:102:ILE:CG2	25:X:113:HIS:HB3	2.51	0.41
34:g:93:HIS:CD2	34:g:95:ARG:HG3	2.55	0.41
1:2:15:U:H2'	1:2:16:G:O4'	2.20	0.41
1:2:42:A:H4'	1:2:98:C:OP1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:153:G:N2	1:2:166:A:C6	2.88	0.41
1:2:563:G:N7	1:2:586:G:N2	2.68	0.41
1:2:641:A:O3'	12:K:41:ARG:NH2	2.54	0.41
1:2:799:U:H2'	1:2:800:U:O4'	2.21	0.41
1:2:946:U:N3	1:2:947:G:N7	2.68	0.41
1:2:1074:C:H2'	1:2:1075:C:C6	2.56	0.41
1:2:1283:C:P	15:N:102:LYS:HZ2	2.43	0.41
1:2:1686:G:H2'	1:2:1687:C:C6	2.55	0.41
8:G:16:ASP:OD1	8:G:16:ASP:N	2.50	0.41
8:G:86:LYS:O	8:G:89:THR:OG1	2.26	0.41
8:G:122:ARG:CZ	31:d:59:LEU:HB2	2.51	0.41
9:H:50:VAL:HG21	9:H:111:LEU:HB3	2.02	0.41
12:K:139:LYS:HD3	12:K:139:LYS:HA	1.83	0.41
16:O:142:GLU:HG2	16:O:145:THR:HG23	2.03	0.41
17:P:139:SER:OG	17:P:140:THR:N	2.53	0.41
20:S:28:PHE:CE2	20:S:32:LYS:HD2	2.56	0.41
22:U:42:HIS:CE1	22:U:79:TYR:HH	2.37	0.41
30:c:11:SER:N	30:c:14:GLU:OE2	2.53	0.41
1:2:30:C:H4'	26:Y:135:LYS:HZ3	1.85	0.41
1:2:445:A:H4'	11:J:50:GLY:C	2.46	0.41
1:2:483:C:P	26:Y:76:LYS:HZ1	2.42	0.41
1:2:816:A:H2'	1:2:817:G:C8	2.56	0.41
1:2:906:U:H2'	1:2:907:G:C8	2.56	0.41
1:2:1098:C:H2'	1:2:1099:G:H8	1.80	0.41
1:2:1204:G:C4	1:2:1205:G:C2	3.09	0.41
1:2:1256:G:H3'	1:2:1256:G:N3	2.35	0.41
1:2:1533:A:H62	1:2:1602:U:H3	1.67	0.41
1:2:1590:C:H42	19:R:77:HIS:CD2	2.38	0.41
1:2:1625:U:C2	1:2:1626:C:C5	3.09	0.41
4:C:148:ASN:OD1	4:C:148:ASN:N	2.52	0.41
7:F:18:TRP:CD1	7:F:18:TRP:H	2.39	0.41
11:J:52:ASN:OD1	11:J:53:LYS:N	2.54	0.41
11:J:54:LYS:HD2	11:J:54:LYS:HA	1.82	0.41
18:Q:124:LYS:HG2	18:Q:125:PRO:O	2.20	0.41
20:S:105:MET:HE3	20:S:105:MET:HB3	1.92	0.41
23:V:81:GLN:HB3	23:V:83:ARG:HH22	1.85	0.41
26:Y:100:VAL:HG13	26:Y:122:VAL:HG23	2.01	0.41
35:h:86:THR:OG1	35:h:87:LEU:N	2.53	0.41
1:2:64:A:N6	1:2:82:G:H3'	2.34	0.41
1:2:96:C:H2'	1:2:97:U:C6	2.56	0.41
1:2:587:A:O2'	1:2:588:G:N2	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:639:C:H2'	1:2:640:A:C8	2.56	0.41
1:2:789:G:H2'	1:2:790:C:H6	1.86	0.41
1:2:830:A:H2'	1:2:831:G:O4'	2.20	0.41
1:2:894:G:N2	1:2:895:G:O4'	2.53	0.41
1:2:969:U:H5'	1:2:970:G:H2'	2.03	0.41
1:2:1041:G:C6	1:2:1042:A:N6	2.88	0.41
1:2:1101:U:OP1	4:C:151:ARG:HG3	2.20	0.41
1:2:1110:G:H2'	1:2:1111:U:H6	1.86	0.41
1:2:1113:A:C6	1:2:1121:G:C6	3.09	0.41
1:2:1178:U:H2'	1:2:1179:G:C8	2.50	0.41
1:2:1335:G:H2'	1:2:1336:C:O4'	2.21	0.41
1:2:1356:G:H2'	1:2:1357:A:C8	2.56	0.41
1:2:1396:A:O2'	1:2:1398:G:N7	2.54	0.41
1:2:1605:G:H2'	1:2:1634:A:H61	1.86	0.41
1:2:1640:A:C2	1:2:1641:A:H1'	2.56	0.41
1:2:1669:G:H1'	23:V:62:ARG:HH22	1.85	0.41
1:2:1684:C:H2'	1:2:1685:U:C6	2.55	0.41
4:C:40:ASN:N	4:C:75:GLN:OE1	2.38	0.41
5:D:94:ILE:HG13	5:D:159:LYS:O	2.21	0.41
5:D:190:SER:O	5:D:190:SER:OG	2.33	0.41
6:E:6:SER:H	6:E:9:ARG:CZ	2.34	0.41
6:E:71:ALA:O	6:E:75:LYS:HG2	2.21	0.41
6:E:190:LEU:HD12	6:E:190:LEU:O	2.20	0.41
7:F:18:TRP:HB2	7:F:20:LEU:HD22	2.03	0.41
7:F:47:PHE:CE2	7:F:90:ILE:HG13	2.56	0.41
7:F:161:GLN:HB3	7:F:170:THR:HB	2.02	0.41
9:H:47:GLY:HA3	9:H:118:GLU:OE1	2.20	0.41
10:I:43:LEU:HD12	10:I:72:PHE:HE1	1.85	0.41
10:I:160:LYS:HE2	10:I:191:GLU:OE1	2.20	0.41
12:K:111:GLN:OE1	12:K:127:ARG:HB2	2.20	0.41
12:K:131:ARG:HA	12:K:131:ARG:HD2	1.88	0.41
14:M:32:LYS:HE2	14:M:32:LYS:HB2	1.94	0.41
16:O:40:LEU:HD11	16:O:53:ILE:HD11	2.03	0.41
19:R:131:LYS:HB2	19:R:137:ALA:O	2.21	0.41
19:R:145:TYR:O	19:R:146:ARG:HB2	2.21	0.41
21:T:16:LEU:HD13	21:T:99:LEU:CD1	2.49	0.41
22:U:28:LEU:HD12	22:U:53:PHE:CE2	2.53	0.41
22:U:87:VAL:C	22:U:88:MET:HE2	2.46	0.41
26:Y:109:GLY:HA2	26:Y:119:ARG:HD3	2.03	0.41
29:b:13:LYS:HA	29:b:13:LYS:HD2	1.93	0.41
35:h:194:TYR:CZ	35:h:212:LYS:HB2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:242:SER:HB2	35:h:245:ARG:O	2.19	0.41
1:2:191:A:OP1	11:J:141:ARG:NH2	2.53	0.41
1:2:377:G:C2	1:2:378:U:C5	3.09	0.41
1:2:482:G:H2'	1:2:484:A:OP2	2.21	0.41
1:2:509:G:H2'	1:2:510:G:C8	2.56	0.41
1:2:862:A:N7	25:X:107:SER:HA	2.36	0.41
1:2:1401:A:H2'	1:2:1402:A:C8	2.52	0.41
1:2:1540:G:C6	1:2:1594:A:C6	3.09	0.41
1:2:1578:U:O2	6:E:9:ARG:NH1	2.54	0.41
1:2:1606:G:C6	1:2:1632:G:C4	3.08	0.41
1:2:1613:G:O5'	18:Q:39:ALA:HB2	2.21	0.41
2:A:9229:U:OP1	2:A:9230:U:H5''	2.20	0.41
2:A:9271:G:H5''	2:A:9272:U:OP2	2.21	0.41
3:B:198:MET:CG	20:S:85:VAL:HG21	2.51	0.41
4:C:73:ASP:OD1	17:P:128:ARG:NH2	2.50	0.41
4:C:97:LEU:HB3	4:C:232:HIS:CD2	2.55	0.41
9:H:230:LYS:HD3	9:H:230:LYS:HA	1.81	0.41
10:I:64:VAL:HG21	10:I:72:PHE:CE2	2.56	0.41
11:J:69:SER:HB2	14:M:21:LYS:HE3	2.03	0.41
17:P:82:ALA:O	17:P:86:LYS:HG2	2.21	0.41
17:P:95:ILE:HB	17:P:129:ILE:HG12	2.02	0.41
20:S:35:CYS:HA	20:S:38:ILE:HG22	2.02	0.41
22:U:134:ILE:HD13	22:U:134:ILE:HA	1.91	0.41
25:X:38:LEU:HD23	25:X:41:MET:HE3	2.03	0.41
25:X:46:TYR:HB3	25:X:69:LEU:HD12	2.03	0.41
32:e:37:ASN:O	32:e:38:MET:HE2	2.20	0.41
35:h:17:TRP:CZ2	35:h:36:ARG:HD2	2.56	0.41
1:2:333:G:OP2	9:H:190:ARG:HG3	2.21	0.40
1:2:801:U:C2	1:2:802:A:C8	3.08	0.40
1:2:1224:G:H2'	1:2:1225:U:H6	1.84	0.40
1:2:1570:G:C2	1:2:1571:G:C5	3.09	0.40
1:2:1640:A:H2'	1:2:1641:A:O4'	2.21	0.40
5:D:83:LEU:HD22	5:D:84:PHE:CE1	2.56	0.40
6:E:5:ILE:HG23	6:E:9:ARG:HE	1.87	0.40
8:G:179:ASN:HA	8:G:184:SER:HB3	2.03	0.40
14:M:38:LYS:HG2	14:M:62:PHE:O	2.21	0.40
27:Z:12:PHE:HD1	27:Z:23:MET:HB3	1.86	0.40
28:a:102:LYS:HA	28:a:107:VAL:HG12	2.03	0.40
1:2:38:A:H2'	1:2:39:A:C8	2.56	0.40
1:2:526:A:H2'	1:2:527:C:C6	2.56	0.40
1:2:651:U:H2'	1:2:652:U:H6	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1041:G:C2	1:2:1042:A:C6	3.10	0.40
1:2:1610:G:O2'	21:T:110:ASP:OD2	2.28	0.40
3:B:154:LEU:HD22	24:W:66:ASP:OD2	2.20	0.40
6:E:169:ASP:OD1	6:E:188:ILE:HG23	2.21	0.40
7:F:71:LYS:HB2	7:F:71:LYS:HE2	1.92	0.40
7:F:154:ILE:O	7:F:155:LYS:HD2	2.21	0.40
8:G:78:MET:O	8:G:79:HIS:CG	2.75	0.40
9:H:64:LYS:O	9:H:100:CYS:HB3	2.20	0.40
11:J:98:LYS:HB3	11:J:179:PRO:HD3	2.03	0.40
15:N:79:VAL:HG12	15:N:81:ASP:H	1.85	0.40
17:P:47:LEU:HD23	17:P:47:LEU:HA	1.96	0.40
19:R:32:ILE:HG13	19:R:39:LEU:HD13	2.03	0.40
25:X:87:GLU:HG3	25:X:117:ARG:HH22	1.85	0.40
27:Z:29:HIS:NE2	27:Z:66:GLY:O	2.54	0.40
35:h:101:PHE:HE1	35:h:136:GLY:HA2	1.85	0.40
36:n:12:ARG:O	36:n:15:ARG:HG2	2.21	0.40
1:2:190:G:N2	1:2:209:A:OP2	2.36	0.40
1:2:430:C:H2'	1:2:431:G:C8	2.56	0.40
1:2:1176:G:C6	1:2:1177:U:C4	3.09	0.40
1:2:1524:G:H2'	1:2:1525:C:O4'	2.22	0.40
1:2:1705:C:H2'	1:2:1706:G:C8	2.56	0.40
1:2:1800:A:C2	1:2:1801:A:H1'	2.56	0.40
1:2:1852:C:H2'	1:2:1853:C:C6	2.55	0.40
6:E:8:LYS:H	6:E:8:LYS:HG2	1.69	0.40
7:F:173:ILE:HG23	7:F:230:LYS:NZ	2.37	0.40
10:I:79:LEU:HD11	10:I:94:PHE:CZ	2.56	0.40
11:J:3:ILE:HB	11:J:30:GLY:O	2.21	0.40
12:K:21:GLU:CD	12:K:24:ARG:HG2	2.46	0.40
13:L:28:HIS:HA	32:e:8:TRP:HZ2	1.87	0.40
14:M:17:PHE:CZ	14:M:19:ASN:HB2	2.57	0.40
16:O:46:THR:HG22	16:O:49:GLN:NE2	2.37	0.40
16:O:88:LEU:O	16:O:92:ILE:HG12	2.22	0.40
26:Y:59:ALA:CB	26:Y:65:ALA:H	2.35	0.40
27:Z:18:LEU:HB3	27:Z:20:ARG:HD3	2.03	0.40
30:c:5:LYS:HE3	30:c:5:LYS:HB3	1.60	0.40
33:f:109:MET:HA	33:f:112:ASN:ND2	2.36	0.40
34:g:141:CYS:CB	34:g:144:CYS:HB2	2.52	0.40
35:h:98:THR:O	35:h:99:ARG:HD2	2.20	0.40
35:h:302:TYR:HE1	35:h:308:ARG:HB2	1.86	0.40
1:2:23:G:OP1	12:K:15:THR:HG21	2.22	0.40
1:2:573:U:H3	1:2:576:A:P	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:816:A:H2'	1:2:817:G:H8	1.86	0.40
1:2:1123:C:OP1	4:C:151:ARG:NH2	2.55	0.40
1:2:1374:C:O2'	1:2:1465:A:H1'	2.22	0.40
1:2:1692:U:H5'	29:b:88:SER:HA	2.03	0.40
3:B:39:TYR:CE2	3:B:40:LYS:HG2	2.57	0.40
4:C:138:PHE:O	4:C:213:ARG:N	2.55	0.40
5:D:171:GLY:HA3	25:X:97:ARG:HH12	1.87	0.40
6:E:120:TYR:HD1	6:E:123:LEU:HD21	1.85	0.40
7:F:87:MET:HE3	7:F:100:ARG:CZ	2.52	0.40
9:H:159:ARG:HD3	9:H:171:THR:HG21	2.03	0.40
12:K:24:ARG:O	12:K:27:GLN:HG2	2.22	0.40
12:K:113:GLN:HG3	12:K:149:VAL:HG21	2.03	0.40
13:L:53:LYS:HE3	13:L:53:LYS:HB3	1.93	0.40
20:S:88:VAL:HG22	20:S:90:ALA:H	1.87	0.40
31:d:55:VAL:C	31:d:56:LEU:HD12	2.46	0.40
35:h:176:VAL:HG22	35:h:186:THR:H	1.86	0.40
1:2:57:U:O2	1:2:499:G:O2'	2.36	0.40
1:2:511:U:H2'	1:2:512:A:H8	1.87	0.40
1:2:679:A:H3'	1:2:680:G:H8	1.86	0.40
1:2:1121:G:C6	1:2:1122:A:C5	3.08	0.40
1:2:1135:C:C4	1:2:1136:U:O4	2.74	0.40
1:2:1475:G:H21	1:2:1475:G:P	2.44	0.40
1:2:1543:U:OP1	22:U:62:ARG:NH1	2.40	0.40
1:2:1823:A:O5'	26:Y:60:LYS:NZ	2.50	0.40
3:B:12:GLU:O	3:B:16:LEU:HD23	2.21	0.40
3:B:77:ILE:HD13	3:B:99:ILE:HB	2.04	0.40
4:C:34:LYS:HD3	4:C:43:ASN:OD1	2.21	0.40
5:D:84:PHE:CE2	5:D:264:SER:HA	2.56	0.40
5:D:187:ARG:HD3	5:D:192:LEU:HD13	2.04	0.40
9:H:67:VAL:HG21	9:H:99:GLY:HA2	2.03	0.40
9:H:176:ILE:HB	9:H:179:LEU:HD11	2.03	0.40
10:I:76:GLN:HE22	10:I:94:PHE:HB2	1.86	0.40
11:J:87:ASN:HB3	11:J:90:LEU:HD13	2.04	0.40
12:K:134:HIS:CE1	12:K:164:PRO:HD2	2.57	0.40
13:L:82:TYR:HD2	13:L:83:LEU:HD22	1.86	0.40
14:M:98:LYS:HD3	14:M:99:TYR:CE1	2.57	0.40
18:Q:130:ARG:HD3	18:Q:130:ARG:H	1.85	0.40
21:T:51:ASP:OD1	21:T:51:ASP:N	2.47	0.40
24:W:32:ILE:HD11	24:W:60:ARG:CD	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	215/295 (73%)	191 (89%)	24 (11%)	0	100	100
4	C	211/264 (80%)	191 (90%)	20 (10%)	0	100	100
5	D	219/221 (99%)	203 (93%)	16 (7%)	0	100	100
6	E	226/281 (80%)	212 (94%)	14 (6%)	0	100	100
7	F	260/263 (99%)	244 (94%)	16 (6%)	0	100	100
8	G	189/204 (93%)	176 (93%)	13 (7%)	0	100	100
9	H	235/249 (94%)	227 (97%)	8 (3%)	0	100	100
10	I	181/432 (42%)	172 (95%)	9 (5%)	0	100	100
11	J	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
12	K	183/194 (94%)	178 (97%)	5 (3%)	0	100	100
13	L	94/149 (63%)	89 (95%)	5 (5%)	0	100	100
14	M	149/158 (94%)	138 (93%)	11 (7%)	0	100	100
15	N	115/132 (87%)	105 (91%)	10 (9%)	0	100	100
16	O	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
17	P	134/168 (80%)	124 (92%)	10 (8%)	0	100	100
18	Q	118/145 (81%)	109 (92%)	9 (8%)	0	100	100
19	R	140/172 (81%)	130 (93%)	10 (7%)	0	100	100
20	S	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
21	T	142/152 (93%)	125 (88%)	17 (12%)	0	100	100
22	U	139/145 (96%)	128 (92%)	11 (8%)	0	100	100
23	V	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
24	W	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
25	X	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
26	Y	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	18	48
27	Z	122/131 (93%)	116 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	a	75/124 (60%)	72 (96%)	3 (4%)	0	100	100
29	b	99/101 (98%)	89 (90%)	10 (10%)	0	100	100
30	c	81/84 (96%)	76 (94%)	5 (6%)	0	100	100
31	d	65/69 (94%)	59 (91%)	6 (9%)	0	100	100
32	e	53/56 (95%)	47 (89%)	6 (11%)	0	100	100
33	f	55/133 (41%)	52 (94%)	3 (6%)	0	100	100
34	g	66/188 (35%)	63 (96%)	3 (4%)	0	100	100
35	h	311/317 (98%)	289 (93%)	22 (7%)	0	100	100
36	n	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4826/5821 (83%)	4492 (93%)	333 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	Y	62	PRO

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	
3	B	180/245 (74%)	180 (100%)	0	100	100
4	C	194/231 (84%)	194 (100%)	0	100	100
5	D	187/187 (100%)	187 (100%)	0	100	100
6	E	190/232 (82%)	190 (100%)	0	100	100
7	F	224/225 (100%)	224 (100%)	0	100	100
8	G	161/170 (95%)	161 (100%)	0	100	100
9	H	207/218 (95%)	207 (100%)	0	100	100
10	I	165/360 (46%)	165 (100%)	0	100	100
11	J	178/180 (99%)	178 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	K	161/168 (96%)	161 (100%)	0	100	100
13	L	87/125 (70%)	87 (100%)	0	100	100
14	M	136/142 (96%)	136 (100%)	0	100	100
15	N	99/108 (92%)	99 (100%)	0	100	100
16	O	130/131 (99%)	130 (100%)	0	100	100
17	P	106/130 (82%)	106 (100%)	0	100	100
18	Q	109/130 (84%)	109 (100%)	0	100	100
19	R	117/140 (84%)	117 (100%)	0	100	100
20	S	119/121 (98%)	119 (100%)	0	100	100
21	T	125/132 (95%)	125 (100%)	0	100	100
22	U	111/116 (96%)	111 (100%)	0	100	100
23	V	92/107 (86%)	92 (100%)	0	100	100
24	W	67/67 (100%)	67 (100%)	0	100	100
25	X	112/113 (99%)	112 (100%)	0	100	100
26	Y	113/115 (98%)	113 (100%)	0	100	100
27	Z	107/113 (95%)	107 (100%)	0	100	100
28	a	68/102 (67%)	68 (100%)	0	100	100
29	b	88/88 (100%)	88 (100%)	0	100	100
30	c	75/76 (99%)	75 (100%)	0	100	100
31	d	60/62 (97%)	60 (100%)	0	100	100
32	e	48/49 (98%)	48 (100%)	0	100	100
33	f	47/106 (44%)	47 (100%)	0	100	100
34	g	61/154 (40%)	61 (100%)	0	100	100
35	h	272/275 (99%)	272 (100%)	0	100	100
36	n	24/24 (100%)	24 (100%)	0	100	100
All	All	4220/4942 (85%)	4220 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	24	HIS

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Mol	Chain	Res	Type
3	B	84	GLN
3	B	111	GLN
3	B	169	HIS
4	C	124	HIS
4	C	149	GLN
4	C	179	ASN
5	D	120	GLN
5	D	134	ASN
5	D	267	GLN
5	D	272	HIS
6	E	22	ASN
6	E	57	ASN
7	F	179	ASN
8	G	83	ASN
10	I	12	ASN
10	I	76	GLN
11	J	22	HIS
11	J	35	ASN
11	J	138	ASN
11	J	168	GLN
12	K	113	GLN
12	K	177	ASN
14	M	18	GLN
15	N	72	HIS
16	O	49	GLN
19	R	11	GLN
19	R	24	HIS
20	S	83	ASN
21	T	10	GLN
21	T	11	HIS
23	V	47	ASN
25	X	120	HIS
26	Y	61	GLN
29	b	17	HIS
29	b	25	ASN
29	b	72	HIS
30	c	9	HIS
30	c	26	GLN
31	d	24	GLN
31	d	29	GLN
33	f	112	ASN
35	h	62	HIS

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Mol	Chain	Res	Type
35	h	117	ASN
35	h	119	GLN
35	h	188	HIS
35	h	196	ASN
35	h	296	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1669/1870 (89%)	414 (24%)	13 (0%)
2	A	105/270 (38%)	38 (36%)	7 (6%)
All	All	1774/2140 (82%)	452 (25%)	20 (1%)

All (452) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	13	C
1	2	14	C
1	2	26	U
1	2	33	G
1	2	41	G
1	2	42	A
1	2	43	U
1	2	44	U
1	2	45	A
1	2	46	A
1	2	49	C
1	2	56	G
1	2	58	C
1	2	61	A
1	2	62	G
1	2	66	G
1	2	67	C
1	2	68	A
1	2	73	C
1	2	74	G
1	2	75	G
1	2	92	A
1	2	102	A

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Mol	Chain	Res	Type
1	2	103	A
1	2	113	G
1	2	114	G
1	2	115	U
1	2	126	G
1	2	128	U
1	2	130	G
1	2	142	C
1	2	143	U
1	2	144	U
1	2	147	A
1	2	158	A
1	2	166	A
1	2	177	G
1	2	180	G
1	2	182	C
1	2	183	G
1	2	184	G
1	2	187	G
1	2	189	U
1	2	191	A
1	2	192	C
1	2	211	G
1	2	291	G
1	2	292	A
1	2	294	U
1	2	302	A
1	2	305	U
1	2	306	C
1	2	307	G
1	2	316	G
1	2	319	C
1	2	335	G
1	2	342	C
1	2	347	G
1	2	356	C
1	2	362	C
1	2	363	A
1	2	364	A
1	2	368	U
1	2	369	C
1	2	381	C

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Mol	Chain	Res	Type
1	2	383	G
1	2	384	U
1	2	385	G
1	2	386	C
1	2	408	A
1	2	409	C
1	2	428	U
1	2	429	C
1	2	435	A
1	2	438	G
1	2	446	G
1	2	447	A
1	2	448	A
1	2	449	A
1	2	450	C
1	2	452	G
1	2	465	A
1	2	468	A
1	2	472	C
1	2	474	G
1	2	485	A
1	2	487	U
1	2	488	U
1	2	492	C
1	2	493	A
1	2	495	U
1	2	502	C
1	2	516	A
1	2	525	A
1	2	532	C
1	2	533	A
1	2	534	G
1	2	541	U
1	2	544	G
1	2	547	G
1	2	548	C
1	2	549	C
1	2	550	C
1	2	551	U
1	2	554	A
1	2	556	U
1	2	560	A

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Mol	Chain	Res	Type
1	2	561	A
1	2	562	U
1	2	567	C
1	2	583	A
1	2	585	C
1	2	587	A
1	2	590	A
1	2	591	U
1	2	593	C
1	2	604	A
1	2	606	G
1	2	608	C
1	2	613	G
1	2	614	C
1	2	617	G
1	2	623	G
1	2	625	G
1	2	628	A
1	2	629	A
1	2	630	U
1	2	631	U
1	2	643	A
1	2	644	G
1	2	649	U
1	2	650	A
1	2	655	A
1	2	659	G
1	2	660	C
1	2	669	A
1	2	671	A
1	2	672	A
1	2	673	G
1	2	688	U
1	2	752	G
1	2	754	G
1	2	756	C
1	2	795	A
1	2	799	U
1	2	800	U
1	2	807	G
1	2	810	A
1	2	811	A

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Mol	Chain	Res	Type
1	2	821	G
1	2	822	U
1	2	827	A
1	2	830	A
1	2	832	G
1	2	844	U
1	2	847	A
1	2	848	U
1	2	849	A
1	2	852	G
1	2	853	C
1	2	860	G
1	2	861	A
1	2	866	U
1	2	868	G
1	2	869	A
1	2	870	A
1	2	871	U
1	2	872	A
1	2	874	G
1	2	875	A
1	2	878	G
1	2	886	A
1	2	887	U
1	2	888	U
1	2	891	G
1	2	893	U
1	2	895	G
1	2	913	A
1	2	914	U
1	2	917	U
1	2	919	A
1	2	920	A
1	2	930	C
1	2	933	G
1	2	939	U
1	2	943	U
1	2	963	A
1	2	968	U
1	2	969	U
1	2	970	G
1	2	971	G

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Mol	Chain	Res	Type
1	2	983	A
1	2	985	G
1	2	990	A
1	2	992	A
1	2	999	G
1	2	1002	U
1	2	1017	U
1	2	1023	A
1	2	1024	A
1	2	1026	C
1	2	1027	A
1	2	1042	A
1	2	1044	G
1	2	1045	U
1	2	1083	A
1	2	1085	C
1	2	1088	U
1	2	1100	A
1	2	1114	U
1	2	1116	C
1	2	1118	C
1	2	1119	A
1	2	1120	U
1	2	1121	G
1	2	1138	C
1	2	1139	C
1	2	1149	A
1	2	1150	A
1	2	1153	C
1	2	1154	U
1	2	1183	A
1	2	1203	U
1	2	1204	G
1	2	1206	C
1	2	1207	G
1	2	1208	A
1	2	1215	C
1	2	1216	C
1	2	1217	A
1	2	1221	G
1	2	1224	G
1	2	1227	G

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Mol	Chain	Res	Type
1	2	1232	U
1	2	1233	G
1	2	1240	A
1	2	1242	U
1	2	1243	U
1	2	1247	C
1	2	1248	U
1	2	1249	C
1	2	1250	A
1	2	1251	A
1	2	1253	A
1	2	1256	G
1	2	1257	G
1	2	1258	A
1	2	1261	C
1	2	1264	C
1	2	1265	A
1	2	1266	C
1	2	1269	G
1	2	1274	G
1	2	1275	G
1	2	1277	C
1	2	1278	A
1	2	1284	A
1	2	1285	G
1	2	1287	A
1	2	1289	U
1	2	1293	A
1	2	1294	G
1	2	1299	A
1	2	1300	U
1	2	1301	A
1	2	1302	G
1	2	1303	C
1	2	1307	U
1	2	1308	U
1	2	1310	U
1	2	1311	C
1	2	1331	C
1	2	1333	U
1	2	1341	C
1	2	1342	U

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Mol	Chain	Res	Type
1	2	1356	G
1	2	1358	U
1	2	1371	U
1	2	1372	U
1	2	1373	C
1	2	1377	U
1	2	1378	A
1	2	1393	G
1	2	1395	C
1	2	1396	A
1	2	1397	U
1	2	1406	G
1	2	1428	G
1	2	1429	G
1	2	1439	A
1	2	1442	U
1	2	1447	G
1	2	1452	A
1	2	1454	A
1	2	1462	U
1	2	1463	U
1	2	1465	A
1	2	1472	C
1	2	1477	U
1	2	1478	U
1	2	1481	G
1	2	1483	A
1	2	1484	A
1	2	1489	A
1	2	1490	G
1	2	1494	U
1	2	1498	A
1	2	1507	G
1	2	1508	A
1	2	1509	U
1	2	1520	G
1	2	1521	C
1	2	1522	A
1	2	1523	C
1	2	1528	G
1	2	1531	A
1	2	1533	A

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Mol	Chain	Res	Type
1	2	1534	C
1	2	1535	U
1	2	1540	G
1	2	1541	G
1	2	1548	G
1	2	1551	U
1	2	1552	G
1	2	1553	C
1	2	1554	C
1	2	1556	A
1	2	1557	C
1	2	1560	U
1	2	1564	C
1	2	1567	G
1	2	1568	C
1	2	1574	C
1	2	1575	G
1	2	1578	U
1	2	1580	A
1	2	1585	U
1	2	1586	U
1	2	1587	G
1	2	1588	A
1	2	1601	A
1	2	1604	G
1	2	1606	G
1	2	1607	A
1	2	1611	G
1	2	1614	A
1	2	1621	U
1	2	1622	U
1	2	1623	A
1	2	1630	A
1	2	1636	G
1	2	1638	G
1	2	1643	U
1	2	1644	C
1	2	1646	C
1	2	1647	A
1	2	1648	G
1	2	1649	U
1	2	1653	U

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Mol	Chain	Res	Type
1	2	1657	G
1	2	1662	U
1	2	1663	A
1	2	1665	G
1	2	1675	A
1	2	1682	C
1	2	1683	C
1	2	1686	G
1	2	1695	A
1	2	1699	A
1	2	1715	A
1	2	1721	U
1	2	1748	G
1	2	1750	C
1	2	1751	C
1	2	1753	C
1	2	1754	G
1	2	1756	C
1	2	1757	G
1	2	1758	G
1	2	1759	G
1	2	1760	G
1	2	1773	C
1	2	1774	C
1	2	1775	U
1	2	1776	G
1	2	1780	G
1	2	1781	A
1	2	1783	C
1	2	1786	U
1	2	1801	A
1	2	1805	G
1	2	1817	G
1	2	1819	A
1	2	1820	G
1	2	1823	A
1	2	1824	A
1	2	1826	G
1	2	1828	C
1	2	1829	G
1	2	1830	U
1	2	1834	A

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Mol	Chain	Res	Type
1	2	1835	A
1	2	1836	G
1	2	1838	U
1	2	1839	U
1	2	1849	G
1	2	1852	C
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1865	C
1	2	1869	A
2	A	9168	A
2	A	9169	G
2	A	9171	A
2	A	9172	G
2	A	9229	U
2	A	9230	U
2	A	9231	G
2	A	9232	G
2	A	9233	G
2	A	9234	A
2	A	9235	A
2	A	9238	C
2	A	9242	C
2	A	9243	C
2	A	9244	U
2	A	9245	U
2	A	9247	G
2	A	9248	A
2	A	9249	C
2	A	9253	A
2	A	9255	G
2	A	9268	G
2	A	9272	U
2	A	9273	U
2	A	9277	A
2	A	9278	C
2	A	9283	A
2	A	9289	U
2	A	9290	U
2	A	9294	G
2	A	9295	A

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Mol	Chain	Res	Type
2	A	9296	U
2	A	9297	C
2	A	9298	C
2	A	9299	G
2	A	9304	G
2	A	9305	G
2	A	9306	G

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	42	A
1	2	383	G
1	2	445	A
1	2	561	A
1	2	612	U
1	2	627	U
1	2	860	G
1	2	874	G
1	2	886	A
1	2	1203	U
1	2	1355	C
1	2	1521	C
1	2	1759	G
2	A	9254	C
2	A	9282	C
2	A	9295	A
2	A	9297	C
2	A	9298	C
2	A	9303	C
2	A	9304	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

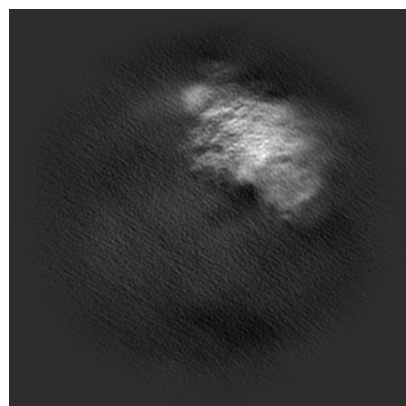
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70479. These allow visual inspection of the internal detail of the map and identification of artifacts.

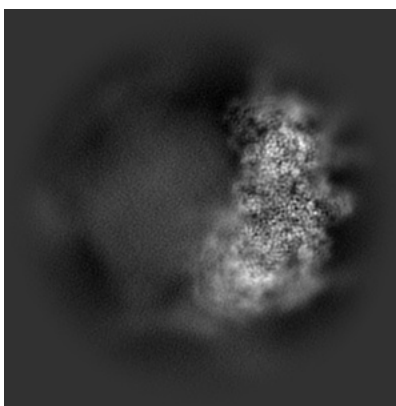
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

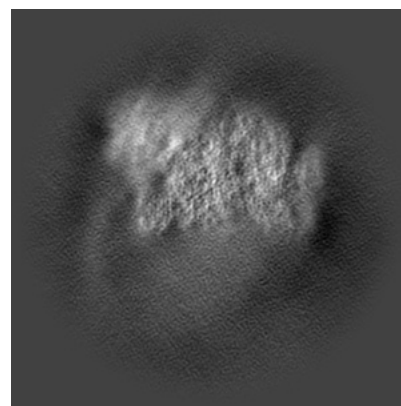
6.1.1 Primary map



X

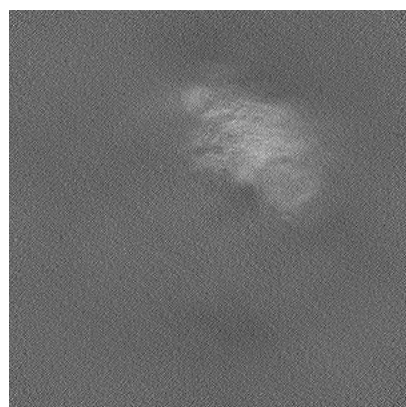


Y

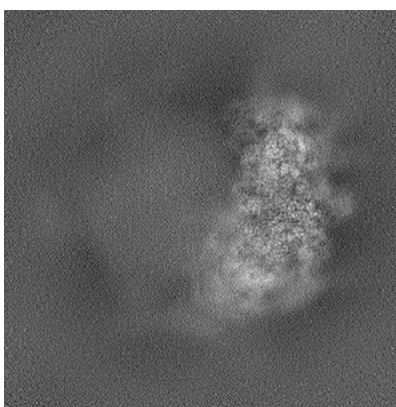


Z

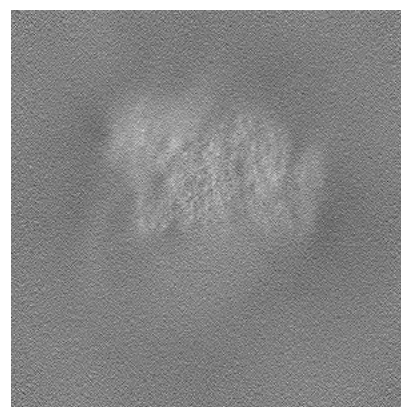
6.1.2 Raw map



X



Y

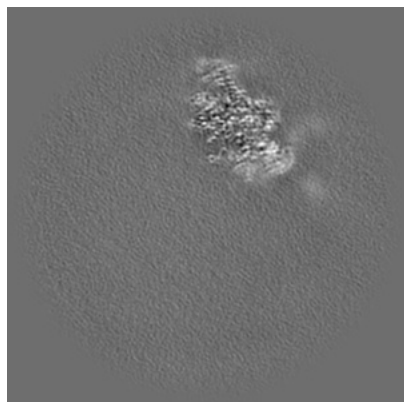


Z

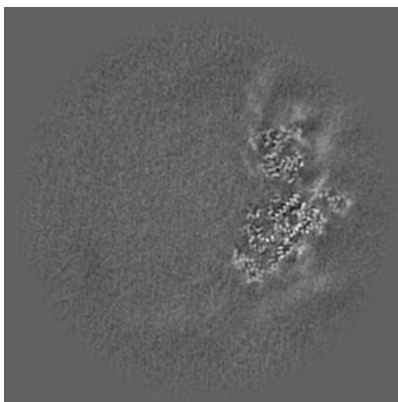
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

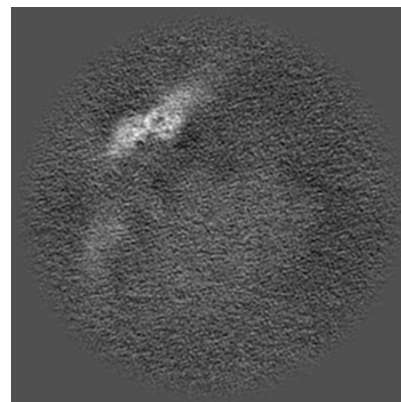
6.2.1 Primary map



X Index: 256

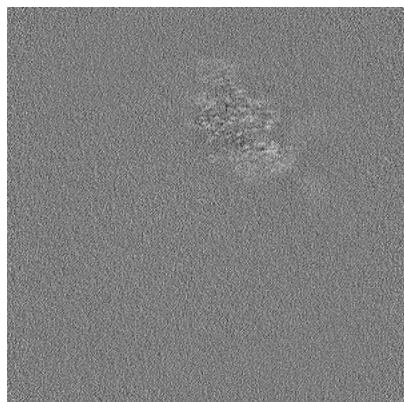


Y Index: 256

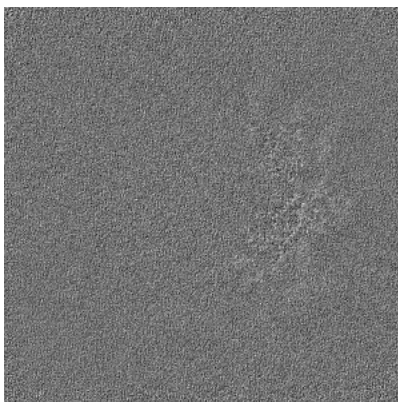


Z Index: 256

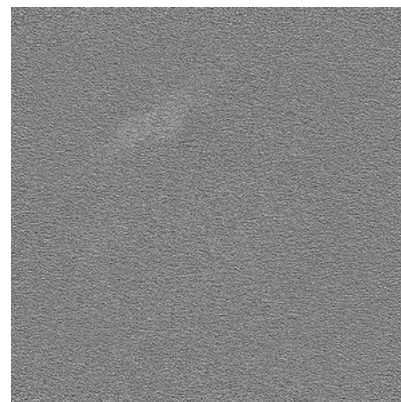
6.2.2 Raw map



X Index: 256



Y Index: 256

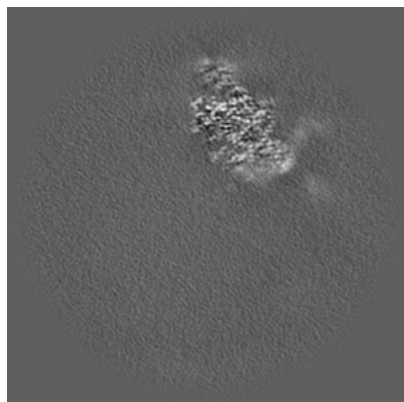


Z Index: 256

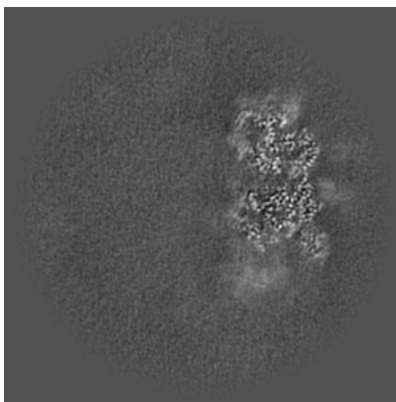
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

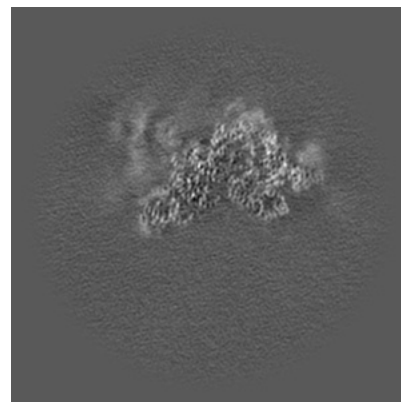
6.3.1 Primary map



X Index: 259

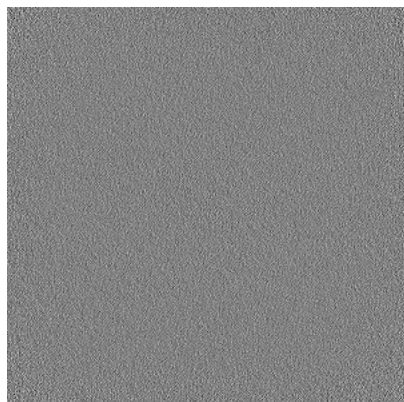


Y Index: 302

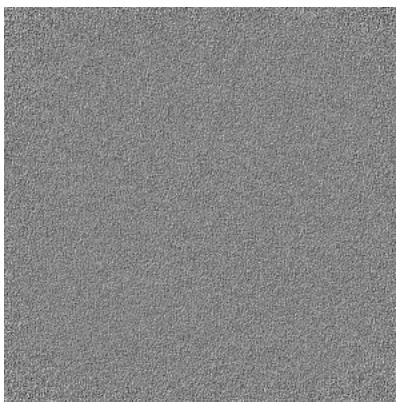


Z Index: 338

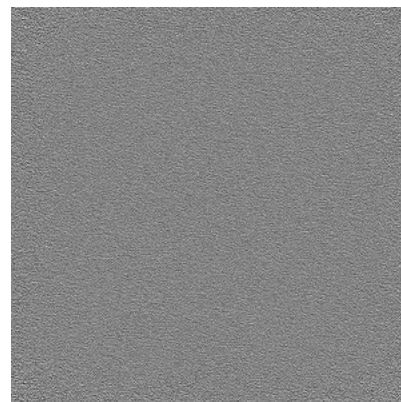
6.3.2 Raw map



X Index: 0



Y Index: 0

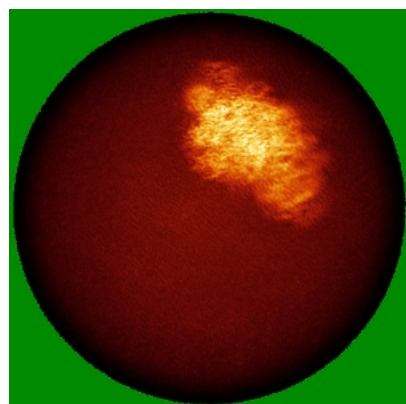


Z Index: 0

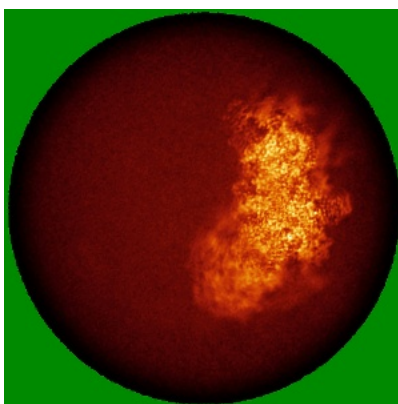
The images above show the largest variance slices of the map in three orthogonal directions.

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

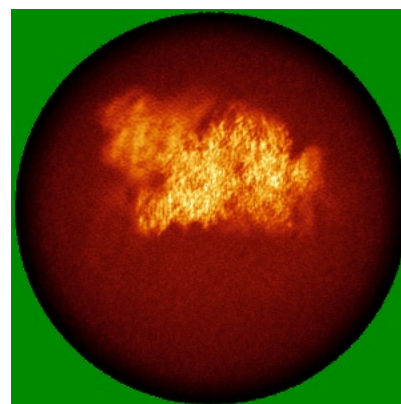
6.4.1 Primary map



X

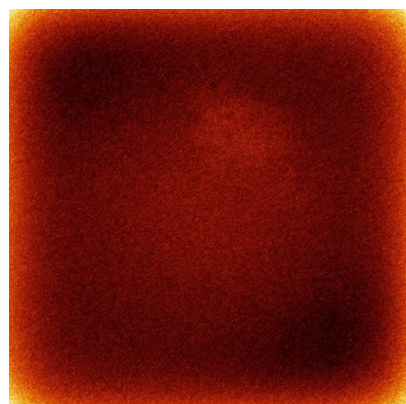


Y

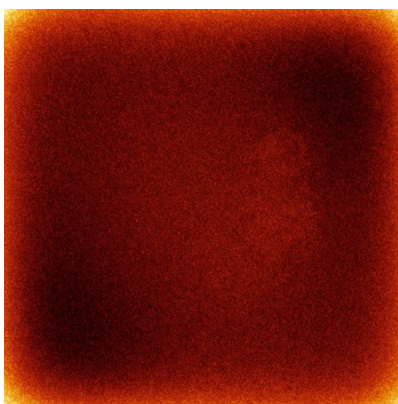


Z

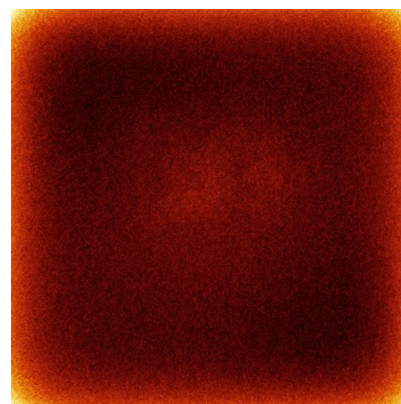
6.4.2 Raw map



X



Y

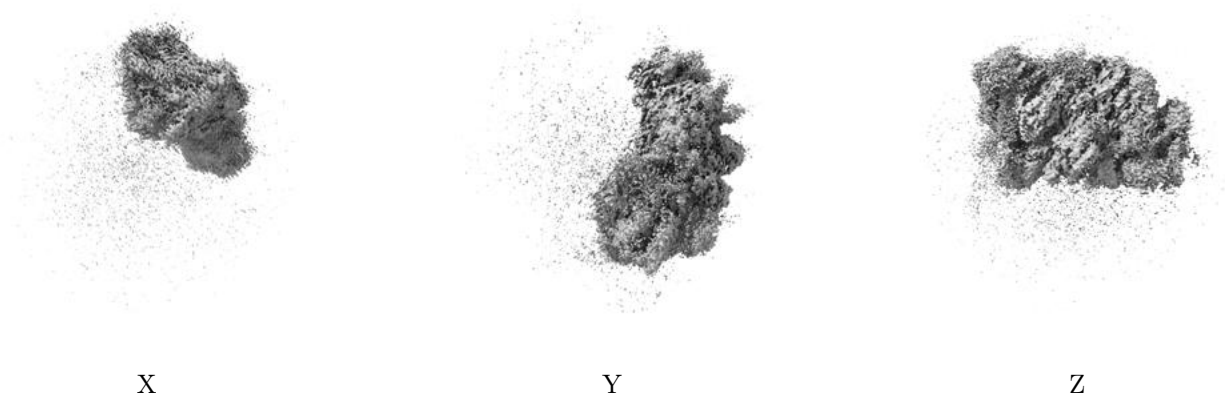


Z

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.

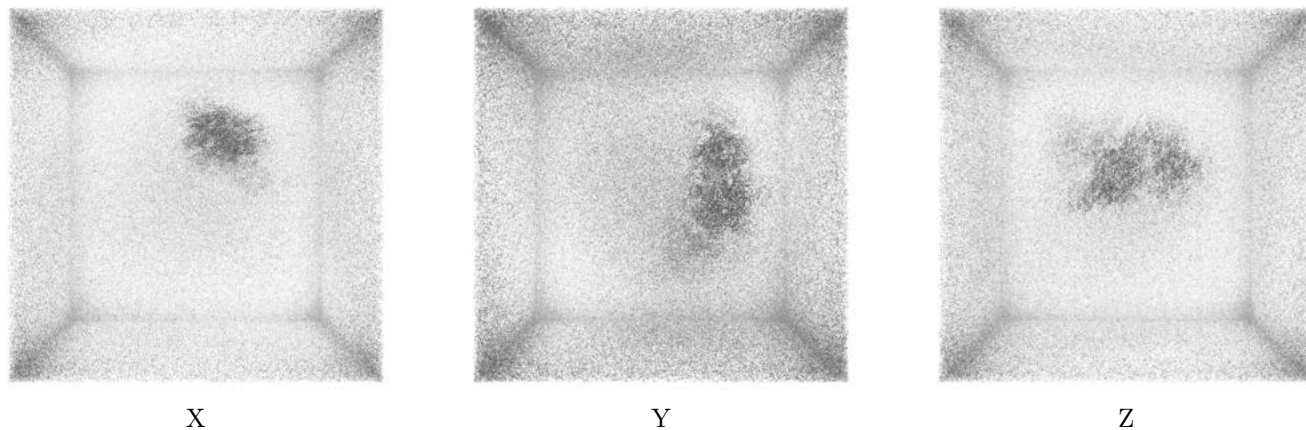
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.26. 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.

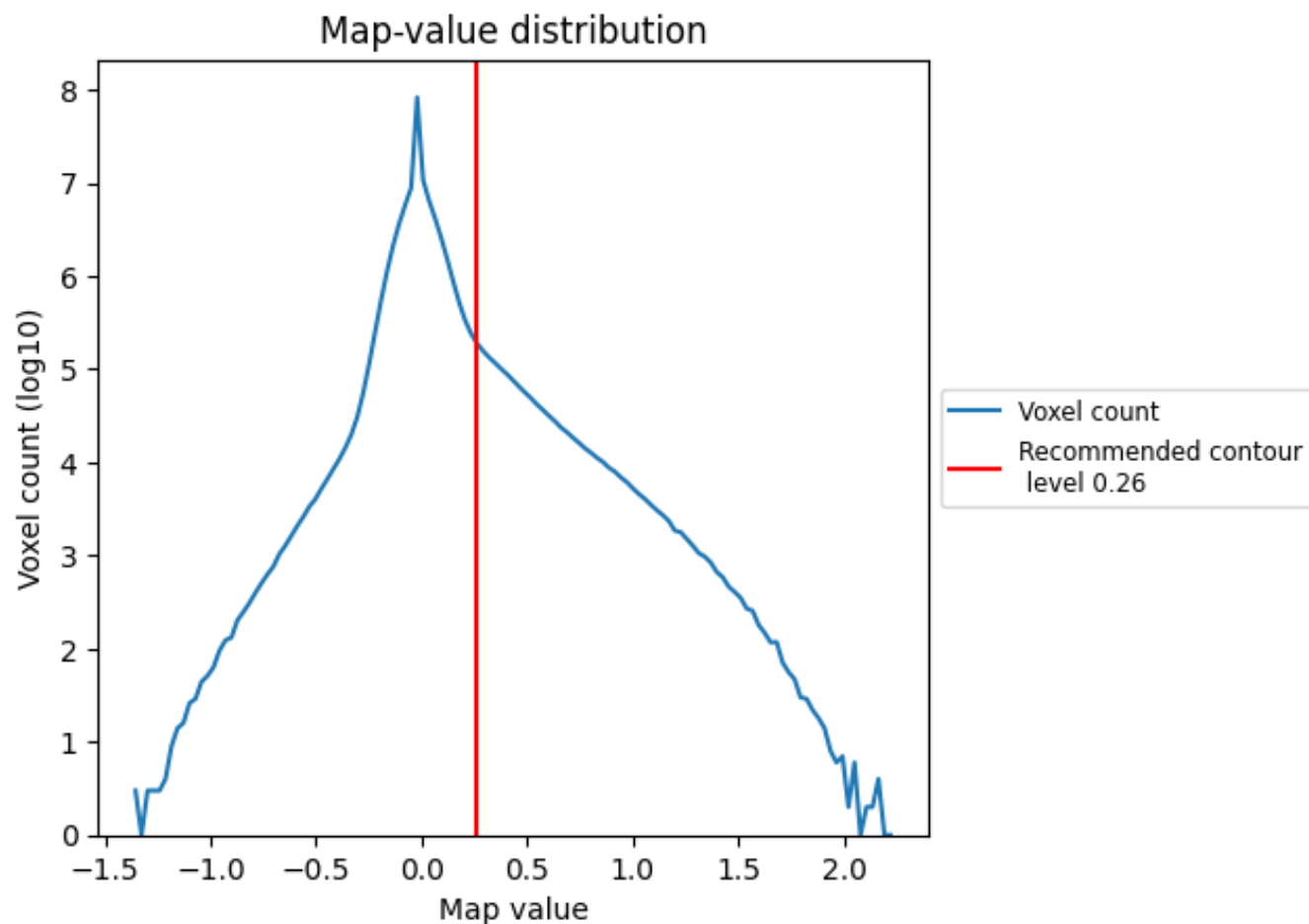
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

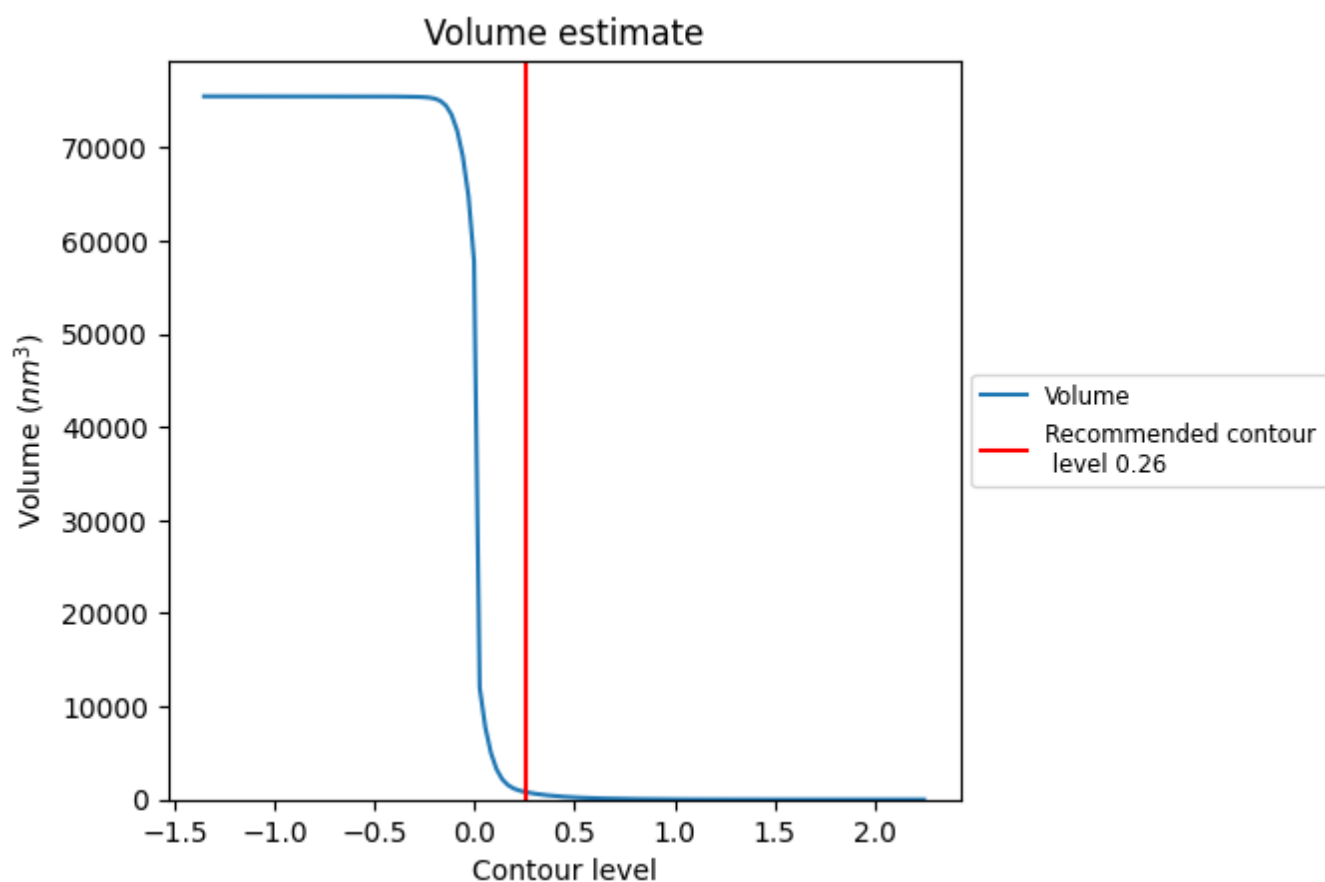
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

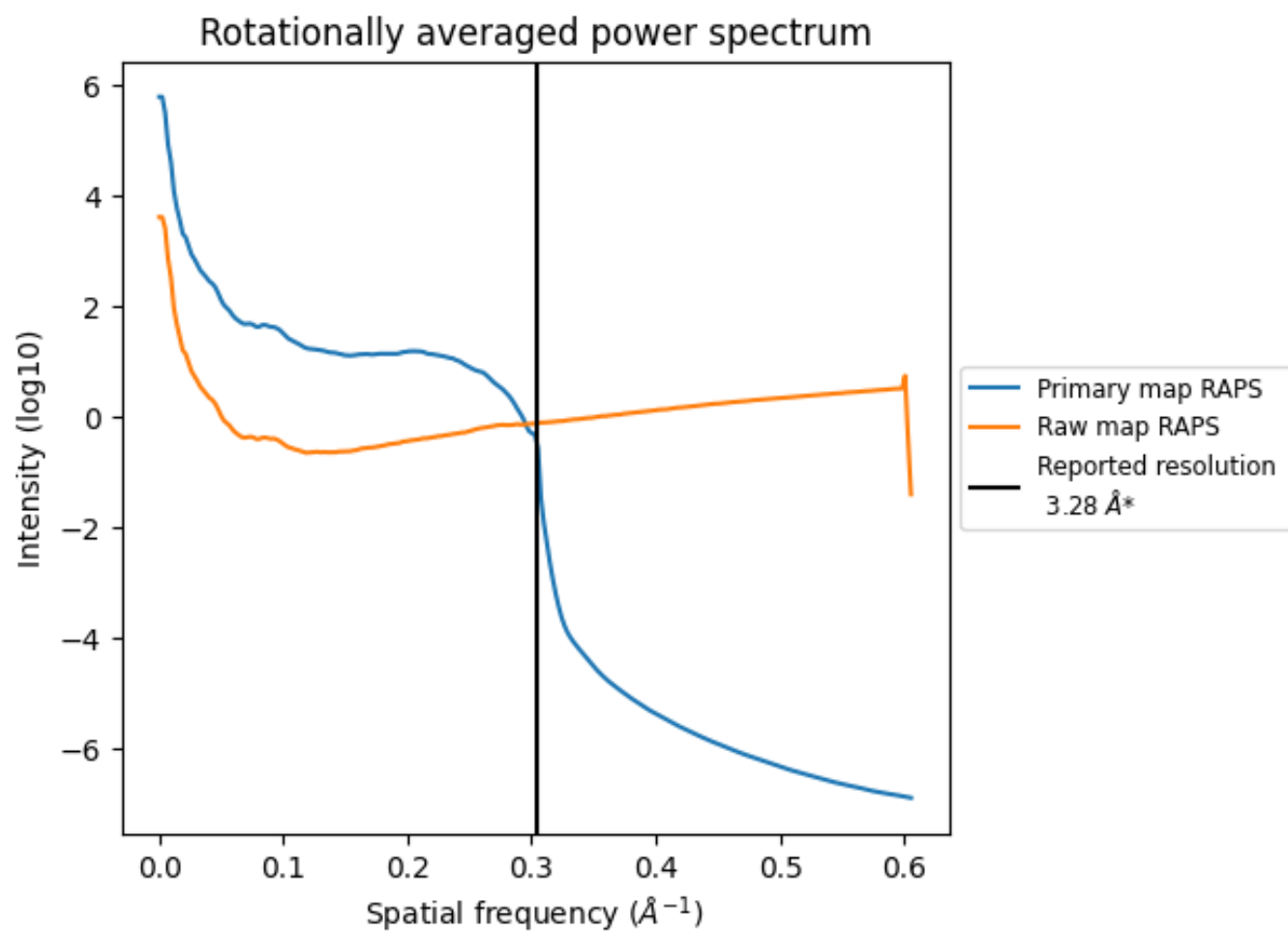
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 782 nm³; this corresponds to an approximate mass of 706 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 ⓘ

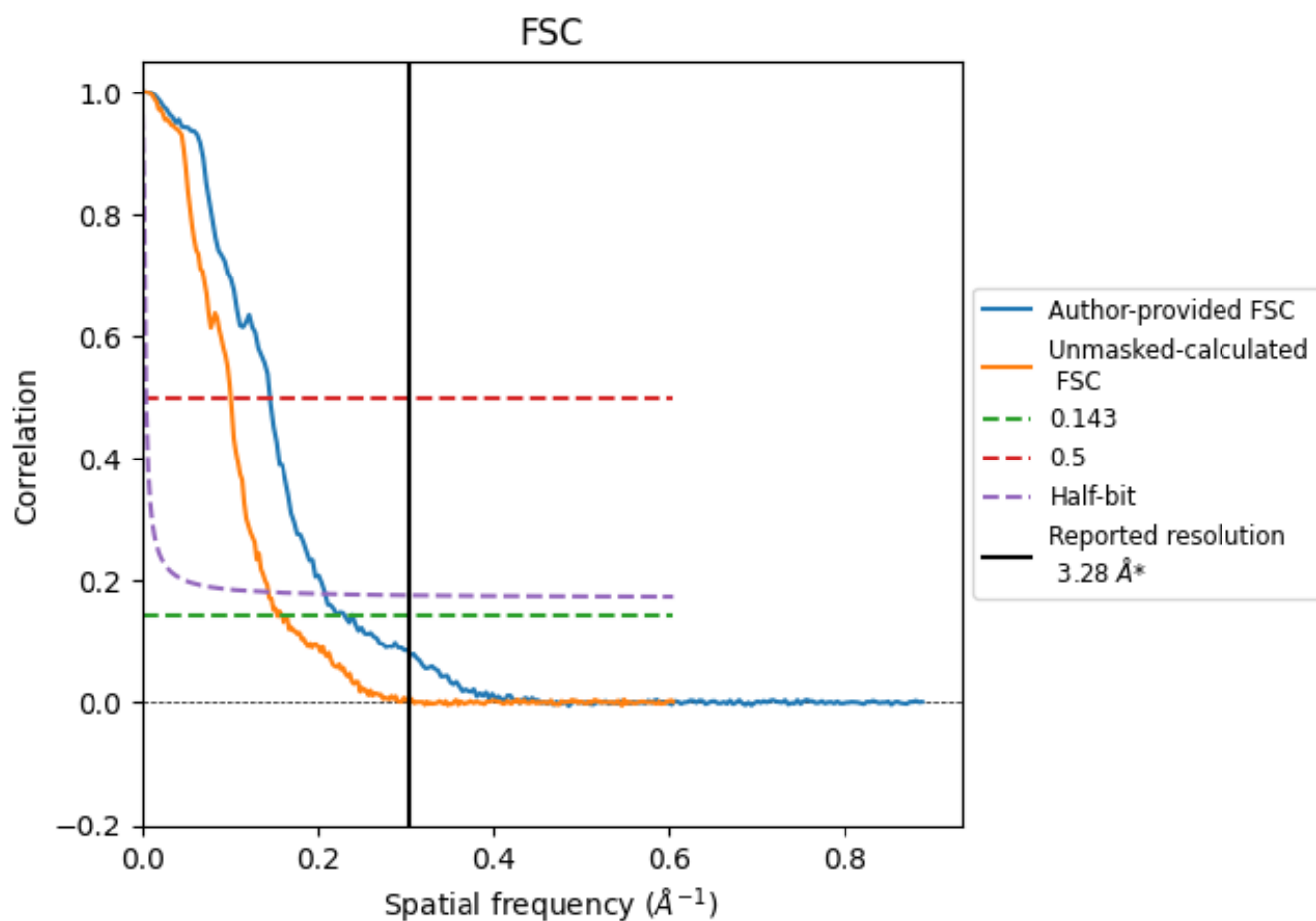


*Reported resolution corresponds to spatial frequency of 0.305 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.305 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	4.33	6.89	4.80
Unmasked-calculated*	6.51	9.94	6.98

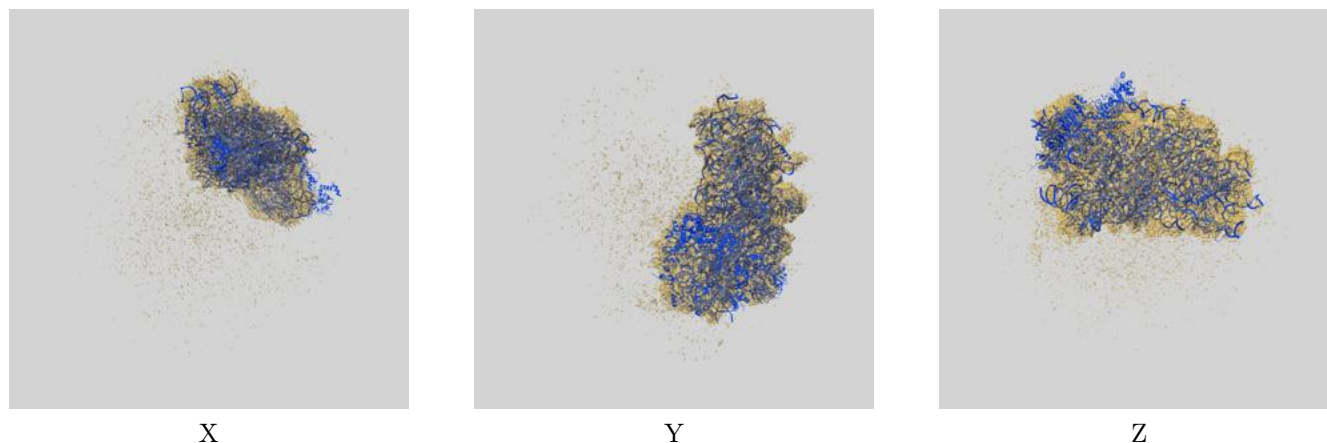
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.33 differs from the reported value 3.28 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.51 differs from the reported value 3.28 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70479 and PDB model 9OGY. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



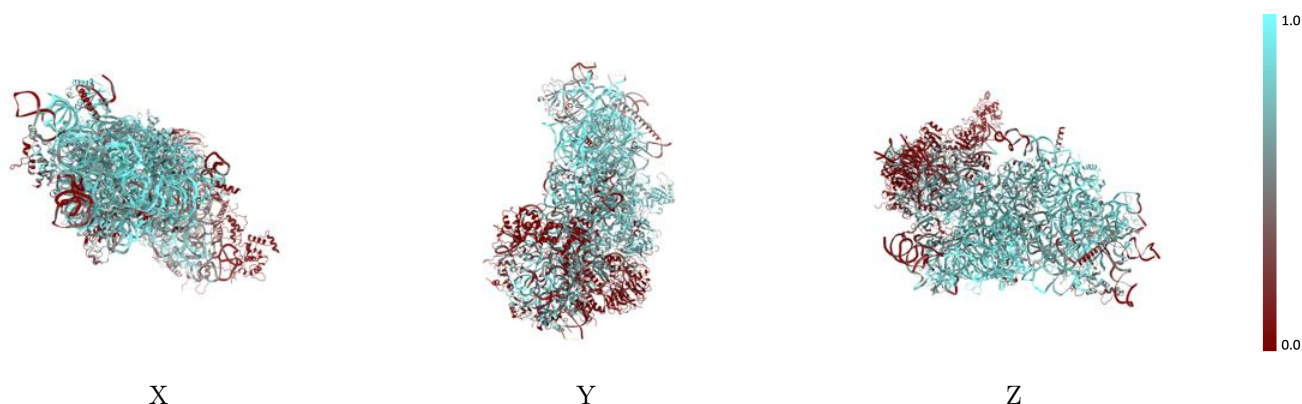
The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



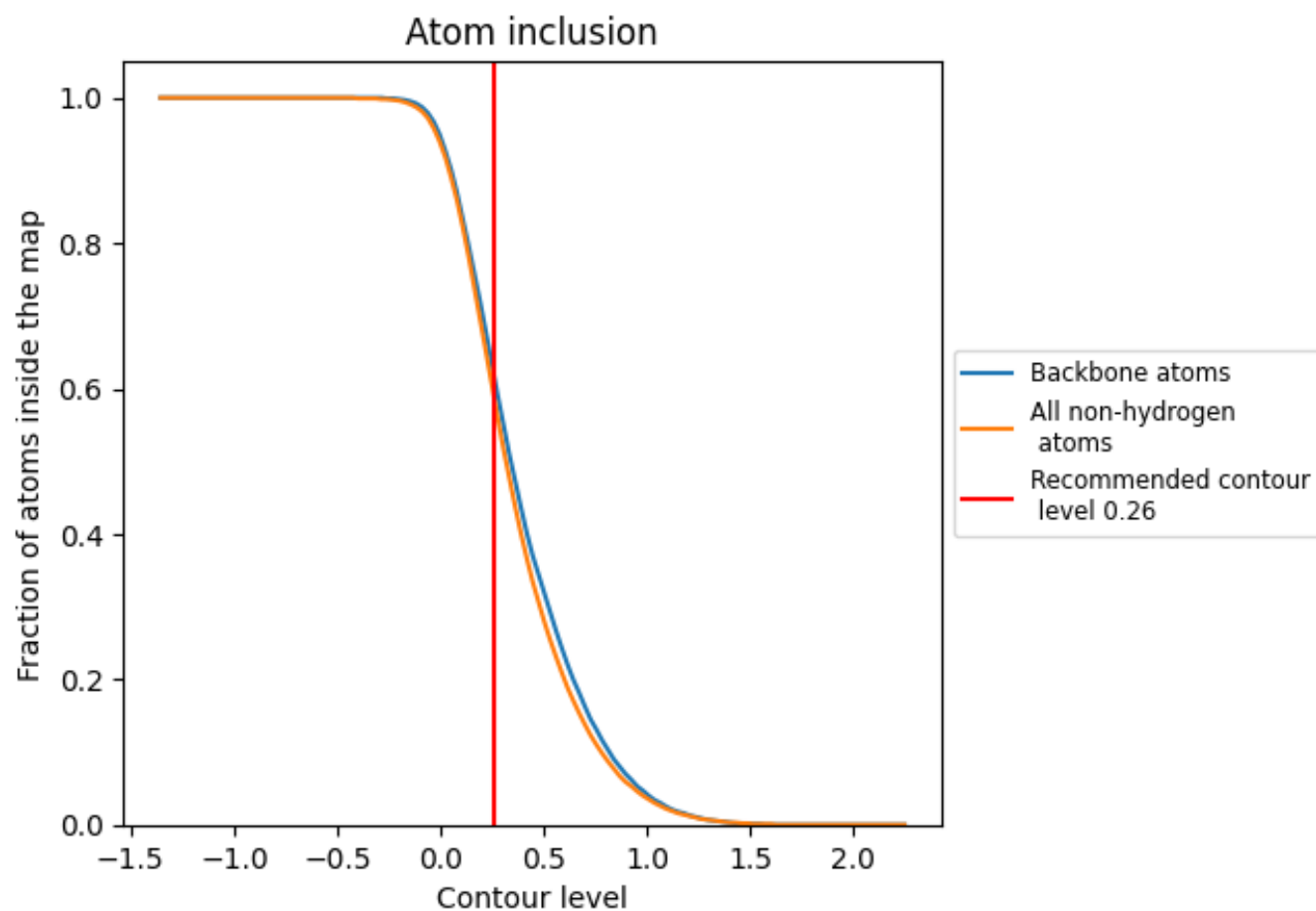
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.26).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 59% 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 (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5880	 0.1720
2	 0.6910	 0.1890
A	 0.2820	 0.0350
B	 0.6930	 0.2280
C	 0.8050	 0.3600
D	 0.6640	 0.2150
E	 0.1930	 0.0330
F	 0.7640	 0.3090
G	 0.5050	 -0.0120
H	 0.4510	 0.1990
I	 0.7410	 0.3000
J	 0.5210	 0.2680
K	 0.6650	 0.1950
L	 0.0630	 0.0050
M	 0.6570	 0.3280
N	 0.0020	 -0.0210
O	 0.7880	 0.4040
P	 0.6270	 0.2160
Q	 0.3910	 0.0350
R	 0.2960	 0.0030
S	 0.2810	 0.0790
T	 0.4880	 -0.0160
U	 0.5150	 0.0410
V	 0.1960	 0.0180
W	 0.7300	 0.2940
X	 0.8190	 0.3750
Y	 0.5450	 0.1980
Z	 0.7260	 0.2220
a	 0.3520	 0.0270
b	 0.6870	 0.2620
c	 0.8560	 0.3850
d	 0.5510	 0.0080
e	 0.4080	 0.0230
f	 0.4410	 0.0810
g	 0.1180	 0.0050



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Chain	Atom inclusion	Q-score
h	 0.0540	 -0.0070
n	 0.0870	 0.1400