



Full wwPDB EM Validation Report ⓘ

Jul 8, 2026 – 01:57 PM JST

PDB ID : 9KMW / pdb_00009kmw
EMDB ID : EMD-62447
Title : SARSr-MpCoV-GX Nsp1 bound to the Human 40S Ribosomal subunit-State2
Authors : Yuan, S.; Yan, R.; Wu, M.
Deposited on : 2024-11-18
Resolution : 2.73 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

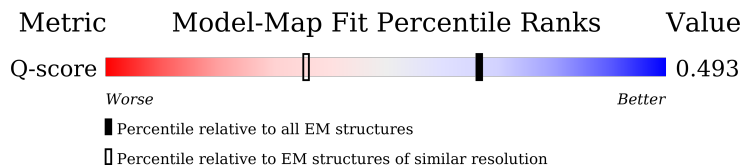
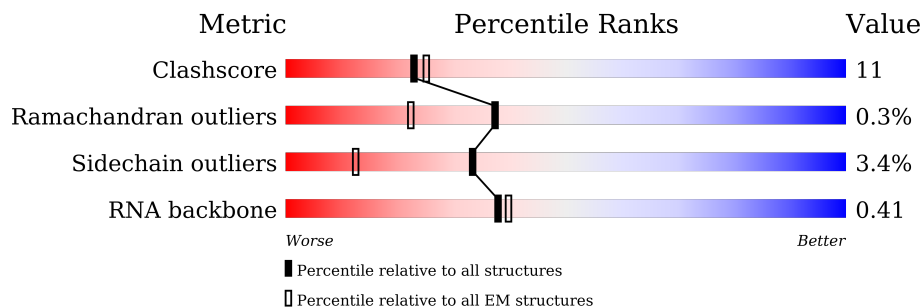
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.73 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.



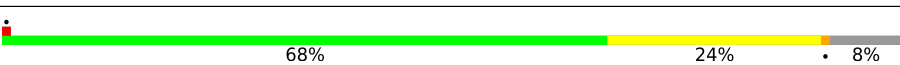
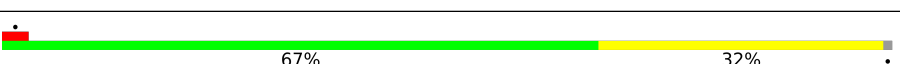
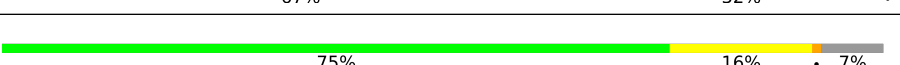
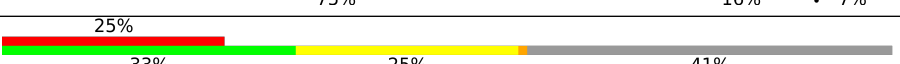
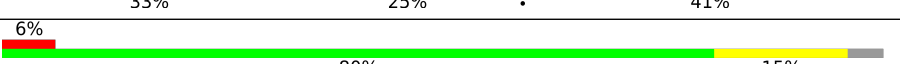
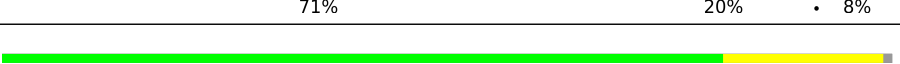
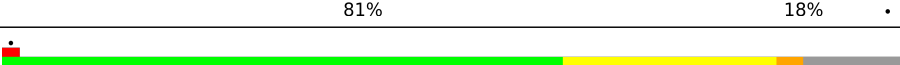
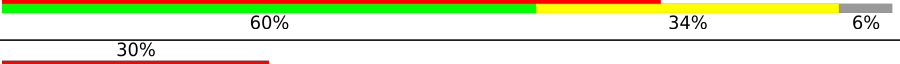
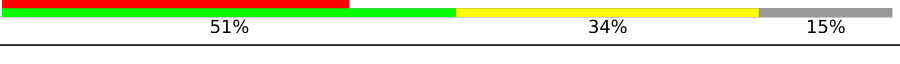
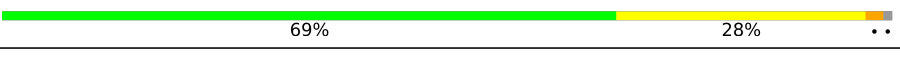
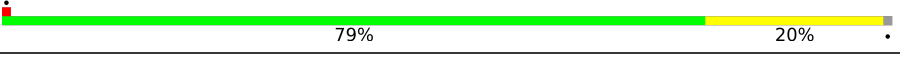
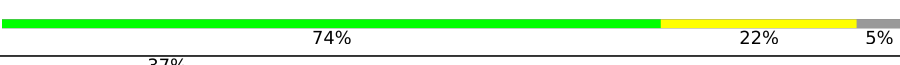
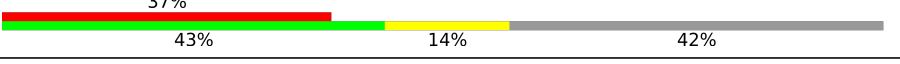
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10432 (2.23 - 3.23)

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	1869	
2	A	295	
3	B	264	

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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	143	
26	Y	130	
27	Z	125	
28	a	101	

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Mol	Chain	Length	Quality of chain
29	b	82	9% 80% 20%
30	c	62	39% 74% 26%
31	d	55	20% 60% 40%
32	e	56	9% 77% 21%
33	f	74	91% 77% 23%
34	g	315	52% 56% 42%
35	h	25	64% 24% 12%
36	n	180	11% 6% 83%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 74798 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	1671	Total	C	N	O	P	0	0
			35647	15925	6406	11655	1661		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	213	Total	C	N	O	S	0	0
			1686	1072	295	311	8		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 6 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 8 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	230	Total	C	N	O	S	0	0
			1864	1164	373	320	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	221	ARG	LYS	variant	UNP P62753

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 10 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 12 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	97	Total	C	N	O	S	0	0
			816	533	144	133	6		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	151	Total	C	N	O	S	0	0
			1229	782	230	211	6		

- Molecule 14 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 17 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			1037	659	196	175	7		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	138	Total	C	N	O	S	0	0
			1097	698	206	190	3		

- Molecule 19 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 21 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	144	Total	C	N	O	S	0	0
			1123	703	217	200	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 24 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 26 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 27 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	99	Total	C	N	O	S	0	0
			794	494	165	130	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	78	VAL	ALA	conflict	UNP P62854

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	82	Total	C	N	O	S	0	0
			641	402	118	114	7		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			489	297	97	93	2		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 32 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	56	Total	C	N	O	S	0	0
			442	273	96	72	1		

- Molecule 33 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	74	Total	C	N	O	S	0	0
			611	385	117	102	7		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2441	1537	425	467	12		

- Molecule 35 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	22	Total	C	N	O	S	0	0
			213	130	57	23	3		

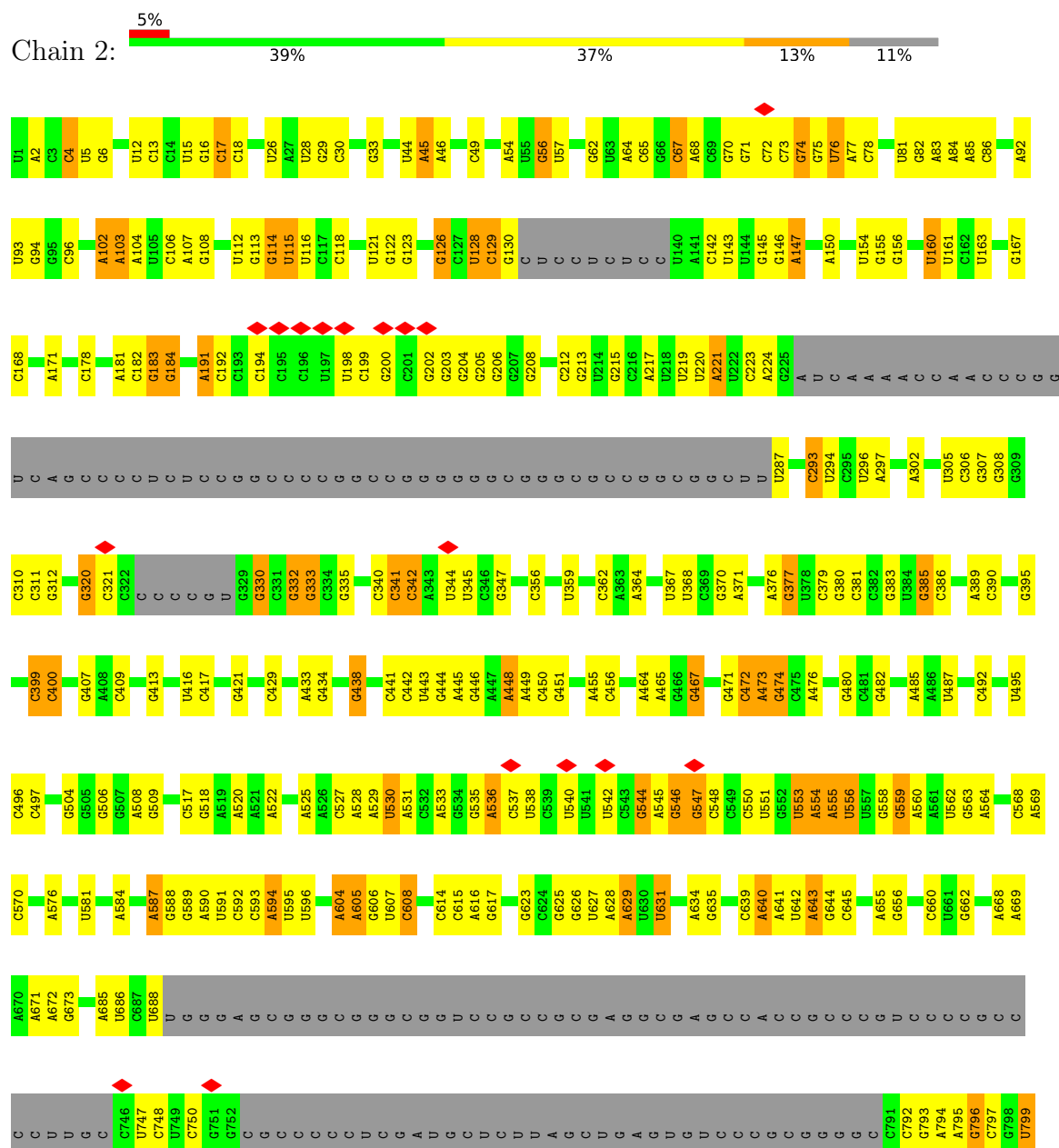
- Molecule 36 is a protein called ORF1ab polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	30	Total	C	N	O	S	0	0
			238	144	44	49	1		

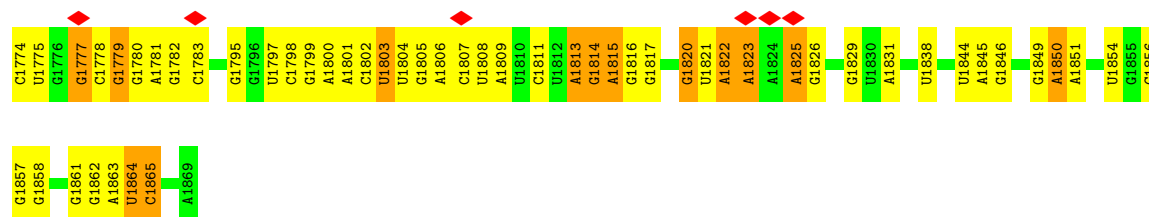
3 Residue-property plots

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

• Molecule 1: 18S ribosomal RNA

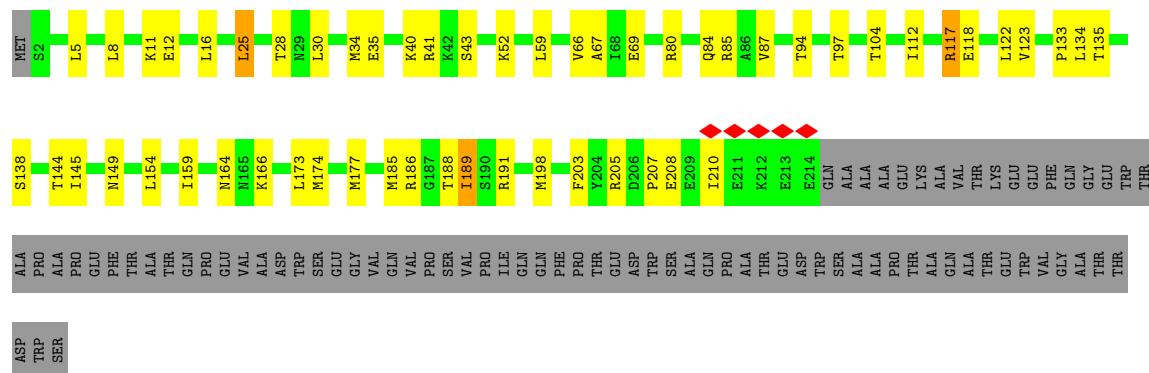






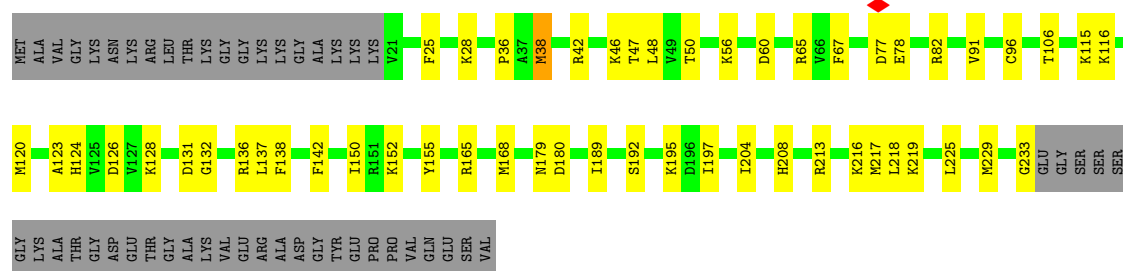
• Molecule 2: Small ribosomal subunit protein uS2

Chain A: 54% 18% 28%



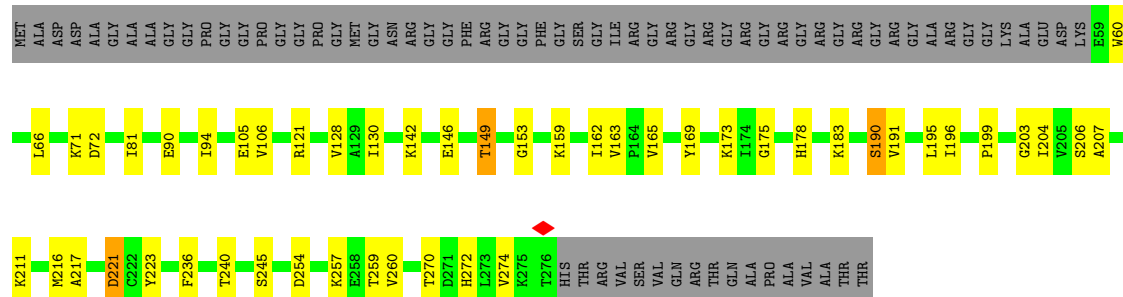
• Molecule 3: Small ribosomal subunit protein eS1

Chain B: 61% 20% 19%

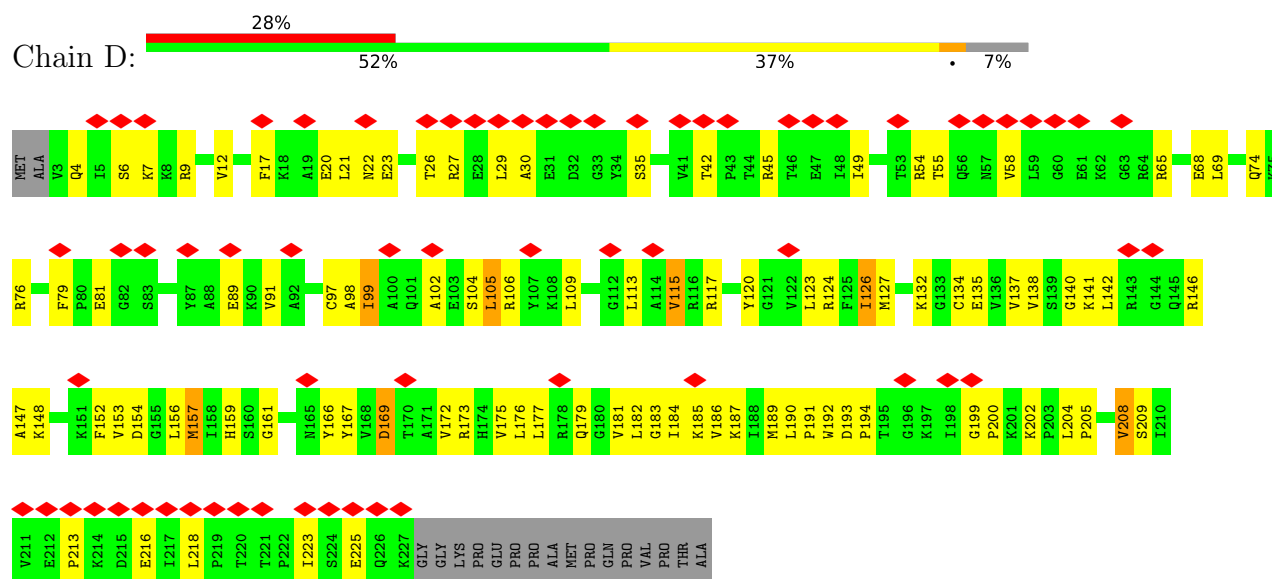


• Molecule 4: Small ribosomal subunit protein uS5

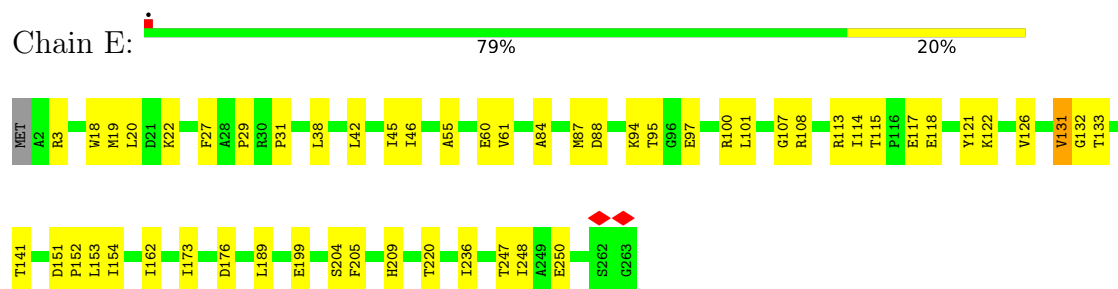
Chain C: 58% 16% 26%



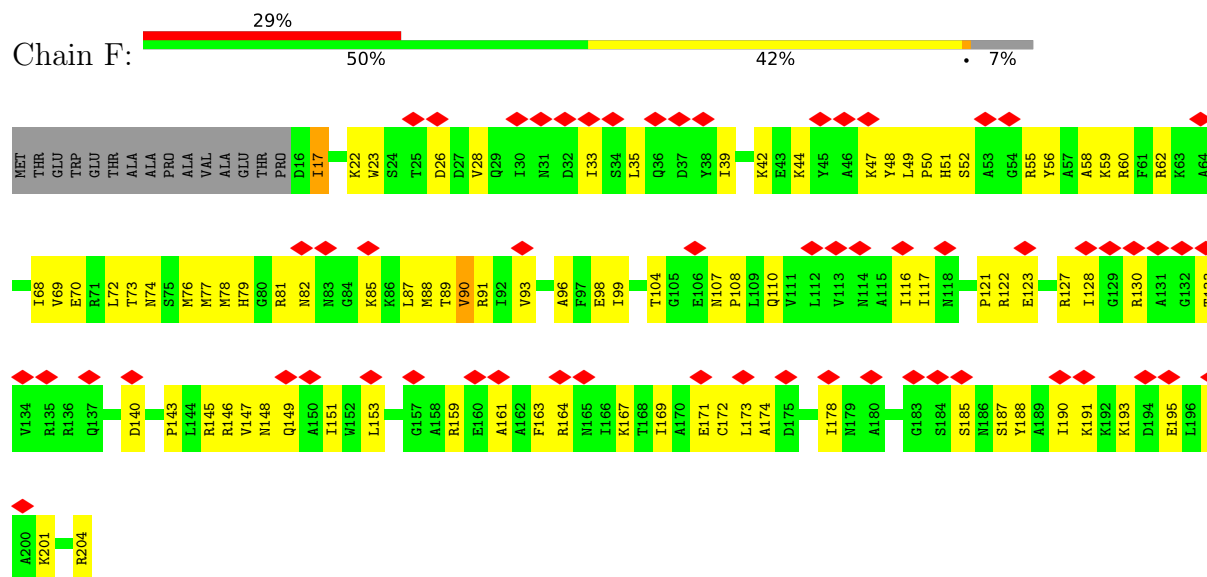
• Molecule 5: Small ribosomal subunit protein uS3



- Molecule 6: Small ribosomal subunit protein eS4, X isoform

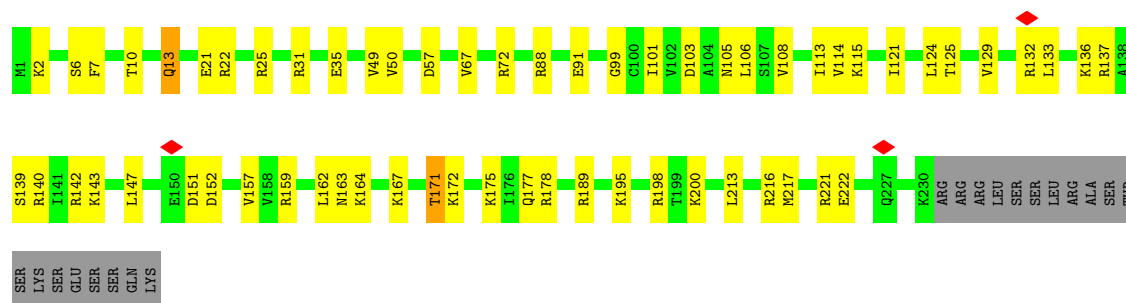


- Molecule 7: Small ribosomal subunit protein uS7

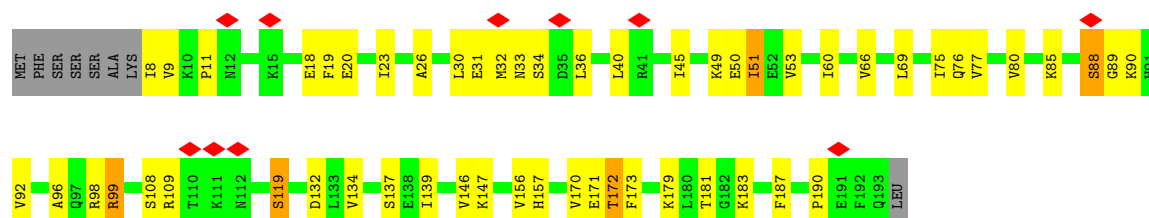


- Molecule 8: Small ribosomal subunit protein eS6

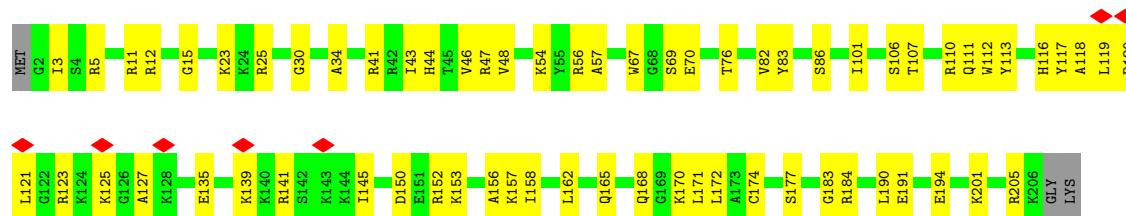




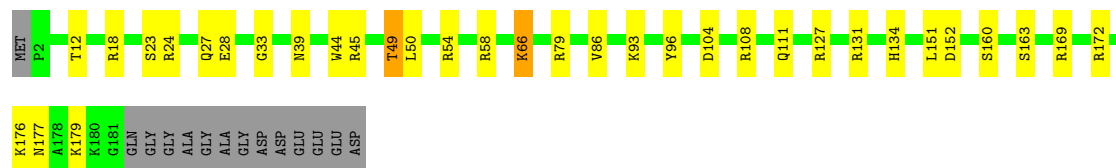
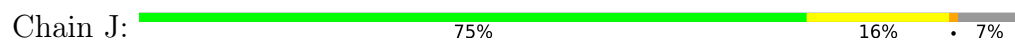
- Molecule 9: Small ribosomal subunit protein eS7



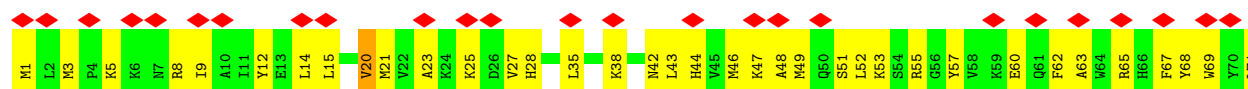
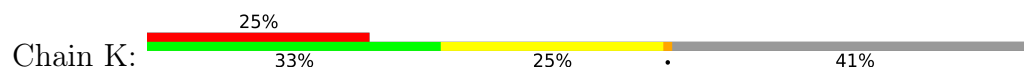
- Molecule 10: Small ribosomal subunit protein eS8

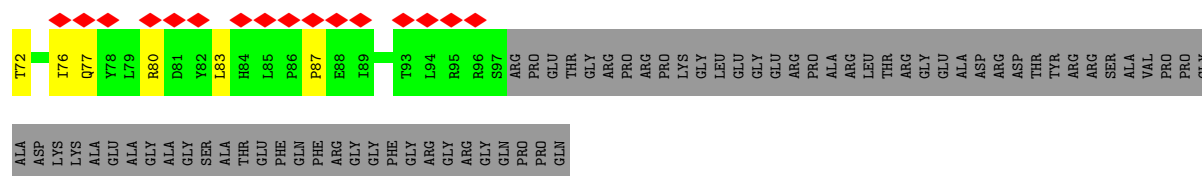


- Molecule 11: Small ribosomal subunit protein uS4

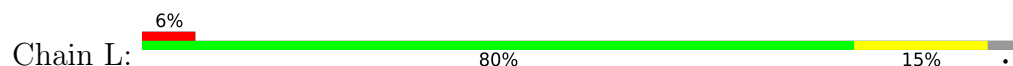


- Molecule 12: Small ribosomal subunit protein eS10

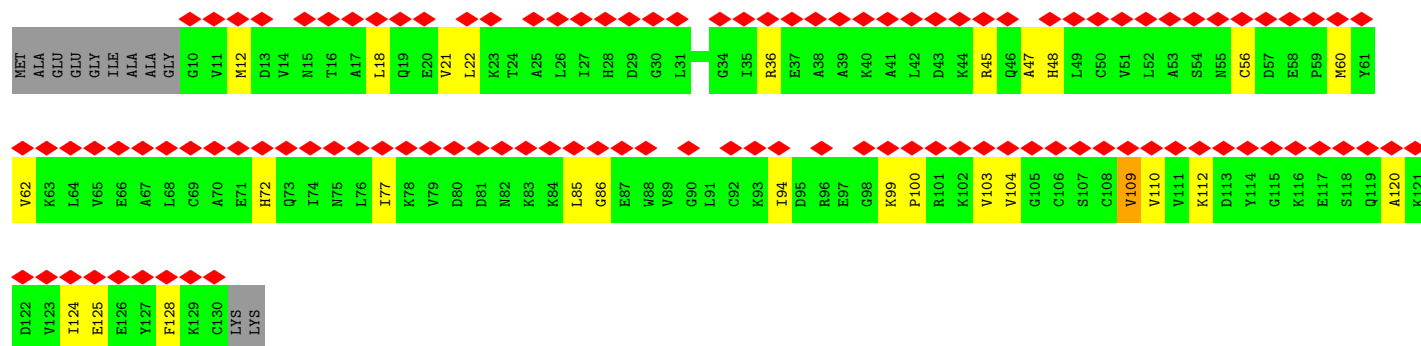
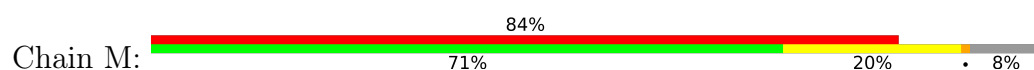




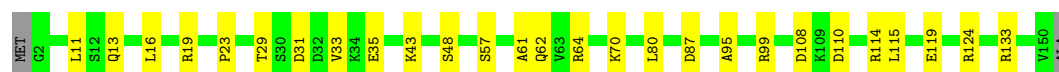
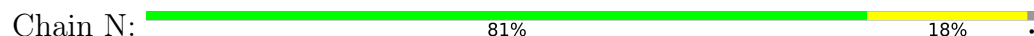
- Molecule 13: Small ribosomal subunit protein uS17



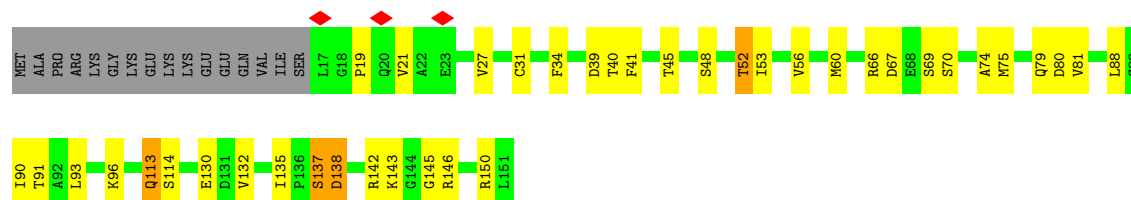
- Molecule 14: Small ribosomal subunit protein eS12



- Molecule 15: Small ribosomal subunit protein uS15

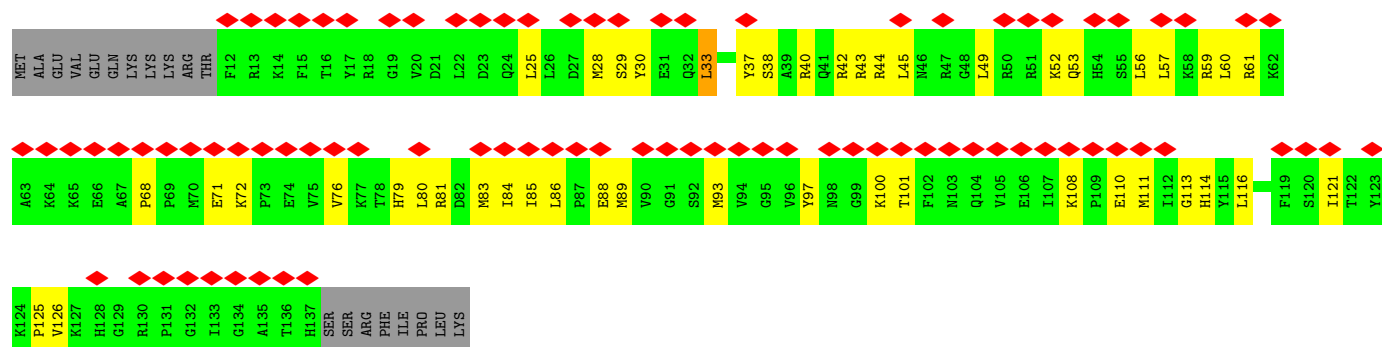


- Molecule 16: Small ribosomal subunit protein uS11

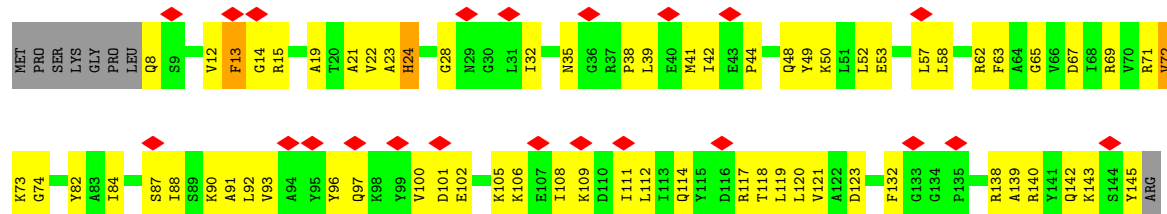


- Molecule 17: Small ribosomal subunit protein uS19

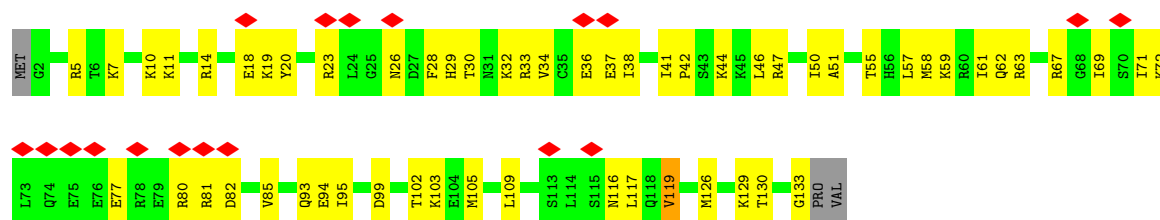




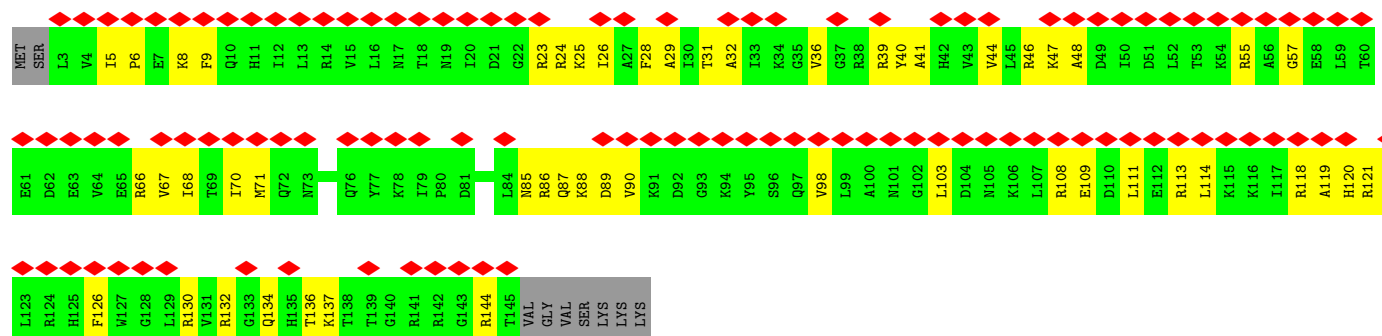
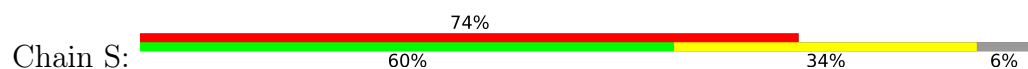
- Molecule 18: Small ribosomal subunit protein uS9



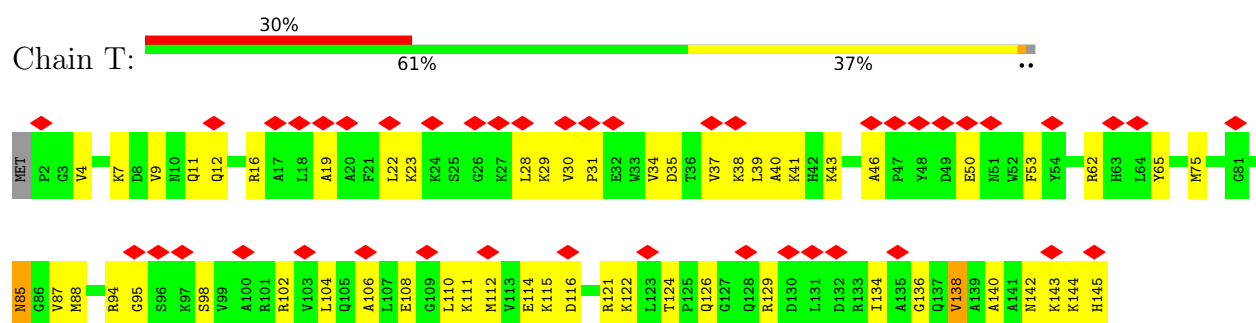
- Molecule 19: Small ribosomal subunit protein eS17



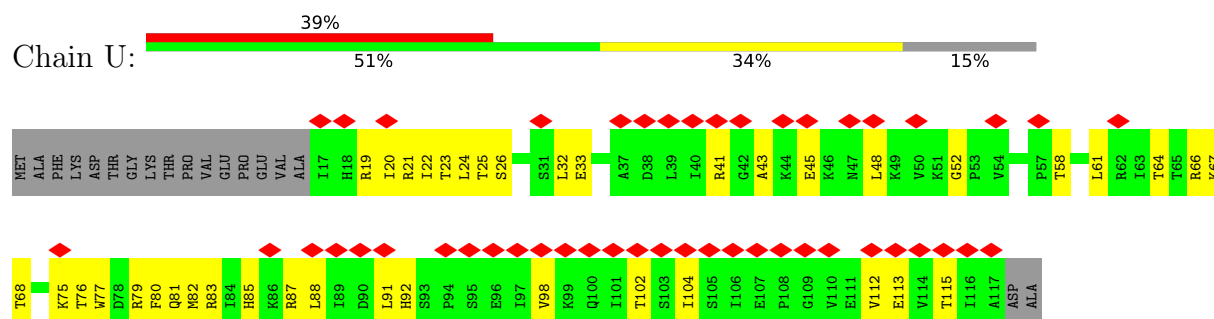
- Molecule 20: Small ribosomal subunit protein uS13



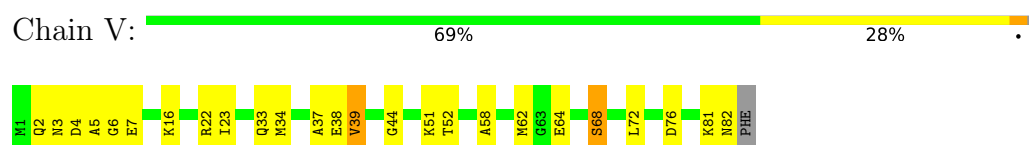
- Molecule 21: Small ribosomal subunit protein eS19



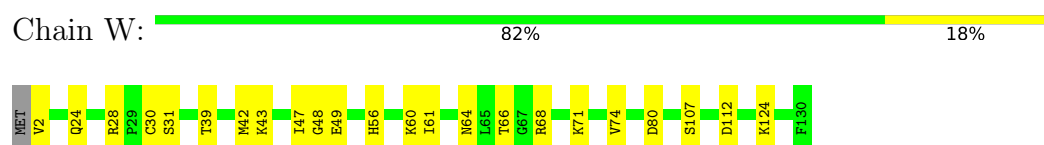
- Molecule 22: Small ribosomal subunit protein uS10



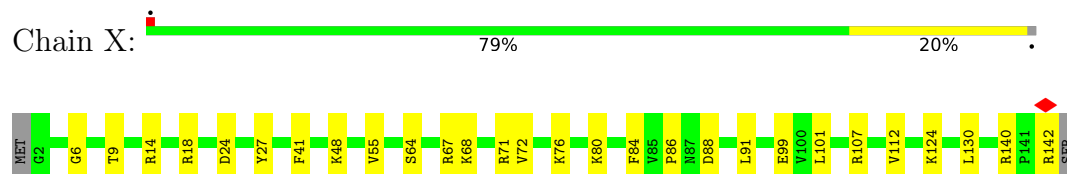
- Molecule 23: Small ribosomal subunit protein eS21



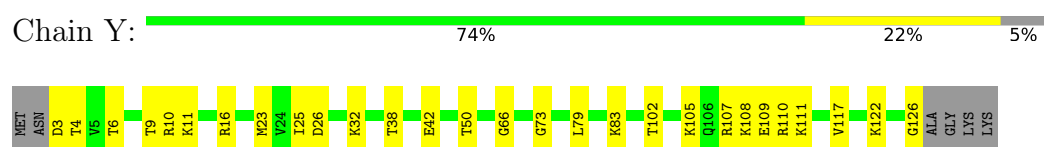
- Molecule 24: Small ribosomal subunit protein uS8



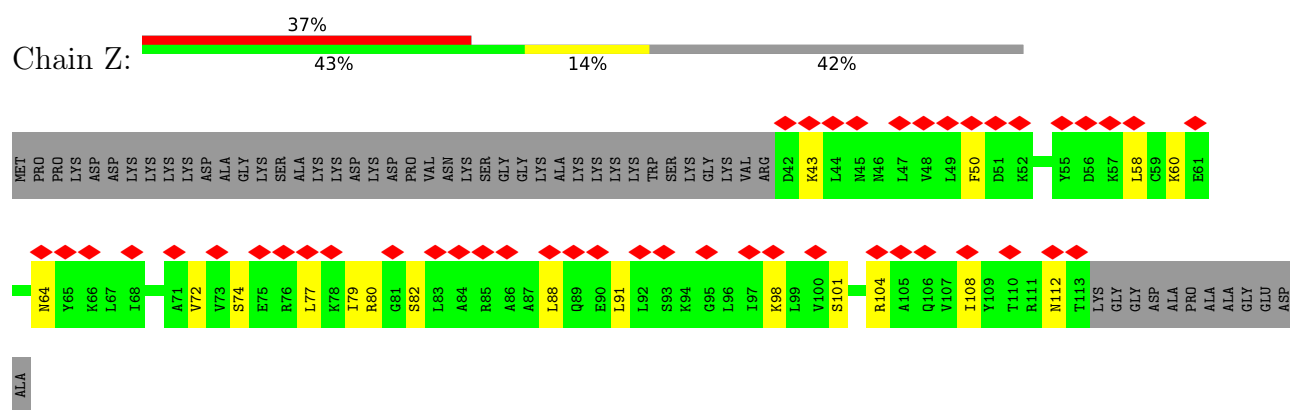
- Molecule 25: Small ribosomal subunit protein uS12



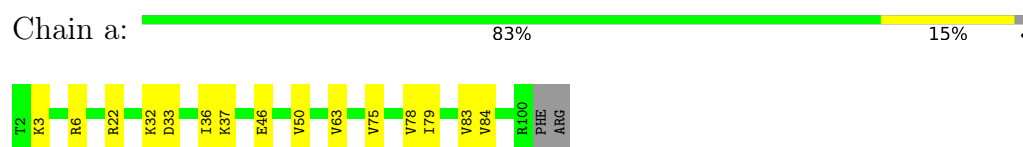
- Molecule 26: Small ribosomal subunit protein eS24



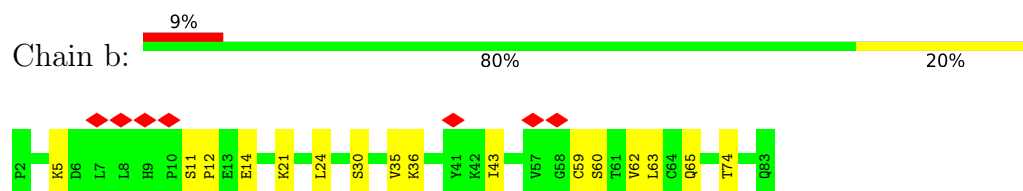
- Molecule 27: Small ribosomal subunit protein eS25



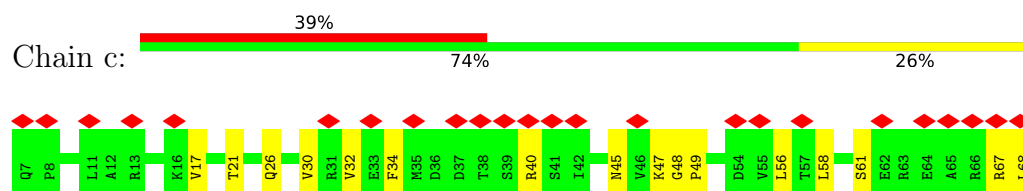
- Molecule 28: Small ribosomal subunit protein eS26



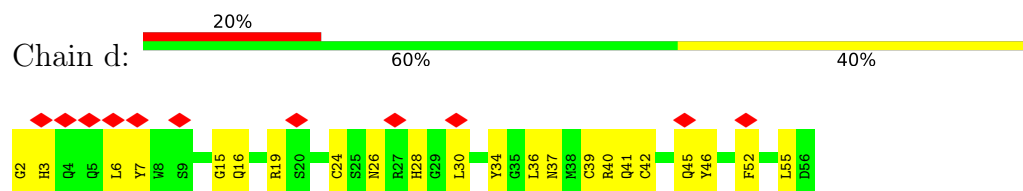
- Molecule 29: Small ribosomal subunit protein eS27



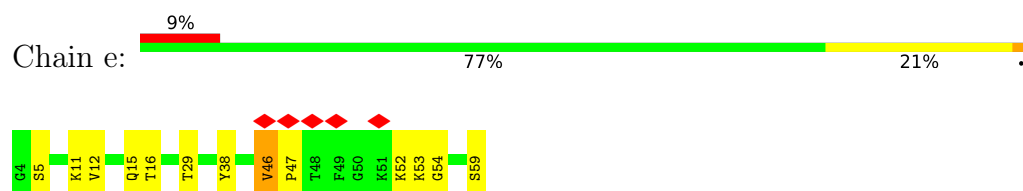
- Molecule 30: Small ribosomal subunit protein eS28



- Molecule 31: Small ribosomal subunit protein uS14



- Molecule 32: Small ribosomal subunit protein eS30



- Molecule 33: Small ribosomal subunit protein eS31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57459	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.348	Depositor
Minimum map value	-0.994	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.158	Depositor
Map size ($\text{\AA}$)	486.4, 486.4, 486.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.95, 0.95, 0.95	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.21	0/39865	0.30	2/62134 (0.0%)
2	A	0.19	0/1723	0.30	0/2341
3	B	0.18	0/1756	0.33	0/2350
4	C	0.22	0/1726	0.37	0/2332
5	D	0.16	0/1780	0.42	0/2397
6	E	0.22	0/2118	0.33	0/2849
7	F	0.18	0/1516	0.50	0/2037
8	G	0.18	0/1887	0.35	0/2513
9	H	0.17	0/1524	0.36	0/2042
10	I	0.19	0/1711	0.38	0/2282
11	J	0.21	0/1524	0.29	0/2035
12	K	0.13	0/840	0.39	0/1133
13	L	0.22	0/1250	0.33	0/1673
14	M	0.11	0/945	0.34	0/1269
15	N	0.18	0/1226	0.28	0/1649
16	O	0.19	0/1023	0.32	0/1372
17	P	0.15	0/1058	0.40	0/1414
18	Q	0.14	0/1114	0.40	0/1492
19	R	0.14	0/1082	0.34	0/1452
20	S	0.12	0/1202	0.40	0/1610
21	T	0.17	0/1143	0.41	0/1530
22	U	0.12	0/813	0.35	0/1092
23	V	0.18	0/631	0.32	0/844
24	W	0.23	0/1051	0.32	0/1406
25	X	0.21	0/1116	0.32	0/1490
26	Y	0.21	0/1031	0.35	0/1370
27	Z	0.12	0/580	0.38	0/780
28	a	0.20	0/807	0.35	0/1082
29	b	0.22	0/654	0.46	1/876 (0.1%)
30	c	0.13	0/491	0.36	0/656
31	d	0.12	0/470	0.39	0/623
32	e	0.19	0/447	0.47	0/587
33	f	0.11	0/623	0.32	0/822
34	g	0.13	0/2498	0.38	1/3399 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.16	0/214	0.32	0/272
36	n	0.21	0/242	0.36	0/325
All	All	0.20	0/79681	0.33	4/115530 (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
16	O	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1501	C	OP1-P-O3'	6.31	126.92	108.00
29	b	12	PRO	CA-N-CD	-5.53	104.26	112.00
1	2	1244	U	OP2-P-O3'	5.15	123.44	108.00
34	g	37	ASP	N-CA-C	-5.07	107.59	112.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
16	O	137	SER	Peptide

5.2 Too-close contacts [i](#)

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	35647	0	18022	611	0
2	A	1686	0	1688	37	0
3	B	1729	0	1803	35	0
4	C	1690	0	1777	30	0
5	D	1752	0	1848	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	2076	0	2177	32	0
7	F	1495	0	1549	86	0
8	G	1864	0	2018	43	0
9	H	1501	0	1593	34	0
10	I	1682	0	1769	58	0
11	J	1499	0	1618	24	0
12	K	816	0	841	40	0
13	L	1229	0	1302	18	0
14	M	935	0	964	15	0
15	N	1202	0	1289	17	0
16	O	1010	0	1034	29	0
17	P	1037	0	1082	47	0
18	Q	1097	0	1161	54	0
19	R	1068	0	1121	39	0
20	S	1184	0	1244	42	0
21	T	1123	0	1153	49	0
22	U	803	0	873	31	0
23	V	625	0	628	16	0
24	W	1034	0	1080	17	0
25	X	1098	0	1167	18	0
26	Y	1014	0	1082	18	0
27	Z	574	0	627	13	0
28	a	794	0	849	14	0
29	b	641	0	665	8	0
30	c	489	0	514	15	0
31	d	459	0	452	25	0
32	e	442	0	487	11	0
33	f	611	0	638	14	0
34	g	2441	0	2396	99	0
35	h	213	0	258	8	0
36	n	238	0	219	6	0
All	All	74798	0	58988	1452	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 11.

All (1452) 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)
1:2:191:A:H62	1:2:208:G:N2	1.61	0.98
1:2:1656:G:H1	1:2:1668:U:H3	1.00	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1091:C:HO2'	24:W:2:VAL:N	1.61	0.97
1:2:1033:G:H1	1:2:1080:A:HO2'	1.15	0.94
1:2:1290:G:H1	1:2:1301:A:HO2'	1.05	0.93
5:D:106:ARG:HE	5:D:175:VAL:HG22	1.33	0.92
1:2:191:A:H62	1:2:208:G:H21	0.95	0.91
1:2:191:A:N6	1:2:208:G:H21	1.70	0.90
28:a:36:ILE:HD12	28:a:78:VAL:HG11	1.58	0.85
5:D:127:MET:HE2	5:D:154:ASP:HB3	1.58	0.84
12:K:15:LEU:HA	12:K:21:MET:HE1	1.61	0.83
1:2:1739:C:H5	1:2:1795:G:H1	1.27	0.83
18:Q:28:GLY:HA3	18:Q:67:ASP:HB2	1.61	0.82
5:D:102:ALA:O	5:D:106:ARG:NH1	2.11	0.82
34:g:112:ALA:HB3	34:g:121:VAL:HB	1.61	0.82
1:2:1221:G:H2'	1:2:1222:G:H8	1.44	0.82
17:P:72:LYS:HD3	17:P:93:MET:HE2	1.64	0.80
5:D:213:PRO:HD3	19:R:19:LYS:HE3	1.63	0.80
20:S:9:PHE:HB2	20:S:57:GLY:HA2	1.63	0.79
17:P:68:PRO:HB2	17:P:71:GLU:HB3	1.63	0.79
21:T:85:ASN:HB2	21:T:88:MET:HB2	1.65	0.78
34:g:177:TRP:HE1	34:g:184:LEU:HG	1.49	0.77
22:U:81:GLN:HE22	31:d:55:LEU:HB2	1.49	0.77
7:F:96:ALA:HA	7:F:99:ILE:HB	1.67	0.76
1:2:1229:G:N2	1:2:1634:A:N3	2.33	0.76
23:V:38:GLU:OE2	23:V:51:LYS:NZ	2.19	0.76
6:E:152:PRO:HG2	8:G:216:ARG:HG2	1.66	0.75
11:J:134:HIS:ND1	11:J:163:SER:OG	2.18	0.75
17:P:30:TYR:HA	17:P:33:LEU:HB2	1.69	0.74
34:g:174:VAL:HG12	34:g:188:HIS:HB2	1.68	0.74
1:2:981:A:H2'	1:2:982:G:C8	2.23	0.74
34:g:196:ASN:ND2	34:g:236:ILE:O	2.21	0.74
1:2:1358:U:OP1	4:C:121:ARG:NH2	2.21	0.74
1:2:874:G:H2'	1:2:875:A:H8	1.53	0.73
6:E:100:ARG:NH2	6:E:121:TYR:O	2.22	0.73
10:I:135:GLU:O	10:I:139:LYS:NZ	2.21	0.72
1:2:587:A:H5'	1:2:592:C:H41	1.54	0.72
9:H:60:ILE:HD11	9:H:90:LYS:HE2	1.69	0.72
1:2:1520:G:H21	17:P:125:PRO:HB3	1.52	0.72
1:2:1335:G:H5'	5:D:185:LYS:HE3	1.69	0.72
1:2:1337:C:H2'	1:2:1338:G:H8	1.54	0.72
9:H:98:ARG:NH1	9:H:132:ASP:OD2	2.22	0.72
1:2:1544:C:N4	1:2:1589:A:OP2	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1454:A:H3'	19:R:5:ARG:HH21	1.53	0.72
19:R:94:GLU:O	19:R:116:ASN:ND2	2.23	0.72
20:S:86:ARG:HH12	20:S:90:VAL:HG23	1.54	0.72
1:2:1263:U:H5''	1:2:1264:C:H2'	1.72	0.71
1:2:1544:C:N3	1:2:1590:C:N4	2.38	0.71
11:J:18:ARG:O	11:J:24:ARG:NH1	2.23	0.71
1:2:907:G:H2'	1:2:908:A:H8	1.54	0.71
27:Z:98:LYS:HB2	27:Z:112:ASN:HB2	1.72	0.71
5:D:106:ARG:HD2	5:D:173:ARG:HB3	1.73	0.71
15:N:31:ASP:O	15:N:35:GLU:HG2	1.90	0.71
1:2:1242:U:H1'	1:2:1518:C:H5'	1.71	0.70
5:D:140:GLY:O	5:D:147:ALA:HA	1.90	0.70
34:g:156:PHE:HE1	34:g:165:ILE:HG22	1.56	0.70
1:2:1253:A:H4'	1:2:1254:C:H5''	1.73	0.70
1:2:928:G:H1	1:2:1013:U:H3	1.39	0.70
6:E:199:GLU:OE2	6:E:209:HIS:NE2	2.18	0.70
1:2:1335:G:H1	1:2:1495:G:H1	1.40	0.70
7:F:193:LYS:NZ	7:F:193:LYS:O	2.25	0.70
1:2:799:U:O4	9:H:108:SER:OG	2.10	0.70
20:S:24:ARG:NH1	20:S:31:THR:OG1	2.25	0.69
1:2:1344:A:N1	1:2:1385:G:O2'	2.23	0.69
9:H:69:LEU:HD22	9:H:96:ALA:HB2	1.73	0.69
5:D:225:GLU:OE1	34:g:187:ASN:ND2	2.24	0.69
31:d:41:GLN:NE2	31:d:42:CYS:SG	2.65	0.69
1:2:1528:G:O2'	1:2:1666:C:OP1	2.11	0.69
32:e:53:LYS:NZ	32:e:59:SER:O	2.25	0.69
1:2:940:U:H3	1:2:1002:U:H3	1.41	0.69
5:D:138:VAL:HG22	5:D:184:ILE:HG22	1.74	0.69
1:2:1143:A:H5'	4:C:190:SER:HB3	1.74	0.69
1:2:1499:U:H4'	5:D:176:LEU:HD11	1.75	0.69
6:E:94:LYS:O	26:Y:16:ARG:NH1	2.26	0.69
21:T:19:ALA:O	21:T:23:LYS:HD3	1.91	0.69
1:2:640:A:H2'	1:2:641:A:C8	2.28	0.69
1:2:64:A:H2	1:2:83:A:H62	1.40	0.68
34:g:256:ILE:HD11	34:g:270:LEU:HD12	1.75	0.68
5:D:27:ARG:HD3	12:K:63:ALA:HB2	1.75	0.68
7:F:59:LYS:HB2	7:F:62:ARG:HE	1.56	0.68
34:g:132:TRP:HD1	34:g:138:CYS:HA	1.58	0.68
30:c:67:ARG:NH1	30:c:68:LEU:O	2.27	0.68
1:2:94:G:HO2'	1:2:508:A:HO2'	1.39	0.68
1:2:1409:A:N6	1:2:1439:A:OP1	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:85:ARG:NH1	19:R:82:ASP:O	2.26	0.68
34:g:20:GLN:NE2	34:g:68:ASP:OD1	2.27	0.68
7:F:143:PRO:HA	7:F:146:ARG:HD3	1.74	0.68
34:g:79:LEU:HD13	34:g:89:LEU:HG	1.74	0.68
1:2:1270:G:H21	1:2:1271:C:H41	1.42	0.68
10:I:11:ARG:NH1	10:I:15:GLY:O	2.27	0.67
1:2:1614:A:H5'	1:2:1615:U:OP2	1.95	0.67
24:W:80:ASP:OD1	24:W:124:LYS:NZ	2.27	0.67
25:X:107:ARG:HG3	25:X:112:VAL:HG22	1.76	0.67
1:2:870:A:H4'	1:2:871:U:H5'	1.76	0.67
7:F:51:HIS:ND1	18:Q:82:TYR:OH	2.23	0.67
18:Q:38:PRO:HG2	18:Q:41:MET:HG3	1.75	0.67
1:2:367:U:H4'	1:2:371:A:C8	2.30	0.67
1:2:1228:A:O2'	1:2:1229:G:N2	2.27	0.67
19:R:26:ASN:HA	19:R:58:MET:HE1	1.75	0.67
1:2:1620:A:O2'	1:2:1624:U:OP2	2.13	0.67
1:2:925:G:H1	1:2:1017:U:H3	1.41	0.67
1:2:1617:G:H22	1:2:1625:U:H3	1.43	0.67
9:H:157:HIS:HB3	9:H:190:PRO:HG3	1.76	0.67
9:H:51:ILE:HG21	9:H:179:LYS:HG2	1.77	0.67
19:R:46:LEU:O	19:R:50:ILE:HG13	1.94	0.67
1:2:1274:G:N2	31:d:7:TYR:OH	2.28	0.67
1:2:1823:A:H2'	1:2:1825:A:H5''	1.77	0.67
34:g:32:LEU:HD22	34:g:40:ILE:HG22	1.77	0.67
5:D:146:ARG:O	5:D:148:LYS:NZ	2.22	0.66
1:2:1758:G:N2	1:2:1779:G:O6	2.29	0.66
29:b:35:VAL:HG11	29:b:63:LEU:HD21	1.76	0.66
1:2:1415:C:N3	1:2:1425:G:N1	2.44	0.66
2:A:69:GLU:HG3	4:C:270:THR:HG21	1.77	0.66
7:F:143:PRO:HD3	30:c:56:LEU:HD22	1.76	0.66
18:Q:117:ARG:HH21	18:Q:121:VAL:HG21	1.59	0.66
1:2:1091:C:O2'	24:W:2:VAL:N	2.28	0.66
3:B:42:ARG:HH12	3:B:233:GLY:H	1.42	0.66
1:2:1446:A:H5''	22:U:58:THR:HG23	1.77	0.66
3:B:126:ASP:OD2	3:B:136:ARG:NH1	2.29	0.66
1:2:1777:G:H2'	1:2:1778:C:O4'	1.94	0.66
5:D:135:GLU:HG3	5:D:153:VAL:HG22	1.77	0.66
7:F:174:ALA:O	7:F:178:ILE:HG12	1.96	0.66
1:2:1864:U:H5'	28:a:79:ILE:HD11	1.76	0.66
22:U:80:PHE:HB3	31:d:52:PHE:HB3	1.78	0.65
22:U:66:ARG:HH22	22:U:75:LYS:HG3	1.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:216:GLU:OE2	34:g:172:LYS:NZ	2.30	0.65
1:2:987:A:OP1	28:a:32:LYS:NZ	2.29	0.65
1:2:1238:U:OP1	1:2:1520:G:N2	2.30	0.65
1:2:1529:C:O2'	21:T:87:VAL:O	2.13	0.65
1:2:1552:G:OP1	5:D:9:ARG:NH2	2.29	0.65
14:M:45:ARG:NH2	14:M:72:HIS:O	2.21	0.65
1:2:1334:G:H2'	1:2:1335:G:H8	1.62	0.65
5:D:55:THR:HA	5:D:58:VAL:HG12	1.77	0.65
5:D:74:GLN:HA	5:D:79:PHE:HB2	1.76	0.65
1:2:1617:G:N2	1:2:1620:A:N7	2.44	0.65
7:F:39:ILE:HG12	7:F:116:ILE:HG21	1.79	0.65
10:I:120:PRO:HG3	10:I:157:LYS:HD2	1.79	0.65
4:C:204:ILE:HB	4:C:211:LYS:HD3	1.78	0.65
1:2:1276:A:H5''	12:K:47:LYS:HE3	1.77	0.64
7:F:55:ARG:NH1	18:Q:123:ASP:OD1	2.29	0.64
1:2:104:A:OP1	10:I:12:ARG:NH1	2.30	0.64
1:2:1260:A:N6	1:2:1617:G:O2'	2.30	0.64
1:2:54:A:OP1	26:Y:111:LYS:NZ	2.29	0.64
1:2:617:G:H4'	25:X:88:ASP:HB3	1.79	0.64
1:2:1261:C:OP1	1:2:1264:C:N4	2.31	0.64
1:2:1276:A:O2'	1:2:1277:C:O4'	2.15	0.64
7:F:140:ASP:O	30:c:47:LYS:N	2.28	0.64
1:2:379:C:O2	10:I:5:ARG:NE	2.29	0.64
5:D:109:LEU:HD21	5:D:115:VAL:HG13	1.78	0.64
27:Z:101:SER:HB2	27:Z:108:ILE:HD12	1.79	0.64
1:2:1643:U:O2'	18:Q:143:LYS:N	2.23	0.64
1:2:1593:C:H41	7:F:91:ARG:HD3	1.61	0.64
1:2:1215:C:O2'	1:2:1645:C:OP2	2.15	0.64
1:2:1391:C:O2'	22:U:83:ARG:NH2	2.31	0.64
1:2:1481:G:H21	31:d:55:LEU:HD22	1.62	0.64
1:2:467:G:H5'	8:G:72:ARG:HH21	1.62	0.63
5:D:172:VAL:O	5:D:173:ARG:NH1	2.24	0.63
14:M:103:VAL:HG12	14:M:104:VAL:HG23	1.81	0.63
18:Q:93:VAL:HG22	18:Q:109:LYS:HE2	1.80	0.63
1:2:928:G:H2'	1:2:929:G:C8	2.33	0.63
1:2:1233:G:N2	1:2:1252:C:O3'	2.31	0.63
7:F:128:ILE:HD13	30:c:45:ASN:HD22	1.63	0.63
8:G:57:ASP:HA	8:G:106:LEU:HA	1.81	0.63
14:M:77:ILE:HD11	14:M:128:PHE:HA	1.81	0.63
17:P:37:TYR:O	17:P:42:ARG:NH2	2.30	0.63
18:Q:111:ILE:O	18:Q:114:GLN:NE2	2.25	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1416:C:H41	1:2:1424:G:H1'	1.62	0.63
5:D:193:ASP:HB3	5:D:199:GLY:H	1.63	0.63
1:2:1302:G:N2	1:2:1306:U:OP2	2.31	0.63
18:Q:19:ALA:HA	18:Q:74:GLY:HA3	1.81	0.63
22:U:33:GLU:OE2	22:U:87:ARG:NH1	2.32	0.63
21:T:29:LYS:HE2	21:T:106:ALA:HA	1.81	0.63
33:f:81:LYS:HD2	33:f:83:LYS:HE3	1.79	0.62
34:g:177:TRP:CD1	34:g:184:LEU:HA	2.34	0.62
1:2:913:A:H1'	9:H:66:VAL:HB	1.80	0.62
1:2:1542:C:OP1	21:T:62:ARG:NH1	2.32	0.62
1:2:1608:U:H2'	1:2:1608:U:O2	1.99	0.62
4:C:146:GLU:HB2	4:C:149:THR:HG22	1.80	0.62
6:E:31:PRO:HG2	6:E:38:LEU:HG	1.80	0.62
1:2:1678:A:H3'	7:F:60:ARG:HH12	1.63	0.62
7:F:28:VAL:HA	7:F:110:GLN:HE22	1.64	0.62
9:H:19:PHE:HZ	9:H:60:ILE:HD12	1.63	0.62
1:2:563:G:HO2'	1:2:564:A:H8	1.47	0.62
1:2:1507:G:O2'	33:f:83:LYS:NZ	2.31	0.62
5:D:157:MET:HE1	5:D:187:LYS:HE3	1.80	0.62
10:I:110:ARG:HG2	10:I:123:ARG:HH21	1.65	0.62
19:R:7:LYS:O	19:R:11:LYS:HB2	2.00	0.62
20:S:24:ARG:HH22	20:S:32:ALA:HB2	1.64	0.62
8:G:35:GLU:OE1	8:G:114:VAL:HG21	2.00	0.62
9:H:181:THR:HG22	9:H:183:LYS:HG3	1.81	0.62
1:2:84:A:N3	1:2:150:A:O2'	2.33	0.62
1:2:1549:U:OP1	31:d:34:TYR:OH	2.15	0.62
7:F:127:ARG:NH2	7:F:133:THR:OG1	2.32	0.62
1:2:857:U:H2'	1:2:858:A:C8	2.35	0.62
5:D:23:GLU:OE1	31:d:46:TYR:OH	2.14	0.62
1:2:376:A:N3	10:I:86:SER:OG	2.30	0.61
1:2:1858:G:OP2	16:O:146:ARG:NH2	2.32	0.61
10:I:119:LEU:HG	10:I:156:ALA:HB1	1.81	0.61
7:F:39:ILE:HD12	7:F:68:ILE:HG21	1.81	0.61
1:2:1256:G:H8	31:d:40:ARG:HD2	1.66	0.61
1:2:1354:G:N2	1:2:1357:A:OP2	2.30	0.61
1:2:1441:U:O2	1:2:1443:C:N4	2.33	0.61
1:2:1643:U:H1'	18:Q:142:GLN:HG3	1.82	0.61
6:E:153:LEU:HD12	8:G:216:ARG:HH21	1.65	0.61
1:2:156:G:OP1	8:G:2:LYS:NZ	2.30	0.61
1:2:907:G:H2'	1:2:908:A:C8	2.36	0.61
8:G:31:ARG:HG2	8:G:101:ILE:HG12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:40:THR:HG21	16:O:74:ALA:HB2	1.81	0.61
1:2:1628:C:H5'	21:T:38:LYS:HG2	1.81	0.61
1:2:1639:G:H2'	1:2:1640:A:C8	2.35	0.61
1:2:1536:G:OP2	27:Z:104:ARG:NH2	2.34	0.61
27:Z:60:LYS:O	27:Z:64:ASN:ND2	2.32	0.61
3:B:152:LYS:HD3	19:R:133:GLY:HA3	1.82	0.61
16:O:31:CYS:HB2	16:O:93:LEU:HD13	1.83	0.61
22:U:20:ILE:HG21	22:U:98:VAL:HG21	1.82	0.61
34:g:145:GLU:O	34:g:175:LYS:NZ	2.33	0.61
1:2:962:A:H5'	16:O:66:ARG:HB3	1.83	0.61
1:2:145:G:H2'	1:2:146:G:C8	2.36	0.61
26:Y:3:ASP:O	26:Y:32:LYS:NZ	2.34	0.61
1:2:943:U:O2'	16:O:135:ILE:O	2.18	0.60
1:2:1289:U:H4'	31:d:2:GLY:HA2	1.83	0.60
1:2:1295:A:N6	1:2:1302:G:OP1	2.33	0.60
34:g:3:GLU:HB2	34:g:247:TRP:HH2	1.66	0.60
1:2:118:C:H1'	1:2:445:A:C5	2.36	0.60
1:2:332:G:O6	8:G:189:ARG:NH2	2.33	0.60
1:2:528:A:H2'	1:2:529:A:H8	1.65	0.60
1:2:1452:A:O2'	1:2:1475:G:N2	2.34	0.60
16:O:113:GLN:OE1	28:a:46:GLU:N	2.34	0.60
20:S:87:GLN:HG3	20:S:88:LYS:H	1.66	0.60
21:T:114:GLU:HB3	21:T:124:THR:HG23	1.82	0.60
13:L:75:GLY:HA3	13:L:88:ILE:HD12	1.83	0.60
1:2:71:G:O2'	1:2:73:C:OP1	2.20	0.60
1:2:1495:G:H21	31:d:41:GLN:HG3	1.67	0.60
5:D:102:ALA:O	5:D:106:ARG:HG2	2.02	0.60
12:K:48:ALA:O	12:K:52:LEU:HD22	2.00	0.60
20:S:98:VAL:HG11	20:S:103:LEU:HD23	1.81	0.60
1:2:73:C:OP2	1:2:74:G:N2	2.34	0.60
1:2:293:C:O2	1:2:293:C:H2'	2.00	0.60
8:G:221:ARG:HD2	8:G:222:GLU:N	2.15	0.60
1:2:297:A:H5'	6:E:132:GLY:HA2	1.84	0.60
8:G:88:ARG:HG3	8:G:91:GLU:HB2	1.83	0.60
30:c:17:VAL:HA	30:c:30:VAL:HG23	1.83	0.60
1:2:1660:C:O2'	1:2:1663:A:N7	2.31	0.60
7:F:77:MET:HE1	7:F:85:LYS:H	1.67	0.60
18:Q:96:TYR:CD1	18:Q:105:LYS:HB2	2.37	0.60
1:2:1572:C:H2'	1:2:1573:G:C8	2.37	0.59
34:g:247:TRP:HE1	34:g:267:VAL:HG11	1.67	0.59
12:K:44:HIS:HA	12:K:47:LYS:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:9:THR:HG23	26:Y:23:MET:HB2	1.84	0.59
1:2:1591:C:H2'	1:2:1592:C:C6	2.38	0.59
20:S:132:ARG:HB2	20:S:134:GLN:HE21	1.66	0.59
1:2:1567:G:HO2'	21:T:98:SER:HG	1.48	0.59
17:P:81:ARG:HH22	17:P:116:LEU:HD13	1.66	0.59
10:I:106:SER:HB3	10:I:171:LEU:HG	1.84	0.59
25:X:41:PHE:O	25:X:76:LYS:NZ	2.31	0.59
30:c:40:ARG:NH2	30:c:61:SER:O	2.35	0.59
4:C:165:VAL:HG21	4:C:217:ALA:HB1	1.83	0.59
7:F:78:MET:O	7:F:82:ASN:ND2	2.24	0.59
9:H:26:ALA:O	9:H:30:LEU:HD22	2.01	0.59
12:K:80:ARG:HD3	12:K:87:PRO:HB3	1.85	0.59
34:g:289:LEU:HD22	34:g:298:LEU:HD11	1.82	0.59
1:2:1342:U:O2'	1:2:1483:A:N1	2.34	0.59
2:A:30:LEU:HD21	2:A:35:GLU:HG2	1.83	0.59
1:2:49:C:N4	1:2:473:A:OP2	2.35	0.59
1:2:1425:G:O2'	1:2:1426:U:OP1	2.21	0.59
7:F:172:CYS:SG	7:F:173:LEU:N	2.75	0.59
9:H:53:VAL:HG11	9:H:172:THR:HG22	1.85	0.59
1:2:1605:G:H2'	1:2:1607:A:H2	1.68	0.58
3:B:136:ARG:HB2	3:B:218:LEU:HD11	1.85	0.58
1:2:1521:C:N4	20:S:137:LYS:O	2.33	0.58
2:A:80:ARG:HH22	2:A:166:LYS:HA	1.67	0.58
7:F:50:PRO:HB3	7:F:69:VAL:HB	1.85	0.58
12:K:51:SER:O	12:K:55:ARG:NH1	2.37	0.58
12:K:77:GLN:HA	12:K:80:ARG:HE	1.68	0.58
34:g:28:PRO:O	34:g:47:ARG:NH2	2.36	0.58
1:2:1298:G:H21	1:2:1299:A:H62	1.50	0.58
21:T:115:LYS:HZ3	21:T:121:ARG:HE	1.52	0.58
36:n:155:ASP:O	36:n:159:VAL:HG23	2.03	0.58
1:2:1314:U:O2'	12:K:1:MET:N	2.35	0.58
5:D:7:LYS:HD2	22:U:25:THR:HG21	1.86	0.58
8:G:50:VAL:HG12	8:G:113:ILE:HA	1.86	0.58
1:2:17:C:O2'	1:2:1194:A:N1	2.35	0.58
1:2:1098:C:H2'	1:2:1099:G:C8	2.38	0.58
5:D:49:ILE:HD11	5:D:89:GLU:HG3	1.85	0.58
6:E:88:ASP:OD1	6:E:122:LYS:NZ	2.37	0.58
17:P:44:ARG:HH21	17:P:83:MET:HB2	1.67	0.58
18:Q:21:ALA:HB2	18:Q:84:ILE:HD12	1.85	0.58
21:T:116:ASP:HB3	21:T:122:LYS:HG3	1.86	0.58
34:g:35:SER:OG	34:g:37:ASP:OD1	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1473:G:N2	1:2:1476:A:OP2	2.34	0.58
10:I:119:LEU:HD11	10:I:152:ARG:HH21	1.68	0.58
1:2:107:A:H2'	1:2:108:G:C8	2.39	0.58
1:2:904:A:N7	1:2:905:C:N4	2.52	0.58
2:A:25:LEU:O	2:A:164:ASN:ND2	2.36	0.58
10:I:57:ALA:HB2	10:I:183:GLY:HA2	1.86	0.58
1:2:1301:A:OP1	17:P:52:LYS:NZ	2.37	0.58
17:P:38:SER:H	17:P:40:ARG:NH1	2.02	0.57
15:N:87:ASP:N	15:N:87:ASP:OD1	2.36	0.57
34:g:256:ILE:HG21	34:g:289:LEU:HD21	1.85	0.57
1:2:877:C:H2'	1:2:878:G:C8	2.39	0.57
1:2:1334:G:H2'	1:2:1335:G:C8	2.38	0.57
2:A:40:LYS:NZ	2:A:41:ARG:O	2.38	0.57
10:I:123:ARG:HB2	10:I:127:ALA:HB3	1.86	0.57
17:P:44:ARG:HH11	17:P:85:ILE:HD12	1.68	0.57
22:U:21:ARG:HB3	22:U:115:THR:HB	1.85	0.57
1:2:1256:G:C8	31:d:40:ARG:HD2	2.39	0.57
1:2:1286:G:O2'	1:2:1315:U:O4	2.22	0.57
1:2:1597:C:OP2	27:Z:82:SER:OG	2.22	0.57
2:A:34:MET:HE3	2:A:154:LEU:HD21	1.85	0.57
5:D:126:ILE:HG21	5:D:134:CYS:HB3	1.85	0.57
22:U:67:LYS:HD3	22:U:76:THR:HB	1.86	0.57
28:a:36:ILE:CD1	28:a:78:VAL:HG11	2.32	0.57
34:g:192:THR:OG1	34:g:213:ASP:OD1	2.20	0.57
1:2:921:G:OP2	29:b:21:LYS:NZ	2.35	0.57
1:2:942:G:H2'	1:2:943:U:C6	2.39	0.57
1:2:1845:A:H2'	1:2:1846:G:C8	2.40	0.57
3:B:28:LYS:HZ3	3:B:50:THR:HG1	1.50	0.57
18:Q:13:PHE:HB3	18:Q:15:ARG:HH21	1.70	0.57
18:Q:108:ILE:O	18:Q:112:LEU:HG	2.04	0.57
3:B:138:PHE:O	3:B:213:ARG:N	2.38	0.57
4:C:60:TRP:O	4:C:71:LYS:NZ	2.26	0.57
21:T:140:ALA:HA	21:T:144:LYS:HB2	1.86	0.57
22:U:23:THR:HA	22:U:88:LEU:HD22	1.87	0.57
5:D:190:LEU:HD23	5:D:199:GLY:HA2	1.87	0.57
10:I:11:ARG:O	13:L:136:LYS:NZ	2.28	0.57
26:Y:105:LYS:O	26:Y:109:GLU:HG3	2.05	0.57
2:A:94:THR:O	2:A:186:ARG:NH2	2.37	0.57
1:2:558:G:H2'	1:2:559:G:C8	2.40	0.57
1:2:919:A:OP2	15:N:64:ARG:NH2	2.35	0.57
1:2:1294:G:C6	1:2:1295:A:H1'	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1820:G:H2'	1:2:1821:U:C6	2.39	0.57
7:F:143:PRO:O	7:F:147:VAL:HG13	2.04	0.57
14:M:18:LEU:HD23	14:M:85:LEU:HD12	1.87	0.57
1:2:952:G:H21	16:O:52:THR:HG21	1.70	0.56
19:R:51:ALA:O	19:R:55:THR:HG23	2.05	0.56
5:D:17:PHE:O	5:D:21:LEU:HG	2.04	0.56
8:G:137:ARG:HB3	8:G:140:ARG:HG3	1.88	0.56
7:F:201:LYS:NZ	7:F:204:ARG:HH12	2.04	0.56
9:H:30:LEU:O	9:H:34:SER:OG	2.18	0.56
14:M:125:GLU:HA	14:M:128:PHE:HB3	1.87	0.56
1:2:1374:C:O2'	1:2:1464:C:O2	2.23	0.56
5:D:17:PHE:CE1	5:D:21:LEU:HD21	2.40	0.56
10:I:110:ARG:HH22	10:I:123:ARG:H	1.54	0.56
10:I:121:LEU:HD11	10:I:125:LYS:H	1.70	0.56
31:d:16:GLN:NE2	31:d:19:ARG:O	2.37	0.56
1:2:996:A:H2'	1:2:997:A:C8	2.40	0.56
16:O:34:PHE:HB3	16:O:41:PHE:HB2	1.86	0.56
1:2:1712:A:H2'	1:2:1713:C:C6	2.41	0.56
12:K:23:ALA:HB3	12:K:67:PHE:HB2	1.88	0.56
22:U:22:ILE:HG23	22:U:112:VAL:HG13	1.87	0.56
1:2:553:U:H2'	1:2:554:A:H4'	1.87	0.56
1:2:1274:G:O2'	12:K:47:LYS:NZ	2.25	0.56
2:A:8:LEU:HD11	23:V:39:VAL:HG11	1.87	0.56
34:g:43:TRP:HZ3	34:g:55:PRO:HG3	1.71	0.56
1:2:1101:U:H2'	1:2:1102:G:C8	2.41	0.56
1:2:1426:U:OP2	18:Q:69:ARG:NH1	2.39	0.56
1:2:544:G:H2'	1:2:545:A:H8	1.71	0.56
1:2:594:A:H61	1:2:643:A:H5''	1.71	0.56
5:D:177:LEU:HG	5:D:179:GLN:H	1.71	0.56
1:2:563:G:N7	11:J:172:ARG:NH2	2.52	0.55
1:2:1219:C:O2'	30:c:26:GLN:OE1	2.22	0.55
6:E:117:GLU:OE2	6:E:117:GLU:N	2.39	0.55
34:g:20:GLN:HG2	34:g:69:VAL:H	1.69	0.55
1:2:5:U:H2'	1:2:6:G:C8	2.41	0.55
1:2:952:G:H2'	1:2:953:C:C6	2.41	0.55
2:A:66:VAL:HG21	2:A:185:MET:HB3	1.88	0.55
5:D:22:ASN:O	5:D:26:THR:OG1	2.20	0.55
1:2:1635:C:O2'	1:2:1638:G:N2	2.40	0.55
31:d:26:ASN:ND2	31:d:39:CYS:SG	2.79	0.55
34:g:46:THR:OG1	34:g:51:ASN:O	2.24	0.55
1:2:1382:A:H2'	1:2:1383:A:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:132:PHE:O	18:Q:140:ARG:NH2	2.40	0.55
29:b:59:CYS:SG	29:b:60:SER:N	2.79	0.55
1:2:448:A:H5''	10:I:25:ARG:HA	1.88	0.55
1:2:588:G:OP2	1:2:588:G:N2	2.30	0.55
11:J:28:GLU:OE2	11:J:44:TRP:NE1	2.27	0.55
32:e:11:LYS:O	32:e:15:GLN:HG2	2.05	0.55
1:2:641:A:O2'	1:2:645:C:OP1	2.25	0.55
5:D:20:GLU:OE2	5:D:76:ARG:NH2	2.39	0.55
9:H:146:VAL:HG12	24:W:42:MET:HE1	1.89	0.55
20:S:46:ARG:HD3	21:T:50:GLU:HA	1.88	0.55
1:2:852:G:O2'	13:L:97:ARG:NH2	2.39	0.55
1:2:1581:C:OP2	1:2:1582:C:N4	2.40	0.55
1:2:1656:G:H2'	1:2:1657:G:H8	1.71	0.55
4:C:142:LYS:HD3	4:C:153:GLY:HA3	1.88	0.55
22:U:26:SER:HB3	22:U:32:LEU:HD13	1.86	0.55
7:F:145:ARG:HE	30:c:48:GLY:HA2	1.70	0.55
34:g:14:HIS:NE2	34:g:35:SER:OG	2.40	0.55
21:T:110:LEU:O	21:T:112:MET:HE2	2.07	0.55
31:d:41:GLN:O	31:d:45:GLN:HG2	2.06	0.55
1:2:128:U:H5'	1:2:129:C:H5	1.71	0.54
1:2:506:G:OP1	26:Y:108:LYS:NZ	2.36	0.54
1:2:1189:A:H2'	1:2:1190:A:C8	2.42	0.54
1:2:1579:A:OP2	5:D:7:LYS:NZ	2.30	0.54
1:2:1717:C:C4	1:2:1718:G:H1'	2.42	0.54
5:D:74:GLN:HE21	5:D:81:GLU:HG3	1.72	0.54
5:D:123:LEU:HD11	5:D:152:PHE:HB3	1.89	0.54
10:I:110:ARG:HH21	10:I:123:ARG:HD3	1.71	0.54
34:g:200:VAL:HG12	34:g:221:LEU:HD21	1.87	0.54
1:2:913:A:H62	9:H:119:SER:HB2	1.72	0.54
1:2:554:A:H5'	1:2:555:A:H4'	1.88	0.54
13:L:103:GLU:OE1	25:X:14:ARG:NH2	2.40	0.54
17:P:59:ARG:HH12	17:P:76:VAL:HG12	1.72	0.54
1:2:123:G:H1	1:2:341:C:H5	1.55	0.54
1:2:1224:G:O2'	1:2:1225:U:O4'	2.26	0.54
1:2:1675:A:H4'	7:F:74:ASN:ND2	2.22	0.54
5:D:68:GLU:HG2	12:K:20:VAL:HG21	1.89	0.54
1:2:1447:G:H2'	1:2:1448:A:C8	2.42	0.54
24:W:30:CYS:HB2	24:W:61:ILE:HG13	1.88	0.54
1:2:562:U:H2'	1:2:563:G:C8	2.42	0.54
1:2:616:A:OP1	25:X:68:LYS:NZ	2.40	0.54
1:2:1139:C:H2'	1:2:1140:G:O4'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:111:VAL:HG12	13:L:140:PHE:HB2	1.89	0.54
18:Q:42:ILE:HG22	18:Q:44:PRO:HD2	1.89	0.54
25:X:140:ARG:O	25:X:142:ARG:NH1	2.39	0.54
1:2:320:G:N2	1:2:330:G:H1	2.06	0.54
1:2:1679:A:C8	7:F:60:ARG:HD3	2.43	0.54
18:Q:132:PHE:HE2	22:U:76:THR:HA	1.73	0.54
5:D:74:GLN:NE2	5:D:81:GLU:HG3	2.23	0.54
1:2:65:C:H4'	8:G:172:LYS:HD3	1.90	0.54
1:2:1310:U:H4'	33:f:143:LYS:HD2	1.90	0.54
1:2:1453:C:H5	1:2:1476:A:H2	1.55	0.54
1:2:1722:G:H1	1:2:1813:A:H5'	1.73	0.54
4:C:199:PRO:HG2	11:J:58:ARG:HD3	1.88	0.54
10:I:34:ALA:HB2	10:I:56:ARG:HE	1.72	0.54
1:2:796:G:H21	9:H:109:ARG:HD3	1.72	0.54
2:A:52:LYS:HG3	19:R:109:LEU:HG	1.90	0.54
2:A:198:MET:HE2	19:R:85:VAL:HG22	1.89	0.54
5:D:190:LEU:HB3	5:D:200:PRO:HD3	1.89	0.54
18:Q:49:TYR:HA	18:Q:52:LEU:HG	1.90	0.54
1:2:809:A:H2'	1:2:810:A:O4'	2.08	0.53
1:2:1183:A:OP2	35:h:18:ARG:NH2	2.35	0.53
5:D:184:ILE:HD12	5:D:186:VAL:HG23	1.89	0.53
1:2:536:A:H62	1:2:546:G:H21	1.56	0.53
18:Q:12:VAL:H	18:Q:90:LYS:HD3	1.72	0.53
1:2:1226:G:HO2'	1:2:1525:C:HO2'	1.57	0.53
1:2:1325:G:H5''	1:2:1326:U:H5'	1.89	0.53
1:2:1607:A:N3	1:2:1633:A:N6	2.57	0.53
1:2:1679:A:N6	7:F:58:ALA:O	2.42	0.53
1:2:1797:U:H2'	1:2:1798:C:C6	2.44	0.53
3:B:47:THR:OG1	3:B:65:ARG:NH1	2.41	0.53
10:I:190:LEU:HD22	10:I:194:GLU:HG2	1.90	0.53
24:W:66:THR:O	24:W:68:ARG:N	2.38	0.53
34:g:7:LEU:HA	34:g:310:TRP:CZ3	2.44	0.53
34:g:237:ASN:ND2	34:g:286:CYS:O	2.42	0.53
1:2:1451:G:H21	1:2:1474:A:H61	1.54	0.53
9:H:134:VAL:HG23	9:H:173:PHE:CE2	2.43	0.53
18:Q:84:ILE:O	18:Q:88:ILE:HG13	2.08	0.53
19:R:63:ARG:O	19:R:63:ARG:NH1	2.41	0.53
1:2:581:U:H4'	26:Y:66:GLY:HA2	1.90	0.53
1:2:814:U:OP1	6:E:22:LYS:NZ	2.42	0.53
1:2:1244:U:H2'	1:2:1244:U:O2	2.07	0.53
1:2:1246:A:H4'	1:2:1491:G:H4'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1554:C:H5'	1:2:1555:U:H5''	1.91	0.53
7:F:195:GLU:HG2	7:F:198:ARG:HE	1.73	0.53
26:Y:10:ARG:NH1	26:Y:26:ASP:OD1	2.41	0.53
1:2:918:U:O2'	24:W:56:HIS:O	2.26	0.53
1:2:1541:G:H22	1:2:1593:C:H4'	1.72	0.53
10:I:3:ILE:O	10:I:30:GLY:N	2.40	0.53
1:2:1798:C:H2'	1:2:1799:G:O4'	2.09	0.53
5:D:204:LEU:HD12	5:D:205:PRO:HD2	1.91	0.53
12:K:60:GLU:HA	12:K:68:TYR:O	2.09	0.53
34:g:67:SER:HB3	34:g:83:TRP:CD1	2.44	0.53
34:g:76:GLN:HB3	34:g:93:THR:HB	1.89	0.53
10:I:107:THR:O	10:I:111:GLN:HG3	2.09	0.53
10:I:110:ARG:HE	10:I:123:ARG:HE	1.57	0.53
18:Q:102:GLU:HA	18:Q:105:LYS:HB3	1.91	0.53
11:J:45:ARG:O	11:J:49:THR:HG22	2.09	0.53
19:R:93:GLN:NE2	19:R:95:ILE:O	2.42	0.53
22:U:41:ARG:O	22:U:45:GLU:N	2.42	0.53
1:2:4:C:H4'	4:C:207:ALA:HB2	1.90	0.53
1:2:900:C:H5''	1:2:901:G:N7	2.24	0.53
1:2:1321:G:H2'	1:2:1322:G:C8	2.44	0.53
3:B:46:LYS:HE3	16:O:21:VAL:HG11	1.90	0.53
5:D:65:ARG:O	5:D:69:LEU:N	2.39	0.53
6:E:151:ASP:HB3	6:E:154:ILE:HG13	1.91	0.53
18:Q:23:ALA:H	18:Q:90:LYS:HZ1	1.57	0.53
1:2:65:C:C2	8:G:133:LEU:HD22	2.44	0.52
6:E:100:ARG:NH1	6:E:118:GLU:OE2	2.41	0.52
28:a:78:VAL:HG13	28:a:84:VAL:HG22	1.92	0.52
34:g:156:PHE:CZ	34:g:163:PRO:HB3	2.44	0.52
1:2:5:U:H2'	1:2:6:G:H8	1.74	0.52
1:2:1295:A:H3'	1:2:1296:U:H5'	1.90	0.52
1:2:1586:U:O2'	1:2:1588:A:N7	2.42	0.52
1:2:1647:A:OP1	18:Q:138:ARG:NH1	2.41	0.52
10:I:117:TYR:CG	10:I:118:ALA:N	2.77	0.52
16:O:145:GLY:O	28:a:22:ARG:NH2	2.41	0.52
18:Q:32:ILE:HB	18:Q:39:LEU:HD22	1.91	0.52
18:Q:112:LEU:HD13	18:Q:120:LEU:HD21	1.91	0.52
19:R:18:GLU:HG3	19:R:69:ILE:HG23	1.91	0.52
21:T:9:VAL:HG21	21:T:138:VAL:HB	1.92	0.52
34:g:132:TRP:CD1	34:g:138:CYS:HA	2.41	0.52
1:2:874:G:H2'	1:2:875:A:C8	2.41	0.52
1:2:1010:G:H2'	1:2:1011:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1499:U:H4'	5:D:176:LEU:CD1	2.39	0.52
7:F:72:LEU:HA	7:F:151:ILE:HD11	1.90	0.52
21:T:111:LYS:O	21:T:124:THR:OG1	2.27	0.52
27:Z:58:LEU:HD12	27:Z:77:LEU:HD22	1.91	0.52
1:2:17:C:H2'	1:2:18:C:C6	2.44	0.52
1:2:115:U:H2'	1:2:116:U:C6	2.45	0.52
1:2:820:U:P	11:J:79:ARG:HH22	2.33	0.52
1:2:871:U:H3'	1:2:872:A:H4'	1.91	0.52
1:2:1590:C:O2'	7:F:85:LYS:NZ	2.42	0.52
4:C:183:LYS:HA	4:C:195:LEU:O	2.10	0.52
7:F:69:VAL:O	7:F:73:THR:HG22	2.08	0.52
1:2:15:U:H2'	1:2:16:G:O4'	2.08	0.52
1:2:608:C:OP1	32:e:59:SER:OG	2.25	0.52
1:2:1465:A:H4'	19:R:10:LYS:HZ1	1.75	0.52
4:C:203:GLY:H	4:C:221:ASP:HB3	1.74	0.52
4:C:254:ASP:OD1	4:C:254:ASP:N	2.38	0.52
5:D:35:SER:O	5:D:99:ILE:HD11	2.09	0.52
8:G:49:VAL:CG1	8:G:115:LYS:HB3	2.40	0.52
1:2:429:C:O2'	1:2:811:A:N1	2.42	0.52
1:2:1618:C:H2'	1:2:1619:A:H5'	1.92	0.52
4:C:72:ASP:HB2	4:C:272:HIS:HE1	1.73	0.52
9:H:88:SER:OG	9:H:89:GLY:N	2.42	0.52
34:g:110:SER:HB2	34:g:153:CYS:HA	1.91	0.52
1:2:1452:A:H4'	1:2:1453:C:O5'	2.10	0.52
1:2:1563:G:OP1	21:T:121:ARG:NH2	2.43	0.52
17:P:113:GLY:O	17:P:114:HIS:ND1	2.42	0.52
1:2:528:A:H2'	1:2:529:A:C8	2.44	0.52
1:2:1277:C:H4'	12:K:55:ARG:NH1	2.25	0.52
1:2:1447:G:H2'	1:2:1448:A:H8	1.75	0.52
1:2:1447:G:OP1	22:U:87:ARG:NH2	2.41	0.52
9:H:170:VAL:HG13	9:H:187:PHE:HB2	1.92	0.52
16:O:75:MET:O	16:O:79:GLN:HG3	2.10	0.52
29:b:62:VAL:HG11	29:b:65:GLN:HE21	1.75	0.52
34:g:114:SER:OG	34:g:118:ARG:N	2.31	0.52
1:2:1496:U:H5'	31:d:26:ASN:HB3	1.91	0.52
1:2:1656:G:N2	1:2:1668:U:O2	2.33	0.52
7:F:122:ARG:NH1	7:F:123:GLU:HG2	2.25	0.52
19:R:30:THR:O	19:R:34:VAL:HG12	2.09	0.52
25:X:101:LEU:HB3	25:X:124:LYS:HB2	1.91	0.52
1:2:28:U:H2'	1:2:29:G:H8	1.75	0.51
1:2:1144:A:H2'	1:2:1145:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1326:U:O4	31:d:28:HIS:ND1	2.43	0.51
1:2:1495:G:H2'	1:2:1496:U:C6	2.45	0.51
14:M:12:MET:HE1	14:M:120:ALA:HB2	1.91	0.51
34:g:76:GLN:O	34:g:92:LEU:N	2.44	0.51
1:2:320:G:H22	1:2:330:G:H22	1.58	0.51
1:2:1216:C:O2'	18:Q:143:LYS:HD2	2.09	0.51
1:2:1220:A:H2'	1:2:1221:G:O4'	2.09	0.51
1:2:1228:A:N1	1:2:1230:C:N4	2.59	0.51
17:P:86:LEU:HG	17:P:88:GLU:H	1.75	0.51
28:a:33:ASP:OD1	28:a:33:ASP:N	2.40	0.51
1:2:639:C:HO2'	1:2:640:A:H8	1.58	0.51
1:2:913:A:N6	9:H:119:SER:HB2	2.25	0.51
6:E:19:MET:SD	6:E:108:ARG:HD2	2.51	0.51
25:X:84:PHE:CE2	25:X:86:PRO:HA	2.44	0.51
1:2:1289:U:O5'	31:d:2:GLY:N	2.43	0.51
1:2:1720:U:H2'	1:2:1721:U:H4'	1.91	0.51
7:F:149:GLN:O	7:F:153:LEU:HG	2.10	0.51
9:H:36:LEU:HD22	9:H:75:ILE:HD12	1.92	0.51
10:I:83:TYR:HB3	10:I:101:ILE:HB	1.91	0.51
15:N:64:ARG:HD3	15:N:70:LYS:HG2	1.91	0.51
1:2:656:G:H5'	1:2:662:G:N2	2.25	0.51
1:2:929:G:H2'	1:2:930:C:O4'	2.11	0.51
1:2:1013:U:OP1	1:2:1129:G:O2'	2.29	0.51
1:2:1509:U:H5'	33:f:78:LYS:HB2	1.91	0.51
1:2:643:A:OP1	11:J:39:ASN:ND2	2.44	0.51
1:2:989:C:OP2	3:B:155:TYR:OH	2.18	0.51
7:F:201:LYS:HZ3	7:F:204:ARG:HH12	1.58	0.51
20:S:109:GLU:O	20:S:113:ARG:NH2	2.33	0.51
20:S:114:LEU:HB3	20:S:119:ALA:HB3	1.93	0.51
1:2:851:C:H5''	1:2:852:G:H5'	1.91	0.51
12:K:43:LEU:O	12:K:46:MET:HG2	2.10	0.51
1:2:1512:C:H5''	12:K:28:HIS:CE1	2.45	0.51
6:E:20:LEU:HD21	6:E:46:ILE:HD12	1.92	0.51
16:O:96:LYS:HG2	16:O:132:VAL:HG11	1.93	0.51
34:g:76:GLN:HA	34:g:92:LEU:HB2	1.93	0.51
1:2:639:C:O2'	1:2:640:A:H8	1.93	0.51
1:2:1222:G:N3	1:2:1222:G:H2'	2.26	0.51
1:2:1648:G:H22	1:2:1674:G:H3'	1.76	0.51
14:M:60:MET:HE2	33:f:107:LYS:HG2	1.93	0.51
21:T:35:ASP:OD1	21:T:35:ASP:N	2.44	0.51
34:g:254:PRO:HB2	34:g:283:PRO:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:10:MET:HE3	35:h:10:MET:O	2.10	0.51
1:2:1395:C:H42	1:2:1450:G:H1	1.58	0.50
6:E:114:ILE:HD12	6:E:118:GLU:HG2	1.93	0.50
7:F:88:MET:N	7:F:88:MET:HE3	2.25	0.50
21:T:7:LYS:HE3	21:T:65:TYR:HE2	1.76	0.50
1:2:30:C:O2'	1:2:596:U:OP1	2.29	0.50
1:2:1610:G:N2	20:S:85:ASN:O	2.39	0.50
3:B:192:SER:HA	3:B:195:LYS:HE2	1.93	0.50
9:H:147:LYS:HA	24:W:49:GLU:OE1	2.10	0.50
34:g:249:CYS:HB2	34:g:289:LEU:HD13	1.93	0.50
1:2:441:C:H2'	1:2:442:C:C6	2.46	0.50
1:2:559:G:O3'	11:J:177:ASN:ND2	2.43	0.50
1:2:1614:A:H2'	1:2:1615:U:C5	2.46	0.50
1:2:1259:A:O2'	1:2:1261:C:OP2	2.20	0.50
1:2:1658:G:OP2	1:2:1660:C:N4	2.45	0.50
5:D:167:TYR:OH	5:D:202:LYS:O	2.24	0.50
7:F:68:ILE:O	7:F:72:LEU:HD23	2.11	0.50
8:G:2:LYS:HB2	8:G:108:VAL:HG23	1.93	0.50
1:2:1024:A:OP2	15:N:124:ARG:NH2	2.44	0.50
1:2:1388:A:O2'	19:R:46:LEU:HD13	2.12	0.50
1:2:1405:A:H2	1:2:1443:C:H41	1.58	0.50
1:2:1440:C:O2'	1:2:1441:U:O5'	2.26	0.50
1:2:1845:A:H2'	1:2:1846:G:H8	1.75	0.50
8:G:136:LYS:NZ	8:G:175:LYS:O	2.33	0.50
1:2:64:A:OP1	8:G:177:GLN:NE2	2.45	0.50
1:2:1114:U:H3	1:2:1119:A:H62	1.58	0.50
1:2:1406:G:N2	1:2:1407:U:O4	2.45	0.50
7:F:195:GLU:HA	7:F:198:ARG:HG2	1.93	0.50
1:2:1642:U:O2'	18:Q:145:TYR:OH	2.28	0.50
1:2:1844:U:P	35:h:11:ARG:HH22	2.34	0.50
18:Q:28:GLY:N	18:Q:65:GLY:O	2.44	0.50
18:Q:73:LYS:HD3	18:Q:74:GLY:H	1.77	0.50
34:g:66:VAL:HA	34:g:82:SER:HA	1.94	0.50
34:g:173:LEU:HD13	34:g:187:ASN:OD1	2.12	0.50
1:2:985:G:H4'	16:O:138:ASP:OD2	2.12	0.50
1:2:1330:G:H4'	1:2:1331:C:H5'	1.93	0.50
1:2:1331:C:O2	1:2:1489:A:N6	2.45	0.50
4:C:191:VAL:HG11	4:C:236:PHE:HA	1.94	0.50
7:F:90:VAL:HA	7:F:93:VAL:HG22	1.94	0.50
34:g:161:SER:OG	34:g:162:ASN:N	2.45	0.50
1:2:554:A:H2'	1:2:556:U:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1234:C:N4	1:2:1526:G:O6	2.45	0.50
1:2:1298:G:H2'	1:2:1301:A:H62	1.77	0.50
9:H:9:VAL:HG22	9:H:11:PRO:HD3	1.93	0.50
1:2:964:A:H2'	1:2:965:U:H6	1.77	0.49
1:2:1495:G:O5'	1:2:1495:G:H8	1.93	0.49
1:2:1617:G:N7	17:P:43:ARG:NH2	2.58	0.49
10:I:69:SER:OG	10:I:191:GLU:OE2	2.24	0.49
23:V:58:ALA:O	23:V:62:MET:HG2	2.11	0.49
1:2:57:U:OP1	1:2:504:G:O2'	2.28	0.49
1:2:942:G:H21	16:O:137:SER:HB2	1.77	0.49
1:2:1315:U:H2'	33:f:92:LYS:HE3	1.94	0.49
2:A:5:LEU:HD12	2:A:8:LEU:HD12	1.94	0.49
10:I:46:VAL:HG21	10:I:56:ARG:HH11	1.77	0.49
10:I:168:GLN:OE1	10:I:168:GLN:HA	2.12	0.49
14:M:47:ALA:HB2	14:M:109:VAL:H	1.77	0.49
17:P:81:ARG:NH2	17:P:116:LEU:HB3	2.27	0.49
18:Q:41:MET:SD	21:T:143:LYS:NZ	2.85	0.49
19:R:37:GLU:OE2	34:g:150:TRP:NE1	2.45	0.49
21:T:94:ARG:NH1	21:T:95:GLY:O	2.45	0.49
1:2:1262:C:N3	31:d:15:GLY:HA3	2.26	0.49
1:2:1650:A:H1'	1:2:1675:A:H61	1.78	0.49
3:B:123:ALA:HB2	3:B:165:ARG:HG3	1.95	0.49
5:D:29:LEU:HD13	5:D:58:VAL:HG23	1.93	0.49
6:E:204:SER:OG	6:E:205:PHE:N	2.45	0.49
7:F:121:PRO:HA	7:F:193:LYS:HE2	1.94	0.49
10:I:141:ARG:HD3	10:I:145:ILE:HG22	1.94	0.49
13:L:23:VAL:HG22	13:L:24:LEU:H	1.76	0.49
34:g:114:SER:HA	34:g:156:PHE:CD2	2.47	0.49
34:g:126:ASP:O	34:g:128:THR:HG23	2.12	0.49
1:2:1537:A:N3	1:2:1604:G:H5'	2.28	0.49
5:D:120:TYR:O	5:D:124:ARG:HG2	2.12	0.49
5:D:132:LYS:HE3	5:D:191:PRO:HB3	1.94	0.49
17:P:40:ARG:HD3	17:P:40:ARG:H	1.78	0.49
31:d:30:LEU:HD21	31:d:37:ASN:HA	1.93	0.49
1:2:1729:U:H3	1:2:1803:U:H3	1.59	0.49
12:K:23:ALA:HB2	12:K:69:TRP:HE1	1.77	0.49
12:K:48:ALA:O	12:K:51:SER:OG	2.26	0.49
20:S:46:ARG:NH2	21:T:35:ASP:HB3	2.27	0.49
34:g:274:VAL:HG23	34:g:284:PRO:HD3	1.94	0.49
1:2:634:A:H2'	1:2:635:G:H8	1.78	0.49
1:2:1084:A:OP1	1:2:1858:G:O2'	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1101:U:H2'	1:2:1102:G:H8	1.77	0.49
1:2:1388:A:H61	5:D:161:GLY:HA2	1.77	0.49
4:C:270:THR:O	4:C:274:VAL:HG23	2.13	0.49
28:a:75:VAL:O	28:a:78:VAL:HG12	2.12	0.49
7:F:17:ILE:HA	7:F:48:TYR:HE1	1.78	0.49
21:T:134:ILE:O	21:T:138:VAL:HG22	2.12	0.49
2:A:12:GLU:OE1	2:A:12:GLU:N	2.45	0.49
4:C:236:PHE:O	4:C:240:THR:HG22	2.12	0.49
35:h:2:ARG:HB3	35:h:5:TRP:CD1	2.48	0.49
1:2:634:A:H2'	1:2:635:G:C8	2.48	0.49
1:2:1174:U:H2'	1:2:1175:G:C8	2.48	0.49
1:2:1457:U:H2'	1:2:1458:G:H8	1.77	0.49
7:F:122:ARG:HH21	30:c:58:LEU:HB3	1.78	0.49
34:g:114:SER:HA	34:g:156:PHE:CE2	2.48	0.49
1:2:385:G:H3'	13:L:136:LYS:HB2	1.95	0.49
1:2:1567:G:O2'	21:T:98:SER:OG	2.16	0.49
12:K:51:SER:O	12:K:55:ARG:HG2	2.12	0.49
18:Q:100:VAL:HG22	18:Q:101:ASP:H	1.77	0.49
28:a:32:LYS:O	28:a:37:LYS:NZ	2.34	0.49
34:g:130:LYS:HE2	34:g:141:THR:HG23	1.94	0.49
1:2:321:C:H41	1:2:330:G:N2	2.10	0.48
1:2:1536:G:N7	27:Z:104:ARG:NH1	2.60	0.48
1:2:1733:U:H2'	1:2:1734:G:O4'	2.13	0.48
4:C:66:LEU:HD21	4:C:81:ILE:HD13	1.95	0.48
16:O:56:VAL:HG21	16:O:80:ASP:HB3	1.95	0.48
23:V:64:GLU:O	23:V:68:SER:OG	2.20	0.48
1:2:154:U:O4'	8:G:13:GLN:HG3	2.12	0.48
1:2:434:G:OP1	10:I:23:LYS:HG2	2.13	0.48
1:2:1010:G:H2'	1:2:1011:A:H8	1.76	0.48
5:D:156:LEU:HD12	5:D:189:MET:HE1	1.94	0.48
10:I:110:ARG:NH2	10:I:123:ARG:H	2.10	0.48
20:S:23:ARG:HH22	27:Z:80:ARG:NH2	2.12	0.48
34:g:156:PHE:CE1	34:g:165:ILE:HG22	2.43	0.48
1:2:455:A:H2'	1:2:456:C:C6	2.48	0.48
1:2:1224:G:O2'	1:2:1225:U:O5'	2.28	0.48
1:2:1864:U:H1'	28:a:36:ILE:HD11	1.96	0.48
4:C:105:GLU:HB3	4:C:216:MET:HE1	1.95	0.48
10:I:165:GLN:HE22	10:I:172:LEU:HG	1.77	0.48
17:P:25:LEU:HD13	17:P:33:LEU:HD21	1.95	0.48
20:S:46:ARG:CD	21:T:50:GLU:HG3	2.43	0.48
1:2:1324:G:H22	1:2:1504:U:H2'	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:31:PRO:HG3	21:T:102:ARG:HE	1.78	0.48
34:g:21:ILE:HG22	34:g:33:SER:HB2	1.95	0.48
1:2:1597:C:H3'	1:2:1598:G:C8	2.48	0.48
1:2:1653:U:H2'	1:2:1654:G:C8	2.49	0.48
2:A:188:THR:O	2:A:189:ILE:HG12	2.14	0.48
10:I:41:ARG:HD3	10:I:43:ILE:HD12	1.96	0.48
25:X:68:LYS:HG2	25:X:91:LEU:HD22	1.94	0.48
1:2:126:G:H5''	8:G:195:LYS:HG2	1.96	0.48
1:2:341:C:H2'	1:2:342:C:C6	2.49	0.48
1:2:1174:U:H2'	1:2:1175:G:H8	1.79	0.48
1:2:1189:A:H2'	1:2:1190:A:H8	1.79	0.48
1:2:1227:G:H2'	1:2:1228:A:H5''	1.95	0.48
1:2:1754:G:N3	1:2:1780:G:O2'	2.38	0.48
16:O:67:ASP:O	16:O:70:SER:OG	2.26	0.48
1:2:341:C:H2'	1:2:342:C:H6	1.78	0.48
1:2:1522:A:H4'	20:S:144:ARG:HG3	1.95	0.48
1:2:1539:U:H5'	21:T:43:LYS:NZ	2.28	0.48
2:A:66:VAL:HG22	2:A:186:ARG:HG2	1.95	0.48
5:D:157:MET:HA	5:D:189:MET:SD	2.53	0.48
5:D:205:PRO:HA	19:R:42:PRO:HG2	1.96	0.48
7:F:122:ARG:HE	30:c:58:LEU:HA	1.79	0.48
7:F:164:ARG:HH11	7:F:164:ARG:HB3	1.78	0.48
27:Z:88:LEU:HD23	27:Z:91:LEU:HD21	1.94	0.48
1:2:604:A:H2'	1:2:605:A:C8	2.49	0.48
1:2:935:G:O2'	15:N:108:ASP:OD1	2.30	0.48
1:2:1688:C:H5''	1:2:1689:C:OP1	2.14	0.48
8:G:124:LEU:HD23	8:G:125:THR:HG23	1.95	0.48
19:R:41:ILE:HG23	19:R:46:LEU:HD23	1.95	0.48
34:g:168:CYS:HB2	34:g:195:LEU:HB2	1.94	0.48
1:2:145:G:O6	8:G:178:ARG:NH2	2.46	0.48
1:2:529:A:H2'	1:2:530:U:C6	2.48	0.48
2:A:207:PRO:HA	2:A:210:ILE:HD12	1.95	0.48
18:Q:112:LEU:HB2	18:Q:119:LEU:HD12	1.96	0.48
34:g:88:ARG:HH21	34:g:100:ARG:HD2	1.78	0.48
1:2:1520:G:H22	17:P:126:VAL:HG12	1.78	0.47
1:2:1545:A:H2	1:2:1671:G:N3	2.12	0.47
22:U:91:LEU:HD11	22:U:98:VAL:HG22	1.95	0.47
26:Y:42:GLU:N	26:Y:42:GLU:OE1	2.47	0.47
1:2:220:U:H2'	1:2:221:A:H8	1.79	0.47
1:2:296:U:O2'	6:E:131:VAL:O	2.31	0.47
1:2:1290:G:H5'	1:2:1291:A:N7	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:218:LEU:HD22	34:g:192:THR:HA	1.97	0.47
7:F:47:LYS:NZ	7:F:52:SER:HB3	2.29	0.47
10:I:48:VAL:HG11	10:I:54:LYS:HD2	1.95	0.47
20:S:25:LYS:O	20:S:29:ALA:N	2.48	0.47
25:X:48:LYS:HD3	25:X:99:GLU:OE2	2.14	0.47
32:e:12:VAL:O	32:e:16:THR:OG1	2.24	0.47
1:2:65:C:N3	8:G:133:LEU:HD22	2.30	0.47
1:2:568:C:H2'	1:2:569:A:C8	2.49	0.47
8:G:7:PHE:HD2	8:G:10:THR:HG22	1.77	0.47
1:2:67:C:C5	8:G:162:LEU:HB3	2.49	0.47
1:2:986:G:C8	16:O:137:SER:O	2.67	0.47
1:2:1733:U:H3	1:2:1801:A:H62	1.62	0.47
1:2:1756:C:H42	1:2:1773:C:H42	1.61	0.47
3:B:136:ARG:HB3	3:B:216:LYS:HG3	1.95	0.47
7:F:78:MET:HE3	7:F:78:MET:N	2.30	0.47
8:G:50:VAL:HG12	8:G:113:ILE:HG12	1.96	0.47
8:G:213:LEU:O	8:G:217:MET:HG3	2.14	0.47
11:J:66:LYS:HD2	11:J:66:LYS:HA	1.57	0.47
34:g:11:LEU:O	34:g:306:LEU:HB2	2.15	0.47
34:g:257:LYS:HD2	34:g:259:TRP:HZ2	1.79	0.47
1:2:294:U:OP1	13:L:36:TYR:OH	2.28	0.47
1:2:902:G:H2'	1:2:903:A:C8	2.49	0.47
1:2:1153:C:OP2	24:W:71:LYS:NZ	2.33	0.47
2:A:191:ARG:NH2	23:V:44:GLY:O	2.44	0.47
3:B:36:PRO:HB2	3:B:38:MET:SD	2.55	0.47
7:F:164:ARG:HB3	7:F:164:ARG:NH1	2.29	0.47
34:g:11:LEU:HB2	34:g:52:TYR:HD2	1.78	0.47
34:g:107:ASP:OD1	34:g:109:LEU:HD22	2.14	0.47
1:2:293:C:O2'	1:2:294:U:H3'	2.15	0.47
1:2:1453:C:C5	1:2:1476:A:H2	2.31	0.47
3:B:28:LYS:NZ	3:B:50:THR:OG1	2.38	0.47
3:B:120:MET:HB2	3:B:142:PHE:CE2	2.50	0.47
3:B:124:HIS:HA	3:B:137:LEU:O	2.14	0.47
4:C:130:ILE:HD13	4:C:159:LYS:HG3	1.95	0.47
4:C:173:LYS:O	23:V:3:ASN:HB2	2.14	0.47
18:Q:50:LYS:HZ3	18:Q:53:GLU:CD	2.22	0.47
19:R:77:GLU:O	19:R:80:ARG:HG3	2.15	0.47
1:2:804:U:H2'	1:2:805:U:C6	2.49	0.47
1:2:1025:U:H2'	1:2:1026:C:O4'	2.15	0.47
1:2:1521:C:OP2	20:S:136:THR:OG1	2.26	0.47
4:C:169:TYR:OH	4:C:175:GLY:O	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:135:GLU:O	10:I:139:LYS:HG2	2.14	0.47
19:R:14:ARG:HG2	19:R:69:ILE:HD11	1.97	0.47
25:X:24:ASP:HB3	25:X:27:TYR:HB3	1.97	0.47
1:2:527:C:H2'	1:2:528:A:C8	2.50	0.47
1:2:913:A:H2	9:H:99:ARG:H	1.62	0.47
1:2:1611:G:O2'	20:S:87:GLN:HB3	2.15	0.47
6:E:87:MET:HE1	6:E:236:ILE:HG21	1.97	0.47
19:R:44:LYS:O	19:R:47:ARG:HG3	2.15	0.47
1:2:16:G:H2'	1:2:17:C:C6	2.50	0.47
1:2:332:G:H4'	1:2:333:G:OP1	2.15	0.47
1:2:1609:C:N4	1:2:1610:G:O6	2.48	0.47
1:2:1814:G:O2'	1:2:1815:A:O5'	2.32	0.47
17:P:52:LYS:HZ1	31:d:6:LEU:HD11	1.80	0.47
20:S:39:ARG:NH1	21:T:38:LYS:HA	2.30	0.47
26:Y:10:ARG:HG2	26:Y:11:LYS:HG2	1.96	0.47
1:2:29:G:H2'	1:2:30:C:C6	2.50	0.47
5:D:113:LEU:HD21	5:D:117:ARG:HD2	1.97	0.47
6:E:97:GLU:OE1	6:E:113:ARG:NH1	2.42	0.47
6:E:107:GLY:HA2	6:E:189:LEU:HG	1.97	0.47
1:2:121:U:H2'	1:2:122:G:C8	2.51	0.46
1:2:443:U:H2'	1:2:444:G:O4'	2.15	0.46
1:2:1233:G:OP2	1:2:1233:G:H8	1.98	0.46
1:2:1480:A:H2'	1:2:1481:G:C8	2.49	0.46
19:R:57:LEU:O	19:R:61:ILE:HG12	2.14	0.46
20:S:36:VAL:HA	20:S:40:TYR:HD2	1.80	0.46
20:S:39:ARG:HB2	21:T:46:ALA:HB2	1.96	0.46
21:T:4:VAL:HG21	21:T:136:GLY:HA2	1.96	0.46
25:X:71:ARG:HH21	25:X:80:LYS:HB2	1.80	0.46
33:f:123:SER:HB3	33:f:144:CYS:SG	2.55	0.46
1:2:1119:A:H2'	1:2:1120:U:O4'	2.15	0.46
1:2:1201:U:H2'	1:2:1202:U:C6	2.50	0.46
1:2:1706:G:N7	1:2:1825:A:N6	2.63	0.46
5:D:166:TYR:OH	5:D:202:LYS:NZ	2.36	0.46
7:F:26:ASP:OD1	7:F:42:LYS:NZ	2.34	0.46
19:R:59:LYS:O	19:R:62:GLN:HG2	2.15	0.46
34:g:196:ASN:OD1	34:g:197:THR:N	2.48	0.46
34:g:228:TYR:CE2	34:g:264:LYS:HG3	2.51	0.46
1:2:223:C:H2'	1:2:224:A:C8	2.50	0.46
1:2:1324:G:H21	33:f:78:LYS:HE2	1.80	0.46
1:2:1600:G:H5'	27:Z:43:LYS:N	2.30	0.46
2:A:145:ILE:HG12	2:A:159:ILE:HB	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:79:HIS:O	7:F:81:ARG:N	2.49	0.46
34:g:17:TRP:CD2	34:g:303:THR:HB	2.49	0.46
34:g:197:THR:HG21	34:g:238:ALA:HA	1.98	0.46
1:2:1218:C:H2'	1:2:1219:C:C6	2.49	0.46
1:2:1531:A:H2'	1:2:1532:C:C6	2.50	0.46
1:2:1601:A:H4'	1:2:1602:U:C5	2.50	0.46
1:2:1605:G:H21	1:2:1634:A:H62	1.63	0.46
5:D:98:ALA:N	5:D:169:ASP:OD2	2.48	0.46
17:P:59:ARG:HH22	17:P:76:VAL:HG12	1.81	0.46
34:g:185:LYS:NZ	34:g:221:LEU:O	2.47	0.46
1:2:212:C:H2'	1:2:213:G:C8	2.50	0.46
1:2:1325:G:O2'	1:2:1327:G:N7	2.42	0.46
7:F:197:GLU:O	7:F:201:LYS:HG2	2.16	0.46
13:L:55:TYR:OH	13:L:116:CYS:HB3	2.15	0.46
1:2:1235:G:H1'	1:2:1236:G:C2	2.50	0.46
1:2:1334:G:O3'	5:D:183:GLY:HA3	2.14	0.46
2:A:205:ARG:HG3	2:A:210:ILE:CG1	2.46	0.46
2:A:205:ARG:HG3	2:A:210:ILE:HG12	1.98	0.46
5:D:6:SER:OG	5:D:9:ARG:NH1	2.49	0.46
31:d:3:HIS:HA	31:d:6:LEU:HB2	1.97	0.46
34:g:158:PRO:HD2	34:g:202:PRO:HA	1.98	0.46
1:2:103:A:OP2	1:2:356:C:N4	2.49	0.46
1:2:848:U:H2'	1:2:849:A:H8	1.81	0.46
1:2:1299:A:H61	17:P:52:LYS:HG3	1.80	0.46
1:2:1365:G:H2'	1:2:1366:G:C8	2.51	0.46
1:2:1569:A:OP1	21:T:94:ARG:NH2	2.48	0.46
1:2:1656:G:C6	1:2:1669:G:C6	3.04	0.46
5:D:141:LYS:HB2	5:D:141:LYS:HE2	1.69	0.46
7:F:130:ARG:HH22	30:c:21:THR:HG22	1.80	0.46
11:J:176:LYS:HD2	11:J:179:LYS:HE2	1.98	0.46
16:O:142:ARG:HG3	16:O:143:LYS:N	2.30	0.46
1:2:383:G:O2'	13:L:133:PRO:O	2.28	0.46
1:2:883:U:O4	1:2:903:A:N6	2.49	0.46
1:2:1567:G:N3	21:T:37:VAL:HG12	2.31	0.46
7:F:87:LEU:O	7:F:91:ARG:HG3	2.15	0.46
7:F:107:ASN:HD22	7:F:108:PRO:HD2	1.79	0.46
10:I:113:TYR:CE1	10:I:119:LEU:HD22	2.51	0.46
11:J:33:GLY:HA3	32:e:38:TYR:CG	2.50	0.46
12:K:52:LEU:HA	12:K:55:ARG:HG2	1.97	0.46
13:L:37:TYR:CE2	13:L:51:ILE:HG23	2.51	0.46
20:S:41:ALA:HA	20:S:44:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:70:G:OP2	8:G:167:LYS:HE3	2.16	0.46
1:2:615:C:O2	32:e:11:LYS:NZ	2.35	0.46
1:2:1139:C:H5	1:2:1149:A:H62	1.61	0.46
1:2:1302:G:H4'	1:2:1303:C:H5	1.81	0.46
1:2:1613:G:C5	1:2:1614:A:H1'	2.51	0.46
7:F:87:LEU:O	7:F:90:VAL:HG12	2.15	0.46
7:F:187:SER:HB3	7:F:190:ILE:HG12	1.98	0.46
20:S:114:LEU:HB2	20:S:122:GLY:HA3	1.97	0.46
24:W:30:CYS:SG	24:W:31:SER:N	2.89	0.46
1:2:220:U:H2'	1:2:221:A:C8	2.51	0.46
1:2:1269:G:H1'	17:P:97:TYR:OH	2.15	0.46
1:2:1380:C:H2'	1:2:1381:G:O4'	2.16	0.46
1:2:1390:U:H2'	1:2:1391:C:C6	2.51	0.46
3:B:106:THR:HB	16:O:130:GLU:OE1	2.16	0.46
7:F:145:ARG:NH2	30:c:49:PRO:HD3	2.30	0.46
21:T:111:LYS:HG3	21:T:126:GLN:HB3	1.98	0.46
34:g:70:VAL:HG23	34:g:79:LEU:HB3	1.98	0.46
34:g:127:LYS:HB2	34:g:147:HIS:O	2.15	0.46
1:2:311:C:H5''	1:2:312:G:H5''	1.99	0.45
1:2:1571:G:O2'	1:2:1572:C:OP1	2.28	0.45
1:2:1673:U:H2'	1:2:1674:G:O4'	2.16	0.45
10:I:162:LEU:HD11	10:I:191:GLU:HG2	1.98	0.45
12:K:55:ARG:HB3	12:K:57:TYR:CE2	2.51	0.45
26:Y:38:THR:O	26:Y:42:GLU:OE1	2.35	0.45
1:2:945:U:H2'	1:2:946:U:C6	2.51	0.45
1:2:1146:C:O2'	1:2:1150:A:N1	2.43	0.45
1:2:1617:G:N2	1:2:1625:U:H3	2.13	0.45
1:2:1850:A:H2'	1:2:1851:A:C8	2.51	0.45
7:F:68:ILE:HD12	7:F:69:VAL:N	2.31	0.45
34:g:238:ALA:O	34:g:251:ALA:N	2.39	0.45
5:D:173:ARG:HD3	5:D:173:ARG:HA	1.70	0.45
7:F:164:ARG:O	7:F:164:ARG:HG2	2.15	0.45
11:J:108:ARG:HA	11:J:108:ARG:HD2	1.79	0.45
24:W:112:ASP:OD1	24:W:112:ASP:N	2.42	0.45
34:g:202:PRO:HG3	34:g:243:PRO:HB3	1.98	0.45
34:g:285:GLN:O	34:g:303:THR:HG23	2.16	0.45
1:2:1516:G:H2'	1:2:1517:G:C2	2.51	0.45
1:2:1556:A:H5''	1:2:1557:C:C5	2.51	0.45
1:2:1678:A:H5'	7:F:145:ARG:HH22	1.80	0.45
17:P:121:ILE:HG12	20:S:120:HIS:HB2	1.97	0.45
19:R:29:HIS:HA	19:R:32:LYS:HE2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Z:74:SER:HA	27:Z:79:ILE:HG22	1.98	0.45
1:2:1181:A:H2'	1:2:1182:A:C8	2.52	0.45
1:2:1293:A:H2'	1:2:1294:G:H8	1.82	0.45
1:2:1592:C:H6	1:2:1592:C:O5'	1.99	0.45
3:B:48:LEU:HD23	3:B:48:LEU:H	1.82	0.45
5:D:9:ARG:O	5:D:12:VAL:HG12	2.16	0.45
17:P:33:LEU:O	17:P:37:TYR:N	2.47	0.45
18:Q:139:ALA:C	18:Q:140:ARG:HD2	2.41	0.45
29:b:11:SER:HB2	29:b:14:GLU:HB2	1.98	0.45
35:h:10:MET:HE1	35:h:17:ARG:NH2	2.31	0.45
1:2:92:A:H1'	6:E:3:ARG:HB2	1.98	0.45
1:2:508:A:H3'	1:2:509:G:H8	1.81	0.45
1:2:544:G:H2'	1:2:545:A:C8	2.50	0.45
1:2:858:A:H2'	1:2:859:G:H8	1.80	0.45
1:2:1109:C:N3	19:R:126:MET:HG3	2.32	0.45
1:2:1172:U:H5''	35:h:10:MET:HE2	1.98	0.45
1:2:1670:C:H2'	1:2:1671:G:C8	2.50	0.45
6:E:55:ALA:HB1	6:E:60:GLU:HB2	1.99	0.45
10:I:46:VAL:HG21	10:I:56:ARG:NH1	2.32	0.45
18:Q:35:ASN:OD1	18:Q:72:VAL:HG13	2.17	0.45
19:R:77:GLU:O	19:R:81:ARG:HG3	2.17	0.45
21:T:104:LEU:HD21	21:T:121:ARG:CZ	2.46	0.45
34:g:5:MET:HE3	34:g:5:MET:HA	1.99	0.45
34:g:152:SER:HG	34:g:168:CYS:HG	1.60	0.45
1:2:126:G:OP1	8:G:198:ARG:NH2	2.47	0.45
1:2:906:U:H2'	1:2:907:G:C8	2.52	0.45
5:D:42:THR:OG1	5:D:45:ARG:HB3	2.16	0.45
7:F:52:SER:OG	7:F:70:GLU:OE1	2.29	0.45
7:F:193:LYS:NZ	7:F:197:GLU:HG2	2.31	0.45
8:G:121:ILE:HB	8:G:124:LEU:HB3	1.98	0.45
8:G:159:ARG:HE	8:G:171:THR:HB	1.82	0.45
9:H:19:PHE:CZ	9:H:60:ILE:HD12	2.48	0.45
10:I:82:VAL:O	10:I:205:ARG:NH1	2.49	0.45
21:T:9:VAL:O	21:T:11:GLN:NE2	2.49	0.45
1:2:103:A:H5'	10:I:12:ARG:CZ	2.46	0.45
1:2:1265:A:N6	1:2:1518:C:O2	2.50	0.45
1:2:1266:C:H5''	1:2:1509:U:H3	1.82	0.45
1:2:1298:G:C5	17:P:79:HIS:HB2	2.51	0.45
7:F:22:LYS:HG3	7:F:23:TRP:CE2	2.52	0.45
7:F:35:LEU:HD11	7:F:143:PRO:HB3	1.98	0.45
10:I:177:SER:OG	10:I:184:ARG:O	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:84:ILE:HG13	17:P:89:MET:SD	2.57	0.45
3:B:82:ARG:NH1	3:B:189:ILE:O	2.50	0.45
11:J:151:LEU:HD23	11:J:151:LEU:HA	1.85	0.45
12:K:49:MET:HE3	12:K:49:MET:HB3	1.89	0.45
12:K:72:THR:O	12:K:76:ILE:HG13	2.17	0.45
21:T:38:LYS:O	21:T:39:LEU:HG	2.17	0.45
22:U:66:ARG:HH22	22:U:75:LYS:HA	1.81	0.45
24:W:47:ILE:HG13	24:W:48:GLY:H	1.81	0.45
34:g:124:SER:OG	34:g:125:ARG:N	2.50	0.45
1:2:527:C:H2'	1:2:528:A:H8	1.79	0.45
1:2:1269:G:H2'	1:2:1269:G:N3	2.32	0.45
1:2:1408:U:O2	18:Q:24:HIS:NE2	2.43	0.45
1:2:1711:U:H2'	1:2:1712:A:C8	2.52	0.45
1:2:1816:G:N3	1:2:1816:G:H2'	2.31	0.45
7:F:72:LEU:HB3	7:F:76:MET:HE1	1.99	0.45
9:H:49:LYS:HE2	9:H:51:ILE:HG23	1.99	0.45
1:2:1365:G:H2'	1:2:1366:G:H8	1.82	0.44
1:2:1665:G:N7	21:T:88:MET:HE1	2.32	0.44
4:C:272:HIS:C	4:C:272:HIS:CD2	2.95	0.44
7:F:49:LEU:HD21	18:Q:49:TYR:CB	2.48	0.44
17:P:57:LEU:HD12	17:P:60:LEU:HD11	1.99	0.44
34:g:89:LEU:HD12	34:g:101:PHE:HE2	1.82	0.44
1:2:297:A:H5''	6:E:133:THR:H	1.83	0.44
1:2:1672:U:H2'	1:2:1673:U:C6	2.52	0.44
1:2:1856:C:H2'	1:2:1857:G:C8	2.53	0.44
19:R:20:TYR:HB3	19:R:23:ARG:HB3	1.99	0.44
19:R:103:LYS:HZ1	19:R:119:VAL:HA	1.81	0.44
19:R:126:MET:HE2	19:R:126:MET:HB3	1.84	0.44
32:e:53:LYS:HB3	32:e:53:LYS:HE3	1.60	0.44
34:g:114:SER:HG	34:g:118:ARG:H	1.62	0.44
1:2:860:G:H21	24:W:107:SER:HB3	1.82	0.44
1:2:864:A:H2'	1:2:865:A:C8	2.52	0.44
1:2:1607:A:C8	1:2:1608:U:C5	3.06	0.44
1:2:1639:G:H2'	1:2:1640:A:H8	1.79	0.44
1:2:1844:U:OP1	35:h:11:ARG:NH2	2.50	0.44
7:F:167:LYS:HB2	7:F:167:LYS:HE2	1.75	0.44
23:V:4:ASP:OD1	23:V:5:ALA:N	2.51	0.44
25:X:6:GLY:O	25:X:9:THR:OG1	2.31	0.44
34:g:38:LYS:HG2	34:g:64:HIS:C	2.43	0.44
1:2:332:G:HO2'	1:2:333:G:C5'	2.27	0.44
1:2:496:C:OP1	6:E:29:PRO:HD3	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:922:A:OP1	24:W:28:ARG:NH2	2.50	0.44
1:2:1613:G:P	17:P:42:ARG:HH12	2.40	0.44
23:V:33:GLN:HE21	23:V:52:THR:HG21	1.81	0.44
1:2:1312:G:N2	1:2:1313:A:H62	2.15	0.44
1:2:1375:G:H2'	1:2:1376:A:C8	2.53	0.44
1:2:1576:G:H2'	1:2:1577:G:H8	1.83	0.44
10:I:113:TYR:CE1	10:I:119:LEU:HD13	2.53	0.44
16:O:19:PRO:HG3	16:O:27:VAL:HG21	2.00	0.44
20:S:108:ARG:HA	20:S:108:ARG:HD3	1.86	0.44
22:U:19:ARG:HE	22:U:92:HIS:HD2	1.65	0.44
23:V:7:GLU:OE1	23:V:7:GLU:N	2.33	0.44
1:2:1005:G:H2'	1:2:1006:C:C6	2.52	0.44
1:2:1221:G:H2'	1:2:1222:G:C8	2.36	0.44
6:E:45:ILE:HA	6:E:61:VAL:HG11	1.99	0.44
15:N:110:ASP:O	15:N:114:ARG:HG2	2.18	0.44
34:g:181:ASN:ND2	34:g:183:LYS:HB3	2.33	0.44
1:2:1016:U:OP1	29:b:30:SER:OG	2.32	0.44
1:2:1280:G:H2'	1:2:1281:G:H5''	2.00	0.44
1:2:1443:C:H1'	18:Q:71:ARG:HH21	1.83	0.44
2:A:34:MET:HE3	2:A:154:LEU:HD11	2.00	0.44
12:K:63:ALA:HB3	12:K:68:TYR:CE2	2.52	0.44
18:Q:13:PHE:HD1	18:Q:14:GLY:H	1.65	0.44
34:g:177:TRP:NE1	34:g:184:LEU:HA	2.33	0.44
1:2:522:A:OP2	11:J:45:ARG:NH2	2.51	0.44
18:Q:50:LYS:HE3	18:Q:82:TYR:CE1	2.53	0.44
18:Q:58:LEU:O	18:Q:62:ARG:NH2	2.48	0.44
23:V:2:GLN:NE2	23:V:6:GLY:O	2.42	0.44
23:V:72:LEU:O	23:V:76:ASP:HB2	2.18	0.44
25:X:130:LEU:HD23	25:X:130:LEU:HA	1.89	0.44
33:f:104:LYS:HE3	33:f:131:PHE:H	1.82	0.44
34:g:164:ILE:HD12	34:g:177:TRP:O	2.17	0.44
1:2:956:G:O5'	16:O:60:MET:HG2	2.18	0.44
1:2:1365:G:O2'	1:2:1462:U:O4	2.26	0.44
1:2:1520:G:N2	17:P:126:VAL:HG12	2.33	0.44
1:2:1760:G:H3'	1:2:1760:G:N3	2.32	0.44
7:F:79:HIS:C	7:F:81:ARG:H	2.25	0.44
10:I:201:LYS:HD3	10:I:201:LYS:HA	1.74	0.44
17:P:121:ILE:HD13	20:S:118:ARG:O	2.17	0.44
34:g:155:ARG:HG2	34:g:199:THR:HG22	1.99	0.44
1:2:1259:A:H1'	1:2:1263:U:H2'	1.99	0.43
7:F:171:GLU:HA	7:F:174:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:67:TRP:HH2	10:I:158:ILE:HD11	1.83	0.43
15:N:16:LEU:HD21	15:N:62:GLN:NE2	2.33	0.43
17:P:49:LEU:HD12	17:P:53:GLN:HG2	1.99	0.43
34:g:217:MET:HB2	34:g:217:MET:HE3	1.81	0.43
1:2:126:G:OP2	8:G:195:LYS:NZ	2.39	0.43
1:2:1265:A:N3	1:2:1494:U:N3	2.52	0.43
2:A:135:THR:O	2:A:138:SER:OG	2.34	0.43
3:B:42:ARG:HA	3:B:42:ARG:HD3	1.57	0.43
7:F:44:LYS:HA	7:F:44:LYS:HD3	1.87	0.43
7:F:188:TYR:O	7:F:191:LYS:HG3	2.18	0.43
33:f:107:LYS:HD3	33:f:107:LYS:HA	1.75	0.43
34:g:41:ILE:HD11	34:g:55:PRO:HB3	2.00	0.43
34:g:226:HIS:NE2	34:g:228:TYR:O	2.52	0.43
1:2:685:A:H2'	1:2:686:U:O4'	2.18	0.43
1:2:872:A:O2'	1:2:873:G:H5'	2.18	0.43
1:2:1514:G:O2'	1:2:1515:G:N7	2.35	0.43
1:2:1568:C:H4'	21:T:41:LYS:HZ1	1.83	0.43
1:2:1745:A:O3'	8:G:31:ARG:NH1	2.46	0.43
10:I:101:ILE:HD12	10:I:190:LEU:HD11	2.00	0.43
20:S:67:VAL:O	20:S:70:ILE:HG22	2.18	0.43
1:2:629:A:O2'	1:2:631:U:OP1	2.37	0.43
1:2:1249:C:H2'	1:2:1250:A:C2	2.53	0.43
1:2:1540:G:H1'	1:2:1594:A:N6	2.34	0.43
1:2:1667:U:H2'	1:2:1668:U:C6	2.53	0.43
2:A:208:GLU:H	2:A:208:GLU:HG2	1.62	0.43
8:G:103:ASP:OD2	8:G:105:ASN:ND2	2.52	0.43
12:K:15:LEU:HD13	12:K:69:TRP:CZ3	2.53	0.43
12:K:25:LYS:HG2	12:K:67:PHE:CE1	2.53	0.43
20:S:46:ARG:HD3	21:T:50:GLU:HG3	2.00	0.43
23:V:16:LYS:HG2	23:V:23:ILE:HD13	2.01	0.43
29:b:5:LYS:HB3	29:b:24:LEU:HD21	2.00	0.43
1:2:595:U:H2'	1:2:596:U:C6	2.54	0.43
1:2:1255:G:OP1	1:2:1256:G:O2'	2.20	0.43
1:2:1672:U:H2'	1:2:1673:U:H6	1.84	0.43
2:A:122:LEU:HD21	2:A:133:PRO:HB2	2.01	0.43
3:B:142:PHE:O	3:B:208:HIS:N	2.52	0.43
7:F:159:ARG:O	7:F:163:PHE:HB2	2.19	0.43
8:G:151:ASP:OD1	8:G:152:ASP:N	2.52	0.43
18:Q:90:LYS:HD2	18:Q:91:ALA:N	2.33	0.43
20:S:55:ARG:HA	20:S:55:ARG:HD3	1.87	0.43
22:U:24:LEU:HD11	22:U:87:ARG:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:24:GLN:NE2	24:W:64:ASN:OD1	2.48	0.43
1:2:28:U:H2'	1:2:29:G:C8	2.54	0.43
1:2:563:G:O2'	1:2:564:A:H5''	2.18	0.43
1:2:1047:C:H5''	16:O:143:LYS:HA	2.00	0.43
1:2:1215:C:O2	1:2:1219:C:N4	2.52	0.43
1:2:1271:C:H4'	1:2:1301:A:C6	2.54	0.43
1:2:1414:A:H2	1:2:1425:G:H22	1.64	0.43
4:C:94:ILE:HG21	4:C:162:ILE:HD12	2.01	0.43
5:D:105:LEU:HA	5:D:105:LEU:HD12	1.75	0.43
7:F:130:ARG:HH22	30:c:21:THR:HA	1.84	0.43
15:N:115:LEU:O	15:N:119:GLU:HG3	2.19	0.43
1:2:1678:A:H3'	7:F:60:ARG:NH1	2.33	0.43
1:2:1731:A:H61	1:2:1803:U:C2'	2.32	0.43
16:O:45:THR:HA	16:O:52:THR:HA	2.00	0.43
18:Q:84:ILE:O	18:Q:87:SER:OG	2.28	0.43
20:S:44:VAL:O	20:S:48:ALA:HB2	2.18	0.43
32:e:52:LYS:HD3	36:n:179:GLY:HA3	2.00	0.43
34:g:52:TYR:CD1	34:g:309:VAL:HG11	2.54	0.43
1:2:12:U:H2'	1:2:13:C:C6	2.53	0.43
1:2:85:A:H2'	1:2:86:C:C6	2.54	0.43
1:2:167:G:H21	8:G:132:ARG:HD3	1.83	0.43
1:2:395:G:H5''	13:L:82:MET:HE2	2.01	0.43
1:2:1100:A:OP1	19:R:129:LYS:NZ	2.35	0.43
2:A:67:ALA:HB2	23:V:37:ALA:HB2	2.01	0.43
3:B:168:MET:HG2	3:B:197:ILE:CG2	2.49	0.43
7:F:148:ASN:O	7:F:151:ILE:HG22	2.19	0.43
10:I:152:ARG:HD2	10:I:156:ALA:HB2	2.00	0.43
12:K:27:VAL:HG23	12:K:28:HIS:CE1	2.54	0.43
16:O:69:SER:O	16:O:69:SER:OG	2.37	0.43
19:R:33:ARG:O	19:R:36:GLU:HG2	2.19	0.43
20:S:26:ILE:C	20:S:28:PHE:H	2.26	0.43
20:S:68:ILE:HA	20:S:71:MET:HG2	2.00	0.43
1:2:1614:A:H2'	1:2:1615:U:H5	1.84	0.43
2:A:149:ASN:HD21	2:A:166:LYS:HE2	1.83	0.43
12:K:15:LEU:HD12	12:K:21:MET:SD	2.58	0.43
16:O:53:ILE:HG13	16:O:90:ILE:HD12	2.00	0.43
17:P:25:LEU:HD23	17:P:25:LEU:HA	1.83	0.43
26:Y:102:THR:HG23	26:Y:107:ARG:HH11	1.83	0.43
28:a:46:GLU:O	28:a:50:VAL:HG23	2.18	0.43
36:n:173:LEU:O	36:n:177:LEU:HG	2.19	0.43
1:2:96:C:O2	1:2:473:A:O2'	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:988:C:H5''	3:B:116:LYS:HG3	2.01	0.43
1:2:1278:A:H3'	1:2:1279:C:H6	1.84	0.43
1:2:1608:U:O2	1:2:1608:U:C2'	2.67	0.43
5:D:26:THR:O	5:D:30:ALA:HB2	2.18	0.43
7:F:127:ARG:NH2	7:F:133:THR:HG1	2.16	0.43
8:G:21:GLU:HG2	8:G:25:ARG:HH12	1.83	0.43
9:H:19:PHE:HE2	9:H:50:GLU:HB3	1.83	0.43
13:L:81:LYS:HB2	13:L:81:LYS:HE3	1.81	0.43
20:S:111:LEU:HD12	20:S:126:PHE:CD1	2.54	0.43
21:T:142:ASN:HA	21:T:145:HIS:CE1	2.54	0.43
31:d:40:ARG:CZ	31:d:40:ARG:HB2	2.46	0.43
34:g:67:SER:HB3	34:g:83:TRP:HD1	1.84	0.43
34:g:298:LEU:HD23	34:g:310:TRP:HD1	1.84	0.43
1:2:183:G:C4	1:2:184:G:HI'	2.54	0.42
1:2:379:C:H2'	1:2:380:G:O4'	2.19	0.42
1:2:625:G:H4'	1:2:629:A:C4	2.54	0.42
1:2:863:U:O4	1:2:864:A:N6	2.52	0.42
1:2:1649:U:O2	1:2:1650:A:C8	2.72	0.42
1:2:1729:U:O4	1:2:1803:U:N3	2.52	0.42
2:A:69:GLU:CG	4:C:270:THR:HG21	2.47	0.42
8:G:143:LYS:HB2	8:G:143:LYS:HE3	1.74	0.42
12:K:3:MET:HG3	12:K:44:HIS:CD2	2.53	0.42
12:K:63:ALA:HB3	12:K:68:TYR:HE2	1.84	0.42
17:P:38:SER:HB2	17:P:40:ARG:HH11	1.84	0.42
20:S:46:ARG:NH1	20:S:47:LYS:HE2	2.34	0.42
33:f:119:ARG:HD2	33:f:119:ARG:HA	1.69	0.42
1:2:1269:G:H5'	17:P:100:LYS:HB2	2.01	0.42
1:2:1298:G:H22	17:P:80:LEU:HD13	1.84	0.42
1:2:1822:A:N3	1:2:1822:A:H2'	2.34	0.42
1:2:1854:U:OP1	16:O:150:ARG:NH2	2.51	0.42
5:D:97:CYS:SG	5:D:99:ILE:HG12	2.59	0.42
10:I:23:LYS:HE2	10:I:23:LYS:HB3	1.79	0.42
10:I:174:CYS:HB2	10:I:190:LEU:HD21	2.00	0.42
17:P:89:MET:HE2	17:P:111:MET:HE2	2.00	0.42
34:g:14:HIS:HE2	34:g:35:SER:CB	2.32	0.42
34:g:99:ARG:HD2	34:g:99:ARG:HA	1.65	0.42
1:2:376:A:H2'	1:2:377:G:O4'	2.18	0.42
1:2:1298:G:N1	17:P:80:LEU:HB2	2.34	0.42
1:2:1389:C:H2'	1:2:1390:U:C6	2.55	0.42
1:2:1457:U:H2'	1:2:1458:G:C8	2.54	0.42
1:2:1650:A:H2'	1:2:1651:A:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:229:MET:HE3	3:B:229:MET:HA	2.02	0.42
5:D:223:ILE:HD12	5:D:223:ILE:O	2.20	0.42
17:P:72:LYS:HD3	17:P:93:MET:CE	2.44	0.42
17:P:108:LYS:O	17:P:110:GLU:N	2.53	0.42
20:S:86:ARG:HD2	20:S:89:ASP:HA	2.01	0.42
1:2:395:G:C5'	13:L:82:MET:HE2	2.49	0.42
1:2:641:A:H2'	1:2:642:U:O4'	2.19	0.42
1:2:1030:A:H2'	1:2:1031:A:H8	1.83	0.42
1:2:1246:A:H4'	1:2:1491:G:H5''	2.01	0.42
1:2:1291:A:OP2	33:f:138:ARG:NH2	2.51	0.42
5:D:81:GLU:N	5:D:81:GLU:OE1	2.52	0.42
11:J:111:GLN:NE2	11:J:127:ARG:HB2	2.35	0.42
12:K:65:ARG:HG3	31:d:24:CYS:HA	2.01	0.42
18:Q:100:VAL:HG22	18:Q:101:ASP:N	2.35	0.42
18:Q:132:PHE:CE2	22:U:76:THR:HA	2.54	0.42
21:T:75:MET:SD	21:T:75:MET:N	2.86	0.42
28:a:78:VAL:HG22	28:a:83:VAL:HB	2.00	0.42
34:g:291:TRP:HB3	34:g:295:GLY:HA2	2.02	0.42
1:2:202:G:H2'	1:2:202:G:N3	2.34	0.42
1:2:293:C:O2	1:2:293:C:C2'	2.67	0.42
1:2:1199:A:H2'	1:2:1200:A:C8	2.54	0.42
2:A:174:MET:HE3	2:A:174:MET:HA	2.02	0.42
7:F:204:ARG:HD2	7:F:204:ARG:HA	1.64	0.42
12:K:5:LYS:HA	12:K:8:ARG:HG2	2.01	0.42
15:N:11:LEU:O	15:N:13:GLN:NE2	2.49	0.42
16:O:53:ILE:HG23	16:O:88:LEU:HD13	2.02	0.42
1:2:56:G:OP1	26:Y:111:LYS:NZ	2.50	0.42
1:2:81:U:H2'	1:2:82:G:O4'	2.19	0.42
1:2:112:U:O2'	1:2:114:G:H2'	2.20	0.42
1:2:433:A:H2'	1:2:434:G:C8	2.54	0.42
1:2:546:G:O2'	1:2:547:G:OP1	2.33	0.42
1:2:943:U:C2	1:2:944:A:C8	3.08	0.42
1:2:1344:A:N6	1:2:1386:A:H5'	2.35	0.42
12:K:9:ILE:HA	12:K:12:TYR:CD2	2.54	0.42
21:T:85:ASN:OD1	21:T:85:ASN:N	2.50	0.42
29:b:36:LYS:NZ	29:b:43:ILE:HG22	2.35	0.42
34:g:12:LYS:HA	34:g:12:LYS:HD3	1.92	0.42
34:g:188:HIS:HB3	34:g:219:TRP:CZ2	2.55	0.42
1:2:416:U:H2'	1:2:417:C:O4'	2.20	0.42
1:2:1060:A:H1'	1:2:1062:A:N7	2.35	0.42
1:2:1530:U:H1'	21:T:87:VAL:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1597:C:H3'	1:2:1598:G:H8	1.85	0.42
1:2:1679:A:H2'	7:F:60:ARG:HG3	2.01	0.42
2:A:69:GLU:OE1	2:A:69:GLU:N	2.45	0.42
2:A:134:LEU:CD2	2:A:144:THR:HG21	2.50	0.42
7:F:60:ARG:C	7:F:62:ARG:H	2.27	0.42
8:G:142:ARG:HA	8:G:147:LEU:HD12	2.01	0.42
9:H:139:ILE:HG23	9:H:156:VAL:HG13	2.02	0.42
17:P:110:GLU:OE2	20:S:113:ARG:HB2	2.20	0.42
21:T:22:LEU:HD21	21:T:28:LEU:HD12	2.01	0.42
26:Y:25:ILE:HD11	26:Y:73:GLY:HA3	2.01	0.42
32:e:46:VAL:HG23	32:e:47:PRO:HD3	2.00	0.42
1:2:472:C:O2'	1:2:474:G:OP1	2.26	0.42
1:2:921:G:O6	24:W:60:LYS:NZ	2.49	0.42
1:2:1037:G:H4'	1:2:1845:A:H4'	2.01	0.42
1:2:1173:A:OP1	35:h:17:ARG:NH2	2.53	0.42
1:2:1290:G:N2	1:2:1301:A:H4'	2.34	0.42
3:B:25:PHE:CD2	16:O:88:LEU:HD11	2.53	0.42
5:D:106:ARG:HG2	5:D:106:ARG:HH11	1.85	0.42
9:H:8:ILE:HD12	9:H:8:ILE:N	2.35	0.42
9:H:31:GLU:HG2	9:H:40:LEU:HB2	2.02	0.42
11:J:152:ASP:OD1	11:J:152:ASP:N	2.51	0.42
12:K:77:GLN:HA	12:K:80:ARG:NE	2.31	0.42
19:R:28:PHE:CE2	19:R:32:LYS:HD3	2.54	0.42
34:g:43:TRP:CZ3	34:g:55:PRO:HG3	2.54	0.42
34:g:146:SER:OG	34:g:147:HIS:N	2.53	0.42
34:g:181:ASN:OD1	34:g:181:ASN:N	2.52	0.42
34:g:270:LEU:HD13	34:g:310:TRP:CD1	2.55	0.42
1:2:563:G:O2'	1:2:564:A:H8	2.01	0.42
1:2:1030:A:H2'	1:2:1031:A:C8	2.55	0.42
1:2:1414:A:H1'	21:T:129:ARG:NH2	2.35	0.42
3:B:67:PHE:CE2	16:O:48:SER:HB3	2.55	0.42
5:D:26:THR:HG21	5:D:173:ARG:HH21	1.85	0.42
12:K:42:ASN:O	12:K:46:MET:HE3	2.20	0.42
14:M:112:LYS:HA	14:M:112:LYS:HD3	1.80	0.42
20:S:26:ILE:HD12	20:S:26:ILE:HA	1.90	0.42
22:U:102:THR:O	22:U:104:ILE:N	2.52	0.42
25:X:107:ARG:CG	25:X:112:VAL:HG22	2.46	0.42
34:g:128:THR:HG22	34:g:143:GLN:HE22	1.84	0.42
34:g:251:ALA:HA	34:g:256:ILE:HG22	2.00	0.42
1:2:146:G:H2'	1:2:147:A:O4'	2.20	0.42
1:2:381:C:OP2	10:I:54:LYS:NZ	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:389:A:H2'	1:2:390:C:C6	2.55	0.42
1:2:399:C:H3'	1:2:400:C:H5'	2.01	0.42
1:2:897:U:H4'	1:2:899:U:C5	2.55	0.42
1:2:1293:A:H2'	1:2:1294:G:C8	2.54	0.42
5:D:192:TRP:CD1	5:D:194:PRO:HD3	2.55	0.42
5:D:208:VAL:HG13	19:R:41:ILE:HG12	2.00	0.42
19:R:19:LYS:C	19:R:20:TYR:HD1	2.27	0.42
22:U:24:LEU:HD12	22:U:32:LEU:HD11	2.02	0.42
24:W:39:THR:O	24:W:43:LYS:HG2	2.19	0.42
1:2:183:G:C5	1:2:184:G:H1'	2.55	0.41
1:2:359:U:OP2	25:X:18:ARG:HD3	2.21	0.41
1:2:495:U:H2'	1:2:496:C:O4'	2.20	0.41
1:2:520:A:H5''	11:J:12:THR:HG23	2.02	0.41
1:2:1338:G:H2'	1:2:1339:U:O4'	2.20	0.41
1:2:1570:G:N1	1:2:1571:G:O6	2.53	0.41
1:2:1597:C:H4'	1:2:1603:G:H1	1.85	0.41
1:2:1669:G:OP1	22:U:79:ARG:NH2	2.53	0.41
1:2:1703:C:H2'	1:2:1704:C:O4'	2.19	0.41
2:A:85:ARG:NE	2:A:203:PHE:O	2.53	0.41
4:C:106:VAL:HA	4:C:128:VAL:HG22	2.02	0.41
6:E:42:LEU:N	6:E:84:ALA:O	2.44	0.41
11:J:50:LEU:O	11:J:54:ARG:HG3	2.20	0.41
12:K:5:LYS:HE2	12:K:9:ILE:HD11	2.02	0.41
14:M:18:LEU:HA	14:M:21:VAL:HG22	2.02	0.41
1:2:45:A:N1	1:2:480:G:O2'	2.50	0.41
1:2:106:C:H2'	1:2:107:A:C8	2.56	0.41
1:2:446:G:P	10:I:47:ARG:HH12	2.44	0.41
1:2:867:G:H2'	1:2:868:G:C8	2.55	0.41
1:2:955:A:C8	1:2:969:U:C4	3.08	0.41
1:2:1016:U:C6	15:N:61:ALA:HB1	2.55	0.41
1:2:1102:G:H2'	1:2:1103:C:C6	2.55	0.41
1:2:1334:G:H4'	5:D:183:GLY:N	2.35	0.41
1:2:1597:C:H4'	1:2:1603:G:N1	2.35	0.41
1:2:1692:U:H2'	1:2:1693:G:C8	2.55	0.41
10:I:118:ALA:HB1	10:I:153:LYS:HB2	2.02	0.41
12:K:71:LEU:HG	12:K:76:ILE:HG12	2.03	0.41
14:M:56:CYS:SG	14:M:62:VAL:HB	2.60	0.41
19:R:67:ARG:HB2	19:R:67:ARG:NH1	2.35	0.41
26:Y:117:VAL:O	26:Y:122:LYS:NZ	2.48	0.41
1:2:76:U:H2'	1:2:78:C:OP2	2.20	0.41
1:2:212:C:H2'	1:2:213:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1113:A:H2'	1:2:1114:U:C6	2.54	0.41
1:2:1249:C:O2'	18:Q:143:LYS:HG2	2.20	0.41
1:2:1285:G:N7	14:M:36:ARG:HB2	2.36	0.41
1:2:1491:G:H2'	1:2:1492:U:C6	2.55	0.41
3:B:77:ASP:O	3:B:78:GLU:HB2	2.20	0.41
5:D:175:VAL:HB	5:D:182:LEU:HB2	2.02	0.41
6:E:247:THR:OG1	6:E:250:GLU:HG3	2.20	0.41
7:F:161:ALA:HB3	7:F:172:CYS:HB2	2.03	0.41
10:I:70:GLU:HB3	10:I:112:TRP:CZ3	2.56	0.41
17:P:81:ARG:CZ	17:P:81:ARG:HA	2.50	0.41
19:R:105:MET:HE2	19:R:105:MET:HB3	1.93	0.41
22:U:43:ALA:HA	22:U:48:LEU:HD12	2.02	0.41
26:Y:110:ARG:HE	26:Y:126:GLY:HA2	1.85	0.41
1:2:617:G:N7	25:X:67:ARG:NH1	2.65	0.41
1:2:912:C:H2'	1:2:914:U:H4'	2.03	0.41
1:2:1278:A:H3'	1:2:1279:C:C6	2.56	0.41
1:2:1470:C:H2'	1:2:1471:C:H6	1.85	0.41
1:2:1622:U:OP2	20:S:121:ARG:HD3	2.19	0.41
1:2:1753:C:N4	1:2:1781:A:OP2	2.35	0.41
3:B:131:ASP:OD2	3:B:180:ASP:HB2	2.21	0.41
7:F:70:GLU:HA	7:F:73:THR:HG22	2.02	0.41
8:G:21:GLU:OE2	8:G:22:ARG:HG3	2.20	0.41
10:I:34:ALA:HB2	10:I:56:ARG:HG3	2.02	0.41
12:K:35:LEU:HA	12:K:38:LYS:HE2	2.02	0.41
15:N:19:ARG:NH2	15:N:23:PRO:HG3	2.35	0.41
20:S:66:ARG:HD2	20:S:66:ARG:HA	1.84	0.41
22:U:23:THR:HB	22:U:113:GLU:HB2	2.02	0.41
34:g:131:LEU:HB3	34:g:139:LYS:NZ	2.36	0.41
1:2:145:G:H2'	1:2:146:G:H8	1.84	0.41
1:2:495:U:O2'	6:E:27:PHE:O	2.29	0.41
1:2:1124:C:H5''	3:B:150:ILE:HG12	2.02	0.41
1:2:1164:G:O2'	1:2:1165:G:H5'	2.21	0.41
11:J:23:SER:O	11:J:27:GLN:HG3	2.21	0.41
13:L:74:SER:O	13:L:90:ARG:HD2	2.21	0.41
17:P:84:ILE:HD13	17:P:84:ILE:HA	1.93	0.41
23:V:22:ARG:HE	23:V:22:ARG:HB3	1.75	0.41
1:2:160:U:O2'	1:2:161:U:H3'	2.21	0.41
1:2:332:G:O2'	1:2:333:G:O5'	2.25	0.41
1:2:1142:G:N2	1:2:1145:A:OP2	2.40	0.41
7:F:169:ILE:HD12	7:F:169:ILE:HA	1.86	0.41
8:G:67:VAL:HB	8:G:99:GLY:HA2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:116:HIS:HB3	10:I:152:ARG:CZ	2.51	0.41
10:I:170:LYS:HE2	10:I:170:LYS:HB2	1.82	0.41
11:J:86:VAL:HG13	11:J:104:ASP:HB3	2.02	0.41
21:T:30:VAL:HG13	21:T:34:VAL:HG11	2.03	0.41
21:T:115:LYS:HA	21:T:115:LYS:HD3	1.89	0.41
32:e:52:LYS:NZ	36:n:178:ASN:O	2.52	0.41
1:2:65:C:C4	8:G:133:LEU:HD22	2.56	0.41
1:2:1016:U:H5	15:N:19:ARG:HH12	1.69	0.41
1:2:1401:A:H5''	22:U:52:GLY:HA3	2.03	0.41
1:2:1448:A:H2'	1:2:1449:G:C8	2.54	0.41
2:A:80:ARG:O	2:A:84:GLN:HG3	2.21	0.41
3:B:128:LYS:HD2	3:B:132:GLY:HA2	2.02	0.41
4:C:257:LYS:O	23:V:16:LYS:NZ	2.37	0.41
9:H:85:LYS:N	9:H:85:LYS:HD3	2.34	0.41
10:I:121:LEU:HD11	10:I:125:LYS:N	2.33	0.41
15:N:43:LYS:HE3	15:N:43:LYS:HB2	1.83	0.41
17:P:45:LEU:HD11	17:P:85:ILE:HD11	2.01	0.41
18:Q:42:ILE:H	18:Q:48:GLN:HE21	1.68	0.41
23:V:81:LYS:HD3	23:V:82:ASN:N	2.35	0.41
25:X:88:ASP:OD1	25:X:88:ASP:C	2.63	0.41
33:f:141:CYS:SG	33:f:146:LEU:HG	2.61	0.41
36:n:157:PHE:O	36:n:161:TRP:HB3	2.20	0.41
1:2:219:U:H5	1:2:302:A:C2	2.39	0.41
1:2:940:U:H2'	1:2:941:C:C6	2.55	0.41
1:2:1177:U:H2'	1:2:1178:U:C6	2.56	0.41
7:F:117:ILE:HD12	7:F:117:ILE:HA	1.78	0.41
9:H:32:MET:HG3	9:H:33:ASN:OD1	2.21	0.41
9:H:77:VAL:O	9:H:80:VAL:HG12	2.20	0.41
19:R:99:ASP:OD1	19:R:99:ASP:N	2.53	0.41
21:T:108:GLU:HG3	21:T:115:LYS:HE3	2.03	0.41
26:Y:79:LEU:HG	26:Y:83:LYS:HE2	2.02	0.41
30:c:34:PHE:HZ	30:c:61:SER:HA	1.85	0.41
36:n:153:PRO:HD2	36:n:176:GLU:OE1	2.21	0.41
1:2:554:A:H2'	1:2:556:U:H6	1.85	0.41
1:2:584:A:OP2	11:J:169:ARG:NH2	2.53	0.41
1:2:904:A:H5'	1:2:905:C:OP2	2.21	0.41
1:2:912:C:C2	1:2:914:U:H1'	2.55	0.41
1:2:1062:A:H2'	1:2:1063:C:C6	2.56	0.41
1:2:1121:G:O2'	3:B:204:ILE:O	2.37	0.41
1:2:1232:U:H2'	1:2:1233:G:O4'	2.20	0.41
1:2:1378:A:H4'	1:2:1379:A:O5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1397:U:H5'	1:2:1442:U:H5'	2.01	0.41
1:2:1515:G:N2	17:P:97:TYR:OH	2.54	0.41
1:2:1588:A:H3'	1:2:1589:A:H8	1.85	0.41
1:2:1739:C:H2'	1:2:1740:C:C6	2.56	0.41
1:2:1740:C:OP1	10:I:44:HIS:ND1	2.35	0.41
1:2:1778:C:H5	1:2:1780:G:C5	2.39	0.41
2:A:59:LEU:HA	2:A:59:LEU:HD23	1.78	0.41
2:A:123:VAL:HA	2:A:145:ILE:O	2.21	0.41
4:C:196:ILE:HB	4:C:223:TYR:HB2	2.02	0.41
5:D:69:LEU:HA	5:D:69:LEU:HD12	1.85	0.41
5:D:190:LEU:CB	5:D:200:PRO:HD3	2.49	0.41
6:E:18:TRP:HH2	6:E:31:PRO:HD3	1.84	0.41
7:F:74:ASN:HA	7:F:77:MET:HB3	2.03	0.41
11:J:93:LYS:HB2	11:J:96:TYR:CD2	2.56	0.41
13:L:88:ILE:HG21	13:L:126:VAL:HG21	2.03	0.41
13:L:126:VAL:HG12	13:L:145:VAL:HG22	2.02	0.41
18:Q:97:GLN:HB2	18:Q:105:LYS:NZ	2.36	0.41
20:S:6:PRO:O	27:Z:50:PHE:HB2	2.21	0.41
21:T:12:GLN:O	21:T:16:ARG:HD3	2.21	0.41
22:U:83:ARG:HB3	22:U:85:HIS:CE1	2.56	0.41
30:c:26:GLN:HE21	30:c:26:GLN:HB3	1.77	0.41
34:g:256:ILE:HB	34:g:289:LEU:HD11	2.03	0.41
1:2:102:A:H5'	1:2:104:A:C4	2.56	0.41
1:2:606:G:OP1	32:e:54:GLY:HA3	2.21	0.41
1:2:864:A:H2'	1:2:865:A:H8	1.85	0.41
1:2:929:G:N2	1:2:1104:G:H4'	2.35	0.41
1:2:1328:G:N2	1:2:1502:C:H42	2.19	0.41
1:2:1577:G:H1'	1:2:1582:C:C2	2.55	0.41
1:2:1645:C:H5'	18:Q:138:ARG:O	2.21	0.41
4:C:178:HIS:HD1	4:C:221:ASP:CG	2.26	0.41
5:D:157:MET:HE2	5:D:159:HIS:HD2	1.85	0.41
5:D:175:VAL:O	5:D:181:VAL:HA	2.21	0.41
7:F:56:TYR:HD1	7:F:62:ARG:HG2	1.85	0.41
9:H:80:VAL:HG23	9:H:92:VAL:HB	2.02	0.41
10:I:110:ARG:HA	10:I:113:TYR:HB3	2.02	0.41
13:L:22:ARG:HD3	13:L:22:ARG:HA	1.84	0.41
15:N:114:ARG:HA	15:N:114:ARG:HD3	1.88	0.41
18:Q:102:GLU:O	18:Q:106:LYS:HG2	2.21	0.41
22:U:61:LEU:HB3	31:d:34:TYR:CE2	2.56	0.41
34:g:78:ALA:HB2	34:g:92:LEU:HD11	2.03	0.41
1:2:438:G:H5''	1:2:438:G:N3	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:496:C:H2'	1:2:497:C:C6	2.56	0.40
1:2:888:U:H1'	1:2:899:U:N3	2.35	0.40
1:2:952:G:OP1	3:B:56:LYS:NZ	2.54	0.40
1:2:1217:A:H2'	1:2:1218:C:C6	2.56	0.40
1:2:1283:C:N3	14:M:99:LYS:HD2	2.37	0.40
1:2:1284:A:H62	14:M:100:PRO:HA	1.86	0.40
1:2:1865:C:H5	28:a:6:ARG:H	1.67	0.40
2:A:173:LEU:HD11	2:A:177:MET:HE2	2.03	0.40
3:B:136:ARG:HG2	3:B:138:PHE:CE1	2.57	0.40
4:C:163:VAL:HG21	4:C:245:SER:HB3	2.04	0.40
6:E:101:LEU:HD23	6:E:101:LEU:HA	1.88	0.40
7:F:73:THR:OG1	7:F:89:THR:OG1	2.31	0.40
12:K:53:LYS:HE2	12:K:60:GLU:HG2	2.02	0.40
14:M:22:LEU:HD13	14:M:86:GLY:HA2	2.02	0.40
17:P:28:MET:HG3	17:P:29:SER:O	2.21	0.40
22:U:61:LEU:HB2	22:U:82:MET:HB3	2.03	0.40
22:U:64:THR:HG22	22:U:77:TRP:CE3	2.56	0.40
33:f:83:LYS:HB3	33:f:88:PRO:HB3	2.03	0.40
34:g:225:LYS:HD2	34:g:226:HIS:H	1.86	0.40
1:2:1012:A:H2'	1:2:1013:U:O4'	2.21	0.40
1:2:1182:A:C5	1:2:1183:A:H1'	2.56	0.40
1:2:1628:C:H2'	1:2:1629:C:C6	2.56	0.40
3:B:217:MET:HE2	3:B:217:MET:HB2	1.78	0.40
8:G:164:LYS:HB3	8:G:167:LYS:HB2	2.03	0.40
11:J:131:ARG:HD2	11:J:131:ARG:HA	1.81	0.40
21:T:38:LYS:HG3	21:T:40:ALA:O	2.20	0.40
1:2:800:U:H5	1:2:865:A:N1	2.19	0.40
1:2:1348:G:C8	1:2:1349:G:C8	3.09	0.40
1:2:1578:U:H2'	5:D:4:GLN:HG2	2.02	0.40
18:Q:39:LEU:H	18:Q:39:LEU:HD23	1.85	0.40
34:g:8:ARG:HA	34:g:8:ARG:CZ	2.51	0.40
1:2:287:U:O2	6:E:131:VAL:HG11	2.21	0.40
1:2:517:C:H2'	1:2:518:G:O4'	2.21	0.40
1:2:1114:U:H3	1:2:1119:A:N6	2.20	0.40
1:2:1295:A:H3'	1:2:1296:U:C5'	2.51	0.40
7:F:73:THR:HG1	7:F:89:THR:HG1	1.62	0.40
7:F:98:GLU:OE1	27:Z:108:ILE:HD13	2.22	0.40
9:H:18:GLU:OE2	9:H:18:GLU:HA	2.20	0.40
15:N:29:THR:O	15:N:33:VAL:HG23	2.21	0.40
15:N:95:ALA:O	15:N:99:ARG:HG3	2.21	0.40
17:P:61:ARG:NE	17:P:88:GLU:OE1	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:100:LYS:HG3	17:P:101:THR:HG23	2.03	0.40
20:S:130:ARG:HA	20:S:130:ARG:HD2	1.67	0.40
31:d:42:CYS:O	31:d:46:TYR:HB2	2.22	0.40
1:2:118:C:H1'	1:2:445:A:C4	2.57	0.40
1:2:1267:C:C5	1:2:1268:C:H1'	2.57	0.40
1:2:1473:G:N2	1:2:1475:G:H3'	2.36	0.40
1:2:1652:G:H1	1:2:1672:U:H3	1.68	0.40
2:A:97:THR:HG22	2:A:117:ARG:HH21	1.86	0.40
3:B:136:ARG:HG2	3:B:138:PHE:CZ	2.56	0.40
6:E:95:THR:HG22	26:Y:16:ARG:HB2	2.03	0.40
7:F:47:LYS:HB3	7:F:47:LYS:HE2	1.66	0.40
10:I:150:ASP:O	10:I:153:LYS:HB3	2.21	0.40
12:K:25:LYS:HG3	12:K:62:PHE:HZ	1.86	0.40
18:Q:63:PHE:CZ	18:Q:92:LEU:HD11	2.57	0.40
18:Q:118:THR:O	18:Q:118:THR:OG1	2.39	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	211/295 (72%)	205 (97%)	5 (2%)	1 (0%)	24	40
3	B	211/264 (80%)	204 (97%)	7 (3%)	0	100	100
4	C	216/293 (74%)	211 (98%)	5 (2%)	0	100	100
5	D	223/243 (92%)	220 (99%)	3 (1%)	0	100	100
6	E	260/263 (99%)	251 (96%)	9 (4%)	0	100	100
7	F	187/204 (92%)	170 (91%)	16 (9%)	1 (0%)	24	40
8	G	228/249 (92%)	221 (97%)	7 (3%)	0	100	100
9	H	184/194 (95%)	174 (95%)	8 (4%)	2 (1%)	11	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	I	203/208 (98%)	194 (96%)	9 (4%)	0	100	100
11	J	178/194 (92%)	172 (97%)	5 (3%)	1 (1%)	21	36
12	K	95/165 (58%)	90 (95%)	5 (5%)	0	100	100
13	L	149/158 (94%)	142 (95%)	6 (4%)	1 (1%)	18	32
14	M	119/132 (90%)	110 (92%)	6 (5%)	3 (2%)	4	7
15	N	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
16	O	133/151 (88%)	128 (96%)	5 (4%)	0	100	100
17	P	124/145 (86%)	112 (90%)	12 (10%)	0	100	100
18	Q	136/146 (93%)	127 (93%)	8 (6%)	1 (1%)	18	32
19	R	130/135 (96%)	127 (98%)	3 (2%)	0	100	100
20	S	141/152 (93%)	124 (88%)	17 (12%)	0	100	100
21	T	142/145 (98%)	136 (96%)	6 (4%)	0	100	100
22	U	99/119 (83%)	94 (95%)	5 (5%)	0	100	100
23	V	80/83 (96%)	80 (100%)	0	0	100	100
24	W	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	X	139/143 (97%)	137 (99%)	2 (1%)	0	100	100
26	Y	122/130 (94%)	121 (99%)	1 (1%)	0	100	100
27	Z	70/125 (56%)	64 (91%)	6 (9%)	0	100	100
28	a	97/101 (96%)	95 (98%)	1 (1%)	1 (1%)	12	22
29	b	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
30	c	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
31	d	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
32	e	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
33	f	72/74 (97%)	60 (83%)	12 (17%)	0	100	100
34	g	312/315 (99%)	278 (89%)	32 (10%)	2 (1%)	21	36
35	h	20/25 (80%)	20 (100%)	0	0	100	100
36	n	28/180 (16%)	28 (100%)	0	0	100	100
All	All	4830/5567 (87%)	4595 (95%)	222 (5%)	13 (0%)	37	54

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	189	ILE

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Mol	Chain	Res	Type
9	H	171	GLU
28	a	63	VAL
14	M	110	VAL
9	H	88	SER
14	M	94	ILE
7	F	33	ILE
14	M	109	VAL
18	Q	13	PHE
34	g	235	ILE
34	g	314	ILE
11	J	160	SER
13	L	32	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	179/243 (74%)	169 (94%)	10 (6%)	19	35
3	B	194/231 (84%)	186 (96%)	8 (4%)	27	48
4	C	184/225 (82%)	177 (96%)	7 (4%)	29	51
5	D	189/202 (94%)	176 (93%)	13 (7%)	14	26
6	E	224/225 (100%)	215 (96%)	9 (4%)	28	49
7	F	159/170 (94%)	155 (98%)	4 (2%)	42	63
8	G	200/218 (92%)	192 (96%)	8 (4%)	28	49
9	H	167/174 (96%)	158 (95%)	9 (5%)	20	36
10	I	178/180 (99%)	177 (99%)	1 (1%)	78	87
11	J	160/168 (95%)	158 (99%)	2 (1%)	61	75
12	K	88/136 (65%)	85 (97%)	3 (3%)	32	55
13	L	135/142 (95%)	134 (99%)	1 (1%)	76	85
14	M	102/108 (94%)	100 (98%)	2 (2%)	48	67
15	N	130/131 (99%)	126 (97%)	4 (3%)	35	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	O	105/119 (88%)	98 (93%)	7 (7%)	15	27
17	P	112/130 (86%)	110 (98%)	2 (2%)	51	69
18	Q	114/121 (94%)	109 (96%)	5 (4%)	25	45
19	R	119/122 (98%)	112 (94%)	7 (6%)	18	32
20	S	124/132 (94%)	122 (98%)	2 (2%)	55	72
21	T	114/115 (99%)	111 (97%)	3 (3%)	40	62
22	U	93/107 (87%)	92 (99%)	1 (1%)	65	79
23	V	66/67 (98%)	63 (96%)	3 (4%)	24	44
24	W	112/113 (99%)	111 (99%)	1 (1%)	70	82
25	X	113/115 (98%)	110 (97%)	3 (3%)	39	61
26	Y	108/112 (96%)	105 (97%)	3 (3%)	38	60
27	Z	64/103 (62%)	63 (98%)	1 (2%)	55	72
28	a	87/89 (98%)	86 (99%)	1 (1%)	65	79
29	b	74/74 (100%)	73 (99%)	1 (1%)	59	74
30	c	55/55 (100%)	54 (98%)	1 (2%)	51	69
31	d	48/48 (100%)	47 (98%)	1 (2%)	47	66
32	e	45/45 (100%)	42 (93%)	3 (7%)	15	27
33	f	67/67 (100%)	65 (97%)	2 (3%)	36	58
34	g	272/273 (100%)	257 (94%)	15 (6%)	19	35
35	h	21/24 (88%)	21 (100%)	0	100	100
36	n	26/150 (17%)	26 (100%)	0	100	100
All	All	4228/4734 (89%)	4085 (97%)	143 (3%)	33	55

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	11	LYS
2	A	16	LEU
2	A	25	LEU
2	A	28	THR
2	A	43	SER
2	A	87	VAL
2	A	104	THR
2	A	112	ILE
2	A	117	ARG

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Mol	Chain	Res	Type
2	A	118	GLU
3	B	38	MET
3	B	60	ASP
3	B	91	VAL
3	B	96	CYS
3	B	115	LYS
3	B	179	ASN
3	B	219	LYS
3	B	225	LEU
4	C	90	GLU
4	C	149	THR
4	C	190	SER
4	C	206	SER
4	C	221	ASP
4	C	259	THR
4	C	260	VAL
5	D	54	ARG
5	D	91	VAL
5	D	99	ILE
5	D	104	SER
5	D	105	LEU
5	D	115	VAL
5	D	126	ILE
5	D	137	VAL
5	D	142	LEU
5	D	157	MET
5	D	169	ASP
5	D	208	VAL
5	D	209	SER
6	E	115	THR
6	E	126	VAL
6	E	131	VAL
6	E	141	THR
6	E	162	ILE
6	E	173	ILE
6	E	176	ASP
6	E	220	THR
6	E	248	ILE
7	F	17	ILE
7	F	90	VAL
7	F	104	THR
7	F	185	SER

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Mol	Chain	Res	Type
8	G	6	SER
8	G	13	GLN
8	G	129	VAL
8	G	139	SER
8	G	157	VAL
8	G	163	ASN
8	G	171	THR
8	G	200	LYS
9	H	20	GLU
9	H	23	ILE
9	H	45	ILE
9	H	51	ILE
9	H	76	GLN
9	H	99	ARG
9	H	119	SER
9	H	137	SER
9	H	172	THR
10	I	76	THR
11	J	49	THR
11	J	66	LYS
12	K	14	LEU
12	K	20	VAL
12	K	83	LEU
13	L	67	SER
14	M	48	HIS
14	M	124	ILE
15	N	48	SER
15	N	57	SER
15	N	80	LEU
15	N	133	ARG
16	O	39	ASP
16	O	52	THR
16	O	81	VAL
16	O	91	THR
16	O	113	GLN
16	O	114	SER
16	O	138	ASP
17	P	33	LEU
17	P	56	LEU
18	Q	8	GLN
18	Q	22	VAL
18	Q	24	HIS

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Mol	Chain	Res	Type
18	Q	57	LEU
18	Q	72	VAL
19	R	38	ILE
19	R	71	ILE
19	R	72	LYS
19	R	102	THR
19	R	117	LEU
19	R	119	VAL
19	R	130	THR
20	S	5	ILE
20	S	8	LYS
21	T	53	PHE
21	T	85	ASN
21	T	138	VAL
22	U	68	THR
23	V	34	MET
23	V	39	VAL
23	V	68	SER
24	W	74	VAL
25	X	55	VAL
25	X	64	SER
25	X	72	VAL
26	Y	4	THR
26	Y	6	THR
26	Y	50	THR
27	Z	72	VAL
28	a	3	LYS
29	b	74	THR
30	c	32	VAL
31	d	36	LEU
32	e	5	SER
32	e	29	THR
32	e	46	VAL
33	f	86	THR
33	f	121	CYS
34	g	18	VAL
34	g	21	ILE
34	g	23	THR
34	g	33	SER
34	g	39	THR
34	g	59	LEU
34	g	73	SER

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Mol	Chain	Res	Type
34	g	89	LEU
34	g	102	VAL
34	g	133	ASN
34	g	199	THR
34	g	237	ASN
34	g	239	LEU
34	g	252	THR
34	g	303	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	70	ASN
2	A	132	GLN
3	B	163	GLN
4	C	272	HIS
6	E	98	ASN
6	E	188	ASN
6	E	197	ASN
7	F	31	ASN
7	F	107	ASN
7	F	110	GLN
7	F	114	ASN
7	F	203	ASN
8	G	105	ASN
9	H	12	ASN
9	H	91	HIS
9	H	114	GLN
9	H	157	HIS
11	J	154	GLN
13	L	83	GLN
14	M	19	GLN
15	N	58	HIS
16	O	38	ASN
16	O	83	GLN
16	O	103	ASN
17	P	46	ASN
17	P	98	ASN
17	P	137	HIS
19	R	56	HIS
19	R	116	ASN
20	S	105	ASN

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Mol	Chain	Res	Type
21	T	126	GLN
25	X	16	HIS
26	Y	15	ASN
26	Y	22	GLN
29	b	65	GLN
30	c	45	ASN
31	d	4	GLN
31	d	26	ASN
31	d	41	GLN
34	g	4	GLN
34	g	20	GLN
34	g	119	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1661/1869 (88%)	511 (30%)	23 (1%)

All (511) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	26	U
1	2	33	G
1	2	44	U
1	2	45	A
1	2	46	A
1	2	56	G
1	2	62	G
1	2	67	C
1	2	68	A
1	2	72	C
1	2	74	G
1	2	75	G
1	2	76	U
1	2	77	A
1	2	93	U
1	2	103	A
1	2	113	G

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Mol	Chain	Res	Type
1	2	114	G
1	2	115	U
1	2	126	G
1	2	128	U
1	2	129	C
1	2	130	G
1	2	142	C
1	2	143	U
1	2	147	A
1	2	155	G
1	2	160	U
1	2	163	U
1	2	168	C
1	2	171	A
1	2	178	C
1	2	181	A
1	2	182	C
1	2	183	G
1	2	184	G
1	2	191	A
1	2	192	C
1	2	194	C
1	2	198	U
1	2	199	C
1	2	200	G
1	2	203	G
1	2	204	G
1	2	205	G
1	2	206	G
1	2	215	G
1	2	217	A
1	2	221	A
1	2	305	U
1	2	306	C
1	2	307	G
1	2	308	G
1	2	310	C
1	2	320	G
1	2	330	G
1	2	333	G
1	2	335	G
1	2	340	C

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Mol	Chain	Res	Type
1	2	342	C
1	2	344	U
1	2	345	U
1	2	347	G
1	2	362	C
1	2	364	A
1	2	368	U
1	2	370	G
1	2	377	G
1	2	385	G
1	2	386	C
1	2	399	C
1	2	400	C
1	2	407	G
1	2	409	C
1	2	413	G
1	2	421	G
1	2	438	G
1	2	448	A
1	2	449	A
1	2	450	C
1	2	451	G
1	2	464	A
1	2	465	A
1	2	467	G
1	2	471	G
1	2	472	C
1	2	473	A
1	2	474	G
1	2	476	A
1	2	482	G
1	2	485	A
1	2	487	U
1	2	492	C
1	2	525	A
1	2	530	U
1	2	531	A
1	2	533	A
1	2	535	G
1	2	536	A
1	2	537	C
1	2	538	U

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Mol	Chain	Res	Type
1	2	540	U
1	2	542	U
1	2	544	G
1	2	546	G
1	2	547	G
1	2	548	C
1	2	551	U
1	2	553	U
1	2	554	A
1	2	555	A
1	2	556	U
1	2	559	G
1	2	560	A
1	2	570	C
1	2	576	A
1	2	587	A
1	2	589	G
1	2	590	A
1	2	591	U
1	2	593	C
1	2	594	A
1	2	604	A
1	2	605	A
1	2	607	U
1	2	608	C
1	2	614	C
1	2	623	G
1	2	626	G
1	2	627	U
1	2	628	A
1	2	629	A
1	2	631	U
1	2	640	A
1	2	643	A
1	2	644	G
1	2	655	A
1	2	660	C
1	2	668	A
1	2	669	A
1	2	671	A
1	2	672	A
1	2	673	G

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Mol	Chain	Res	Type
1	2	688	U
1	2	747	U
1	2	748	C
1	2	750	C
1	2	792	C
1	2	793	G
1	2	794	A
1	2	795	A
1	2	796	G
1	2	797	C
1	2	799	U
1	2	811	A
1	2	821	G
1	2	822	U
1	2	823	U
1	2	824	C
1	2	830	A
1	2	831	G
1	2	847	A
1	2	862	A
1	2	870	A
1	2	871	U
1	2	872	A
1	2	873	G
1	2	874	G
1	2	878	G
1	2	879	C
1	2	881	G
1	2	882	U
1	2	884	C
1	2	885	U
1	2	886	A
1	2	888	U
1	2	890	U
1	2	891	G
1	2	892	U
1	2	894	G
1	2	895	G
1	2	896	U
1	2	897	U
1	2	899	U
1	2	901	G

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Mol	Chain	Res	Type
1	2	902	G
1	2	903	A
1	2	909	G
1	2	912	C
1	2	913	A
1	2	914	U
1	2	920	A
1	2	922	A
1	2	930	C
1	2	933	G
1	2	943	U
1	2	962	A
1	2	963	A
1	2	970	G
1	2	971	G
1	2	990	A
1	2	992	A
1	2	999	G
1	2	1017	U
1	2	1023	A
1	2	1026	C
1	2	1049	A
1	2	1050	A
1	2	1061	U
1	2	1062	A
1	2	1078	C
1	2	1083	A
1	2	1085	C
1	2	1115	U
1	2	1116	C
1	2	1118	C
1	2	1121	G
1	2	1123	C
1	2	1130	G
1	2	1133	A
1	2	1138	C
1	2	1146	C
1	2	1148	A
1	2	1149	A
1	2	1154	U
1	2	1157	G
1	2	1171	G

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Mol	Chain	Res	Type
1	2	1195	A
1	2	1207	G
1	2	1215	C
1	2	1216	C
1	2	1220	A
1	2	1223	A
1	2	1224	G
1	2	1225	U
1	2	1226	G
1	2	1227	G
1	2	1228	A
1	2	1230	C
1	2	1231	C
1	2	1232	U
1	2	1233	G
1	2	1234	C
1	2	1235	G
1	2	1237	C
1	2	1238	U
1	2	1239	U
1	2	1240	A
1	2	1241	A
1	2	1242	U
1	2	1243	U
1	2	1244	U
1	2	1247	C
1	2	1248	U
1	2	1249	C
1	2	1251	A
1	2	1256	G
1	2	1257	G
1	2	1258	A
1	2	1259	A
1	2	1260	A
1	2	1262	C
1	2	1264	C
1	2	1265	A
1	2	1266	C
1	2	1268	C
1	2	1270	G
1	2	1271	C
1	2	1272	C

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Mol	Chain	Res	Type
1	2	1273	C
1	2	1274	G
1	2	1275	G
1	2	1276	A
1	2	1277	C
1	2	1280	G
1	2	1283	C
1	2	1285	G
1	2	1286	G
1	2	1287	A
1	2	1289	U
1	2	1290	G
1	2	1292	C
1	2	1293	A
1	2	1294	G
1	2	1295	A
1	2	1296	U
1	2	1300	U
1	2	1301	A
1	2	1302	G
1	2	1304	U
1	2	1305	C
1	2	1311	C
1	2	1312	G
1	2	1313	A
1	2	1316	C
1	2	1319	U
1	2	1321	G
1	2	1324	G
1	2	1326	U
1	2	1327	G
1	2	1330	G
1	2	1331	C
1	2	1333	U
1	2	1335	G
1	2	1336	C
1	2	1340	U
1	2	1341	C
1	2	1342	U
1	2	1348	G
1	2	1371	U
1	2	1372	U

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Mol	Chain	Res	Type
1	2	1378	A
1	2	1382	A
1	2	1392	U
1	2	1401	A
1	2	1402	A
1	2	1403	C
1	2	1404	U
1	2	1405	A
1	2	1407	U
1	2	1408	U
1	2	1410	C
1	2	1413	G
1	2	1414	A
1	2	1415	C
1	2	1425	G
1	2	1426	U
1	2	1428	G
1	2	1430	C
1	2	1431	G
1	2	1439	A
1	2	1441	U
1	2	1444	U
1	2	1447	G
1	2	1454	A
1	2	1463	U
1	2	1465	A
1	2	1466	G
1	2	1474	A
1	2	1477	U
1	2	1480	A
1	2	1483	A
1	2	1485	U
1	2	1490	G
1	2	1491	G
1	2	1494	U
1	2	1497	G
1	2	1498	A
1	2	1500	G
1	2	1501	C
1	2	1503	C
1	2	1504	U
1	2	1505	U

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Mol	Chain	Res	Type
1	2	1506	A
1	2	1507	G
1	2	1509	U
1	2	1510	G
1	2	1512	C
1	2	1513	C
1	2	1516	G
1	2	1517	G
1	2	1518	C
1	2	1520	G
1	2	1521	C
1	2	1522	A
1	2	1525	C
1	2	1526	G
1	2	1529	C
1	2	1530	U
1	2	1533	A
1	2	1535	U
1	2	1536	G
1	2	1537	A
1	2	1538	C
1	2	1539	U
1	2	1540	G
1	2	1543	U
1	2	1548	G
1	2	1551	U
1	2	1552	G
1	2	1553	C
1	2	1556	A
1	2	1557	C
1	2	1558	C
1	2	1559	C
1	2	1561	A
1	2	1562	C
1	2	1567	G
1	2	1568	C
1	2	1569	A
1	2	1570	G
1	2	1571	G
1	2	1572	C
1	2	1575	G
1	2	1576	G

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Mol	Chain	Res	Type
1	2	1578	U
1	2	1579	A
1	2	1580	A
1	2	1581	C
1	2	1583	C
1	2	1587	G
1	2	1588	A
1	2	1593	C
1	2	1594	A
1	2	1597	C
1	2	1598	G
1	2	1600	G
1	2	1601	A
1	2	1602	U
1	2	1605	G
1	2	1608	U
1	2	1609	C
1	2	1615	U
1	2	1617	G
1	2	1618	C
1	2	1619	A
1	2	1620	A
1	2	1621	U
1	2	1623	A
1	2	1624	U
1	2	1625	U
1	2	1626	C
1	2	1627	C
1	2	1628	C
1	2	1629	C
1	2	1630	A
1	2	1636	G
1	2	1637	A
1	2	1638	G
1	2	1642	U
1	2	1643	U
1	2	1644	C
1	2	1645	C
1	2	1646	C
1	2	1647	A
1	2	1654	G
1	2	1660	C

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Mol	Chain	Res	Type
1	2	1661	A
1	2	1662	U
1	2	1664	A
1	2	1665	G
1	2	1671	G
1	2	1672	U
1	2	1675	A
1	2	1676	U
1	2	1678	A
1	2	1679	A
1	2	1680	G
1	2	1682	C
1	2	1683	C
1	2	1684	C
1	2	1686	G
1	2	1688	C
1	2	1689	C
1	2	1695	A
1	2	1698	C
1	2	1715	A
1	2	1719	A
1	2	1720	U
1	2	1721	U
1	2	1722	G
1	2	1723	G
1	2	1725	U
1	2	1726	G
1	2	1748	G
1	2	1755	C
1	2	1756	C
1	2	1757	G
1	2	1758	G
1	2	1760	G
1	2	1761	U
1	2	1772	C
1	2	1773	C
1	2	1774	C
1	2	1775	U
1	2	1777	G
1	2	1779	G
1	2	1782	G
1	2	1783	C

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Mol	Chain	Res	Type
1	2	1800	A
1	2	1802	C
1	2	1803	U
1	2	1804	U
1	2	1805	G
1	2	1806	A
1	2	1807	C
1	2	1808	U
1	2	1809	A
1	2	1811	C
1	2	1813	A
1	2	1814	G
1	2	1815	A
1	2	1817	G
1	2	1820	G
1	2	1822	A
1	2	1823	A
1	2	1825	A
1	2	1826	G
1	2	1829	G
1	2	1831	A
1	2	1838	U
1	2	1849	G
1	2	1850	A
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	102	A
1	2	293	C
1	2	332	G
1	2	341	C
1	2	546	G
1	2	550	C
1	2	559	G
1	2	604	A
1	2	873	G

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Mol	Chain	Res	Type
1	2	961	G
1	2	1224	G
1	2	1234	C
1	2	1263	U
1	2	1285	G
1	2	1409	A
1	2	1425	G
1	2	1428	G
1	2	1464	C
1	2	1517	G
1	2	1571	G
1	2	1627	C
1	2	1677	U
1	2	1814	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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

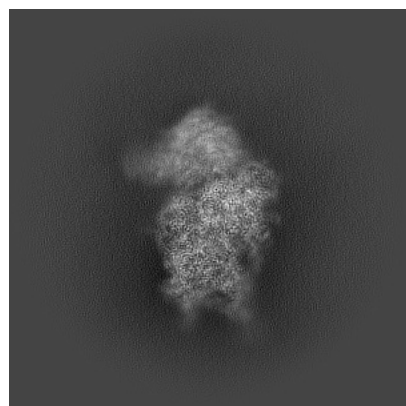
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62447. These allow visual inspection of the internal detail of the map and identification of artifacts.

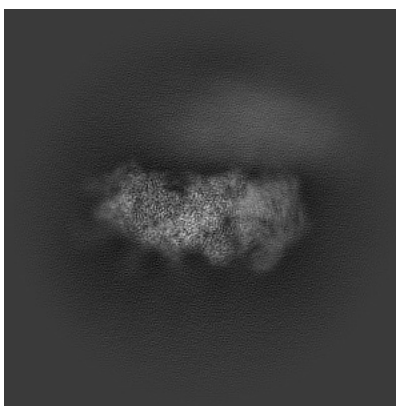
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

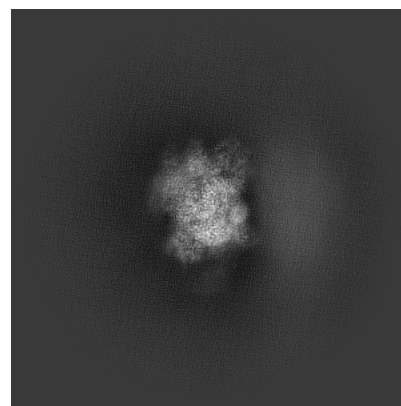
6.1.1 Primary map



X

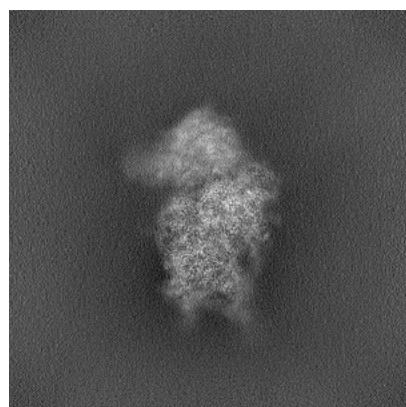


Y

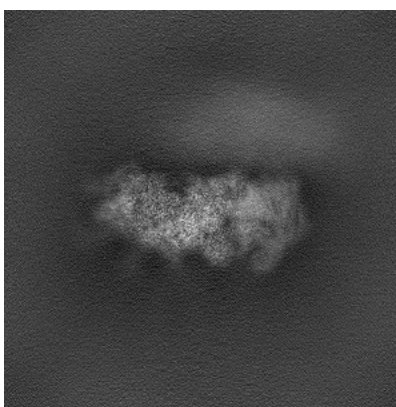


Z

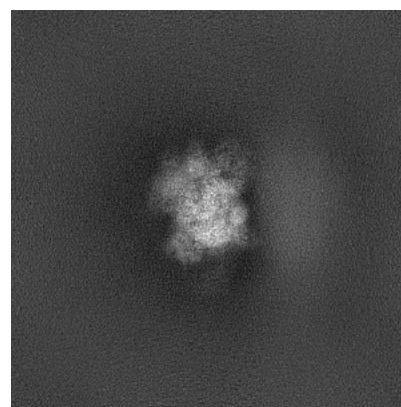
6.1.2 Raw map



X



Y

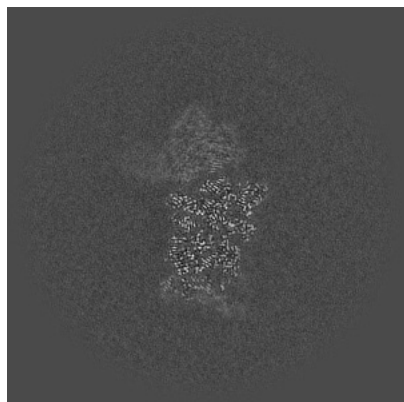


Z

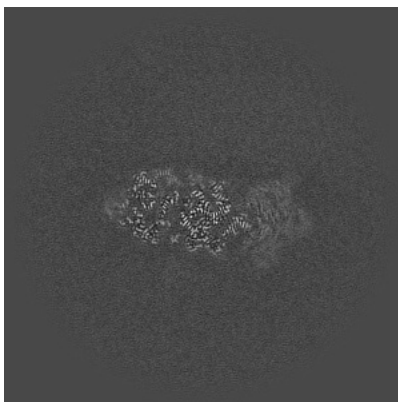
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

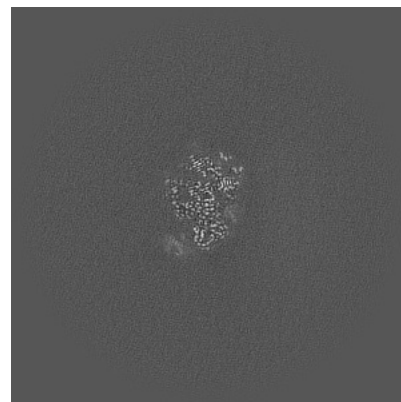
6.2.1 Primary map



X Index: 256

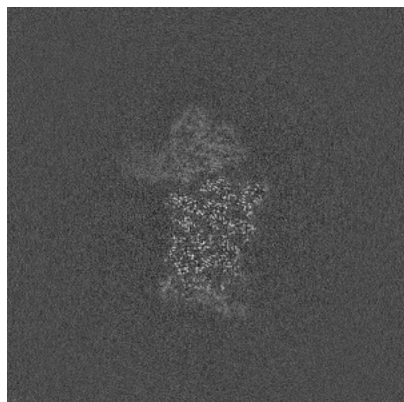


Y Index: 256

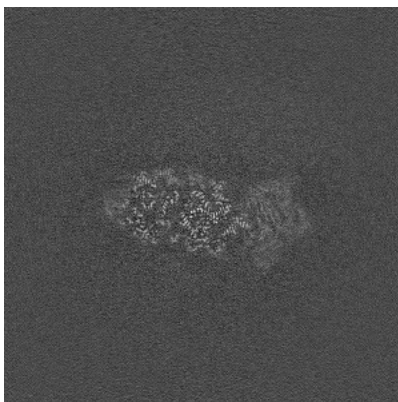


Z Index: 256

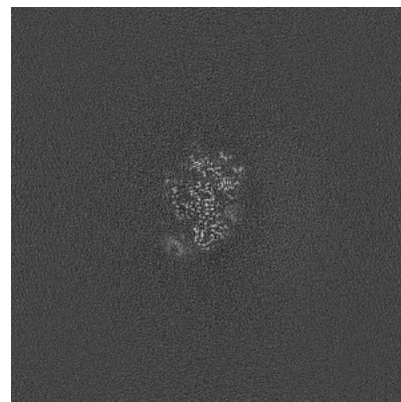
6.2.2 Raw map



X Index: 256



Y Index: 256

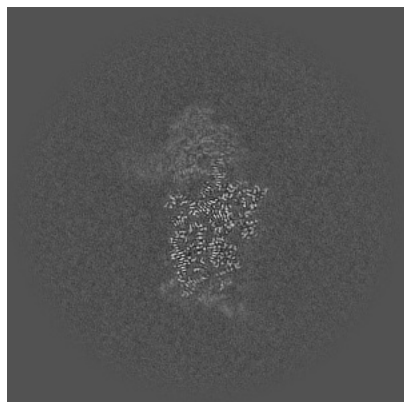


Z Index: 256

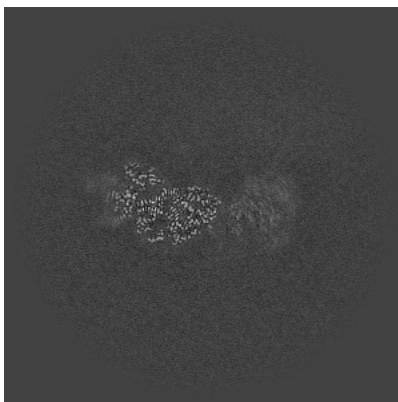
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

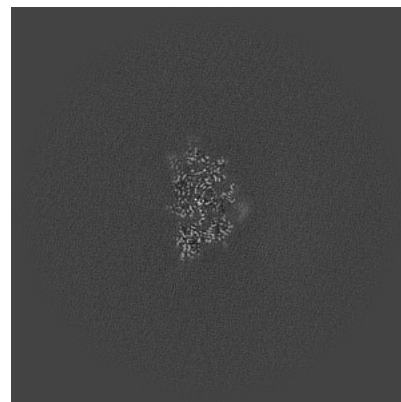
6.3.1 Primary map



X Index: 252

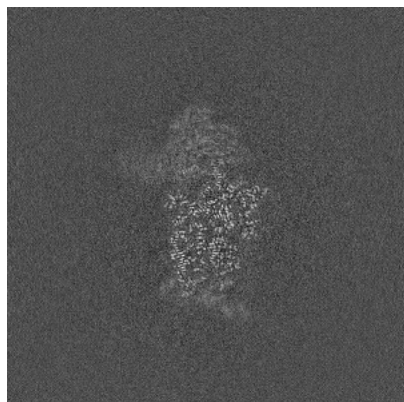


Y Index: 224

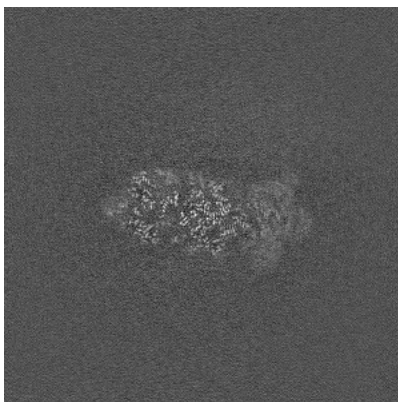


Z Index: 237

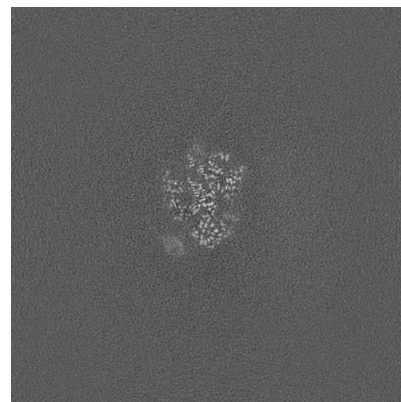
6.3.2 Raw map



X Index: 252



Y Index: 257

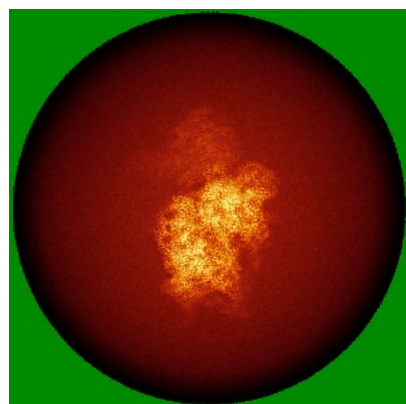


Z Index: 260

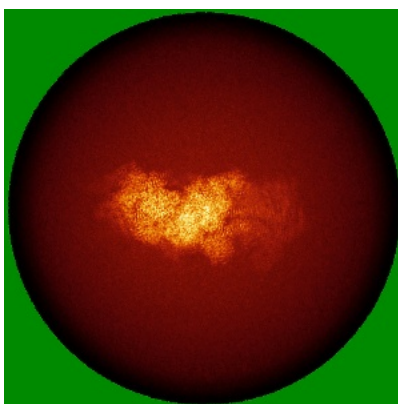
The images above show the largest variance slices of the map in three orthogonal directions.

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

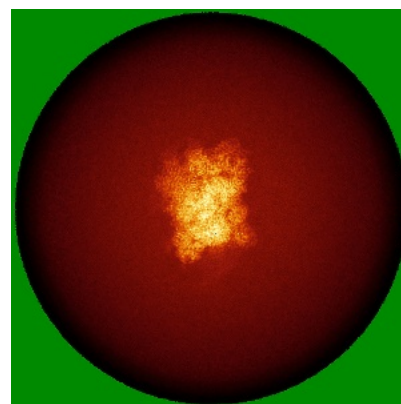
6.4.1 Primary map



X

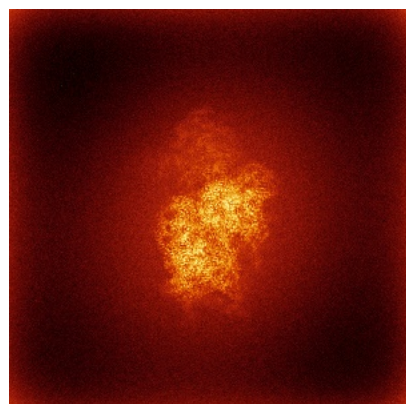


Y

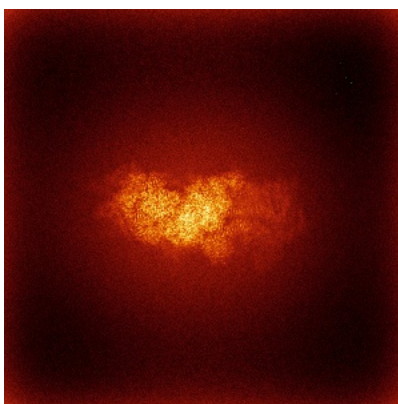


Z

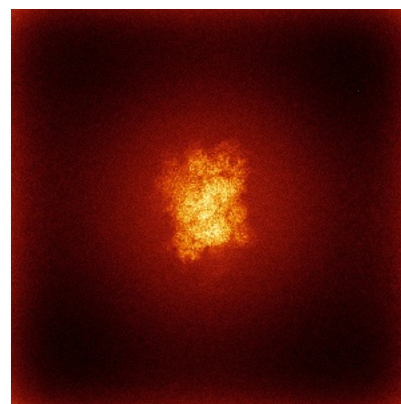
6.4.2 Raw map



X



Y

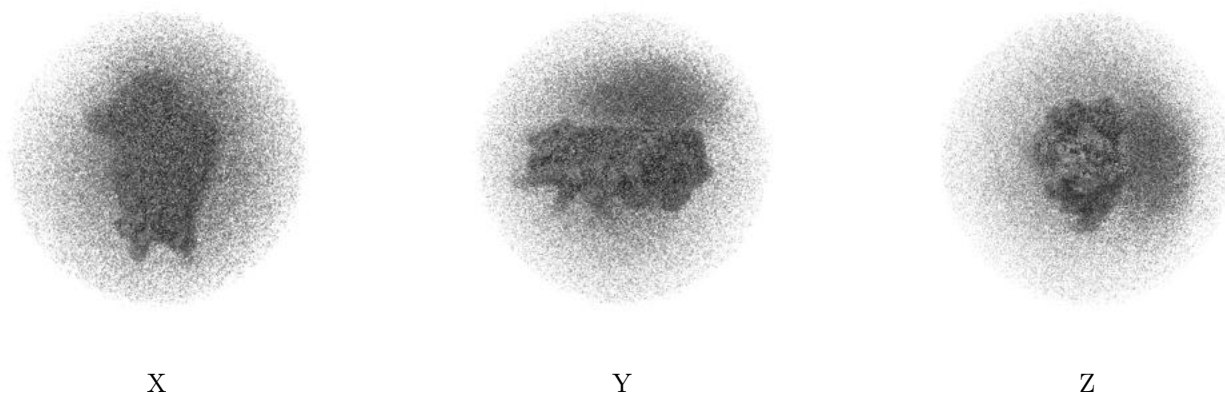


Z

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.

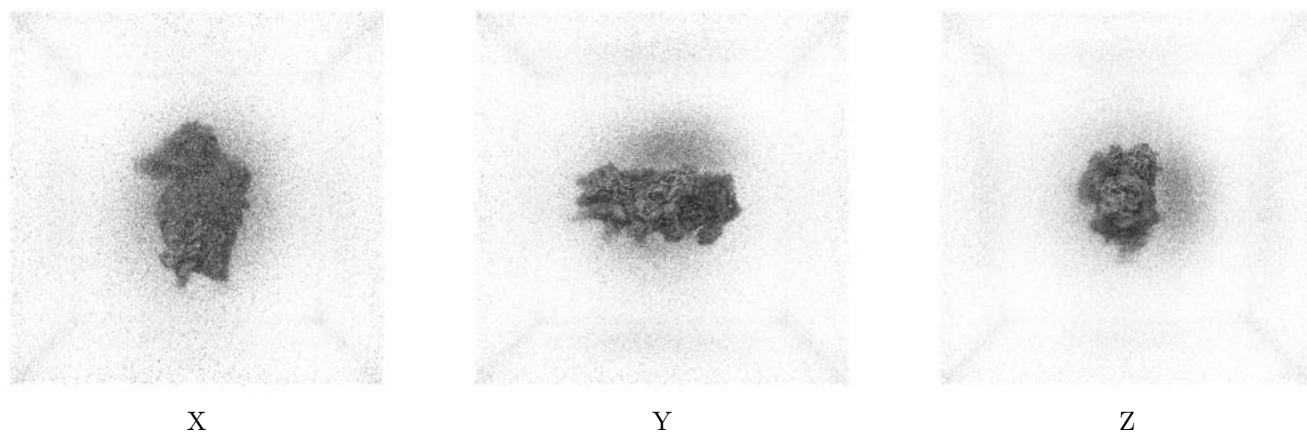
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.158. 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.

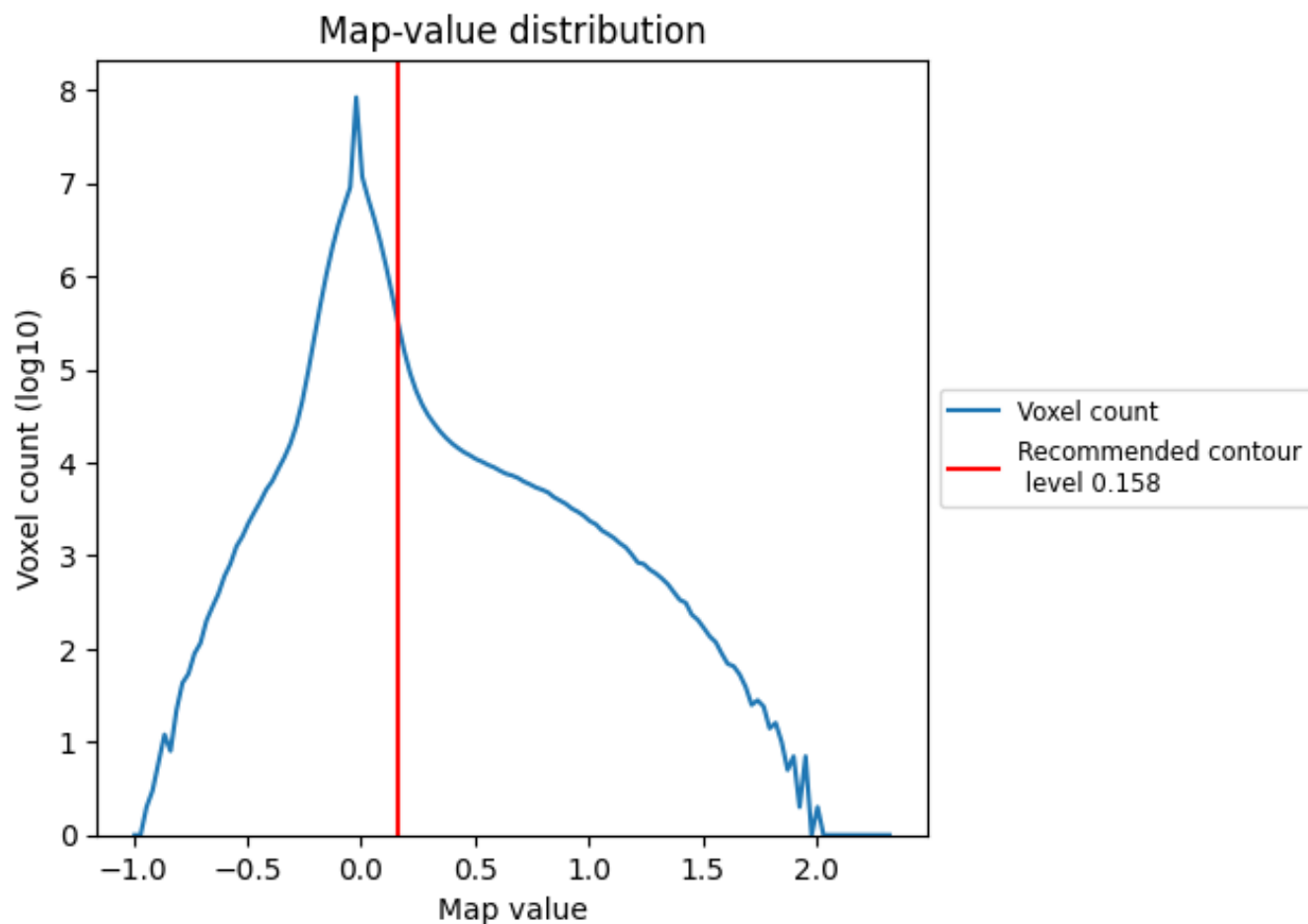
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

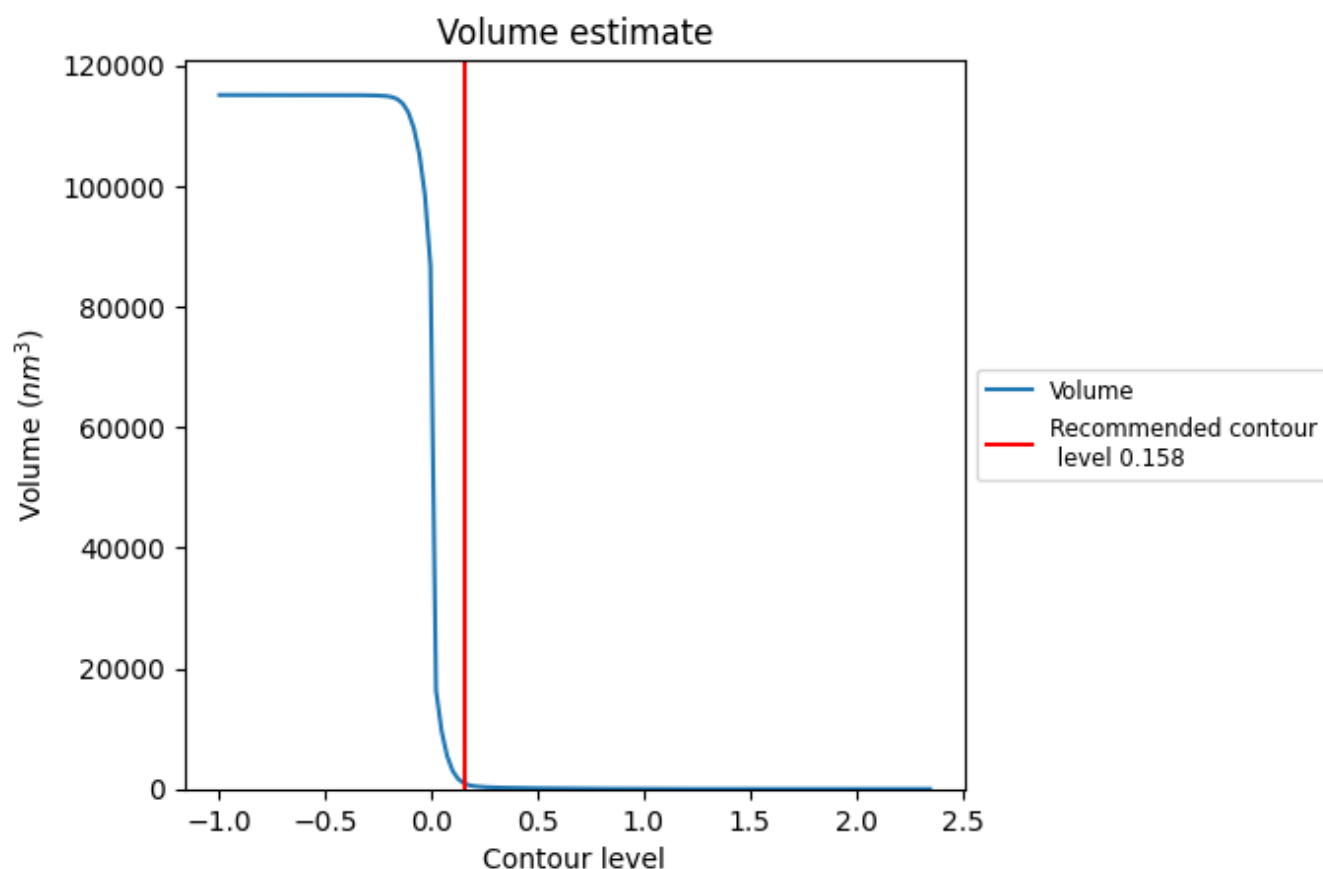
This section contains the results of statistical analysis of the map.

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.

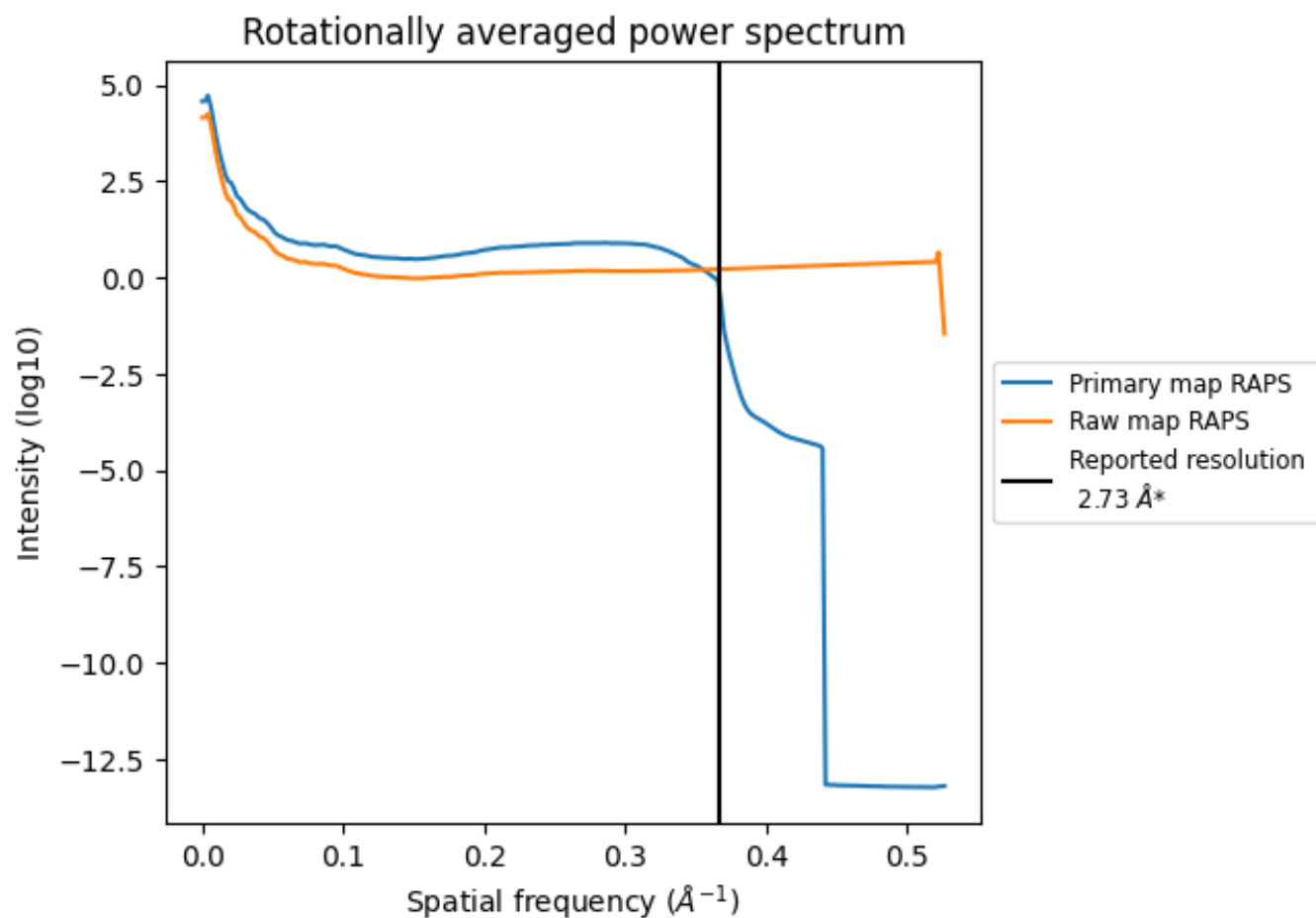
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 919 nm^3 ; this corresponds to an approximate mass of 831 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 ⓘ

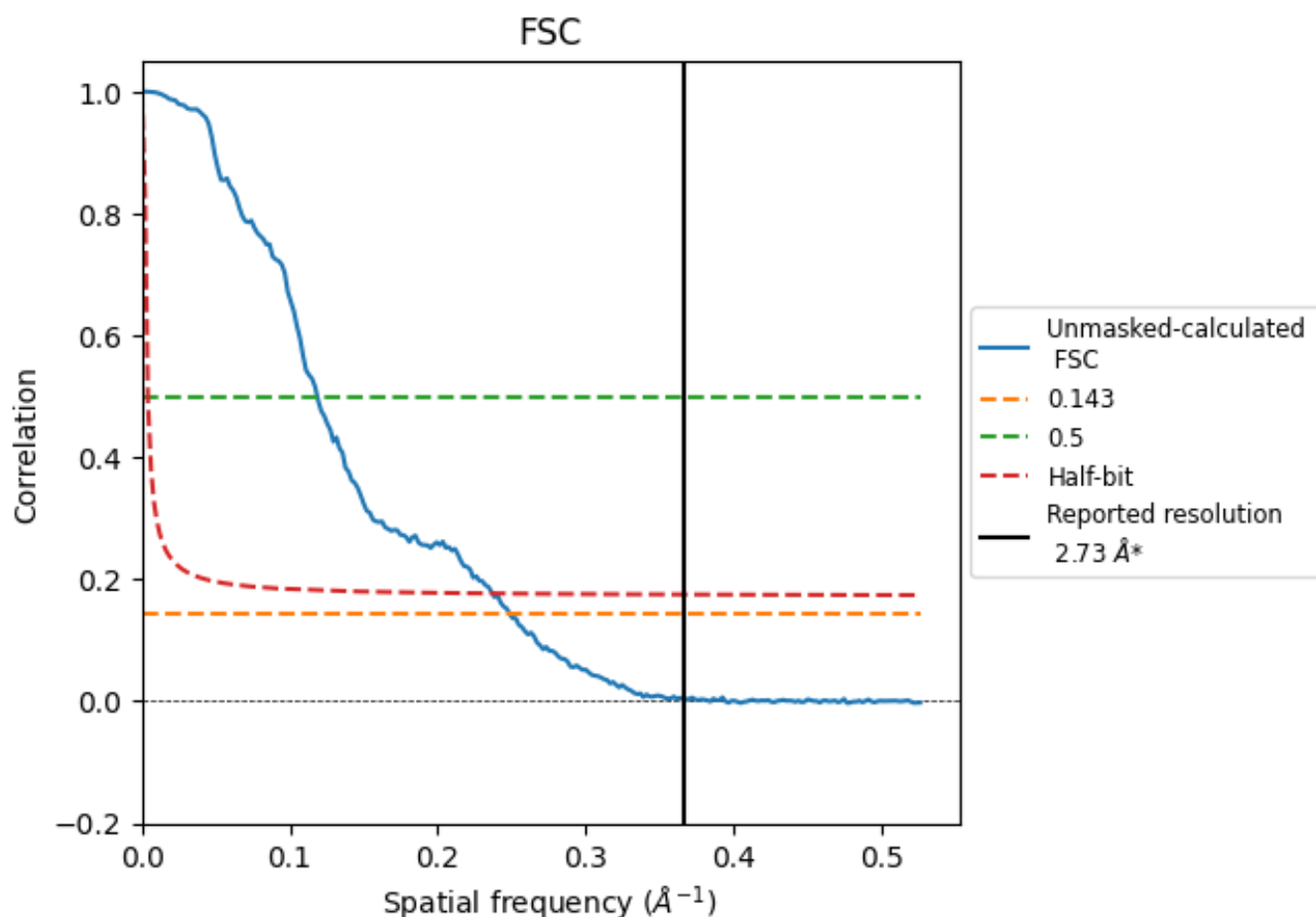


*Reported resolution corresponds to spatial frequency of 0.366 Å⁻¹

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 0.366 Å⁻¹

8.2 Resolution estimates [i](#)

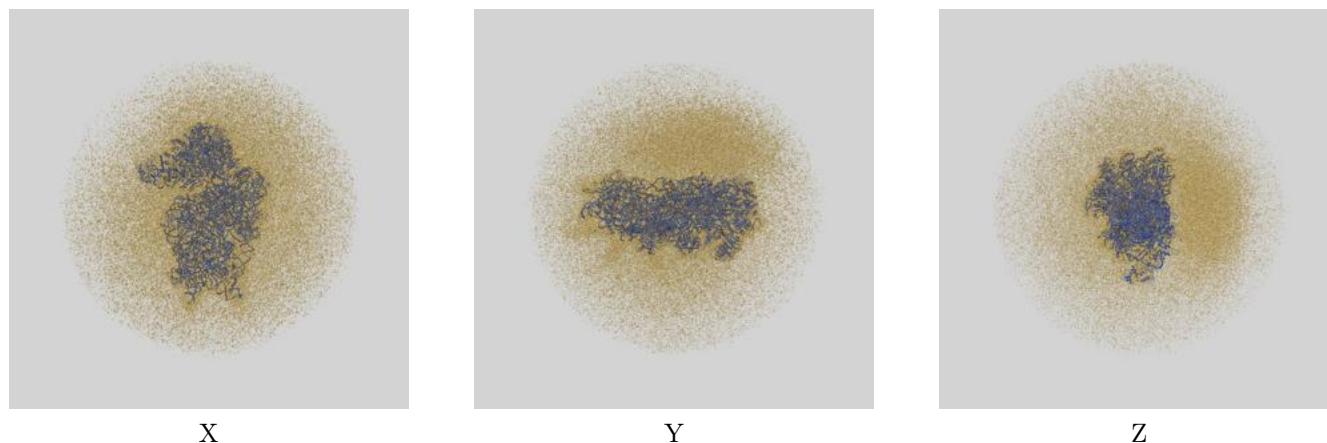
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.73	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.02	8.43	4.22

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.02 differs from the reported value 2.73 by more than 10 %

9 Map-model fit [i](#)

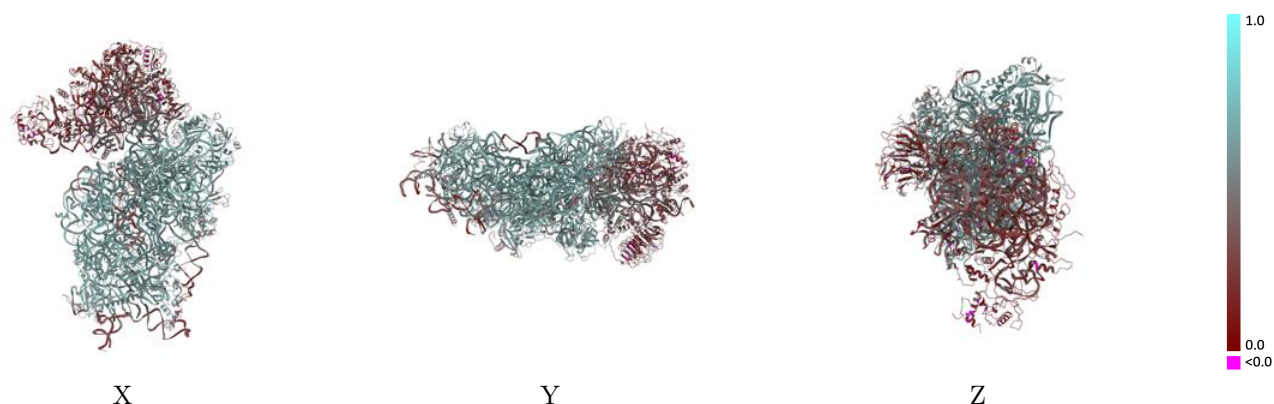
This section contains information regarding the fit between EMDB map EMD-62447 and PDB model 9KMW. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



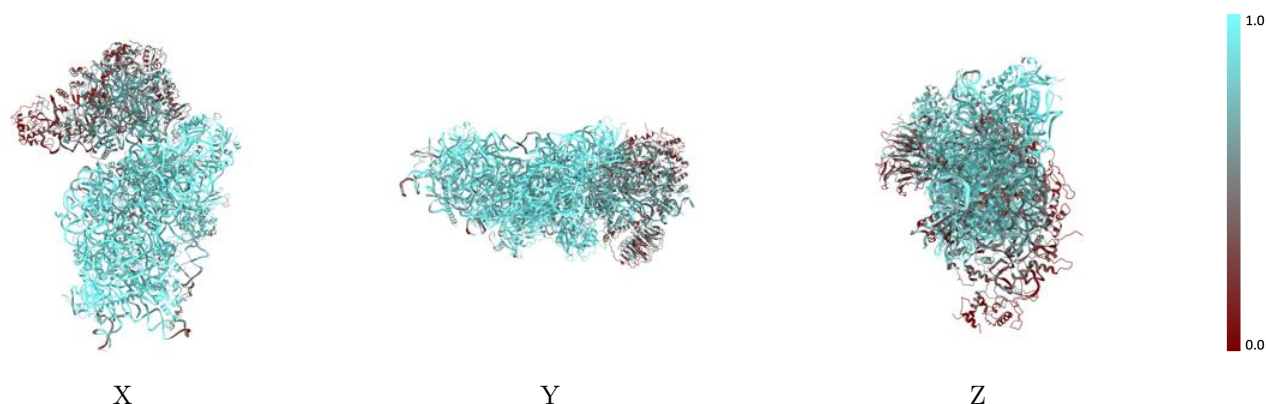
The images above show the 3D surface view of the map at the recommended contour level 0.158 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



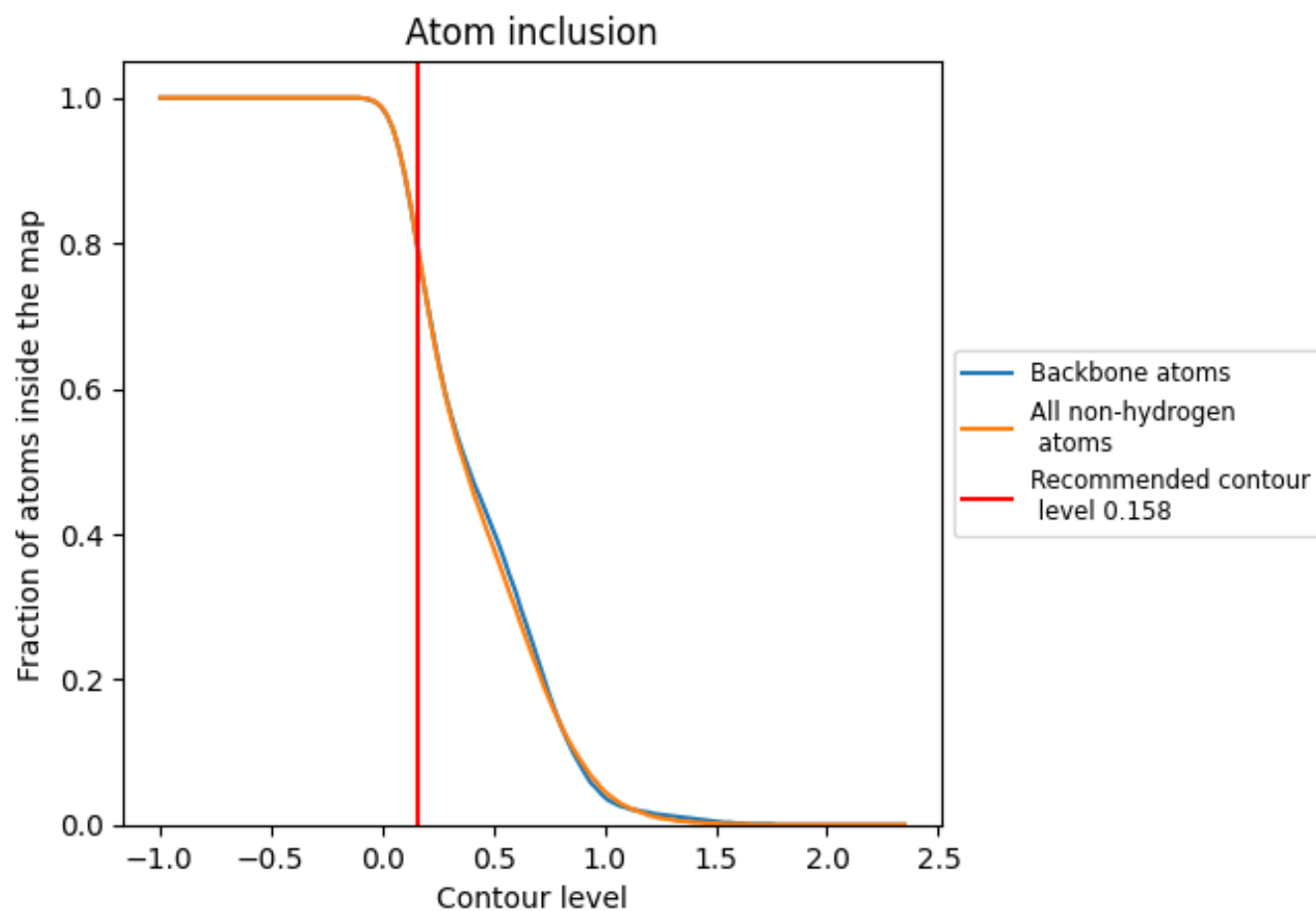
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.158).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 80% 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 (0.158) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.4930
2	 0.8670	 0.5090
A	 0.9360	 0.5980
B	 0.9390	 0.5900
C	 0.9610	 0.6200
D	 0.5520	 0.3530
E	 0.9690	 0.6260
F	 0.5310	 0.3090
G	 0.9230	 0.5630
H	 0.8100	 0.5160
I	 0.9000	 0.5730
J	 0.9760	 0.6250
K	 0.4660	 0.2880
L	 0.9150	 0.6030
M	 0.1540	 0.2340
N	 0.9570	 0.6060
O	 0.9360	 0.5910
P	 0.2900	 0.2600
Q	 0.6570	 0.3620
R	 0.7000	 0.4510
S	 0.2470	 0.2750
T	 0.5420	 0.3040
U	 0.4580	 0.3320
V	 0.9660	 0.6140
W	 0.9800	 0.6360
X	 0.9700	 0.6260
Y	 0.9670	 0.6210
Z	 0.3300	 0.2550
a	 0.9520	 0.6080
b	 0.8320	 0.5120
c	 0.5120	 0.3460
d	 0.6240	 0.3390
e	 0.8810	 0.5820
f	 0.1430	 0.2520
g	 0.4170	 0.2720



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Chain	Atom inclusion	Q-score
h	 0.9120	 0.5910
n	 0.9060	 0.5990