



Full wwPDB EM Validation Report ⓘ

Jul 8, 2026 – 12:53 PM JST

PDB ID : 9KMV / pdb_00009kmv
EMDB ID : EMD-62446
Title : SARSr-MpCoV-GX Nsp1 bound to the Human 40S Ribosomal subunit-State1
Authors : Yuan, S.; Yan, R.; Wu, M.
Deposited on : 2024-11-18
Resolution : 2.65 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

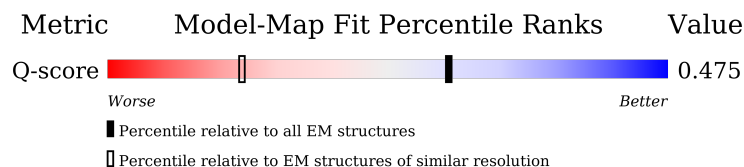
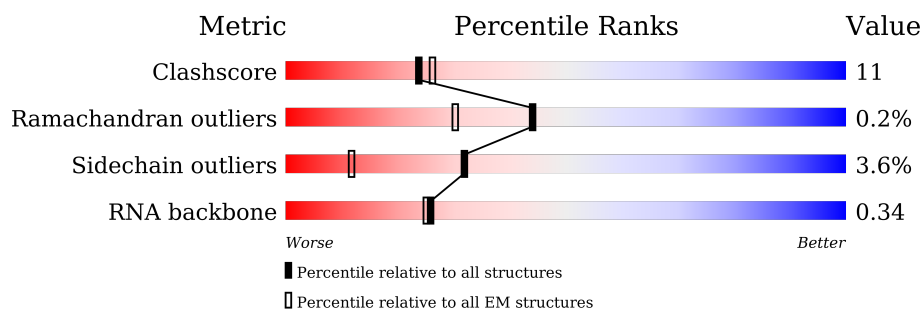
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

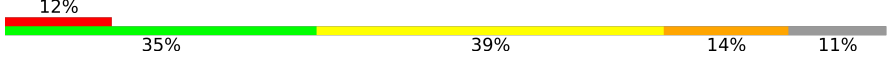
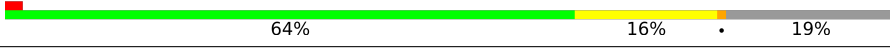
The reported resolution of this entry is 2.65 Å.

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.



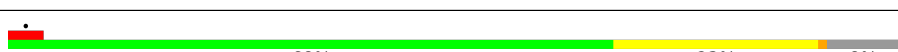
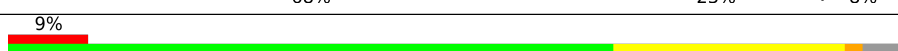
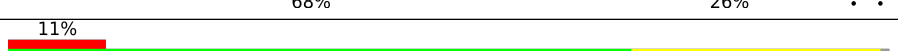
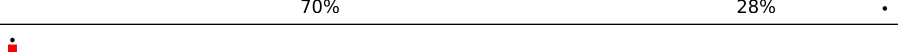
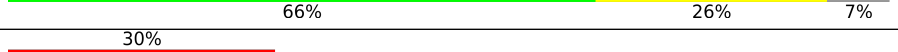
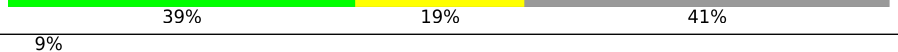
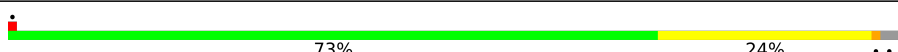
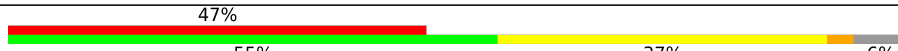
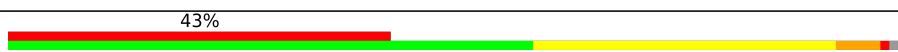
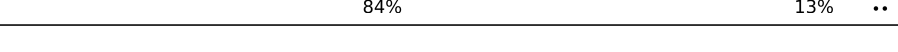
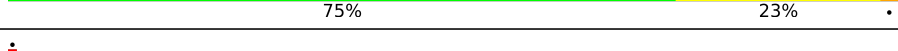
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9050 (2.15 - 3.15)

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% 18%
30	c	62	50% 66% 32%
31	d	55	13% 78% 20%
32	e	56	12% 82% 16%
33	f	74	95% 80% 20%
34	g	315	63% 72% 24%
35	h	25	60% 28% 12%
36	n	180	15% 83%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 74606 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	1662	Total	C	N	O	P	0	0
			35455	15839	6371	11592	1653		

- 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		

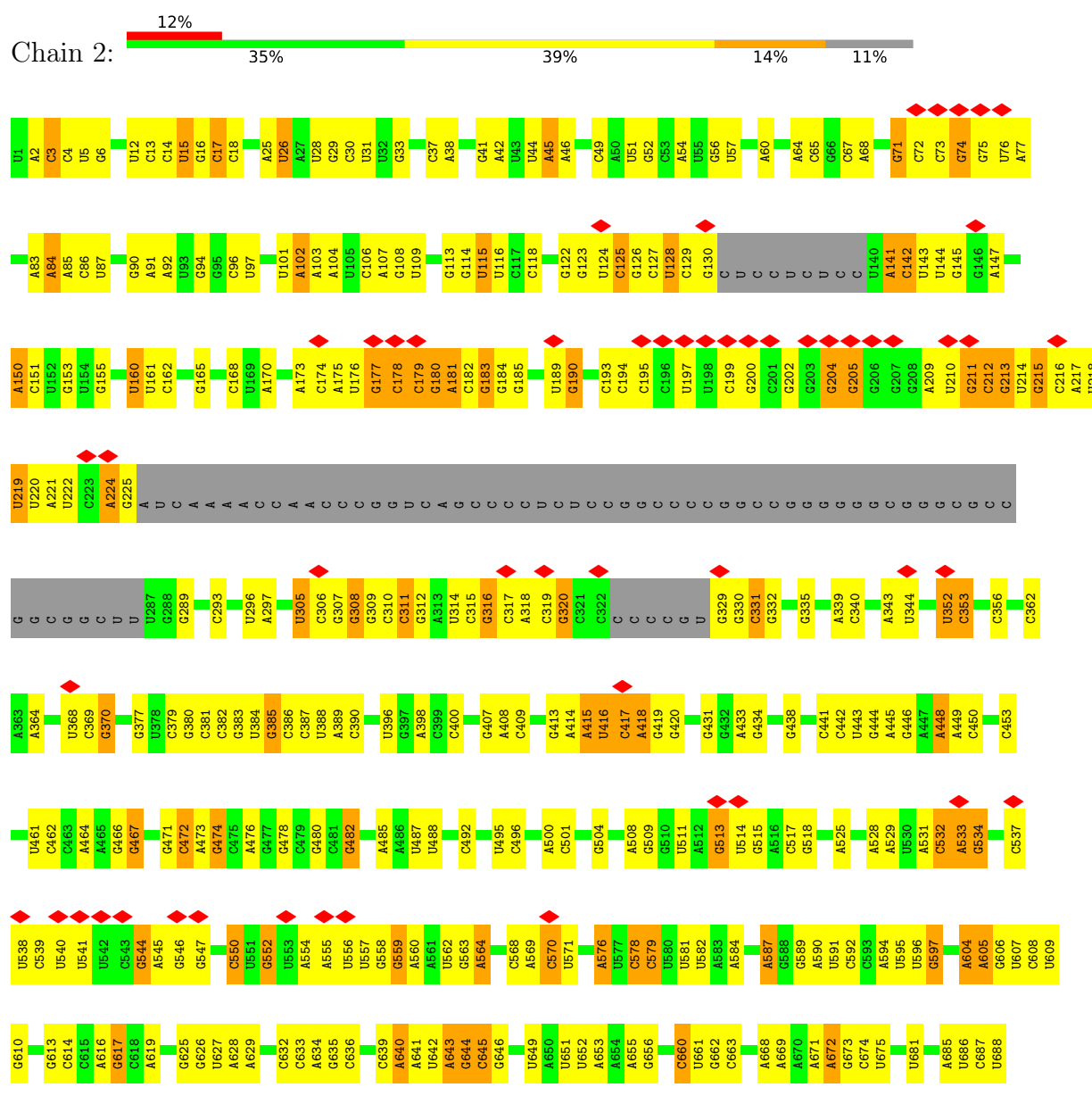
- Molecule 36 is a protein called ORF1ab polyprotein.

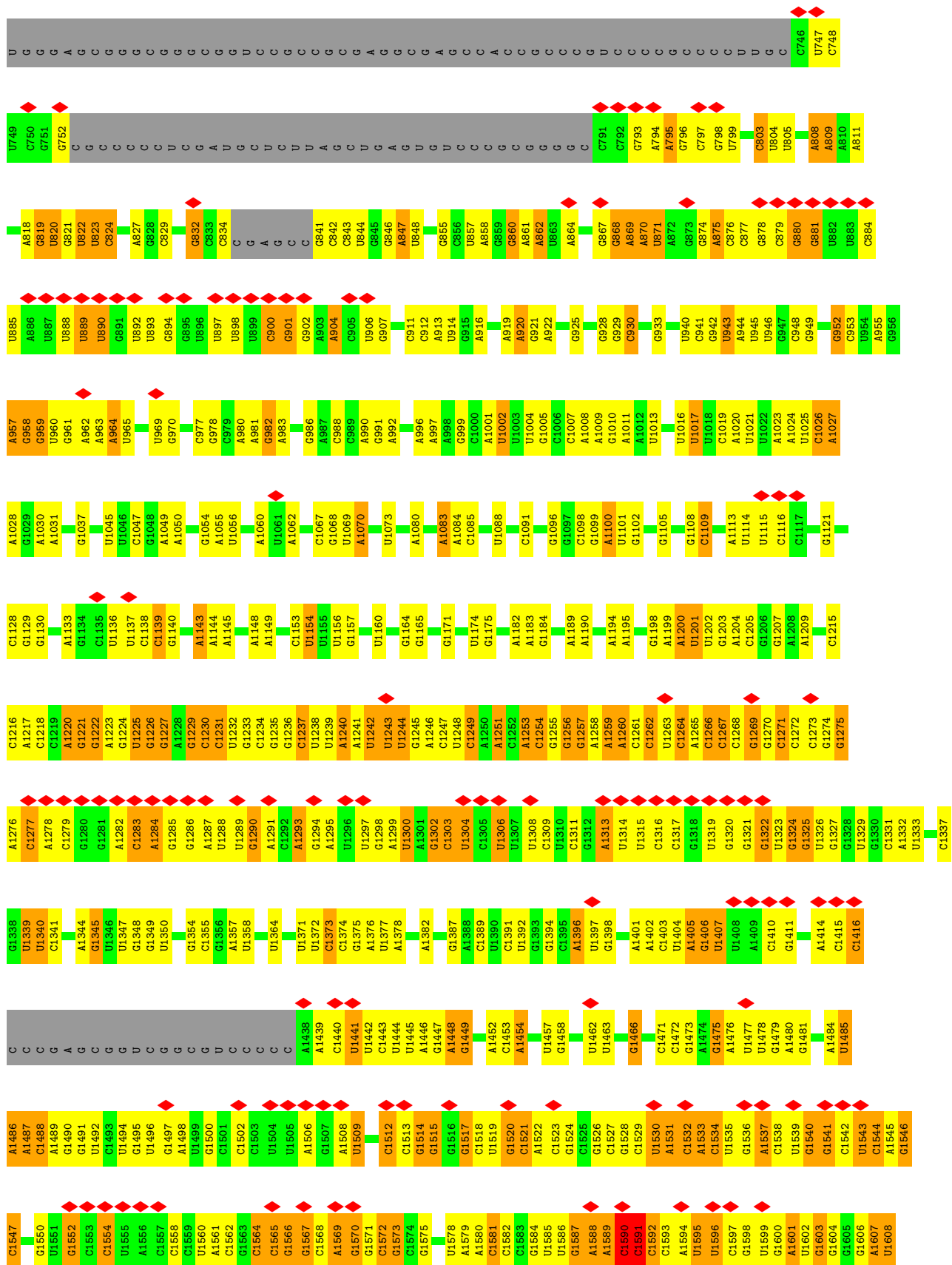
Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	30	Total	C	N	O	S	0	0
			238	144	44	49	1		

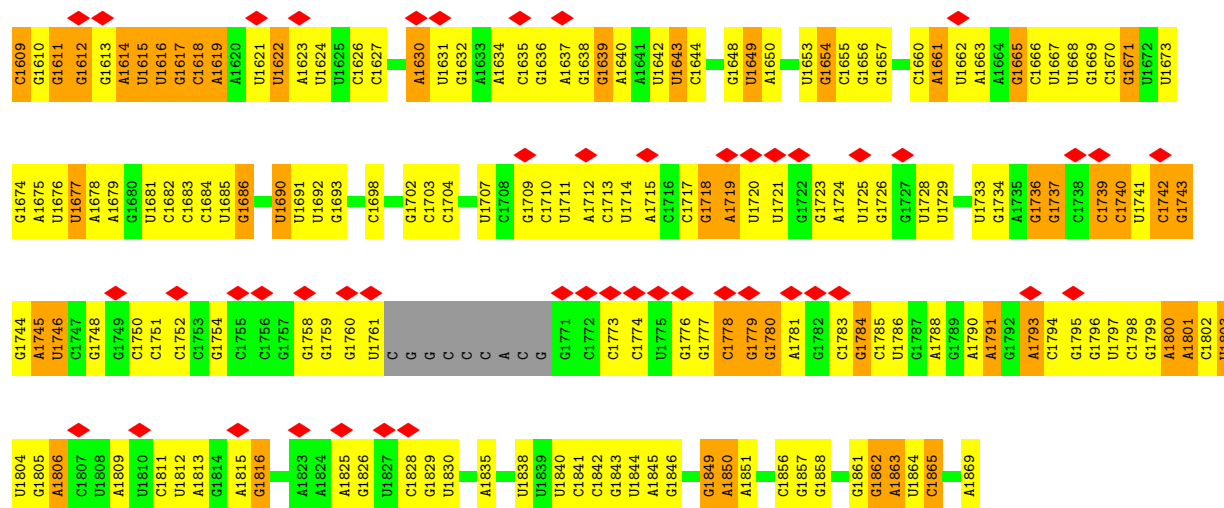
3 Residue-property plots

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.

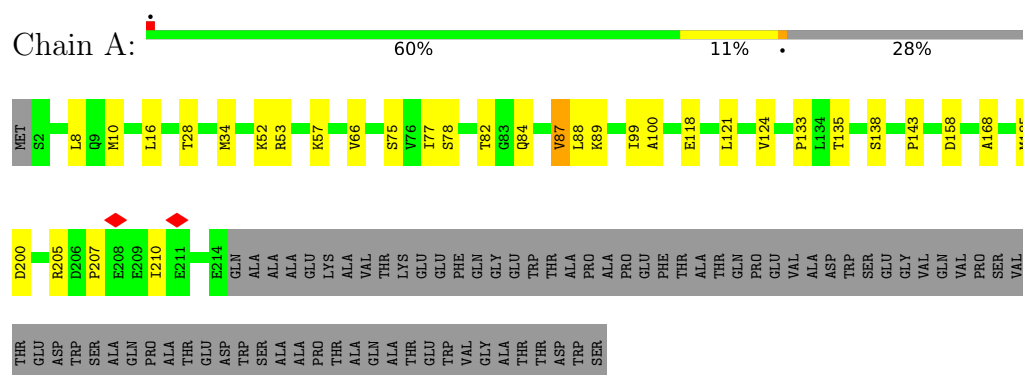
• Molecule 1: 18S ribosomal RNA



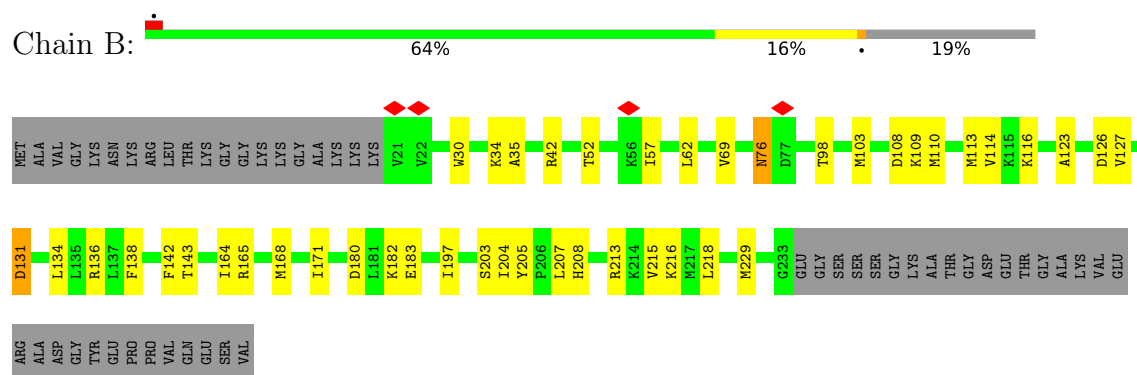




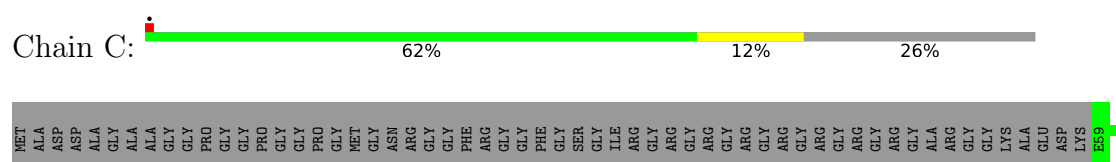
• Molecule 2: Small ribosomal subunit protein uS2



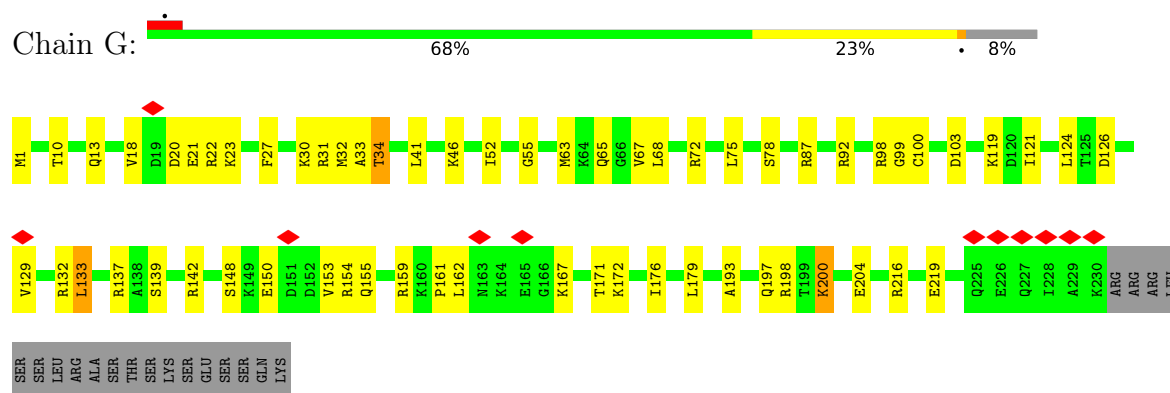
• Molecule 3: Small ribosomal subunit protein eS1



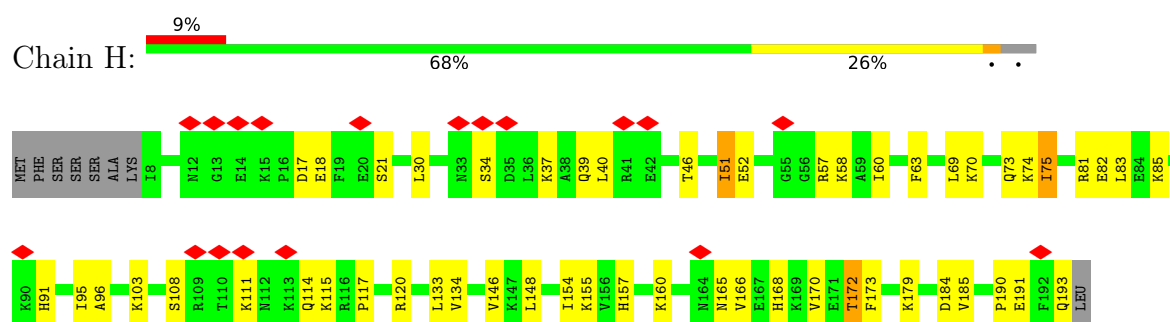
• Molecule 4: Small ribosomal subunit protein uS5



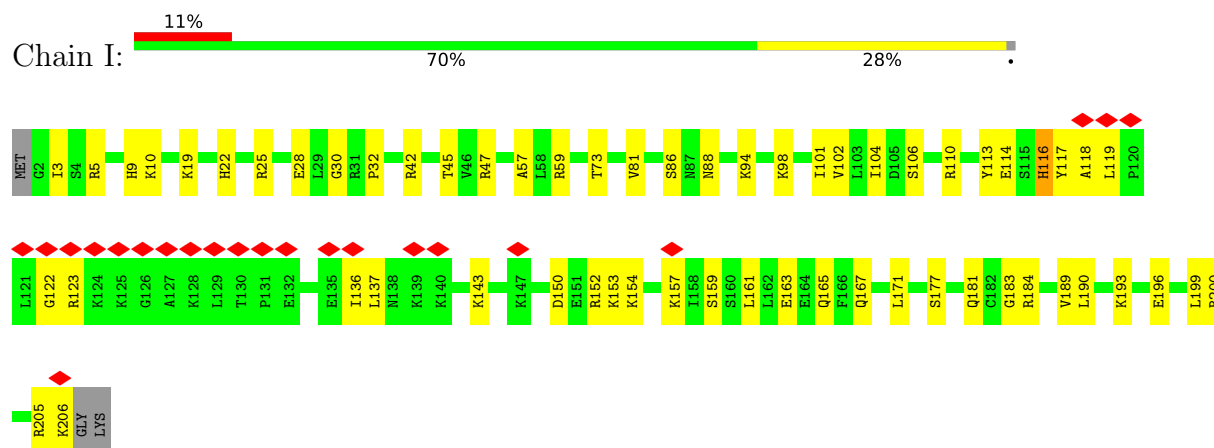
- Molecule 8: Small ribosomal subunit protein eS6



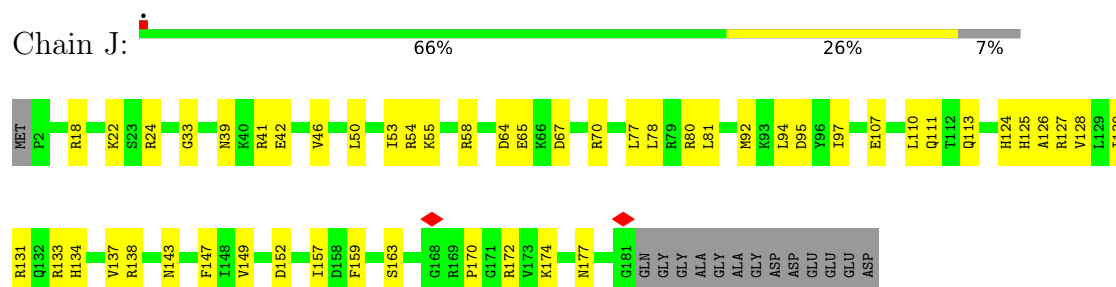
- Molecule 9: Small ribosomal subunit protein eS7



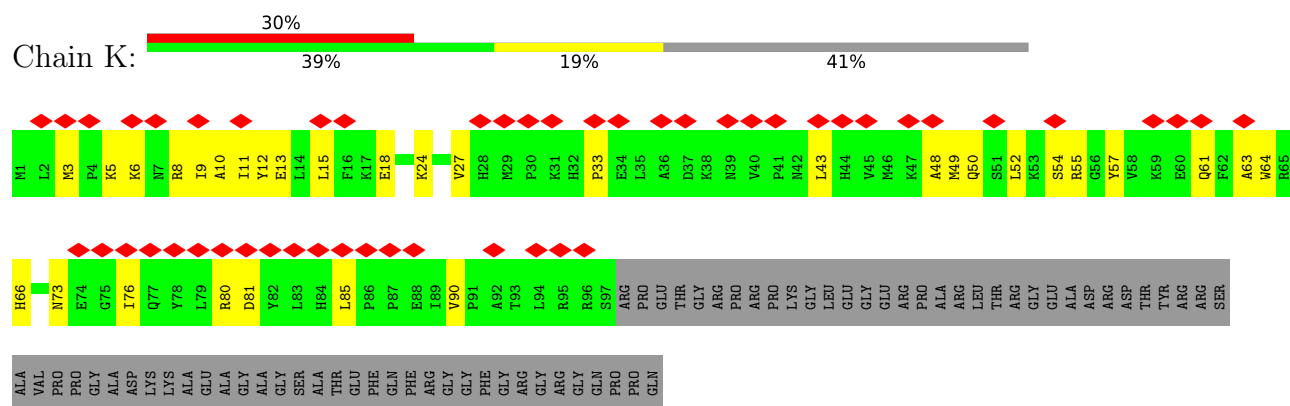
- Molecule 10: Small ribosomal subunit protein eS8



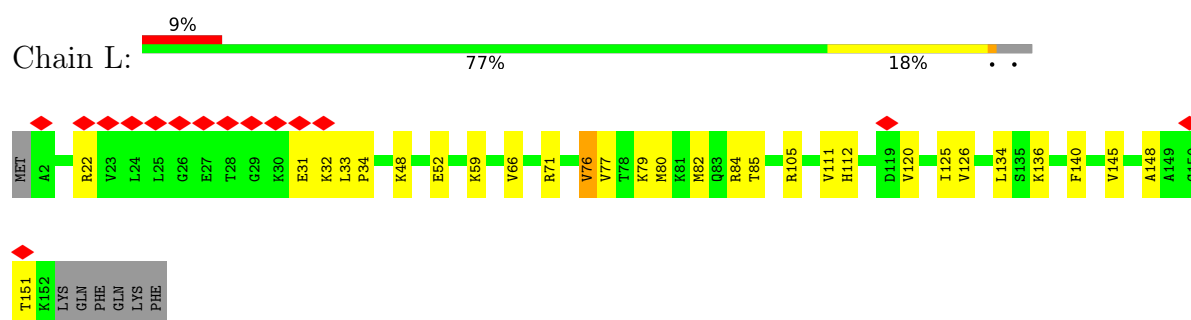
- Molecule 11: Small ribosomal subunit protein uS4



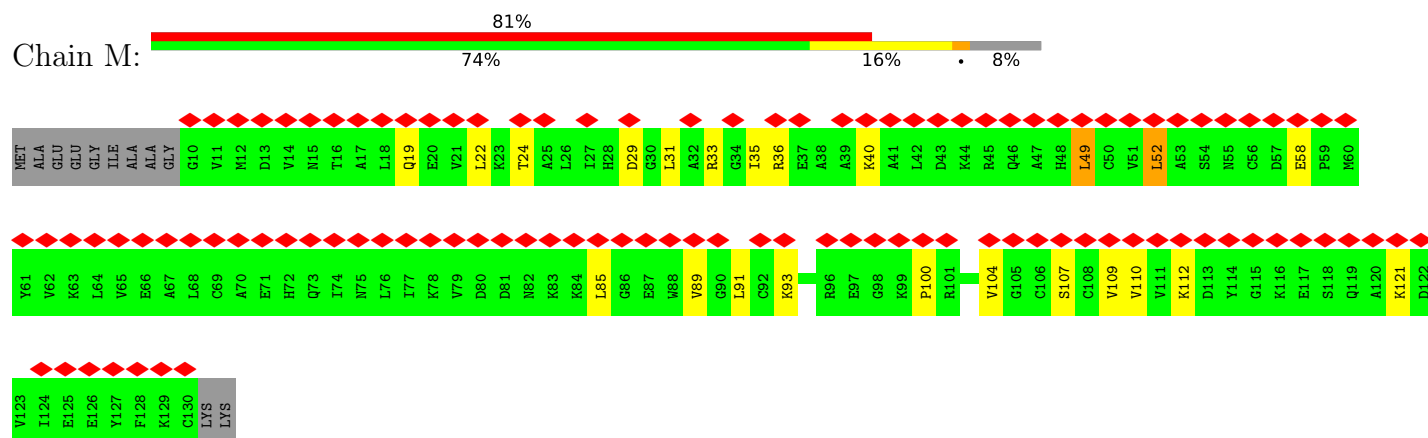
- Molecule 12: Small ribosomal subunit protein eS10



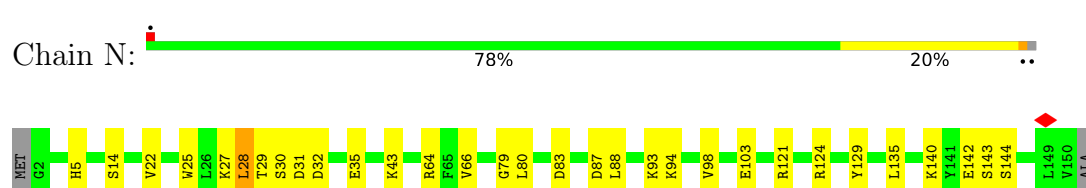
- Molecule 13: Small ribosomal subunit protein uS17



- Molecule 14: Small ribosomal subunit protein eS12



- Molecule 15: Small ribosomal subunit protein uS15

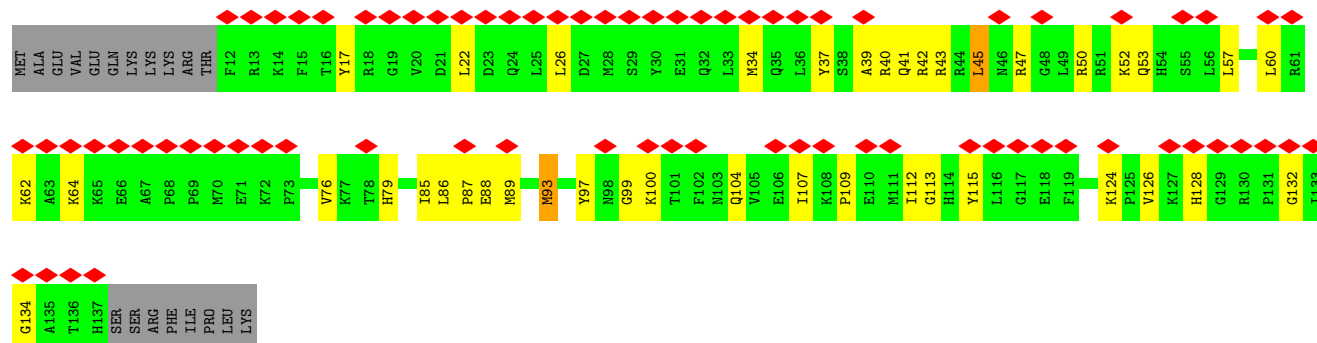


- Molecule 16: Small ribosomal subunit protein uS11

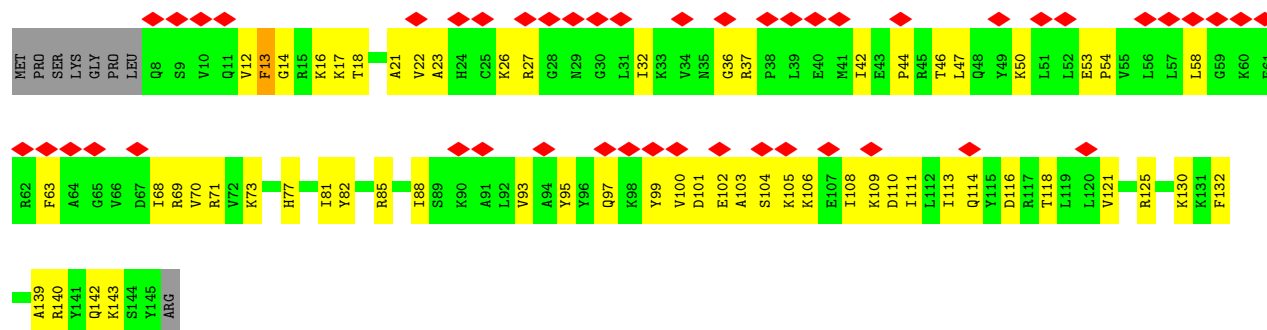




• Molecule 17: Small ribosomal subunit protein uS19



• Molecule 18: Small ribosomal subunit protein uS9

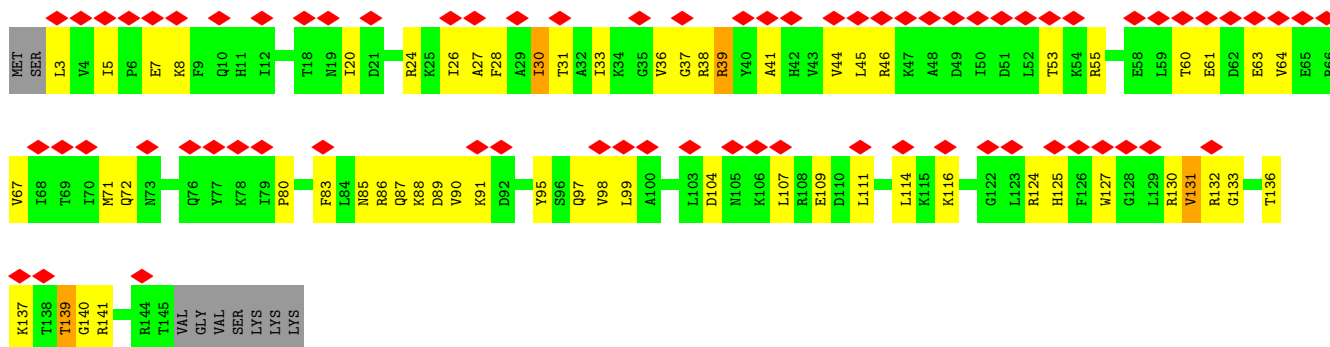


• Molecule 19: Small ribosomal subunit protein eS17



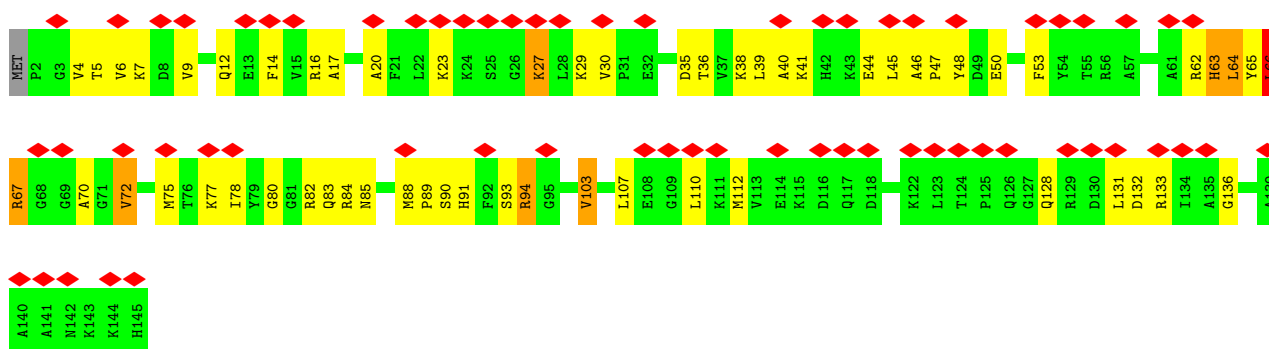
• Molecule 20: Small ribosomal subunit protein uS13





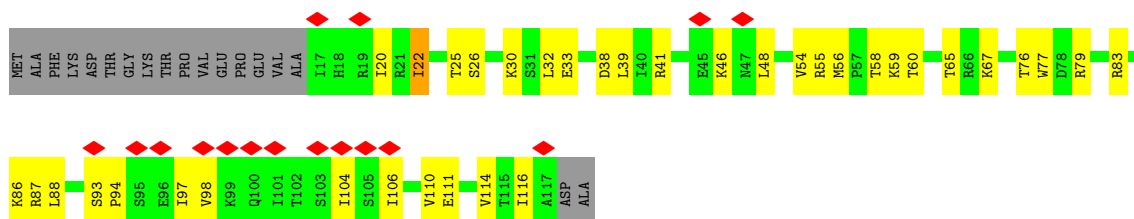
- Molecule 21: Small ribosomal subunit protein eS19

Chain T:



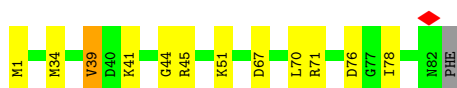
- Molecule 22: Small ribosomal subunit protein uS10

Chain U:



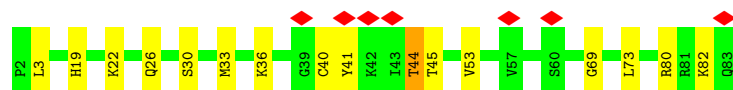
- Molecule 23: Small ribosomal subunit protein eS21

Chain V:

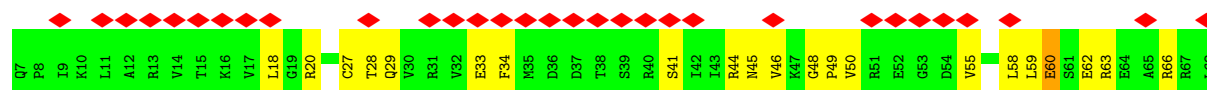


- Molecule 24: Small ribosomal subunit protein uS8

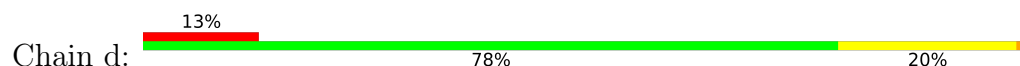
Chain W:



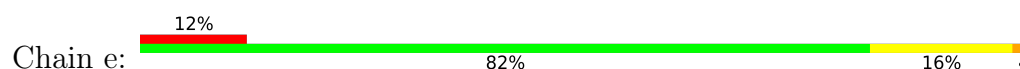
- Molecule 30: Small ribosomal subunit protein eS28



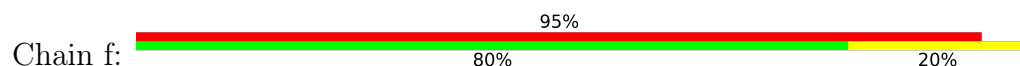
- Molecule 31: Small ribosomal subunit protein uS14



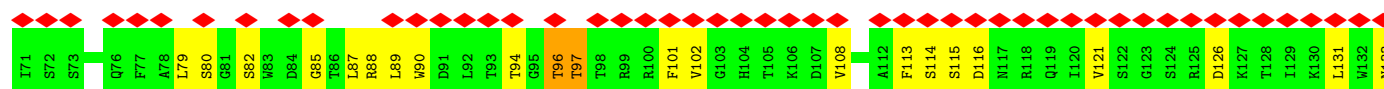
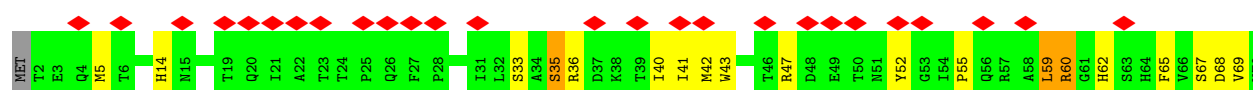
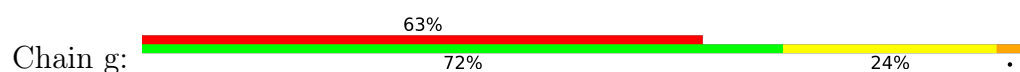
- Molecule 32: Small ribosomal subunit protein eS30

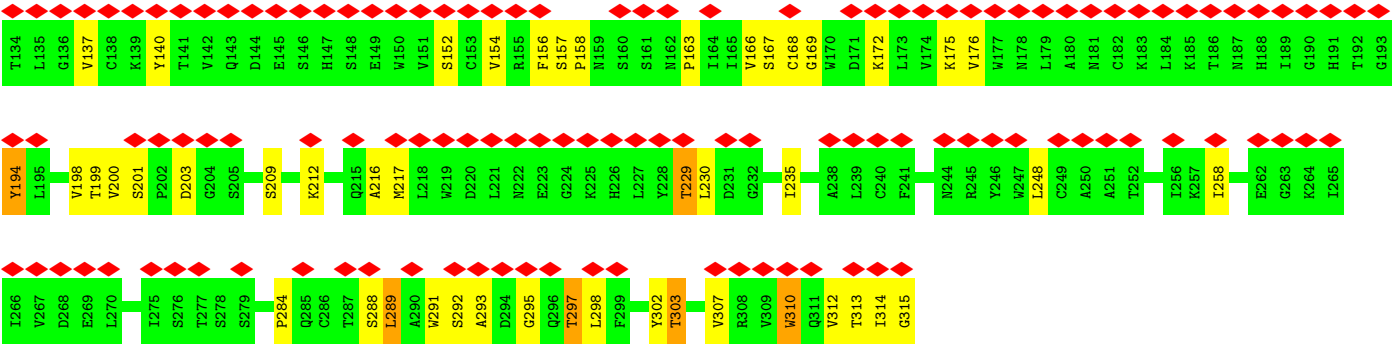


- Molecule 33: Small ribosomal subunit protein eS31



- Molecule 34: Small ribosomal subunit protein RACK1

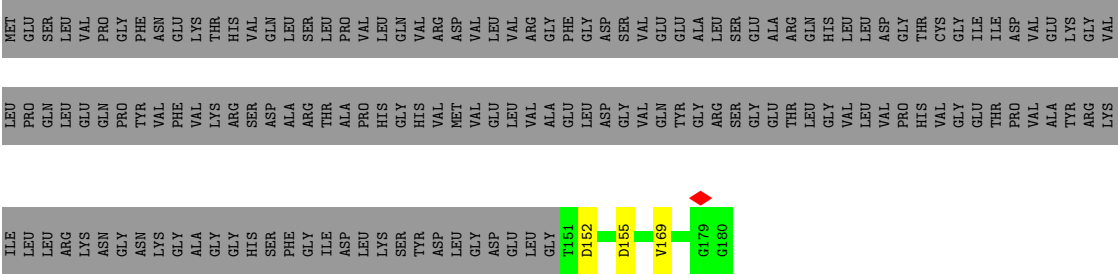




• Molecule 35: Small ribosomal subunit protein eS32



• Molecule 36: ORF1ab polypeptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91626	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	2.495	Depositor
Minimum map value	-1.191	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.2	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	0.17	0/39651	0.31	4/61801 (0.0%)
2	A	0.15	0/1723	0.30	0/2341
3	B	0.15	0/1756	0.32	0/2350
4	C	0.16	0/1726	0.34	0/2332
5	D	0.18	0/1780	0.42	0/2397
6	E	0.16	0/2118	0.32	0/2849
7	F	0.24	0/1516	0.65	1/2037 (0.0%)
8	G	0.16	0/1887	0.35	0/2513
9	H	0.17	0/1524	0.37	0/2042
10	I	0.15	0/1711	0.35	0/2282
11	J	0.15	0/1524	0.34	0/2035
12	K	0.20	0/840	0.46	0/1133
13	L	0.15	0/1250	0.31	0/1673
14	M	0.11	0/945	0.35	0/1269
15	N	0.16	0/1226	0.33	0/1649
16	O	0.17	0/1023	0.38	0/1372
17	P	0.18	0/1058	0.43	0/1414
18	Q	0.19	0/1114	0.52	1/1492 (0.1%)
19	R	0.15	0/1082	0.38	0/1452
20	S	0.18	0/1202	0.49	0/1610
21	T	0.37	0/1143	0.70	3/1530 (0.2%)
22	U	0.16	0/813	0.39	0/1092
23	V	0.17	0/631	0.36	0/844
24	W	0.18	0/1051	0.35	0/1406
25	X	0.15	0/1116	0.33	0/1490
26	Y	0.15	0/1031	0.32	0/1370
27	Z	0.16	0/580	0.40	0/780
28	a	0.18	0/807	0.36	0/1082
29	b	0.14	0/654	0.33	0/876
30	c	0.15	0/491	0.37	0/656
31	d	0.15	0/470	0.38	0/623
32	e	0.14	0/447	0.36	0/587
33	f	0.12	0/623	0.34	0/822
34	g	0.15	0/2498	0.39	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.13	0/214	0.27	0/272
36	n	0.14	0/242	0.26	0/325
All	All	0.17	0/79467	0.35	9/115197 (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
7	F	0	3
16	O	0	1
All	All	0	4

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	T	72	VAL	N-CA-C	7.89	120.96	111.09
1	2	1591	C	C2'-C3'-O3'	-7.79	102.01	113.70
18	Q	12	VAL	N-CA-C	-6.19	107.25	113.20
21	T	66	LEU	N-CA-C	-6.06	105.80	113.43
7	F	183	GLY	N-CA-C	5.48	126.16	113.18
1	2	1590	C	P-O3'-C3'	5.42	128.33	120.20
21	T	63	HIS	CB-CA-C	5.41	119.88	110.68
1	2	1591	C	C4'-C3'-O3'	5.33	120.99	113.00
1	2	550	C	O3'-P-O5'	-5.08	96.38	104.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	F	142	SER	Peptide
7	F	180	ALA	Peptide
7	F	183	GLY	Peptide
16	O	137	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	35455	0	17923	645	0
2	A	1686	0	1688	26	0
3	B	1729	0	1803	27	0
4	C	1690	0	1777	23	0
5	D	1752	0	1848	66	0
6	E	2076	0	2177	46	0
7	F	1495	0	1549	91	0
8	G	1864	0	2018	48	0
9	H	1501	0	1593	36	0
10	I	1682	0	1769	51	0
11	J	1499	0	1618	37	0
12	K	816	0	841	23	0
13	L	1229	0	1302	20	0
14	M	935	0	964	17	0
15	N	1202	0	1289	22	0
16	O	1010	0	1034	29	0
17	P	1037	0	1082	32	0
18	Q	1097	0	1161	53	0
19	R	1068	0	1121	33	0
20	S	1184	0	1244	52	0
21	T	1123	0	1153	63	0
22	U	803	0	873	33	0
23	V	625	0	628	12	0
24	W	1034	0	1080	24	0
25	X	1098	0	1167	21	0
26	Y	1014	0	1082	28	0
27	Z	574	0	627	14	0
28	a	794	0	849	20	0
29	b	641	0	665	12	0
30	c	489	0	514	19	0
31	d	459	0	452	13	0
32	e	442	0	487	10	0
33	f	611	0	638	12	0
34	g	2441	0	2396	61	0
35	h	213	0	258	5	0
36	n	238	0	219	2	0
All	All	74606	0	58889	1447	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 (1447) 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)
1:2:531:A:N6	1:2:552:G:H1	1.45	1.12
1:2:1590:C:H3'	1:2:1591:C:C2	2.01	0.94
1:2:1243:U:H3	1:2:1264:C:H42	0.94	0.92
1:2:1243:U:H3	1:2:1264:C:N4	1.68	0.90
1:2:141:A:N6	1:2:177:G:C4	2.42	0.88
1:2:1484:A:H2'	1:2:1485:U:H5	1.37	0.87
1:2:1538:C:H3'	1:2:1593:C:H5	1.39	0.85
21:T:64:LEU:C	21:T:66:LEU:H	1.82	0.83
1:2:13:C:H5	1:2:1198:G:H1	1.24	0.83
1:2:531:A:H61	1:2:552:G:H1	0.82	0.81
1:2:1748:G:H1	1:2:1786:U:H3	1.27	0.81
1:2:925:G:H1	1:2:1017:U:H3	1.28	0.79
8:G:22:ARG:H	8:G:22:ARG:HD3	1.49	0.78
18:Q:132:PHE:O	18:Q:140:ARG:NH1	2.17	0.77
1:2:1581:C:H5'	1:2:1582:C:H5	1.49	0.77
1:2:581:U:OP1	11:J:133:ARG:NH2	2.17	0.77
1:2:560:A:OP2	11:J:177:ASN:ND2	2.18	0.77
1:2:64:A:H2	1:2:83:A:H62	1.30	0.77
7:F:159:ARG:O	7:F:163:PHE:N	2.12	0.77
5:D:99:ILE:HG23	5:D:173:ARG:HH12	1.51	0.76
1:2:1543:U:OP2	21:T:78:ILE:HD13	1.85	0.76
1:2:962:A:OP2	1:2:963:A:N6	2.13	0.75
1:2:1611:G:H1'	20:S:87:GLN:HG3	1.66	0.75
1:2:1544:C:N4	21:T:80:GLY:O	2.19	0.75
1:2:1607:A:H2'	1:2:1608:U:C6	2.22	0.75
1:2:1591:C:OP2	21:T:82:ARG:HG2	1.87	0.75
21:T:64:LEU:C	21:T:66:LEU:N	2.44	0.75
5:D:59:LEU:HA	5:D:66:ILE:HG12	1.69	0.74
1:2:1223:A:H61	1:2:1644:C:H42	1.34	0.74
1:2:1546:G:O6	1:2:1655:C:O2'	2.06	0.73
7:F:112:LEU:HA	7:F:178:ILE:HD13	1.70	0.73
1:2:919:A:OP2	15:N:64:ARG:NH2	2.19	0.73
5:D:116:ARG:NH1	36:n:152:ASP:OD2	2.22	0.73
1:2:870:A:H4'	1:2:871:U:H5'	1.71	0.72
34:g:152:SER:H	34:g:169:GLY:HA2	1.53	0.72
1:2:1537:A:H5''	1:2:1591:C:H41	1.52	0.72
1:2:1233:G:N2	1:2:1235:G:H22	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1538:C:H5''	1:2:1593:C:H41	1.54	0.72
1:2:1024:A:OP2	15:N:124:ARG:NH2	2.23	0.71
7:F:108:PRO:O	7:F:112:LEU:HB2	1.90	0.71
10:I:119:LEU:HA	10:I:153:LYS:HG3	1.73	0.71
7:F:145:ARG:NH1	7:F:149:GLN:OE1	2.24	0.70
9:H:154:ILE:HB	9:H:185:VAL:HG22	1.73	0.70
1:2:1453:C:H5	1:2:1476:A:H2	1.40	0.70
18:Q:58:LEU:HD22	18:Q:108:ILE:HD11	1.71	0.70
1:2:928:G:H1	1:2:1013:U:H3	1.40	0.70
1:2:1533:A:OP1	7:F:81:ARG:NH2	2.25	0.70
10:I:81:VAL:HG12	10:I:102:VAL:HG12	1.74	0.70
1:2:377:G:H5'	10:I:98:LYS:HB3	1.71	0.70
5:D:135:GLU:HB2	5:D:153:VAL:HG12	1.72	0.70
1:2:320:G:H1	1:2:331:C:H42	1.37	0.70
1:2:587:A:H5'	1:2:592:C:H41	1.57	0.69
24:W:111:MET:HG3	24:W:115:GLU:HB3	1.73	0.69
34:g:209:SER:HB3	34:g:217:MET:HB2	1.74	0.69
19:R:22:THR:HB	34:g:212:LYS:HG2	1.73	0.69
1:2:880:G:O2'	1:2:881:G:OP2	2.08	0.69
1:2:1143:A:H5'	4:C:190:SER:HB3	1.74	0.69
1:2:1406:G:N2	1:2:1442:U:O4	2.23	0.69
1:2:1293:A:O3'	17:P:62:LYS:NZ	2.26	0.69
34:g:152:SER:OG	34:g:168:CYS:SG	2.47	0.69
1:2:1243:U:O2	1:2:1264:C:N3	2.26	0.69
7:F:174:ALA:O	7:F:178:ILE:HG12	1.92	0.69
4:C:76:LYS:HA	4:C:76:LYS:HE3	1.74	0.69
9:H:155:LYS:NZ	24:W:51:GLU:OE2	2.23	0.69
20:S:131:VAL:O	20:S:132:ARG:NH1	2.26	0.69
1:2:818:A:OP1	11:J:80:ARG:NH2	2.26	0.69
7:F:104:THR:HG21	7:F:108:PRO:HG3	1.73	0.69
1:2:1290:G:N2	1:2:1302:G:O2'	2.24	0.68
1:2:1537:A:H5''	1:2:1591:C:N4	2.08	0.68
1:2:1648:G:N2	1:2:1675:A:OP2	2.20	0.68
15:N:29:THR:OG1	15:N:32:ASP:OD1	2.10	0.68
34:g:114:SER:OG	34:g:116:ASP:OD1	2.12	0.68
1:2:570:C:N4	1:2:576:A:OP1	2.26	0.68
5:D:16:ILE:HG21	31:d:22:ARG:HH11	1.59	0.68
22:U:25:THR:HG22	22:U:86:LYS:HG3	1.74	0.68
1:2:1265:A:H5'	1:2:1267:C:H5	1.58	0.68
16:O:40:THR:HG21	16:O:74:ALA:HB2	1.75	0.68
1:2:104:A:OP2	1:2:352:U:N3	2.25	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:640:A:H2'	1:2:641:A:C8	2.28	0.68
1:2:1538:C:H3'	1:2:1593:C:C5	2.27	0.68
1:2:957:A:H3'	1:2:958:G:H21	1.58	0.68
21:T:62:ARG:HH22	21:T:63:HIS:HD2	1.39	0.68
7:F:117:ILE:HB	7:F:183:GLY:H	1.57	0.67
5:D:69:LEU:HA	5:D:72:VAL:HG22	1.75	0.67
22:U:98:VAL:HG11	22:U:114:VAL:HG11	1.74	0.67
1:2:1653:U:H2'	1:2:1654:G:C8	2.30	0.67
6:E:100:ARG:NH2	6:E:121:TYR:O	2.27	0.67
1:2:1609:C:H5'	20:S:131:VAL:HG12	1.77	0.67
20:S:36:VAL:HG23	20:S:67:VAL:HG11	1.77	0.67
1:2:1739:C:H5	10:I:32:PRO:HG2	1.59	0.67
20:S:90:VAL:HG13	20:S:91:LYS:HG3	1.75	0.67
1:2:1484:A:H2'	1:2:1485:U:C5	2.24	0.67
1:2:1616:U:O2'	1:2:1617:G:N7	2.27	0.67
8:G:193:ALA:O	8:G:197:GLN:HG3	1.95	0.67
16:O:34:PHE:HB3	16:O:41:PHE:HB2	1.77	0.67
20:S:86:ARG:HD2	20:S:89:ASP:HB2	1.77	0.67
1:2:1512:C:O2	1:2:1514:G:N2	2.27	0.66
7:F:77:MET:HE2	7:F:84:GLY:HA2	1.77	0.66
7:F:110:GLN:O	7:F:114:ASN:HB2	1.95	0.66
1:2:928:G:H2'	1:2:929:G:C8	2.30	0.66
16:O:84:ARG:NH1	16:O:87:GLU:OE2	2.28	0.66
1:2:1569:A:H61	1:2:1613:G:H21	1.42	0.66
7:F:110:GLN:OE1	7:F:114:ASN:ND2	2.29	0.66
1:2:379:C:O2	10:I:5:ARG:NE	2.28	0.66
26:Y:20:ARG:HE	26:Y:22:GLN:HE21	1.42	0.66
6:E:117:GLU:N	6:E:117:GLU:OE1	2.29	0.66
34:g:168:CYS:HB3	34:g:198:VAL:HG22	1.78	0.65
1:2:1590:C:HO2'	1:2:1591:C:P	2.20	0.65
6:E:87:MET:HE3	6:E:123:LEU:HB2	1.78	0.65
7:F:77:MET:HB2	7:F:84:GLY:H	1.60	0.65
34:g:42:MET:HE1	34:g:59:LEU:HG	1.77	0.65
1:2:1589:A:H5''	21:T:93:SER:HB2	1.77	0.65
16:O:53:ILE:HG23	16:O:88:LEU:HD23	1.78	0.65
1:2:562:U:H2'	1:2:563:G:C8	2.31	0.65
1:2:875:A:H62	1:2:911:C:H42	1.43	0.65
1:2:1327:G:H22	1:2:1502:C:H42	1.43	0.65
1:2:1650:A:H5''	18:Q:139:ALA:HB2	1.77	0.65
18:Q:104:SER:O	18:Q:108:ILE:HG22	1.96	0.65
1:2:433:A:H5''	10:I:22:HIS:HB3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:798:G:O2'	9:H:108:SER:OG	2.12	0.65
1:2:1260:A:OP1	1:2:1261:C:N4	2.29	0.65
1:2:1751:C:N4	1:2:1784:G:O6	2.30	0.65
1:2:1286:G:O2'	33:f:94:LYS:NZ	2.30	0.65
1:2:1253:A:H61	1:2:1665:G:H8	1.45	0.64
1:2:1591:C:H3'	1:2:1591:C:H6	1.62	0.64
20:S:72:GLN:OE1	20:S:97:GLN:NE2	2.30	0.64
1:2:1591:C:H2'	1:2:1592:C:C6	2.33	0.64
1:2:1544:C:H5	21:T:80:GLY:H	1.45	0.64
1:2:880:G:H21	1:2:904:A:H62	1.46	0.64
1:2:1091:C:HO2'	24:W:2:VAL:N	1.96	0.64
1:2:1531:A:N6	7:F:80:GLY:O	2.30	0.64
35:h:1:MET:HE1	35:h:9:ARG:HD3	1.79	0.64
1:2:861:A:H1'	1:2:862:A:H2	1.63	0.64
6:E:54:TYR:O	26:Y:15:ASN:ND2	2.29	0.64
7:F:51:HIS:HB2	7:F:90:VAL:HG11	1.80	0.64
34:g:79:LEU:HD11	34:g:113:PHE:HB2	1.78	0.64
1:2:628:A:N6	5:D:144:GLY:O	2.31	0.64
1:2:1590:C:H3'	1:2:1591:C:N1	2.12	0.64
7:F:141:VAL:HG11	7:F:145:ARG:HB3	1.79	0.64
5:D:10:LYS:HE3	22:U:111:GLU:HG2	1.80	0.64
35:h:19:LYS:O	35:h:22:GLN:NE2	2.30	0.64
1:2:1546:G:O2'	1:2:1547:C:O4'	2.15	0.64
1:2:1406:G:N2	1:2:1441:U:O2	2.30	0.64
7:F:114:ASN:HA	7:F:184:SER:HB3	1.80	0.64
12:K:11:ILE:HG21	12:K:48:ALA:HB1	1.80	0.64
1:2:867:G:O2'	1:2:868:G:N7	2.30	0.64
1:2:1591:C:H2'	1:2:1592:C:H6	1.62	0.64
6:E:88:ASP:OD1	6:E:122:LYS:NZ	2.31	0.63
6:E:159:THR:HG23	6:E:227:VAL:HG13	1.79	0.63
34:g:201:SER:OG	34:g:203:ASP:OD1	2.15	0.63
2:A:77:ILE:HB	2:A:124:VAL:HG12	1.81	0.63
7:F:113:VAL:HB	7:F:182:LYS:O	1.97	0.63
1:2:1587:G:N3	21:T:94:ARG:HD3	2.13	0.63
1:2:224:A:N6	1:2:297:A:N1	2.46	0.63
10:I:25:ARG:HB2	10:I:28:GLU:HG3	1.79	0.63
1:2:107:A:H2'	1:2:108:G:C8	2.34	0.63
1:2:1534:C:O2'	27:Z:104:ARG:NH1	2.22	0.63
9:H:165:ASN:O	9:H:168:HIS:NE2	2.32	0.63
1:2:860:G:N2	24:W:107:SER:OG	2.31	0.63
6:E:192:ILE:HB	6:E:243:GLY:HA3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:3:ARG:NH1	24:W:9:ASP:OD2	2.32	0.63
1:2:1758:G:N3	1:2:1759:G:N1	2.47	0.62
11:J:107:GLU:O	11:J:113:GLN:NE2	2.31	0.62
1:2:161:U:O2'	8:G:87:ARG:NH1	2.33	0.62
1:2:1570:G:O2'	1:2:1615:U:OP1	2.15	0.62
16:O:99:ALA:H	16:O:133:THR:HB	1.64	0.62
17:P:26:LEU:HD13	17:P:88:GLU:HB2	1.80	0.62
17:P:93:MET:HE1	17:P:104:GLN:HB2	1.81	0.62
1:2:1453:C:C5	1:2:1476:A:H2	2.17	0.62
1:2:1740:C:O2'	1:2:1742:C:OP2	2.13	0.62
10:I:57:ALA:HB2	10:I:183:GLY:HA2	1.79	0.62
19:R:109:LEU:HG	19:R:111:PHE:HD2	1.64	0.62
18:Q:132:PHE:HZ	22:U:77:TRP:H	1.46	0.62
34:g:166:VAL:HG13	34:g:176:VAL:HG22	1.82	0.62
36:n:152:ASP:HB3	36:n:155:ASP:HB2	1.81	0.62
1:2:14:C:H2'	1:2:15:U:C6	2.35	0.62
1:2:1100:A:OP1	19:R:132:ARG:NH1	2.33	0.62
7:F:160:GLU:HA	7:F:163:PHE:HB3	1.80	0.62
1:2:1013:U:OP1	1:2:1129:G:O2'	2.18	0.62
1:2:1590:C:C3'	1:2:1591:C:C2	2.81	0.62
13:L:77:VAL:HG11	13:L:80:MET:HE3	1.81	0.62
34:g:35:SER:OG	34:g:36:ARG:N	2.28	0.62
1:2:370:G:O2'	10:I:10:LYS:NZ	2.31	0.62
1:2:1203:G:H2'	1:2:1204:A:C8	2.35	0.62
1:2:1446:A:H5''	22:U:58:THR:HG23	1.82	0.62
15:N:79:GLY:O	15:N:80:LEU:HD23	1.99	0.62
1:2:165:G:OP2	1:2:165:G:N2	2.25	0.61
1:2:1221:G:N3	1:2:1677:U:O2'	2.32	0.61
10:I:122:GLY:O	10:I:123:ARG:NH1	2.33	0.61
21:T:4:VAL:HG11	21:T:136:GLY:HA3	1.82	0.61
1:2:846:G:H2'	6:E:19:MET:HG2	1.80	0.61
6:E:182:MET:HB2	6:E:228:ILE:HD11	1.81	0.61
6:E:199:GLU:OE1	6:E:209:HIS:NE2	2.30	0.61
30:c:66:ARG:H	30:c:66:ARG:HD2	1.64	0.61
1:2:122:G:C5	1:2:123:G:H1'	2.35	0.61
6:E:160:ILE:HD12	6:E:169:ILE:HG12	1.81	0.61
21:T:64:LEU:HD13	21:T:70:ALA:HB2	1.83	0.61
16:O:131:ASP:OD1	16:O:133:THR:HG22	2.00	0.61
11:J:53:ILE:HD13	11:J:81:LEU:HD21	1.82	0.61
20:S:36:VAL:HG21	20:S:64:VAL:HG23	1.82	0.61
34:g:216:ALA:HB3	34:g:230:LEU:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:380:G:OP2	10:I:181:GLN:NE2	2.33	0.61
1:2:212:C:H2'	1:2:213:G:C8	2.36	0.61
1:2:1745:A:H61	8:G:65:GLN:CD	2.09	0.61
1:2:305:U:O2'	1:2:308:G:OP1	2.15	0.61
11:J:65:GLU:OE1	11:J:65:GLU:N	2.26	0.61
6:E:122:LYS:NZ	6:E:143:ASP:OD2	2.21	0.60
9:H:51:ILE:HG21	9:H:179:LYS:HE3	1.83	0.60
1:2:190:G:H21	1:2:209:A:H62	1.48	0.60
1:2:532:C:O2	1:2:552:G:N2	2.33	0.60
1:2:963:A:N3	1:2:1055:A:O2'	2.33	0.60
1:2:1862:G:O2'	28:a:5:ARG:NH2	2.34	0.60
27:Z:73:VAL:HG23	27:Z:77:LEU:HD22	1.82	0.60
1:2:1514:G:OP2	31:d:12:ARG:NH2	2.34	0.60
5:D:55:THR:HA	5:D:58:VAL:HG12	1.83	0.60
18:Q:105:LYS:O	18:Q:109:LYS:HB3	2.01	0.60
1:2:1541:G:O2'	21:T:12:GLN:OE1	2.16	0.60
6:E:100:ARG:HG2	6:E:102:ILE:HG12	1.83	0.60
1:2:857:U:H2'	1:2:858:A:C8	2.37	0.60
2:A:84:GLN:HG2	2:A:100:ALA:HB1	1.83	0.60
1:2:1520:G:C5	17:P:126:VAL:HG22	2.36	0.60
1:2:1674:G:H2'	1:2:1675:A:C8	2.37	0.60
3:B:76:ASN:OD1	3:B:76:ASN:N	2.25	0.60
1:2:185:G:H1	1:2:214:U:H3	1.48	0.60
2:A:84:GLN:O	2:A:88:LEU:HD22	2.00	0.60
6:E:143:ASP:HB3	6:E:145:ARG:HG3	1.82	0.60
12:K:10:ALA:HA	12:K:13:GLU:OE2	2.01	0.60
1:2:1445:U:O4	1:2:1446:A:N6	2.34	0.60
5:D:105:LEU:HG	5:D:122:VAL:HG21	1.83	0.60
5:D:138:VAL:HG13	5:D:182:LEU:HD13	1.84	0.60
7:F:80:GLY:H	7:F:83:ASN:CG	2.10	0.60
10:I:110:ARG:O	10:I:114:GLU:HG2	2.00	0.60
21:T:90:SER:OG	21:T:91:HIS:N	2.35	0.60
1:2:387:C:OP2	10:I:10:LYS:NZ	2.32	0.60
1:2:1590:C:H3'	1:2:1591:C:O2	2.00	0.60
1:2:1610:G:N2	20:S:85:ASN:O	2.34	0.60
8:G:78:SER:HB3	8:G:92:ARG:HG2	1.84	0.60
18:Q:71:ARG:HB3	18:Q:73:LYS:HE3	1.83	0.60
21:T:82:ARG:O	21:T:82:ARG:NH1	2.35	0.60
1:2:943:U:O2'	16:O:135:ILE:O	2.19	0.59
18:Q:102:GLU:HB2	34:g:55:PRO:HB2	1.84	0.59
31:d:10:HIS:HD2	31:d:11:PRO:HD2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:33:SER:HB3	34:g:43:TRP:HE1	1.67	0.59
21:T:5:THR:HG22	21:T:7:LYS:H	1.67	0.59
24:W:80:ASP:OD1	24:W:80:ASP:N	2.34	0.59
1:2:142:C:OP1	1:2:179:C:N4	2.36	0.59
1:2:1858:G:OP2	16:O:146:ARG:NH2	2.36	0.59
10:I:101:ILE:HD12	10:I:190:LEU:HD11	1.82	0.59
22:U:46:LYS:HZ3	22:U:97:ILE:HG12	1.66	0.59
1:2:96:C:H1'	1:2:474:G:H5'	1.84	0.59
30:c:18:LEU:HB2	30:c:29:GLN:HB3	1.82	0.59
2:A:53:ARG:HH22	23:V:70:LEU:HD21	1.66	0.59
34:g:172:LYS:HE2	34:g:194:TYR:HA	1.83	0.59
1:2:495:U:O2'	6:E:27:PHE:O	2.21	0.59
1:2:563:G:N7	11:J:172:ARG:NH2	2.51	0.59
7:F:121:PRO:O	7:F:146:ARG:NH1	2.35	0.59
33:f:126:CYS:HB3	33:f:130:VAL:HG21	1.82	0.59
1:2:1244:U:O5'	33:f:78:LYS:NZ	2.28	0.59
1:2:1534:C:HO2'	27:Z:104:ARG:HH12	1.48	0.59
1:2:1545:A:N3	1:2:1671:G:O2'	2.30	0.59
2:A:121:LEU:HD12	2:A:143:PRO:HG2	1.85	0.59
3:B:52:THR:HG23	3:B:57:ILE:HA	1.84	0.59
33:f:133:ALA:O	33:f:139:HIS:ND1	2.36	0.59
1:2:1528:G:O2'	1:2:1666:C:OP1	2.18	0.59
1:2:1607:A:H2'	1:2:1608:U:H6	1.64	0.59
1:2:1610:G:H2'	1:2:1611:G:C8	2.38	0.59
1:2:1797:U:H2'	1:2:1798:C:C6	2.38	0.59
22:U:22:ILE:HG22	22:U:114:VAL:HG22	1.85	0.59
1:2:212:C:H2'	1:2:213:G:H8	1.67	0.58
1:2:531:A:N6	1:2:552:G:N1	2.28	0.58
1:2:1227:G:H21	1:2:1639:G:H21	1.49	0.58
1:2:1569:A:H61	1:2:1613:G:N2	2.00	0.58
11:J:170:PRO:HB3	11:J:174:LYS:HG2	1.84	0.58
1:2:1354:G:N2	1:2:1357:A:OP2	2.33	0.58
1:2:1591:C:N4	21:T:82:ARG:NH1	2.52	0.58
34:g:87:LEU:HD22	34:g:88:ARG:H	1.68	0.58
9:H:74:LYS:HD2	9:H:75:ILE:HG23	1.84	0.58
1:2:1389:C:OP1	19:R:43:SER:OG	2.17	0.58
10:I:163:GLU:O	10:I:167:GLN:HG2	2.03	0.58
21:T:35:ASP:HA	21:T:47:PRO:HD2	1.84	0.58
25:X:98:ASP:OD2	25:X:140:ARG:NH2	2.37	0.58
7:F:78:MET:O	7:F:79:HIS:HB2	2.04	0.58
19:R:26:ASN:HD22	19:R:26:ASN:C	2.12	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:639:C:HO2'	1:2:640:A:H8	1.49	0.58
1:2:1521:C:N4	20:S:137:LYS:HB3	2.18	0.58
1:2:1201:U:H2'	1:2:1202:U:C6	2.37	0.58
7:F:115:ALA:HB3	7:F:178:ILE:CG2	2.34	0.58
8:G:121:ILE:HB	8:G:124:LEU:HB3	1.85	0.58
7:F:145:ARG:HG2	30:c:48:GLY:HA3	1.84	0.58
1:2:1324:G:H1'	1:2:1325:G:H5'	1.84	0.58
1:2:1596:U:OP1	1:2:1603:G:N2	2.37	0.58
1:2:1538:C:OP2	1:2:1591:C:N4	2.37	0.58
7:F:77:MET:HB2	7:F:84:GLY:N	2.19	0.58
16:O:104:ARG:HG3	16:O:104:ARG:HH11	1.69	0.58
1:2:594:A:H61	1:2:643:A:H5''	1.69	0.57
1:2:1536:G:OP2	1:2:1592:C:P	2.62	0.57
6:E:181:CYS:HA	6:E:227:VAL:HA	1.85	0.57
13:L:80:MET:HE1	13:L:120:VAL:HB	1.86	0.57
1:2:1129:G:H3'	1:2:1130:G:H21	1.69	0.57
3:B:229:MET:HE3	3:B:229:MET:HA	1.85	0.57
20:S:46:ARG:HH21	21:T:50:GLU:HG2	1.69	0.57
11:J:18:ARG:O	11:J:24:ARG:NH1	2.37	0.57
4:C:196:ILE:HB	4:C:223:TYR:HB2	1.87	0.57
18:Q:26:LYS:HD3	18:Q:27:ARG:N	2.19	0.57
18:Q:132:PHE:HE2	22:U:76:THR:HG23	1.69	0.57
1:2:1244:U:O4	1:2:1257:G:N2	2.36	0.57
1:2:1590:C:H3'	1:2:1591:C:C1'	2.33	0.57
8:G:142:ARG:HH21	8:G:153:VAL:HG21	1.70	0.57
1:2:1589:A:OP2	21:T:40:ALA:HB1	2.04	0.57
6:E:151:ASP:HB3	6:E:154:ILE:HG13	1.86	0.57
12:K:80:ARG:NH2	12:K:81:ASP:OD1	2.37	0.57
15:N:142:GLU:OE1	15:N:144:SER:OG	2.23	0.57
3:B:110:MET:HA	3:B:113:MET:HE2	1.86	0.57
5:D:23:GLU:HG2	12:K:64:TRP:CD1	2.40	0.57
22:U:54:VAL:HB	22:U:88:LEU:HD12	1.87	0.57
1:2:1224:G:H1	1:2:1643:U:H3	1.53	0.56
28:a:36:ILE:HD13	28:a:78:VAL:HG11	1.87	0.56
3:B:138:PHE:O	3:B:213:ARG:N	2.37	0.56
5:D:125:PHE:O	5:D:129:SER:OG	2.23	0.56
23:V:71:ARG:HH21	24:W:23:ARG:HH21	1.53	0.56
30:c:28:THR:O	30:c:46:VAL:N	2.38	0.56
1:2:832:G:OP1	26:Y:11:LYS:NZ	2.38	0.56
1:2:1230:C:H2'	1:2:1529:C:O2'	2.05	0.56
1:2:1487:A:H4'	1:2:1488:C:OP1	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1532:C:N4	7:F:79:HIS:O	2.39	0.56
1:2:1550:G:H3'	1:2:1579:A:H61	1.71	0.56
4:C:172:ASN:ND2	11:J:95:ASP:OD1	2.38	0.56
29:b:19:HIS:HB3	29:b:22:LYS:HG3	1.87	0.56
5:D:42:THR:HG23	5:D:43:PRO:HD2	1.87	0.56
15:N:140:LYS:NZ	15:N:142:GLU:OE2	2.39	0.56
15:N:22:VAL:HG13	15:N:66:VAL:HG22	1.86	0.56
22:U:33:GLU:OE1	22:U:55:ARG:NH1	2.38	0.56
28:a:36:ILE:HG21	28:a:78:VAL:HG21	1.88	0.56
1:2:77:A:OP2	8:G:155:GLN:NE2	2.38	0.56
1:2:434:G:OP2	10:I:25:ARG:NH2	2.38	0.56
1:2:942:G:H2'	1:2:943:U:C6	2.40	0.56
1:2:964:A:H2'	1:2:965:U:O2	2.06	0.56
22:U:32:LEU:HD21	22:U:87:ARG:HG3	1.88	0.56
1:2:118:C:H1'	1:2:445:A:C5	2.40	0.56
1:2:125:C:H5''	8:G:198:ARG:HD2	1.87	0.56
1:2:558:G:H2'	1:2:559:G:C8	2.41	0.56
1:2:996:A:H2'	1:2:997:A:C8	2.40	0.56
1:2:1567:G:H1	1:2:1612:G:H21	1.51	0.56
9:H:95:ILE:HD11	9:H:133:LEU:HD13	1.87	0.56
19:R:106:LEU:HD23	19:R:109:LEU:HD23	1.88	0.56
21:T:64:LEU:O	21:T:66:LEU:N	2.39	0.56
24:W:30:CYS:SG	24:W:31:SER:N	2.79	0.56
1:2:1121:G:O2'	3:B:204:ILE:O	2.23	0.56
7:F:115:ALA:O	7:F:119:SER:OG	2.23	0.56
34:g:62:HIS:CE1	34:g:82:SER:HB2	2.41	0.56
1:2:1231:C:O2'	1:2:1232:U:O2	2.22	0.56
1:2:1396:A:N6	1:2:1449:G:O6	2.39	0.56
1:2:1520:G:H5'	20:S:130:ARG:NH2	2.21	0.56
1:2:1544:C:OP2	1:2:1585:U:N3	2.39	0.56
1:2:1587:G:H21	21:T:94:ARG:HH11	1.54	0.56
1:2:1742:C:H42	1:2:1793:A:H62	1.54	0.56
2:A:187:GLY:HA2	23:V:45:ARG:HD3	1.88	0.56
7:F:119:SER:OG	7:F:186:ASN:N	2.39	0.56
34:g:80:SER:OG	34:g:88:ARG:NH1	2.39	0.56
1:2:1098:C:H2'	1:2:1099:G:C8	2.40	0.55
1:2:1454:A:H5''	19:R:3:ARG:HD2	1.88	0.55
1:2:1591:C:H3'	1:2:1591:C:C6	2.41	0.55
5:D:58:VAL:HG22	5:D:66:ILE:HD11	1.88	0.55
8:G:67:VAL:HG23	8:G:99:GLY:HA2	1.88	0.55
7:F:115:ALA:HB3	7:F:178:ILE:HG21	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:191:GLU:O	9:H:193:GLN:NE2	2.38	0.55
34:g:284:PRO:HB3	34:g:303:THR:H	1.72	0.55
1:2:453:C:O2'	8:G:92:ARG:O	2.18	0.55
1:2:643:A:OP1	11:J:39:ASN:ND2	2.40	0.55
1:2:1129:G:OP1	29:b:22:LYS:NZ	2.39	0.55
1:2:1587:G:N2	21:T:94:ARG:HH11	2.04	0.55
5:D:64:ARG:O	5:D:68:GLU:HG2	2.07	0.55
26:Y:86:GLU:OE2	26:Y:90:ARG:NE	2.39	0.55
34:g:96:THR:OG1	34:g:97:THR:N	2.39	0.55
1:2:51:U:H2'	1:2:52:G:H8	1.71	0.55
1:2:1189:A:H2'	1:2:1190:A:C8	2.41	0.55
1:2:1217:A:H2'	1:2:1218:C:C6	2.42	0.55
1:2:1261:C:H1'	1:2:1514:G:OP2	2.06	0.55
7:F:51:HIS:O	18:Q:82:TYR:OH	2.19	0.55
14:M:112:LYS:HB2	14:M:121:LYS:HB2	1.88	0.55
22:U:26:SER:OG	22:U:32:LEU:HB2	2.07	0.55
22:U:48:LEU:HD21	22:U:93:SER:HB3	1.88	0.55
1:2:1591:C:C6	1:2:1591:C:C3'	2.90	0.55
10:I:116:HIS:HA	10:I:152:ARG:HH21	1.71	0.55
22:U:56:MET:HB2	22:U:86:LYS:HB3	1.89	0.55
1:2:1139:C:N4	1:2:1149:A:H62	2.04	0.55
2:A:77:ILE:HD13	2:A:99:ILE:HB	1.87	0.55
7:F:114:ASN:CA	7:F:184:SER:HB3	2.37	0.55
9:H:30:LEU:O	9:H:34:SER:OG	2.16	0.55
1:2:1324:G:O2'	1:2:1325:G:N2	2.37	0.55
1:2:1595:U:C2	21:T:45:LEU:HD21	2.42	0.55
20:S:39:ARG:HD2	20:S:83:PHE:HE1	1.71	0.55
1:2:656:G:H5'	1:2:662:G:N2	2.22	0.54
1:2:1648:G:C8	18:Q:125:ARG:HB3	2.42	0.54
6:E:104:ASP:HB3	6:E:110:ALA:HB2	1.88	0.54
8:G:148:SER:OG	8:G:150:GLU:OE1	2.25	0.54
1:2:1608:U:H5''	1:2:1609:C:C5	2.42	0.54
1:2:5:U:H2'	1:2:6:G:H8	1.72	0.54
1:2:847:A:OP1	6:E:108:ARG:NH1	2.40	0.54
7:F:116:ILE:HD13	7:F:187:SER:HB2	1.89	0.54
18:Q:26:LYS:HD3	18:Q:27:ARG:H	1.72	0.54
1:2:617:G:H4'	25:X:88:ASP:HB3	1.88	0.54
7:F:122:ARG:HB3	30:c:59:LEU:HD13	1.90	0.54
21:T:53:PHE:CD1	21:T:103:VAL:HG22	2.42	0.54
22:U:83:ARG:HH21	31:d:55:LEU:HD13	1.72	0.54
1:2:448:A:H5''	10:I:25:ARG:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1007:C:H2'	1:2:1008:A:C8	2.42	0.54
1:2:1101:U:H2'	1:2:1102:G:C8	2.42	0.54
23:V:51:LYS:HG3	23:V:78:ILE:HD11	1.90	0.54
1:2:636:C:H5''	32:e:22:GLN:HG2	1.90	0.54
1:2:1538:C:H1'	21:T:44:GLU:HB2	1.89	0.54
11:J:94:LEU:HA	11:J:97:ILE:HD12	1.90	0.54
16:O:65:ASP:OD1	16:O:66:ARG:N	2.40	0.54
19:R:26:ASN:O	19:R:26:ASN:ND2	2.28	0.54
1:2:958:G:H2'	1:2:959:G:O4'	2.08	0.54
1:2:1534:C:H5'	7:F:169:ILE:HG22	1.89	0.54
7:F:92:ILE:HG23	7:F:170:ALA:HA	1.89	0.54
21:T:35:ASP:HB2	21:T:46:ALA:HB1	1.89	0.54
1:2:1737:G:H4'	8:G:92:ARG:HH22	1.73	0.54
10:I:177:SER:OG	10:I:184:ARG:O	2.24	0.54
1:2:115:U:H2'	1:2:116:U:C6	2.43	0.54
20:S:139:THR:OG1	20:S:140:GLY:N	2.40	0.54
1:2:1139:C:H41	1:2:1149:A:H62	1.56	0.54
1:2:1401:A:N6	1:2:1442:U:OP2	2.41	0.54
6:E:107:GLY:HA2	6:E:189:LEU:HG	1.90	0.54
10:I:81:VAL:HG22	10:I:94:LYS:HD3	1.90	0.54
15:N:83:ASP:OD1	15:N:83:ASP:N	2.41	0.54
17:P:132:GLY:O	17:P:134:GLY:N	2.39	0.54
20:S:30:ILE:O	20:S:33:ILE:N	2.39	0.53
1:2:289:G:OP1	6:E:155:LYS:NZ	2.41	0.53
1:2:1225:U:O2'	1:2:1226:G:H5'	2.07	0.53
1:2:1374:C:H2'	1:2:1375:G:O4'	2.08	0.53
1:2:1407:U:OP1	18:Q:71:ARG:NH1	2.41	0.53
5:D:157:MET:HE3	5:D:187:LYS:HE3	1.90	0.53
1:2:12:U:H2'	1:2:13:C:O2	2.09	0.53
1:2:150:A:H5''	1:2:151:C:H5	1.72	0.53
1:2:420:G:O2'	1:2:660:C:N3	2.39	0.53
1:2:1303:C:H2'	1:2:1304:U:H4'	1.88	0.53
13:L:76:VAL:HG12	13:L:125:ILE:HD13	1.91	0.53
32:e:36:MET:HE3	32:e:40:ARG:NH1	2.24	0.53
1:2:296:U:O2'	6:E:131:VAL:O	2.25	0.53
1:2:1591:C:C2	1:2:1592:C:C5	2.96	0.53
13:L:48:LYS:HZ2	13:L:52:GLU:HG2	1.73	0.53
34:g:298:LEU:HD23	34:g:310:TRP:HE1	1.72	0.53
1:2:101:U:H5''	10:I:19:LYS:HD2	1.91	0.53
1:2:1591:C:P	21:T:82:ARG:HG2	2.48	0.53
12:K:6:LYS:O	12:K:9:ILE:HG13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:855:G:O2'	13:L:71:ARG:NH1	2.42	0.53
1:2:1016:U:H5''	15:N:14:SER:HB3	1.89	0.53
1:2:1339:U:H2'	1:2:1340:U:C6	2.43	0.53
34:g:152:SER:HG	34:g:168:CYS:HG	1.51	0.53
1:2:1016:U:O2	29:b:30:SER:OG	2.26	0.53
1:2:1674:G:O3'	7:F:84:GLY:HA3	2.09	0.53
7:F:117:ILE:HB	7:F:183:GLY:N	2.24	0.53
7:F:188:TYR:O	7:F:191:LYS:HG2	2.09	0.53
20:S:5:ILE:HG12	20:S:7:GLU:H	1.74	0.53
1:2:880:G:HO2'	1:2:881:G:P	2.32	0.53
11:J:149:VAL:HG11	11:J:157:ILE:HD11	1.91	0.53
1:2:1718:G:H21	1:2:1813:A:N6	2.07	0.53
2:A:200:ASP:OD1	19:R:89:SER:OG	2.20	0.53
16:O:131:ASP:OD2	28:a:67:LEU:HD21	2.08	0.53
17:P:57:LEU:HD21	17:P:89:MET:HE2	1.90	0.53
18:Q:110:ASP:O	18:Q:114:GLN:HB3	2.09	0.53
34:g:47:ARG:NH1	34:g:297:THR:OG1	2.41	0.53
1:2:1266:C:H4'	33:f:79:LYS:H	1.74	0.52
1:2:1603:G:O5'	1:2:1630:A:N6	2.42	0.52
3:B:131:ASP:OD1	3:B:131:ASP:N	2.34	0.52
18:Q:46:THR:HG23	18:Q:47:LEU:HG	1.91	0.52
21:T:62:ARG:HH22	21:T:63:HIS:CD2	2.24	0.52
1:2:109:U:O2	13:L:71:ARG:NH2	2.42	0.52
1:2:1144:A:H2'	1:2:1145:A:C8	2.44	0.52
1:2:1239:U:O2	17:P:100:LYS:NZ	2.42	0.52
2:A:135:THR:O	2:A:138:SER:OG	2.27	0.52
1:2:1189:A:H2'	1:2:1190:A:H8	1.74	0.52
1:2:1230:C:O2	1:2:1665:G:N2	2.27	0.52
1:2:1261:C:O2	31:d:12:ARG:NH1	2.43	0.52
1:2:1679:A:H5'	7:F:60:ARG:HD3	1.92	0.52
21:T:6:VAL:HG22	21:T:14:PHE:CE1	2.45	0.52
22:U:26:SER:HB3	22:U:110:VAL:HA	1.92	0.52
1:2:57:U:OP1	1:2:504:G:O2'	2.25	0.52
1:2:180:G:H4'	1:2:181:A:OP1	2.09	0.52
1:2:568:C:H2'	1:2:569:A:C8	2.44	0.52
1:2:1589:A:O2'	1:2:1590:C:OP1	2.23	0.52
1:2:1606:G:O2'	1:2:1607:A:O5'	2.27	0.52
16:O:22:ALA:HB1	16:O:25:GLU:HG3	1.92	0.52
28:a:42:ARG:O	28:a:67:LEU:N	2.33	0.52
34:g:291:TRP:CE3	34:g:295:GLY:HA2	2.45	0.52
1:2:28:U:H2'	1:2:29:G:H8	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:104:A:H62	1:2:356:C:H5	1.53	0.52
1:2:1153:C:OP2	24:W:71:LYS:NZ	2.43	0.52
1:2:1515:G:OP1	1:2:1618:C:N4	2.42	0.52
4:C:166:ARG:NH2	4:C:254:ASP:OD1	2.39	0.52
4:C:254:ASP:HB2	23:V:1:MET:HG2	1.91	0.52
6:E:128:LYS:HG2	6:E:140:VAL:HB	1.91	0.52
20:S:37:GLY:H	20:S:41:ALA:HB2	1.75	0.52
32:e:36:MET:HE3	32:e:40:ARG:HH12	1.74	0.52
1:2:30:C:O2'	1:2:596:U:OP1	2.26	0.52
1:2:1373:C:OP1	19:R:7:LYS:N	2.37	0.52
1:2:1590:C:O2'	1:2:1591:C:OP1	2.26	0.52
26:Y:117:VAL:HG23	26:Y:122:LYS:HG2	1.91	0.52
1:2:595:U:H2'	1:2:596:U:C6	2.44	0.52
1:2:1004:U:H2'	1:2:1005:G:H8	1.74	0.52
11:J:127:ARG:HD3	32:e:31:ARG:HD3	1.91	0.52
16:O:61:LYS:HD3	16:O:76:LEU:HB3	1.91	0.52
19:R:63:ARG:O	19:R:63:ARG:HG2	2.10	0.52
23:V:51:LYS:HD3	23:V:76:ASP:OD2	2.10	0.52
9:H:168:HIS:CD2	9:H:168:HIS:H	2.25	0.52
10:I:3:ILE:O	10:I:30:GLY:N	2.39	0.52
10:I:196:GLU:O	10:I:200:ARG:HG3	2.10	0.52
13:L:111:VAL:HG12	13:L:140:PHE:HB2	1.92	0.52
25:X:84:PHE:CE2	25:X:86:PRO:HA	2.44	0.52
1:2:1534:C:O2	27:Z:104:ARG:NH1	2.42	0.52
1:2:1717:C:N4	1:2:1816:G:O6	2.43	0.52
7:F:197:GLU:O	7:F:201:LYS:HB2	2.10	0.52
13:L:148:ALA:O	13:L:151:THR:OG1	2.20	0.52
26:Y:57:VAL:HB	26:Y:60:PHE:HE2	1.74	0.52
1:2:307:G:N2	10:I:45:THR:O	2.32	0.52
1:2:443:U:H2'	1:2:444:G:O4'	2.09	0.52
1:2:1587:G:OP1	21:T:77:LYS:HD3	2.09	0.52
7:F:113:VAL:HB	7:F:182:LYS:C	2.34	0.52
8:G:32:MET:HG3	8:G:100:CYS:HB2	1.91	0.52
13:L:126:VAL:HG12	13:L:145:VAL:HG22	1.91	0.52
18:Q:53:GLU:HB2	18:Q:54:PRO:HD3	1.92	0.52
1:2:808:A:O2'	1:2:809:A:OP1	2.26	0.51
1:2:1538:C:C6	1:2:1593:C:C5	2.98	0.51
1:2:1554:C:H4'	12:K:33:PRO:HG3	1.92	0.51
10:I:106:SER:HB3	10:I:171:LEU:HG	1.90	0.51
20:S:8:LYS:NZ	27:Z:50:PHE:O	2.42	0.51
21:T:103:VAL:O	21:T:107:LEU:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:46:LYS:NZ	22:U:97:ILE:HG12	2.25	0.51
1:2:1242:U:H3	1:2:1518:C:H4'	1.75	0.51
15:N:28:LEU:HG	15:N:32:ASP:HB2	1.90	0.51
26:Y:42:GLU:HA	26:Y:42:GLU:OE1	2.10	0.51
1:2:190:G:N2	1:2:209:A:H62	2.08	0.51
1:2:921:G:C6	24:W:28:ARG:HD3	2.45	0.51
1:2:929:G:H2'	1:2:930:C:O4'	2.09	0.51
1:2:962:A:H61	7:F:134:VAL:HG11	1.76	0.51
7:F:150:ALA:HB1	7:F:190:ILE:HG12	1.92	0.51
17:P:40:ARG:HB2	17:P:113:GLY:HA2	1.93	0.51
18:Q:97:GLN:HB2	18:Q:105:LYS:HD3	1.92	0.51
20:S:44:VAL:HG11	20:S:67:VAL:HG22	1.92	0.51
21:T:27:LYS:HE3	21:T:110:LEU:HD21	1.91	0.51
26:Y:10:ARG:HG3	26:Y:26:ASP:OD1	2.09	0.51
30:c:46:VAL:HG21	30:c:50:VAL:HG21	1.91	0.51
1:2:672:A:N6	1:2:1027:A:OP1	2.41	0.51
1:2:819:G:O2'	1:2:820:U:OP1	2.26	0.51
1:2:1589:A:OP1	21:T:91:HIS:HB2	2.10	0.51
1:2:625:G:O6	25:X:63:ASN:HB2	2.11	0.51
1:2:5:U:H2'	1:2:6:G:C8	2.45	0.51
1:2:952:G:N3	16:O:52:THR:HG21	2.26	0.51
2:A:66:VAL:HG21	2:A:185:MET:HB3	1.92	0.51
4:C:130:ILE:HG23	4:C:162:ILE:HD11	1.93	0.51
10:I:157:LYS:HZ1	13:L:22:ARG:HB2	1.75	0.51
12:K:55:ARG:HG3	12:K:57:TYR:CE2	2.45	0.51
20:S:130:ARG:NH1	20:S:136:THR:OG1	2.43	0.51
21:T:63:HIS:NE2	21:T:75:MET:HA	2.26	0.51
1:2:1184:G:OP1	35:h:11:ARG:NH2	2.44	0.51
1:2:1389:C:H5	1:2:1481:G:H1	1.59	0.51
1:2:1590:C:O2'	1:2:1591:C:P	2.68	0.51
7:F:148:ASN:HA	7:F:151:ILE:HB	1.92	0.51
18:Q:22:VAL:O	18:Q:70:VAL:HA	2.11	0.51
1:2:83:A:H2	26:Y:120:THR:HG22	1.75	0.51
1:2:1522:A:N1	17:P:126:VAL:HG11	2.25	0.51
3:B:35:ALA:O	3:B:42:ARG:NH1	2.44	0.51
6:E:11:ARG:HA	6:E:28:ALA:HB2	1.92	0.51
10:I:88:ASN:OD1	10:I:205:ARG:NH1	2.44	0.51
20:S:111:LEU:HD23	20:S:114:LEU:HD21	1.93	0.51
34:g:313:THR:O	34:g:315:GLY:N	2.42	0.51
1:2:1589:A:O2'	21:T:82:ARG:O	2.28	0.51
1:2:1283:C:H2'	14:M:100:PRO:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1536:G:OP2	1:2:1592:C:OP1	2.29	0.51
6:E:45:ILE:HA	6:E:61:VAL:HG11	1.93	0.51
12:K:55:ARG:HG3	12:K:57:TYR:HE2	1.75	0.51
23:V:39:VAL:HG13	23:V:44:GLY:HA2	1.93	0.51
1:2:446:G:P	10:I:47:ARG:HH12	2.34	0.50
1:2:1653:U:O2'	21:T:82:ARG:HB3	2.11	0.50
7:F:61:PHE:CD1	30:c:49:PRO:HB3	2.45	0.50
8:G:154:ARG:NH2	8:G:179:LEU:HD21	2.27	0.50
18:Q:14:GLY:O	18:Q:21:ALA:N	2.44	0.50
1:2:467:G:H5'	8:G:72:ARG:HH12	1.76	0.50
1:2:1030:A:H2'	1:2:1031:A:C8	2.46	0.50
1:2:1313:A:C8	14:M:33:ARG:HD3	2.47	0.50
5:D:215:ASP:N	5:D:215:ASP:OD1	2.43	0.50
7:F:51:HIS:HB3	18:Q:50:LYS:NZ	2.26	0.50
10:I:116:HIS:HD1	10:I:116:HIS:C	2.17	0.50
10:I:150:ASP:O	10:I:154:LYS:HG2	2.11	0.50
18:Q:82:TYR:HD2	18:Q:85:ARG:CZ	2.24	0.50
18:Q:95:TYR:O	18:Q:99:TYR:HB2	2.11	0.50
34:g:194:TYR:HE1	34:g:235:ILE:HG22	1.75	0.50
1:2:51:U:H2'	1:2:52:G:C8	2.46	0.50
1:2:581:U:H4'	26:Y:66:GLY:HA2	1.93	0.50
1:2:619:A:N6	25:X:114:ASP:OD1	2.43	0.50
23:V:67:ASP:OD2	23:V:71:ARG:NH1	2.45	0.50
1:2:1010:G:H2'	1:2:1011:A:C8	2.47	0.50
1:2:1083:A:N7	1:2:1841:C:O2'	2.37	0.50
9:H:17:ASP:OD1	9:H:18:GLU:N	2.44	0.50
11:J:64:ASP:O	11:J:70:ARG:HD3	2.12	0.50
18:Q:16:LYS:NZ	18:Q:82:TYR:HB2	2.27	0.50
1:2:106:C:H2'	1:2:107:A:H8	1.75	0.50
1:2:643:A:OP1	11:J:41:ARG:NH2	2.44	0.50
1:2:1101:U:H2'	1:2:1102:G:H8	1.76	0.50
1:2:1673:U:H2'	1:2:1674:G:O4'	2.11	0.50
5:D:79:PHE:HB3	5:D:83:SER:HB2	1.94	0.50
7:F:59:LYS:HG2	7:F:60:ARG:O	2.11	0.50
13:L:33:LEU:HD12	13:L:34:PRO:HD2	1.93	0.50
34:g:298:LEU:HB3	34:g:310:TRP:CD1	2.46	0.50
1:2:293:C:O2	1:2:293:C:H2'	2.11	0.50
1:2:1222:G:O2'	1:2:1676:U:O2	2.28	0.50
1:2:1271:C:H2'	1:2:1272:C:C6	2.46	0.50
5:D:16:ILE:HG21	31:d:22:ARG:NH1	2.26	0.50
25:X:57:VAL:HG22	25:X:67:ARG:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:508:A:H3'	1:2:509:G:H8	1.76	0.50
1:2:796:G:N2	9:H:108:SER:O	2.45	0.50
1:2:980:A:H2'	1:2:981:A:C8	2.46	0.50
1:2:1004:U:H2'	1:2:1005:G:C8	2.46	0.50
1:2:1084:A:OP1	1:2:1858:G:O2'	2.25	0.50
20:S:45:LEU:HD21	20:S:63:GLU:HB3	1.94	0.50
1:2:150:A:H5'	1:2:151:C:OP2	2.11	0.50
1:2:649:U:H1'	25:X:45:SER:HB3	1.92	0.50
1:2:1546:G:H2'	1:2:1547:C:C6	2.47	0.50
7:F:116:ILE:HG21	7:F:179:ASN:HA	1.94	0.50
16:O:119:LEU:O	16:O:124:MET:HB2	2.12	0.50
1:2:418:A:H2'	1:2:419:G:C8	2.47	0.50
1:2:962:A:O2'	16:O:65:ASP:OD2	2.25	0.50
1:2:1522:A:C8	17:P:128:HIS:HB3	2.46	0.50
5:D:20:GLU:OE1	5:D:76:ARG:NH2	2.39	0.50
5:D:45:ARG:HH12	5:D:83:SER:HA	1.76	0.50
17:P:42:ARG:HD2	17:P:43:ARG:H	1.76	0.50
1:2:141:A:N6	1:2:177:G:C5	2.80	0.49
4:C:209:VAL:HB	4:C:210:PRO:HD3	1.94	0.49
7:F:71:ARG:NH1	7:F:75:SER:OG	2.45	0.49
1:2:122:G:C6	1:2:123:G:H1'	2.46	0.49
1:2:533:A:H2'	1:2:534:G:O4'	2.12	0.49
1:2:920:A:OP1	24:W:57:ARG:NH2	2.42	0.49
1:2:983:A:OP1	1:2:1073:U:O2'	2.30	0.49
1:2:1231:C:H4'	1:2:1665:G:C8	2.47	0.49
7:F:118:ASN:HB2	7:F:184:SER:N	2.27	0.49
9:H:46:THR:OG1	9:H:63:PHE:O	2.29	0.49
17:P:37:TYR:HB3	17:P:112:ILE:HG21	1.93	0.49
19:R:57:LEU:O	19:R:61:ILE:HG23	2.12	0.49
24:W:30:CYS:HB2	24:W:61:ILE:HG13	1.94	0.49
1:2:49:C:H2'	1:2:472:C:H41	1.78	0.49
1:2:1030:A:H2'	1:2:1031:A:H8	1.77	0.49
1:2:1262:C:H2'	31:d:27:ARG:HH12	1.77	0.49
9:H:57:ARG:HG3	9:H:57:ARG:HH11	1.77	0.49
1:2:948:C:H2'	1:2:949:G:H8	1.78	0.49
1:2:1267:C:OP2	33:f:82:LYS:NZ	2.46	0.49
1:2:1485:U:O2'	1:2:1486:A:O5'	2.24	0.49
5:D:27:ARG:HE	12:K:61:GLN:HG3	1.77	0.49
8:G:159:ARG:HH21	8:G:171:THR:HG23	1.77	0.49
11:J:78:LEU:HB3	11:J:92:MET:HG2	1.94	0.49
34:g:5:MET:HB3	34:g:312:VAL:HG13	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:560:A:H5''	11:J:174:LYS:HB2	1.95	0.49
1:2:940:U:H3	1:2:1002:U:H3	1.60	0.49
3:B:30:TRP:CE2	16:O:19:PRO:HD3	2.48	0.49
3:B:142:PHE:O	3:B:208:HIS:N	2.46	0.49
7:F:142:SER:O	7:F:144:LEU:N	2.44	0.49
8:G:162:LEU:HD11	8:G:172:LYS:HE3	1.95	0.49
9:H:157:HIS:ND1	9:H:190:PRO:HG3	2.26	0.49
34:g:303:THR:O	34:g:303:THR:OG1	2.30	0.49
1:2:160:U:O2'	1:2:162:C:OP2	2.24	0.49
1:2:1863:A:OP2	28:a:4:LYS:NZ	2.39	0.49
3:B:116:LYS:HG3	3:B:116:LYS:O	2.13	0.49
7:F:59:LYS:HD2	7:F:62:ARG:HH21	1.77	0.49
1:2:142:C:N4	1:2:329:G:O5'	2.46	0.49
1:2:1517:G:OP2	1:2:1622:U:H1'	2.13	0.49
7:F:194:ASP:HA	7:F:197:GLU:HB3	1.93	0.49
18:Q:85:ARG:HA	18:Q:88:ILE:HG22	1.94	0.49
26:Y:79:LEU:HG	26:Y:83:LYS:HE3	1.95	0.49
1:2:1227:G:H21	1:2:1639:G:N2	2.11	0.49
1:2:1249:C:O3'	18:Q:143:LYS:NZ	2.46	0.49
1:2:1316:C:H2'	1:2:1317:C:C6	2.47	0.49
17:P:45:LEU:HD13	17:P:85:ILE:HG23	1.94	0.49
26:Y:7:ILE:HG22	26:Y:47:MET:HE1	1.94	0.49
29:b:44:THR:O	29:b:44:THR:OG1	2.25	0.49
1:2:921:G:O6	24:W:60:LYS:NZ	2.45	0.49
1:2:1572:C:H2'	1:2:1573:G:C8	2.47	0.49
10:I:117:TYR:HE1	10:I:119:LEU:HB2	1.78	0.49
25:X:34:THR:HG23	25:X:37:LYS:HE3	1.95	0.49
30:c:20:ARG:HA	30:c:27:CYS:O	2.13	0.49
34:g:115:SER:HB2	34:g:163:PRO:HB3	1.95	0.49
1:2:1667:U:H2'	1:2:1668:U:C6	2.48	0.48
19:R:31:ASN:N	19:R:31:ASN:HD22	2.11	0.48
1:2:74:G:H5'	1:2:75:G:H21	1.78	0.48
1:2:106:C:OP1	1:2:431:G:O2'	2.29	0.48
1:2:128:U:O4'	1:2:215:G:N2	2.46	0.48
1:2:641:A:O2'	1:2:645:C:OP1	2.30	0.48
1:2:1128:C:H2'	1:2:1129:G:H8	1.78	0.48
1:2:1618:C:H2'	1:2:1619:A:H5'	1.95	0.48
1:2:1643:U:H2'	1:2:1644:C:C6	2.48	0.48
2:A:77:ILE:HG21	2:A:133:PRO:HG3	1.94	0.48
12:K:24:LYS:HB2	12:K:66:HIS:CD2	2.48	0.48
1:2:106:C:H2'	1:2:107:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:34:SER:H	9:H:37:LYS:HD3	1.78	0.48
11:J:110:LEU:HB2	11:J:147:PHE:HB3	1.95	0.48
24:W:90:GLN:HB3	24:W:94:LEU:HD12	1.96	0.48
28:a:44:ILE:HD12	28:a:65:PRO:HG2	1.95	0.48
1:2:674:C:H2'	1:2:675:U:C6	2.48	0.48
1:2:1144:A:H5'	1:2:1355:C:H41	1.79	0.48
1:2:1617:G:O2'	1:2:1619:A:N1	2.43	0.48
4:C:163:VAL:HG21	4:C:245:SER:HB3	1.96	0.48
5:D:40:ARG:NH2	22:U:106:ILE:O	2.27	0.48
5:D:102:ALA:HA	5:D:184:ILE:HD11	1.94	0.48
7:F:59:LYS:HB2	7:F:59:LYS:NZ	2.28	0.48
8:G:176:ILE:HG22	8:G:179:LEU:HB2	1.95	0.48
1:2:841:G:H5''	26:Y:12:PHE:HD1	1.78	0.48
1:2:1779:G:H5''	1:2:1780:G:N7	2.29	0.48
8:G:20:ASP:HB3	8:G:22:ARG:CZ	2.43	0.48
30:c:45:ASN:HB2	30:c:63:ARG:HH12	1.79	0.48
1:2:177:G:H2'	1:2:178:C:H4'	1.94	0.48
1:2:1253:A:H4'	1:2:1254:C:H5''	1.95	0.48
1:2:1402:A:H2'	1:2:1405:A:H61	1.79	0.48
18:Q:69:ARG:NH2	18:Q:71:ARG:HH12	2.12	0.48
1:2:210:U:H6	1:2:211:G:H8	1.60	0.48
1:2:219:U:O4	10:I:184:ARG:NH1	2.46	0.48
4:C:191:VAL:HG11	4:C:236:PHE:HA	1.95	0.48
5:D:16:ILE:HD11	31:d:36:LEU:HD13	1.96	0.48
7:F:41:VAL:HG13	7:F:46:ALA:HB2	1.96	0.48
8:G:216:ARG:O	8:G:219:GLU:HG2	2.14	0.48
9:H:117:PRO:HG2	9:H:120:ARG:HD2	1.96	0.48
10:I:113:TYR:O	10:I:117:TYR:N	2.47	0.48
18:Q:77:HIS:O	18:Q:81:ILE:HB	2.13	0.48
1:2:29:G:H2'	1:2:30:C:C6	2.48	0.48
1:2:809:A:OP2	6:E:186:GLY:HA3	2.13	0.48
1:2:1588:A:H5'	21:T:94:ARG:HE	1.78	0.48
1:2:1610:G:H2'	1:2:1611:G:H8	1.79	0.48
1:2:1739:C:C5	10:I:32:PRO:HG2	2.44	0.48
10:I:117:TYR:CE1	10:I:119:LEU:HB2	2.48	0.48
11:J:134:HIS:ND1	11:J:163:SER:HB2	2.28	0.48
1:2:14:C:H2'	1:2:15:U:H6	1.79	0.48
1:2:57:U:H2'	1:2:500:A:H2	1.78	0.48
1:2:441:C:H2'	1:2:442:C:C6	2.49	0.48
1:2:495:U:H2'	1:2:496:C:O4'	2.13	0.48
1:2:528:A:H2'	1:2:529:A:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1324:G:HO2'	1:2:1325:G:N2	2.12	0.48
1:2:1448:A:H5'	22:U:30:LYS:NZ	2.29	0.48
34:g:121:VAL:HG21	34:g:154:VAL:HB	1.95	0.48
1:2:388:U:H2'	1:2:389:A:C8	2.48	0.48
6:E:54:TYR:OH	6:E:97:GLU:OE1	2.25	0.48
24:W:86:LEU:O	24:W:90:GLN:HG3	2.14	0.48
1:2:85:A:H2'	1:2:86:C:H6	1.78	0.47
1:2:1589:A:HO2'	1:2:1590:C:P	2.36	0.47
3:B:180:ASP:OD1	3:B:183:GLU:HG3	2.14	0.47
5:D:185:LYS:HB2	5:D:185:LYS:HE3	1.52	0.47
18:Q:32:ILE:HD11	18:Q:63:PHE:HB3	1.95	0.47
22:U:20:ILE:HG22	22:U:116:ILE:HG23	1.96	0.47
1:2:900:C:O2'	1:2:901:G:OP1	2.31	0.47
1:2:1588:A:H5'	21:T:94:ARG:HH21	1.79	0.47
1:2:1849:G:H5''	1:2:1850:A:OP1	2.14	0.47
6:E:62:LYS:HE2	6:E:62:LYS:HB3	1.68	0.47
12:K:73:ASN:HA	12:K:76:ILE:HD12	1.95	0.47
18:Q:54:PRO:O	18:Q:58:LEU:HG	2.14	0.47
18:Q:103:ALA:HA	18:Q:106:LYS:HE3	1.95	0.47
20:S:24:ARG:H	20:S:24:ARG:HD3	1.79	0.47
20:S:130:ARG:HD2	20:S:133:GLY:HA2	1.96	0.47
1:2:1231:C:O2'	1:2:1232:U:OP2	2.32	0.47
1:2:1742:C:H42	1:2:1793:A:N6	2.12	0.47
18:Q:109:LYS:O	18:Q:113:ILE:HG13	2.13	0.47
21:T:27:LYS:HD3	21:T:27:LYS:H	1.79	0.47
1:2:4:C:H4'	4:C:207:ALA:HB2	1.97	0.47
1:2:54:A:OP1	26:Y:111:LYS:NZ	2.30	0.47
1:2:96:C:H2'	1:2:97:U:C6	2.49	0.47
1:2:107:A:H2'	1:2:108:G:H8	1.78	0.47
1:2:141:A:C6	1:2:177:G:N3	2.82	0.47
1:2:1313:A:H8	14:M:33:ARG:HH11	1.62	0.47
1:2:1416:C:O4'	21:T:133:ARG:NH2	2.47	0.47
1:2:1669:G:OP1	22:U:79:ARG:NH1	2.48	0.47
1:2:1745:A:H1'	8:G:31:ARG:NH2	2.29	0.47
2:A:188:THR:O	2:A:189:ILE:HG12	2.14	0.47
5:D:90:LYS:HB3	5:D:90:LYS:HE3	1.70	0.47
16:O:74:ALA:HB1	16:O:115:ALA:HB2	1.96	0.47
17:P:22:LEU:HD11	17:P:109:PRO:HB3	1.95	0.47
25:X:107:ARG:HB3	25:X:110:HIS:HB3	1.95	0.47
26:Y:15:ASN:HD22	26:Y:22:GLN:NE2	2.13	0.47
34:g:291:TRP:CE3	34:g:298:LEU:HD13	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:127:MET:HG3	5:D:154:ASP:OD2	2.13	0.47
7:F:143:PRO:O	7:F:147:VAL:HG23	2.15	0.47
8:G:154:ARG:HH21	8:G:179:LEU:HD21	1.80	0.47
10:I:104:ILE:HD11	10:I:189:VAL:HG22	1.96	0.47
20:S:30:ILE:HD12	20:S:36:VAL:HG13	1.97	0.47
20:S:125:HIS:CE1	20:S:131:VAL:HG21	2.49	0.47
34:g:133:ASN:HD21	34:g:137:VAL:HB	1.80	0.47
1:2:3:C:O2	11:J:18:ARG:NH2	2.43	0.47
1:2:219:U:H5	1:2:220:U:H3	1.60	0.47
1:2:1265:A:H8	33:f:78:LYS:HE2	1.80	0.47
6:E:20:LEU:HD21	6:E:46:ILE:HD12	1.96	0.47
7:F:194:ASP:O	7:F:197:GLU:HB3	2.14	0.47
10:I:193:LYS:HA	10:I:196:GLU:HG3	1.96	0.47
18:Q:100:VAL:HG13	18:Q:101:ASP:N	2.30	0.47
26:Y:76:TYR:OH	26:Y:86:GLU:OE1	2.28	0.47
1:2:144:U:OP2	8:G:139:SER:OG	2.33	0.47
1:2:352:U:H4'	1:2:353:C:C5	2.49	0.47
1:2:604:A:H2'	1:2:605:A:C8	2.49	0.47
1:2:1019:C:H2'	1:2:1020:A:O4'	2.14	0.47
1:2:1300:U:H5''	17:P:52:LYS:NZ	2.30	0.47
1:2:1656:G:H1	1:2:1668:U:H3	1.63	0.47
1:2:1805:G:H2'	1:2:1806:A:O4'	2.15	0.47
3:B:34:LYS:O	3:B:98:THR:OG1	2.22	0.47
7:F:81:ARG:O	7:F:85:LYS:NZ	2.27	0.47
10:I:114:GLU:HA	10:I:117:TYR:HB2	1.95	0.47
10:I:116:HIS:C	10:I:116:HIS:ND1	2.71	0.47
10:I:116:HIS:ND1	10:I:116:HIS:O	2.42	0.47
13:L:82:MET:HE3	13:L:85:THR:HB	1.95	0.47
25:X:68:LYS:HB3	25:X:91:LEU:HD22	1.97	0.47
34:g:33:SER:HB3	34:g:43:TRP:NE1	2.30	0.47
34:g:60:ARG:HE	34:g:60:ARG:HB3	1.21	0.47
1:2:15:U:H2'	1:2:16:G:O4'	2.15	0.47
1:2:1544:C:N4	1:2:1590:C:H1'	2.29	0.47
1:2:1666:C:H2'	1:2:1667:U:C6	2.50	0.47
1:2:1718:G:H21	1:2:1813:A:H62	1.63	0.47
4:C:98:LEU:O	4:C:101:SER:OG	2.33	0.47
1:2:45:A:N1	1:2:480:G:O2'	2.46	0.47
1:2:84:A:N3	1:2:150:A:O2'	2.45	0.47
1:2:160:U:O2'	1:2:161:U:H3'	2.15	0.47
1:2:957:A:H3'	1:2:958:G:N2	2.26	0.47
1:2:1453:C:O2	19:R:28:PHE:CE2	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:108:PRO:O	7:F:112:LEU:CB	2.60	0.47
9:H:69:LEU:O	9:H:73:GLN:HG3	2.14	0.47
11:J:22:LYS:HA	11:J:22:LYS:HD2	1.72	0.47
20:S:131:VAL:HG13	20:S:132:ARG:HD2	1.96	0.47
21:T:64:LEU:HD12	21:T:67:ARG:O	2.15	0.47
22:U:20:ILE:HD12	22:U:20:ILE:O	2.14	0.47
30:c:44:ARG:NH2	30:c:63:ARG:HB3	2.30	0.47
34:g:312:VAL:HG12	34:g:314:ILE:H	1.80	0.47
1:2:28:U:H2'	1:2:29:G:C8	2.50	0.47
1:2:528:A:H2'	1:2:529:A:C8	2.50	0.47
1:2:609:U:H2'	1:2:610:G:H8	1.79	0.47
1:2:1316:C:H2'	1:2:1317:C:H6	1.80	0.47
1:2:1320:G:N7	1:2:1322:G:N2	2.63	0.47
1:2:1742:C:H3'	1:2:1743:G:C5'	2.45	0.47
3:B:164:ILE:HD13	3:B:207:LEU:HD21	1.97	0.47
7:F:61:PHE:HD1	30:c:49:PRO:HB3	1.78	0.47
7:F:142:SER:OG	30:c:55:VAL:O	2.25	0.47
7:F:154:LEU:HG	7:F:189:ALA:HB3	1.97	0.47
11:J:111:GLN:NE2	11:J:127:ARG:HB2	2.31	0.47
16:O:106:LYS:HD2	16:O:135:ILE:HD13	1.97	0.47
26:Y:11:LYS:HB2	26:Y:24:VAL:HG23	1.97	0.47
29:b:36:LYS:HG2	29:b:80:ARG:HH12	1.80	0.47
1:2:60:A:N3	1:2:316:G:O2'	2.31	0.46
1:2:795:A:H3'	1:2:796:G:H5''	1.96	0.46
1:2:1240:A:N6	17:P:99:GLY:O	2.47	0.46
1:2:1259:A:H1'	1:2:1264:C:H5	1.80	0.46
1:2:1533:A:N3	1:2:1533:A:H2'	2.31	0.46
1:2:1585:U:C5	21:T:67:ARG:HD3	2.50	0.46
7:F:161:ALA:HA	7:F:165:ASN:HD22	1.80	0.46
8:G:126:ASP:OD1	8:G:126:ASP:N	2.47	0.46
15:N:43:LYS:HE3	15:N:43:LYS:HB3	1.72	0.46
18:Q:82:TYR:O	18:Q:85:ARG:HG2	2.14	0.46
18:Q:93:VAL:HG22	18:Q:109:LYS:HB2	1.97	0.46
20:S:55:ARG:HB3	20:S:55:ARG:NH1	2.30	0.46
28:a:51:ARG:HG2	28:a:55:GLU:OE2	2.15	0.46
1:2:1236:G:H3'	1:2:1237:C:C6	2.50	0.46
12:K:12:TYR:O	12:K:15:LEU:HG	2.16	0.46
14:M:93:LYS:HD3	14:M:93:LYS:HA	1.70	0.46
20:S:63:GLU:O	20:S:67:VAL:HG23	2.15	0.46
27:Z:67:LEU:HB3	27:Z:72:VAL:HG21	1.97	0.46
34:g:284:PRO:HB2	34:g:302:TYR:HD2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:352:U:H4'	1:2:353:C:H5	1.80	0.46
1:2:414:A:H2'	1:2:415:A:C8	2.49	0.46
1:2:1217:A:H2'	1:2:1218:C:H6	1.80	0.46
1:2:1300:U:H5''	17:P:52:LYS:HZ3	1.79	0.46
1:2:1333:U:OP1	5:D:147:ALA:N	2.48	0.46
5:D:45:ARG:HH22	5:D:83:SER:HA	1.81	0.46
7:F:159:ARG:HG2	7:F:163:PHE:HB2	1.98	0.46
15:N:25:TRP:HB3	29:b:82:LYS:HD2	1.97	0.46
18:Q:42:ILE:HG22	18:Q:44:PRO:HD2	1.97	0.46
18:Q:47:LEU:HB2	18:Q:81:ILE:HD13	1.97	0.46
25:X:124:LYS:HG2	25:X:129:SER:HA	1.96	0.46
1:2:1733:U:H3	1:2:1801:A:H62	1.64	0.46
1:2:1844:U:OP1	35:h:11:ARG:NH2	2.45	0.46
1:2:1865:C:OP2	28:a:5:ARG:NH1	2.48	0.46
5:D:27:ARG:CZ	12:K:63:ALA:HB3	2.46	0.46
11:J:138:ARG:NH2	11:J:152:ASP:OD1	2.49	0.46
28:a:60:ASP:OD1	28:a:60:ASP:N	2.37	0.46
29:b:40:CYS:SG	29:b:41:TYR:N	2.89	0.46
1:2:1009:A:H5'	15:N:98:VAL:HG12	1.97	0.46
1:2:1235:G:H2'	1:2:1236:G:H8	1.80	0.46
1:2:1661:A:C8	31:d:14:PHE:HB3	2.51	0.46
7:F:72:LEU:HD11	7:F:179:ASN:HB3	1.97	0.46
19:R:107:LYS:HD2	19:R:107:LYS:O	2.16	0.46
1:2:17:C:O2'	1:2:1194:A:N1	2.36	0.46
1:2:94:G:O2'	1:2:508:A:O2'	2.23	0.46
1:2:417:C:C4	11:J:55:LYS:HE2	2.50	0.46
1:2:1284:A:H4'	1:2:1285:G:H5'	1.96	0.46
1:2:1485:U:H5'	5:D:151:LYS:HZ1	1.79	0.46
5:D:210:ILE:HG21	19:R:19:LYS:HD3	1.98	0.46
18:Q:17:LYS:HB3	18:Q:18:THR:H	1.63	0.46
22:U:60:THR:HG23	22:U:83:ARG:HG2	1.98	0.46
1:2:352:U:H5''	1:2:353:C:OP1	2.16	0.46
1:2:948:C:H2'	1:2:949:G:C8	2.51	0.46
1:2:1265:A:P	1:2:1267:C:H41	2.37	0.46
1:2:1590:C:H5'	1:2:1591:C:N3	2.31	0.46
1:2:1681:U:H2'	1:2:1682:C:C6	2.51	0.46
2:A:8:LEU:HD11	23:V:39:VAL:HG11	1.97	0.46
3:B:168:MET:HG2	3:B:197:ILE:HG21	1.97	0.46
7:F:125:SER:HB2	7:F:136:ARG:HB3	1.97	0.46
8:G:132:ARG:HH21	8:G:161:PRO:HD2	1.81	0.46
19:R:106:LEU:HA	19:R:109:LEU:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Z:96:LEU:HD12	27:Z:96:LEU:HA	1.83	0.46
1:2:1220:A:OP2	1:2:1221:G:H8	1.99	0.46
1:2:1581:C:H5'	1:2:1582:C:C5	2.39	0.46
1:2:1611:G:H2'	1:2:1612:G:C8	2.50	0.46
7:F:115:ALA:HB1	7:F:186:ASN:HB2	1.97	0.46
9:H:146:VAL:HG12	24:W:42:MET:HE1	1.98	0.46
10:I:118:ALA:HB3	10:I:153:LYS:HB2	1.98	0.46
1:2:1269:G:N2	1:2:1270:G:N3	2.64	0.46
1:2:1487:A:O2'	1:2:1488:C:H5'	2.16	0.46
1:2:1863:A:H1'	28:a:79:ILE:HD13	1.98	0.46
7:F:154:LEU:HD11	7:F:190:ILE:HG13	1.98	0.46
1:2:957:A:OP1	16:O:57:THR:OG1	2.31	0.46
1:2:1736:G:N2	1:2:1798:C:H42	2.14	0.46
3:B:109:LYS:HE3	3:B:113:MET:SD	2.56	0.46
3:B:123:ALA:HB2	3:B:165:ARG:HG3	1.97	0.46
5:D:45:ARG:HD2	5:D:45:ARG:HA	1.66	0.46
8:G:20:ASP:HB2	8:G:23:LYS:HG3	1.98	0.46
34:g:156:PHE:O	34:g:200:VAL:HG21	2.16	0.46
34:g:289:LEU:HB3	34:g:298:LEU:HD21	1.98	0.46
1:2:388:U:H2'	1:2:389:A:H8	1.81	0.45
1:2:416:U:N3	1:2:417:C:O2'	2.48	0.45
1:2:921:G:C2	29:b:22:LYS:HD3	2.51	0.45
1:2:1129:G:H3'	1:2:1130:G:N2	2.31	0.45
1:2:1164:G:O2'	1:2:1165:G:H5'	2.16	0.45
1:2:1304:U:H5	1:2:1306:U:H1'	1.81	0.45
1:2:1734:G:O2'	1:2:1800:A:N6	2.45	0.45
3:B:103:MET:HE2	3:B:103:MET:HB3	1.80	0.45
6:E:19:MET:HE3	6:E:19:MET:HB2	1.79	0.45
1:2:606:G:O2'	32:e:58:ASN:ND2	2.45	0.45
1:2:808:A:HO2'	1:2:809:A:P	2.39	0.45
1:2:1285:G:N2	1:2:1314:U:O4	2.50	0.45
1:2:1329:U:O2'	1:2:1332:A:OP2	2.18	0.45
1:2:1798:C:H2'	1:2:1799:G:O4'	2.16	0.45
6:E:94:LYS:O	26:Y:16:ARG:NH1	2.49	0.45
9:H:39:GLN:HG2	9:H:74:LYS:NZ	2.31	0.45
21:T:112:MET:HE2	21:T:112:MET:HB3	1.83	0.45
27:Z:80:ARG:HG3	27:Z:82:SER:H	1.80	0.45
28:a:33:ASP:N	28:a:33:ASP:OD1	2.50	0.45
1:2:153:G:H21	8:G:13:GLN:NE2	2.14	0.45
1:2:980:A:H2'	1:2:981:A:H8	1.81	0.45
1:2:1284:A:H8	14:M:104:VAL:HB	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:200:LYS:HE3	8:G:204:GLU:OE2	2.15	0.45
14:M:58:GLU:OE2	33:f:100:LEU:HD11	2.17	0.45
30:c:33:GLU:HG2	30:c:41:SER:HA	1.98	0.45
34:g:229:THR:O	34:g:229:THR:OG1	2.31	0.45
1:2:17:C:H2'	1:2:18:C:C6	2.52	0.45
1:2:219:U:H3	10:I:184:ARG:HD2	1.81	0.45
1:2:964:A:H1'	1:2:1054:G:O2'	2.16	0.45
1:2:1265:A:OP2	1:2:1267:C:N4	2.43	0.45
6:E:22:LYS:HG3	6:E:23:LEU:HD23	1.97	0.45
10:I:206:LYS:HB2	10:I:206:LYS:HE3	1.69	0.45
15:N:94:LYS:HB2	15:N:94:LYS:HE3	1.76	0.45
20:S:61:GLU:O	20:S:64:VAL:HG12	2.16	0.45
27:Z:99:LEU:HD13	27:Z:109:TYR:CZ	2.51	0.45
1:2:85:A:H2'	1:2:86:C:C6	2.52	0.45
1:2:804:U:H2'	1:2:805:U:C6	2.52	0.45
1:2:1480:A:O2'	31:d:56:ASP:O	2.32	0.45
1:2:1538:C:C6	1:2:1593:C:C4	3.04	0.45
1:2:1745:A:N3	8:G:31:ARG:NH2	2.65	0.45
3:B:134:LEU:HD23	3:B:218:LEU:HB2	1.99	0.45
5:D:59:LEU:HD23	5:D:66:ILE:HG13	1.98	0.45
8:G:30:LYS:HB3	8:G:34:THR:HG21	1.98	0.45
19:R:21:TYR:HE1	19:R:58:MET:HE1	1.80	0.45
19:R:60:ARG:HG3	19:R:60:ARG:HH11	1.81	0.45
21:T:6:VAL:HG22	21:T:14:PHE:HE1	1.82	0.45
1:2:1249:C:OP1	1:2:1251:A:H5''	2.17	0.45
2:A:53:ARG:NH2	23:V:70:LEU:HD11	2.32	0.45
8:G:27:PHE:HE2	8:G:41:LEU:HD21	1.81	0.45
9:H:63:PHE:HA	9:H:95:ILE:O	2.17	0.45
13:L:48:LYS:O	13:L:52:GLU:HG3	2.16	0.45
1:2:517:C:H2'	1:2:518:G:O4'	2.16	0.45
1:2:1222:G:H2'	1:2:1223:A:C8	2.52	0.45
1:2:1591:C:OP2	21:T:82:ARG:CG	2.61	0.45
1:2:1743:G:H2'	1:2:1744:G:C8	2.52	0.45
5:D:163:PRO:O	5:D:167:TYR:HB2	2.17	0.45
7:F:187:SER:HB3	7:F:190:ILE:HB	1.98	0.45
25:X:123:VAL:HG12	25:X:124:LYS:HG3	1.98	0.45
1:2:803:C:H3'	1:2:804:U:O2	2.16	0.45
1:2:1128:C:H2'	1:2:1129:G:C8	2.52	0.45
1:2:1274:G:H4'	1:2:1275:G:O5'	2.17	0.45
1:2:1538:C:O2	21:T:45:LEU:HD23	2.17	0.45
1:2:1644:C:H4'	18:Q:140:ARG:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:35:ILE:HG12	33:f:104:LYS:HE3	1.99	0.45
17:P:26:LEU:HD21	17:P:87:PRO:HD2	1.99	0.45
17:P:43:ARG:HG2	17:P:43:ARG:O	2.17	0.45
30:c:46:VAL:CG2	30:c:50:VAL:HG21	2.47	0.45
34:g:166:VAL:HG22	34:g:176:VAL:HG13	1.99	0.45
1:2:544:G:H2'	1:2:544:G:N3	2.32	0.45
1:2:641:A:H2'	1:2:642:U:O4'	2.17	0.45
1:2:1485:U:H5'	5:D:151:LYS:NZ	2.32	0.45
1:2:1630:A:N6	20:S:28:PHE:O	2.43	0.45
3:B:110:MET:O	3:B:114:VAL:HG23	2.17	0.45
18:Q:85:ARG:NH2	18:Q:118:THR:HB	2.32	0.45
26:Y:39:GLU:O	26:Y:43:LYS:HD2	2.17	0.45
1:2:385:G:H3'	13:L:136:LYS:HB2	1.98	0.45
1:2:681:U:O2'	1:2:1160:U:OP1	2.29	0.45
1:2:822:U:H2'	1:2:824:C:OP2	2.17	0.45
1:2:1616:U:H2'	17:P:47:ARG:NH1	2.32	0.45
2:A:34:MET:HE3	2:A:34:MET:HB3	1.80	0.45
25:X:6:GLY:O	25:X:9:THR:OG1	2.31	0.45
1:2:182:C:H4'	1:2:183:G:C8	2.52	0.44
1:2:482:G:OP1	25:X:76:LYS:HA	2.17	0.44
1:2:570:C:HO2'	1:2:571:U:H6	1.60	0.44
1:2:1025:U:H2'	1:2:1026:C:O4'	2.17	0.44
1:2:1174:U:H2'	1:2:1175:G:C8	2.52	0.44
5:D:74:GLN:NE2	5:D:79:PHE:O	2.42	0.44
5:D:99:ILE:O	5:D:103:GLU:HG2	2.17	0.44
5:D:132:LYS:HG2	5:D:156:LEU:HD11	1.98	0.44
6:E:44:LEU:HD13	6:E:72:ILE:HD11	1.99	0.44
7:F:115:ALA:CB	7:F:186:ASN:HB2	2.46	0.44
7:F:171:GLU:HB3	27:Z:106:GLN:HE22	1.82	0.44
1:2:1552:G:OP1	5:D:9:ARG:NH2	2.45	0.44
1:2:1683:C:H2'	1:2:1684:C:H6	1.81	0.44
4:C:199:PRO:HG2	11:J:58:ARG:HD3	1.99	0.44
5:D:132:LYS:HD2	5:D:189:MET:HE2	1.98	0.44
6:E:126:VAL:HA	6:E:141:THR:HA	2.00	0.44
8:G:22:ARG:HD3	8:G:22:ARG:N	2.26	0.44
15:N:103:GLU:OE1	15:N:103:GLU:HA	2.17	0.44
17:P:43:ARG:O	17:P:47:ARG:N	2.50	0.44
25:X:73:GLN:HG3	25:X:80:LYS:HD2	1.97	0.44
1:2:513:G:H2'	1:2:513:G:N3	2.33	0.44
1:2:633:C:O2'	32:e:16:THR:HG21	2.18	0.44
1:2:1266:C:OP2	1:2:1267:C:H6	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1778:C:N4	1:2:1781:A:OP2	2.50	0.44
5:D:202:LYS:H	5:D:202:LYS:HG2	1.65	0.44
7:F:119:SER:OG	7:F:187:SER:N	2.46	0.44
26:Y:6:THR:HB	26:Y:28:LEU:HB2	2.00	0.44
28:a:67:LEU:HD23	28:a:67:LEU:HA	1.65	0.44
30:c:59:LEU:HD23	30:c:59:LEU:H	1.82	0.44
1:2:417:C:H3'	1:2:418:A:H5''	2.00	0.44
1:2:1349:G:H2'	1:2:1350:U:C6	2.52	0.44
1:2:1491:G:H2'	1:2:1492:U:C6	2.51	0.44
1:2:1617:G:N2	1:2:1619:A:OP2	2.51	0.44
7:F:49:LEU:HB3	18:Q:50:LYS:HZ2	1.82	0.44
16:O:88:LEU:HD12	16:O:88:LEU:HA	1.81	0.44
20:S:26:ILE:HG13	20:S:27:ALA:H	1.82	0.44
1:2:1452:A:H5''	19:R:48:ASN:ND2	2.32	0.44
7:F:121:PRO:HD3	7:F:190:ILE:HG23	1.98	0.44
13:L:59:LYS:HD3	13:L:134:LEU:HB3	2.00	0.44
1:2:889:U:O2'	1:2:890:U:O4'	2.36	0.44
1:2:1277:C:O2'	1:2:1278:A:O4'	2.31	0.44
1:2:1457:U:H2'	1:2:1458:G:H8	1.83	0.44
5:D:65:ARG:HG3	5:D:69:LEU:HD23	1.98	0.44
10:I:136:ILE:HG23	10:I:137:LEU:HD12	1.98	0.44
12:K:5:LYS:HB3	14:M:29:ASP:CG	2.43	0.44
12:K:10:ALA:HA	12:K:13:GLU:CD	2.43	0.44
14:M:91:LEU:HD22	14:M:100:PRO:HD2	1.99	0.44
17:P:126:VAL:HB	17:P:128:HIS:CE1	2.53	0.44
20:S:124:ARG:HB2	20:S:131:VAL:HG23	1.99	0.44
21:T:72:VAL:HG13	21:T:94:ARG:HG2	1.99	0.44
22:U:94:PRO:HD2	22:U:97:ILE:HD13	2.00	0.44
35:h:17:ARG:O	35:h:20:MET:HG2	2.17	0.44
1:2:87:U:H3	1:2:500:A:H62	1.66	0.44
1:2:616:A:N3	32:e:12:VAL:HG21	2.32	0.44
1:2:1174:U:H2'	1:2:1175:G:H8	1.82	0.44
1:2:1486:A:OP2	1:2:1486:A:H3'	2.18	0.44
3:B:103:MET:HE2	3:B:215:VAL:HG23	1.98	0.44
5:D:132:LYS:HE2	5:D:191:PRO:HA	1.99	0.44
5:D:205:PRO:HA	19:R:42:PRO:HG2	2.00	0.44
6:E:211:LYS:HB3	6:E:211:LYS:HE3	1.79	0.44
11:J:53:ILE:HG23	11:J:77:LEU:HD11	2.00	0.44
20:S:30:ILE:H	20:S:30:ILE:HG12	1.69	0.44
20:S:89:ASP:OD1	20:S:90:VAL:N	2.50	0.44
27:Z:70:PRO:HA	27:Z:73:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:461:U:H2'	1:2:462:C:C6	2.53	0.44
1:2:639:C:O2'	1:2:640:A:H8	2.00	0.44
8:G:10:THR:O	8:G:129:VAL:HB	2.18	0.44
18:Q:13:PHE:HB3	18:Q:22:VAL:HA	1.99	0.44
20:S:61:GLU:O	20:S:61:GLU:HG3	2.18	0.44
26:Y:20:ARG:HH21	26:Y:22:GLN:NE2	2.15	0.44
32:e:58:ASN:ND2	32:e:58:ASN:H	2.14	0.44
1:2:1105:G:O3'	29:b:69:GLY:HA3	2.17	0.44
1:2:1564:C:H5	1:2:1565:C:N3	2.16	0.44
6:E:250:GLU:O	6:E:254:LYS:HG3	2.17	0.44
7:F:147:VAL:O	7:F:151:ILE:HG12	2.18	0.44
16:O:46:ASP:HB2	16:O:51:GLU:HB2	1.99	0.44
16:O:47:LEU:HD12	16:O:47:LEU:HA	1.83	0.44
19:R:10:LYS:HD3	19:R:53:TYR:CZ	2.53	0.44
20:S:39:ARG:NH2	21:T:38:LYS:HB2	2.32	0.44
22:U:67:LYS:HD2	22:U:76:THR:HG22	1.99	0.44
28:a:45:VAL:HG21	28:a:64:LEU:HD22	1.98	0.44
28:a:73:TYR:HB3	28:a:78:VAL:HB	2.00	0.44
1:2:25:A:H2'	1:2:26:U:C6	2.53	0.43
1:2:433:A:H2'	1:2:434:G:C8	2.53	0.43
1:2:685:A:H2'	1:2:686:U:O4'	2.18	0.43
1:2:868:G:C5	9:H:115:LYS:HB3	2.53	0.43
20:S:20:ILE:HD12	20:S:20:ILE:HA	1.89	0.43
20:S:38:ARG:NH2	21:T:44:GLU:O	2.51	0.43
1:2:145:G:N7	8:G:137:ARG:NH1	2.66	0.43
1:2:1690:U:H2'	1:2:1691:U:C6	2.53	0.43
1:2:1733:U:H2'	1:2:1734:G:O4'	2.18	0.43
24:W:84:LYS:HB3	24:W:84:LYS:HE3	1.82	0.43
1:2:1615:U:H3'	1:2:1616:U:O4'	2.18	0.43
1:2:1692:U:H2'	1:2:1693:G:C8	2.53	0.43
2:A:52:LYS:HG2	19:R:109:LEU:HD13	1.99	0.43
8:G:21:GLU:OE2	8:G:21:GLU:C	2.62	0.43
15:N:87:ASP:OD1	15:N:88:LEU:N	2.51	0.43
18:Q:13:PHE:HA	18:Q:23:ALA:HB3	2.00	0.43
20:S:8:LYS:HD3	27:Z:49:LEU:HD21	2.00	0.43
20:S:72:GLN:O	20:S:72:GLN:NE2	2.50	0.43
21:T:64:LEU:HA	21:T:67:ARG:O	2.18	0.43
24:W:57:ARG:HG2	24:W:58:ALA:H	1.83	0.43
26:Y:55:ILE:HG12	26:Y:75:ILE:HG12	1.99	0.43
27:Z:102:LYS:HD3	27:Z:103:HIS:N	2.33	0.43
34:g:79:LEU:CD1	34:g:113:PHE:HB2	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:180:G:O2'	1:2:181:A:O5'	2.33	0.43
1:2:823:U:H5	11:J:143:ASN:HB3	1.83	0.43
1:2:1802:C:H2'	1:2:1803:U:C6	2.53	0.43
5:D:135:GLU:HG2	5:D:187:LYS:HE2	2.01	0.43
7:F:117:ILE:HD11	7:F:179:ASN:C	2.44	0.43
7:F:119:SER:HG	7:F:186:ASN:H	1.64	0.43
16:O:104:ARG:HG3	16:O:104:ARG:NH1	2.33	0.43
17:P:39:ALA:HA	17:P:42:ARG:HB3	1.99	0.43
17:P:50:ARG:H	17:P:53:GLN:NE2	2.15	0.43
21:T:40:ALA:HB2	21:T:94:ARG:O	2.18	0.43
21:T:85:ASN:ND2	21:T:90:SER:HA	2.32	0.43
26:Y:9:THR:HA	26:Y:24:VAL:O	2.18	0.43
26:Y:57:VAL:HB	26:Y:60:PHE:CE2	2.52	0.43
1:2:1108:G:H2'	1:2:1109:C:H5''	2.01	0.43
1:2:1275:G:H2'	1:2:1277:C:N4	2.34	0.43
4:C:103:LYS:HB2	4:C:103:LYS:HE2	1.81	0.43
6:E:37:LYS:HB2	6:E:40:GLU:HG2	2.00	0.43
9:H:69:LEU:HG	9:H:96:ALA:HB2	2.00	0.43
14:M:22:LEU:HD23	14:M:85:LEU:HD21	2.00	0.43
19:R:109:LEU:HG	19:R:111:PHE:CD2	2.51	0.43
34:g:59:LEU:HD22	34:g:59:LEU:HA	1.85	0.43
1:2:382:C:H2'	1:2:383:G:H8	1.84	0.43
1:2:643:A:H4'	1:2:644:G:H5'	1.99	0.43
1:2:981:A:H2'	1:2:982:G:C8	2.54	0.43
1:2:1269:G:N7	33:f:83:LYS:HD2	2.33	0.43
1:2:1542:C:O2'	18:Q:37:ARG:NH2	2.49	0.43
1:2:1703:C:H2'	1:2:1704:C:O4'	2.19	0.43
4:C:200:ARG:O	11:J:54:ARG:NH2	2.41	0.43
10:I:42:ARG:HH21	10:I:59:ARG:NH2	2.16	0.43
14:M:19:GLN:HB3	14:M:89:VAL:HA	2.01	0.43
1:2:829:C:OP1	6:E:21:ASP:HB2	2.18	0.43
1:2:875:A:N6	1:2:911:C:H42	2.14	0.43
1:2:1550:G:O2'	1:2:1558:C:O2	2.33	0.43
1:2:1669:G:OP2	18:Q:130:LYS:HD3	2.19	0.43
7:F:117:ILE:HD11	7:F:179:ASN:O	2.18	0.43
9:H:91:HIS:CD2	9:H:172:THR:HG21	2.53	0.43
22:U:22:ILE:HD12	22:U:39:LEU:HD23	1.99	0.43
26:Y:10:ARG:NH2	26:Y:24:VAL:HG11	2.34	0.43
1:2:1204:A:H2'	1:2:1205:C:C6	2.54	0.43
2:A:16:LEU:HD21	19:R:114:LEU:HD22	2.00	0.43
2:A:89:LYS:HA	2:A:89:LYS:HD3	1.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:49:LEU:HA	7:F:50:PRO:HD3	1.89	0.43
7:F:67:PRO:HG2	7:F:70:GLU:HB2	1.99	0.43
34:g:194:TYR:CE1	34:g:235:ILE:HG22	2.54	0.43
1:2:625:G:H4'	1:2:629:A:C4	2.53	0.43
1:2:1545:A:H2'	1:2:1546:G:O4'	2.19	0.43
11:J:33:GLY:HA3	32:e:38:TYR:CG	2.54	0.43
13:L:105:ARG:HG3	25:X:11:ARG:HH22	1.83	0.43
20:S:61:GLU:OE1	20:S:64:VAL:HG11	2.19	0.43
20:S:141:ARG:HG2	20:S:141:ARG:HH11	1.83	0.43
1:2:563:G:O2'	1:2:564:A:H8	2.01	0.43
1:2:1256:G:O6	22:U:65:THR:HG22	2.18	0.43
5:D:126:ILE:HG21	5:D:188:ILE:HG12	2.00	0.43
8:G:98:ARG:NH2	8:G:103:ASP:OD1	2.52	0.43
9:H:70:LYS:HB3	9:H:70:LYS:HE3	1.64	0.43
9:H:83:LEU:HD23	9:H:83:LEU:HA	1.81	0.43
13:L:31:GLU:C	13:L:32:LYS:HD2	2.44	0.43
14:M:40:LYS:H	14:M:40:LYS:HG2	1.66	0.43
16:O:60:MET:H	16:O:60:MET:HG2	1.72	0.43
1:2:511:U:O2'	1:2:576:A:N6	2.52	0.42
1:2:1231:C:H4'	1:2:1665:G:N7	2.33	0.42
4:C:125:LYS:HG3	4:C:143:CYS:HB2	2.00	0.42
5:D:103:GLU:OE1	5:D:173:ARG:NH1	2.52	0.42
11:J:131:ARG:HD2	11:J:131:ARG:HA	1.62	0.42
12:K:49:MET:HA	12:K:52:LEU:HD12	2.01	0.42
15:N:27:LYS:HA	15:N:27:LYS:HD3	1.85	0.42
21:T:66:LEU:C	21:T:67:ARG:HD2	2.44	0.42
22:U:20:ILE:HD12	22:U:20:ILE:C	2.44	0.42
22:U:38:ASP:OD1	22:U:41:ARG:NH2	2.52	0.42
1:2:37:C:H2'	1:2:38:A:O4'	2.19	0.42
1:2:1237:C:N3	1:2:1242:U:H2'	2.34	0.42
1:2:1277:C:H2'	1:2:1278:A:C8	2.54	0.42
1:2:1649:U:C5	1:2:1675:A:H2	2.38	0.42
1:2:1791:A:H4'	8:G:75:LEU:HD22	2.00	0.42
5:D:71:ALA:O	5:D:75:LYS:HG3	2.19	0.42
8:G:132:ARG:NH2	8:G:161:PRO:HD2	2.34	0.42
18:Q:100:VAL:HG13	18:Q:101:ASP:OD1	2.19	0.42
34:g:292:SER:OG	34:g:293:ALA:N	2.53	0.42
1:2:297:A:C5'	6:E:132:GLY:HA2	2.49	0.42
1:2:1067:C:H2'	1:2:1068:G:O4'	2.19	0.42
1:2:1391:C:O3'	22:U:83:ARG:NH2	2.48	0.42
3:B:126:ASP:OD1	3:B:126:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:140:ASP:O	30:c:46:VAL:HG23	2.19	0.42
9:H:170:VAL:C	9:H:172:THR:H	2.27	0.42
12:K:8:ARG:O	12:K:11:ILE:HG22	2.20	0.42
12:K:85:LEU:HD23	12:K:85:LEU:HA	1.90	0.42
14:M:52:LEU:HD12	14:M:52:LEU:HA	1.77	0.42
15:N:93:LYS:HE3	15:N:93:LYS:HB3	1.75	0.42
30:c:34:PHE:HE1	30:c:58:LEU:HD22	1.83	0.42
34:g:89:LEU:HD12	34:g:101:PHE:HE2	1.84	0.42
1:2:31:U:O2'	1:2:643:A:N1	2.49	0.42
1:2:71:G:H1'	1:2:72:C:C5	2.53	0.42
1:2:220:U:H6	1:2:220:U:H2'	1.70	0.42
1:2:597:G:H4'	1:2:646:G:H4'	2.01	0.42
1:2:921:G:N2	29:b:22:LYS:HD3	2.34	0.42
1:2:1540:G:O2'	1:2:1541:G:H5''	2.19	0.42
3:B:143:THR:HG23	3:B:205:TYR:CE1	2.54	0.42
5:D:95:GLY:HA2	5:D:125:PHE:CE2	2.54	0.42
5:D:141:LYS:NZ	5:D:179:GLN:O	2.50	0.42
19:R:107:LYS:HD2	19:R:107:LYS:C	2.43	0.42
21:T:128:GLN:O	21:T:131:LEU:HG	2.18	0.42
23:V:41:LYS:CD	23:V:41:LYS:H	2.33	0.42
28:a:78:VAL:HG13	28:a:84:VAL:HG22	2.02	0.42
34:g:167:SER:N	34:g:175:LYS:O	2.51	0.42
1:2:1037:G:H4'	1:2:1845:A:H4'	2.00	0.42
1:2:1199:A:H2'	1:2:1200:A:C8	2.53	0.42
1:2:1203:G:H2'	1:2:1204:A:H8	1.82	0.42
1:2:1614:A:C8	17:P:42:ARG:HD3	2.55	0.42
2:A:158:ASP:HB3	23:V:34:MET:HE1	2.01	0.42
2:A:207:PRO:O	2:A:210:ILE:HG13	2.19	0.42
4:C:132:ASP:OD1	4:C:136:HIS:HB2	2.20	0.42
16:O:120:ALA:HB2	28:a:53:ILE:HD13	2.00	0.42
18:Q:36:GLY:C	18:Q:37:ARG:HG3	2.44	0.42
20:S:124:ARG:CB	20:S:131:VAL:HG23	2.49	0.42
31:d:33:LYS:O	31:d:36:LEU:HD23	2.19	0.42
1:2:869:A:C6	9:H:114:GLN:HG3	2.55	0.42
1:2:1227:G:N2	1:2:1639:G:H21	2.15	0.42
1:2:1273:C:N3	1:2:1506:A:O2'	2.51	0.42
6:E:31:PRO:HG2	6:E:38:LEU:HG	2.02	0.42
7:F:123:GLU:N	7:F:197:GLU:OE1	2.50	0.42
13:L:48:LYS:NZ	13:L:52:GLU:HG2	2.33	0.42
15:N:31:ASP:O	15:N:35:GLU:HG2	2.18	0.42
17:P:89:MET:SD	17:P:89:MET:N	2.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:41:PHE:O	25:X:76:LYS:NZ	2.46	0.42
1:2:92:A:H1'	6:E:3:ARG:HB3	2.00	0.42
1:2:320:G:H1	1:2:331:C:N4	2.11	0.42
1:2:578:C:H2'	1:2:579:C:H6	1.85	0.42
1:2:945:U:H2'	1:2:946:U:C6	2.55	0.42
1:2:1856:C:H2'	1:2:1857:G:C8	2.54	0.42
2:A:10:MET:HE3	19:R:109:LEU:HD11	2.02	0.42
2:A:52:LYS:HE3	2:A:52:LYS:HB3	1.86	0.42
2:A:78:SER:HB2	2:A:87:VAL:HG21	2.00	0.42
4:C:244:ILE:O	4:C:247:THR:OG1	2.29	0.42
7:F:119:SER:C	7:F:190:ILE:HG21	2.45	0.42
13:L:84:ARG:HB3	13:L:112:HIS:CE1	2.54	0.42
14:M:36:ARG:NH1	33:f:105:TYR:OH	2.52	0.42
21:T:35:ASP:OD1	21:T:36:THR:N	2.52	0.42
1:2:65:C:C4	8:G:133:LEU:HG	2.55	0.42
1:2:77:A:C8	8:G:154:ARG:HB2	2.55	0.42
1:2:102:A:H4'	1:2:104:A:C8	2.55	0.42
1:2:943:U:C2	1:2:944:A:C8	3.08	0.42
1:2:1154:U:H2'	4:C:192:LEU:HD11	2.01	0.42
1:2:1472:C:H2'	1:2:1473:G:O4'	2.18	0.42
1:2:1603:G:OP1	20:S:31:THR:OG1	2.38	0.42
5:D:122:VAL:O	5:D:126:ILE:HG13	2.19	0.42
6:E:56:LEU:HD22	26:Y:74:MET:HE1	2.01	0.42
8:G:31:ARG:HE	8:G:31:ARG:HB2	1.58	0.42
17:P:41:GLN:N	17:P:115:TYR:OH	2.53	0.42
1:2:1182:A:C5	1:2:1183:A:H1'	2.54	0.42
1:2:1565:C:HO2'	1:2:1566:G:H8	1.65	0.42
10:I:161:LEU:O	10:I:165:GLN:HG3	2.20	0.42
20:S:141:ARG:HG2	20:S:141:ARG:NH1	2.34	0.42
26:Y:44:LEU:HD23	26:Y:44:LEU:HA	1.94	0.42
34:g:166:VAL:HG21	34:g:200:VAL:HG12	2.02	0.42
1:2:1339:U:H2'	1:2:1340:U:H6	1.85	0.42
1:2:1587:G:O2'	1:2:1588:A:OP2	2.35	0.42
1:2:1591:C:C2	1:2:1592:C:C4	3.08	0.42
1:2:1608:U:H5''	1:2:1609:C:C6	2.55	0.42
1:2:1674:G:H4'	7:F:83:ASN:O	2.20	0.42
1:2:1865:C:O2	28:a:92:ARG:HB3	2.20	0.42
6:E:44:LEU:HD11	6:E:70:ILE:HG21	2.02	0.42
9:H:81:ARG:O	9:H:85:LYS:HG2	2.20	0.42
10:I:9:HIS:ND1	10:I:9:HIS:C	2.78	0.42
10:I:199:LEU:HD23	10:I:199:LEU:HA	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:50:GLN:O	12:K:54:SER:OG	2.20	0.42
17:P:17:TYR:OH	17:P:112:ILE:HB	2.20	0.42
21:T:29:LYS:HD3	21:T:30:VAL:H	1.85	0.42
24:W:105:THR:HB	24:W:126:LEU:HD11	2.01	0.42
25:X:81:ILE:HD12	25:X:120:PHE:CE2	2.55	0.42
1:2:311:C:H5'	1:2:312:G:H5''	2.02	0.41
1:2:651:U:H2'	1:2:652:U:C6	2.55	0.41
1:2:656:G:N2	1:2:663:C:H5''	2.35	0.41
1:2:870:A:H62	1:2:916:A:H5'	1.85	0.41
1:2:988:C:H5''	3:B:116:LYS:HA	2.02	0.41
1:2:1069:U:H2'	1:2:1070:A:C8	2.55	0.41
1:2:1376:A:H2'	1:2:1377:U:O4'	2.20	0.41
1:2:1538:C:OP2	1:2:1592:C:N4	2.53	0.41
1:2:1670:C:H2'	1:2:1671:G:C8	2.55	0.41
3:B:136:ARG:HB3	3:B:216:LYS:HG3	2.01	0.41
4:C:256:TRP:CE2	24:W:68:ARG:HB3	2.55	0.41
5:D:20:GLU:CD	5:D:76:ARG:HH21	2.25	0.41
7:F:116:ILE:HG12	7:F:178:ILE:HG22	2.01	0.41
12:K:27:VAL:HG13	12:K:43:LEU:HD13	2.01	0.41
15:N:94:LYS:O	15:N:98:VAL:HG13	2.19	0.41
31:d:48:LYS:HB2	31:d:48:LYS:HE2	1.63	0.41
1:2:1246:A:N3	1:2:1251:A:O2'	2.44	0.41
1:2:1347:U:H2'	1:2:1348:G:N3	2.34	0.41
7:F:112:LEU:HG	7:F:177:LEU:HB3	2.03	0.41
8:G:119:LYS:HD2	8:G:119:LYS:HA	1.92	0.41
8:G:167:LYS:HE2	8:G:167:LYS:HB2	1.87	0.41
9:H:134:VAL:HG12	9:H:173:PHE:CE2	2.54	0.41
18:Q:46:THR:O	18:Q:47:LEU:HD23	2.20	0.41
21:T:20:ALA:HA	21:T:23:LYS:HE3	2.03	0.41
1:2:141:A:C6	1:2:177:G:C4	3.07	0.41
1:2:384:U:O4	10:I:5:ARG:NH2	2.46	0.41
1:2:389:A:H2'	1:2:390:C:C6	2.54	0.41
1:2:1257:G:H4'	1:2:1258:A:C5'	2.51	0.41
1:2:1685:U:H2'	1:2:1686:G:O4'	2.20	0.41
2:A:57:LYS:HA	2:A:57:LYS:HD2	1.82	0.41
4:C:194:ARG:HD3	4:C:196:ILE:HD11	2.01	0.41
5:D:12:VAL:HG11	31:d:36:LEU:HD22	2.01	0.41
5:D:106:ARG:HB2	5:D:175:VAL:HG22	2.02	0.41
11:J:50:LEU:O	11:J:54:ARG:HG3	2.20	0.41
17:P:60:LEU:O	17:P:64:LYS:HB2	2.20	0.41
20:S:88:LYS:H	20:S:95:TYR:HE1	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:84:ARG:HH22	21:T:89:PRO:HA	1.86	0.41
24:W:39:THR:O	24:W:43:LYS:HG2	2.20	0.41
29:b:33:MET:HE1	29:b:73:LEU:HD21	2.02	0.41
34:g:67:SER:OG	34:g:68:ASP:N	2.54	0.41
1:2:1232:U:H5	1:2:1526:G:H1	1.69	0.41
1:2:1265:A:H1'	1:2:1509:U:H3	1.84	0.41
5:D:206:ASP:OD1	5:D:206:ASP:N	2.42	0.41
6:E:180:LEU:N	6:E:231:GLY:O	2.53	0.41
7:F:72:LEU:HD11	7:F:179:ASN:C	2.46	0.41
7:F:94:LYS:NZ	18:Q:46:THR:O	2.53	0.41
21:T:6:VAL:HB	21:T:132:ASP:OD1	2.20	0.41
1:2:617:G:N7	25:X:67:ARG:NH1	2.67	0.41
1:2:1284:A:C8	14:M:104:VAL:HB	2.55	0.41
1:2:1401:A:N6	1:2:1446:A:N1	2.68	0.41
1:2:1601:A:C2	1:2:1602:U:H5	2.38	0.41
5:D:99:ILE:HD13	5:D:171:ALA:HB2	2.02	0.41
10:I:143:LYS:HD2	10:I:143:LYS:HA	1.82	0.41
11:J:137:VAL:HG22	11:J:157:ILE:HG12	2.02	0.41
20:S:85:ASN:N	20:S:85:ASN:OD1	2.52	0.41
21:T:16:ARG:NH2	21:T:17:ALA:HA	2.35	0.41
34:g:157:SER:HA	34:g:158:PRO:HD3	1.93	0.41
1:2:582:U:H1'	26:Y:33:ALA:HB2	2.03	0.41
4:C:167:ARG:HB3	4:C:177:PRO:HB2	2.01	0.41
18:Q:111:ILE:HD13	18:Q:111:ILE:HA	1.91	0.41
22:U:59:LYS:H	22:U:59:LYS:HG2	1.67	0.41
34:g:158:PRO:HG3	34:g:200:VAL:HG23	2.01	0.41
1:2:211:G:H2'	1:2:211:G:N3	2.36	0.41
1:2:1287:A:N1	33:f:95:ARG:HB2	2.36	0.41
1:2:1678:A:H2'	1:2:1679:A:H5''	2.03	0.41
2:A:205:ARG:NH2	2:A:210:ILE:HG22	2.35	0.41
5:D:21:LEU:O	5:D:25:LEU:HG	2.20	0.41
7:F:76:MET:HA	7:F:76:MET:HE2	2.01	0.41
8:G:55:GLY:O	8:G:63:MET:HG3	2.21	0.41
11:J:124:HIS:CE1	32:e:35:ARG:HB2	2.56	0.41
15:N:129:TYR:HB3	15:N:135:LEU:HG	2.03	0.41
21:T:41:LYS:HB2	21:T:83:GLN:HE21	1.86	0.41
21:T:84:ARG:NH1	21:T:88:MET:O	2.44	0.41
30:c:34:PHE:CE1	30:c:58:LEU:HD22	2.55	0.41
34:g:59:LEU:HD11	34:g:90:TRP:NE1	2.35	0.41
34:g:85:GLY:HA2	34:g:108:VAL:HB	2.02	0.41
34:g:94:THR:HG23	34:g:96:THR:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1391:C:H2'	1:2:1392:U:O4'	2.21	0.41
1:2:1520:G:O2'	17:P:124:LYS:O	2.34	0.41
1:2:1815:A:C6	1:2:1816:G:H1'	2.56	0.41
5:D:12:VAL:O	5:D:16:ILE:HG12	2.21	0.41
7:F:112:LEU:O	7:F:178:ILE:HA	2.19	0.41
9:H:52:GLU:HG3	9:H:58:LYS:HD3	2.02	0.41
14:M:49:LEU:HD21	14:M:107:SER:HB2	2.03	0.41
1:2:613:G:N2	1:2:626:G:OP1	2.50	0.41
1:2:986:G:C8	16:O:137:SER:O	2.74	0.41
1:2:1475:G:H8	1:2:1475:G:OP2	2.03	0.41
1:2:1591:C:O2'	1:2:1592:C:O5'	2.37	0.41
1:2:1609:C:O2'	20:S:109:GLU:OE2	2.35	0.41
1:2:1649:U:C6	1:2:1675:A:H2	2.39	0.41
1:2:1745:A:N6	1:2:1746:U:H1'	2.35	0.41
2:A:82:THR:HG23	2:A:168:ALA:HA	2.03	0.41
3:B:171:ILE:HD12	3:B:197:ILE:HA	2.02	0.41
5:D:48:ILE:HB	5:D:86:LEU:HB3	2.03	0.41
8:G:31:ARG:HD2	8:G:68:LEU:HD22	2.02	0.41
8:G:33:ALA:N	8:G:52:ILE:O	2.32	0.41
10:I:123:ARG:HA	10:I:123:ARG:HD3	1.82	0.41
19:R:10:LYS:HD3	19:R:53:TYR:CE2	2.56	0.41
20:S:104:ASP:O	20:S:107:LEU:HG	2.20	0.41
28:a:12:LYS:HG3	28:a:15:ARG:HG2	2.03	0.41
30:c:60:GLU:HG2	30:c:62:GLU:H	1.85	0.41
34:g:126:ASP:OD1	34:g:126:ASP:N	2.53	0.41
34:g:131:LEU:HD12	34:g:140:TYR:HB3	2.02	0.41
1:2:204:G:C2	1:2:205:G:N7	2.89	0.41
1:2:1613:G:H5''	17:P:34:MET:HE1	2.02	0.41
5:D:55:THR:HA	5:D:58:VAL:CG1	2.51	0.41
7:F:49:LEU:HB3	18:Q:50:LYS:NZ	2.35	0.41
9:H:82:GLU:H	9:H:82:GLU:HG2	1.70	0.41
24:W:83:LEU:HD12	24:W:83:LEU:HA	1.85	0.41
25:X:101:LEU:HB3	25:X:124:LYS:HB2	2.03	0.41
34:g:284:PRO:HB2	34:g:302:TYR:HB3	2.02	0.41
1:2:396:U:OP2	13:L:79:LYS:NZ	2.32	0.40
1:2:472:C:H4'	1:2:474:G:OP1	2.21	0.40
1:2:652:U:H2'	1:2:653:A:C8	2.56	0.40
1:2:820:U:OP1	6:E:259:LYS:NZ	2.54	0.40
1:2:941:C:H2'	1:2:942:G:C8	2.56	0.40
1:2:1253:A:N6	1:2:1665:G:O2'	2.54	0.40
1:2:1527:C:H5''	18:Q:142:GLN:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1842:C:H2'	1:2:1843:G:C8	2.56	0.40
5:D:25:LEU:HD12	5:D:34:TYR:CE1	2.56	0.40
9:H:148:LEU:HD21	24:W:48:GLY:HA2	2.04	0.40
12:K:18:GLU:HA	12:K:18:GLU:OE1	2.21	0.40
19:R:20:TYR:O	19:R:24:LEU:HG	2.21	0.40
19:R:111:PHE:HB3	19:R:114:LEU:HD11	2.03	0.40
22:U:104:ILE:HD12	22:U:104:ILE:HA	1.89	0.40
34:g:203:ASP:OD1	34:g:203:ASP:N	2.51	0.40
34:g:288:SER:C	34:g:289:LEU:HD13	2.46	0.40
1:2:90:G:H2'	1:2:91:A:O4'	2.21	0.40
1:2:419:G:N2	1:2:661:U:O2	2.54	0.40
1:2:1047:C:H5''	16:O:143:LYS:HA	2.03	0.40
1:2:1345:G:H21	1:2:1484:A:H8	1.66	0.40
1:2:1466:G:H5'	19:R:4:VAL:HG22	2.03	0.40
1:2:1590:C:C3'	1:2:1591:C:N1	2.84	0.40
5:D:179:GLN:OE1	5:D:179:GLN:HA	2.21	0.40
7:F:51:HIS:CD2	18:Q:47:LEU:HD11	2.57	0.40
12:K:3:MET:SD	12:K:8:ARG:HB2	2.61	0.40
19:R:25:GLY:H	19:R:31:ASN:HD21	1.69	0.40
20:S:80:PRO:HG2	21:T:36:THR:OG1	2.20	0.40
20:S:116:LYS:HB3	20:S:116:LYS:HE2	1.85	0.40
27:Z:79:ILE:HG21	27:Z:83:LEU:HD23	2.02	0.40
1:2:687:C:O2'	9:H:103:LYS:HD3	2.22	0.40
1:2:819:G:HO2'	1:2:820:U:P	2.42	0.40
1:2:1229:G:P	1:2:1530:U:H1'	2.62	0.40
1:2:1538:C:H5''	1:2:1593:C:N4	2.29	0.40
1:2:1538:C:H42	1:2:1595:U:H5''	1.85	0.40
1:2:1718:G:H4'	1:2:1719:A:OP2	2.21	0.40
3:B:182:LYS:NZ	3:B:182:LYS:HB3	2.37	0.40
5:D:197:LYS:HD3	5:D:197:LYS:HA	1.96	0.40
9:H:111:LYS:HA	9:H:111:LYS:HD3	1.68	0.40
11:J:42:GLU:O	11:J:46:VAL:HG23	2.22	0.40
11:J:126:ALA:O	11:J:130:ILE:HG13	2.22	0.40
12:K:48:ALA:O	12:K:52:LEU:HG	2.21	0.40
15:N:5:HIS:ND1	15:N:121:ARG:HD3	2.36	0.40
22:U:30:LYS:HA	22:U:30:LYS:HD2	1.70	0.40
25:X:37:LYS:HD2	25:X:38:ALA:N	2.36	0.40
28:a:32:LYS:O	28:a:37:LYS:NZ	2.41	0.40
34:g:248:LEU:O	34:g:258:ILE:HD12	2.21	0.40
1:2:14:C:H5''	4:C:190:SER:HB3	2.04	0.40
1:2:482:G:N1	1:2:485:A:OP2	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1538:C:C6	1:2:1593:C:N4	2.89	0.40
6:E:129:ILE:HG13	6:E:129:ILE:O	2.21	0.40
8:G:1:MET:HE2	8:G:1:MET:HB3	1.85	0.40
11:J:125:HIS:HA	11:J:128:VAL:HG22	2.03	0.40
24:W:66:THR:C	24:W:68:ARG:H	2.28	0.40
29:b:82:LYS:HE2	29:b:82:LYS:HB2	1.97	0.40
34:g:65:PHE:CD1	34:g:65:PHE:N	2.88	0.40
1:2:634:A:H2'	1:2:635:G:H8	1.87	0.40
1:2:1269:G:N1	1:2:1270:G:C4	2.89	0.40
1:2:1515:G:N3	1:2:1515:G:H2'	2.35	0.40
1:2:1702:G:H2'	1:2:1703:C:O4'	2.21	0.40
1:2:1785:C:H2'	1:2:1786:U:C6	2.57	0.40
9:H:160:LYS:HD2	9:H:160:LYS:HA	1.67	0.40
16:O:45:THR:CG2	16:O:49:GLY:HA2	2.51	0.40
17:P:79:HIS:CE1	17:P:97:TYR:HD1	2.40	0.40
19:R:99:ASP:O	19:R:102:THR:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	211/295 (72%)	208 (99%)	2 (1%)	1 (0%)	24	39
3	B	211/264 (80%)	206 (98%)	5 (2%)	0	100	100
4	C	216/293 (74%)	212 (98%)	4 (2%)	0	100	100
5	D	223/243 (92%)	217 (97%)	6 (3%)	0	100	100
6	E	260/263 (99%)	253 (97%)	7 (3%)	0	100	100
7	F	187/204 (92%)	157 (84%)	29 (16%)	1 (0%)	24	39
8	G	228/249 (92%)	222 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	H	184/194 (95%)	176 (96%)	8 (4%)	0	100	100
10	I	203/208 (98%)	193 (95%)	10 (5%)	0	100	100
11	J	178/194 (92%)	172 (97%)	6 (3%)	0	100	100
12	K	95/165 (58%)	90 (95%)	5 (5%)	0	100	100
13	L	149/158 (94%)	146 (98%)	3 (2%)	0	100	100
14	M	119/132 (90%)	109 (92%)	7 (6%)	3 (2%)	4	7
15	N	147/151 (97%)	144 (98%)	3 (2%)	0	100	100
16	O	133/151 (88%)	127 (96%)	6 (4%)	0	100	100
17	P	124/145 (86%)	115 (93%)	9 (7%)	0	100	100
18	Q	136/146 (93%)	121 (89%)	14 (10%)	1 (1%)	18	30
19	R	130/135 (96%)	128 (98%)	2 (2%)	0	100	100
20	S	141/152 (93%)	120 (85%)	21 (15%)	0	100	100
21	T	142/145 (98%)	128 (90%)	12 (8%)	2 (1%)	9	14
22	U	99/119 (83%)	93 (94%)	6 (6%)	0	100	100
23	V	80/83 (96%)	80 (100%)	0	0	100	100
24	W	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
25	X	139/143 (97%)	137 (99%)	2 (1%)	0	100	100
26	Y	122/130 (94%)	120 (98%)	2 (2%)	0	100	100
27	Z	70/125 (56%)	66 (94%)	4 (6%)	0	100	100
28	a	97/101 (96%)	95 (98%)	1 (1%)	1 (1%)	12	20
29	b	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
30	c	60/62 (97%)	54 (90%)	6 (10%)	0	100	100
31	d	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
32	e	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
33	f	72/74 (97%)	65 (90%)	7 (10%)	0	100	100
34	g	312/315 (99%)	282 (90%)	30 (10%)	0	100	100
35	h	20/25 (80%)	20 (100%)	0	0	100	100
36	n	28/180 (16%)	25 (89%)	3 (11%)	0	100	100
All	All	4830/5567 (87%)	4588 (95%)	233 (5%)	9 (0%)	44	60

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	M	109	VAL
21	T	65	TYR
28	a	63	VAL
2	A	189	ILE
7	F	79	HIS
14	M	110	VAL
18	Q	13	PHE
14	M	31	LEU
21	T	39	LEU

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%)	173 (97%)	6 (3%)	32	53
3	B	194/231 (84%)	187 (96%)	7 (4%)	31	51
4	C	184/225 (82%)	180 (98%)	4 (2%)	45	67
5	D	189/202 (94%)	176 (93%)	13 (7%)	14	24
6	E	224/225 (100%)	223 (100%)	1 (0%)	84	93
7	F	159/170 (94%)	154 (97%)	5 (3%)	35	56
8	G	200/218 (92%)	195 (98%)	5 (2%)	42	64
9	H	167/174 (96%)	159 (95%)	8 (5%)	23	39
10	I	178/180 (99%)	174 (98%)	4 (2%)	45	67
11	J	160/168 (95%)	158 (99%)	2 (1%)	61	77
12	K	88/136 (65%)	87 (99%)	1 (1%)	65	80
13	L	135/142 (95%)	133 (98%)	2 (2%)	57	75
14	M	102/108 (94%)	99 (97%)	3 (3%)	37	58
15	N	130/131 (99%)	127 (98%)	3 (2%)	44	66
16	O	105/119 (88%)	99 (94%)	6 (6%)	18	32
17	P	112/130 (86%)	107 (96%)	5 (4%)	24	42
18	Q	114/121 (94%)	111 (97%)	3 (3%)	40	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	R	119/122 (98%)	115 (97%)	4 (3%)	32	53
20	S	124/132 (94%)	113 (91%)	11 (9%)	9	15
21	T	114/115 (99%)	106 (93%)	8 (7%)	14	24
22	U	93/107 (87%)	92 (99%)	1 (1%)	65	80
23	V	66/67 (98%)	65 (98%)	1 (2%)	57	75
24	W	112/113 (99%)	108 (96%)	4 (4%)	31	51
25	X	113/115 (98%)	109 (96%)	4 (4%)	32	52
26	Y	108/112 (96%)	105 (97%)	3 (3%)	38	60
27	Z	64/103 (62%)	63 (98%)	1 (2%)	55	74
28	a	87/89 (98%)	82 (94%)	5 (6%)	18	32
29	b	74/74 (100%)	69 (93%)	5 (7%)	14	25
30	c	55/55 (100%)	54 (98%)	1 (2%)	51	72
31	d	48/48 (100%)	46 (96%)	2 (4%)	26	45
32	e	45/45 (100%)	43 (96%)	2 (4%)	25	43
33	f	67/67 (100%)	65 (97%)	2 (3%)	36	57
34	g	272/273 (100%)	253 (93%)	19 (7%)	14	24
35	h	21/24 (88%)	21 (100%)	0	100	100
36	n	26/150 (17%)	25 (96%)	1 (4%)	29	49
All	All	4228/4734 (89%)	4076 (96%)	152 (4%)	32	51

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	28	THR
2	A	75	SER
2	A	87	VAL
2	A	118	GLU
2	A	188	THR
2	A	189	ILE
3	B	62	LEU
3	B	69	VAL
3	B	76	ASN
3	B	108	ASP
3	B	127	VAL
3	B	131	ASP
3	B	203	SER

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Mol	Chain	Res	Type
4	C	74	LYS
4	C	162	ILE
4	C	180	VAL
4	C	248	TYR
5	D	25	LEU
5	D	35	SER
5	D	41	VAL
5	D	42	THR
5	D	86	LEU
5	D	91	VAL
5	D	96	LEU
5	D	115	VAL
5	D	156	LEU
5	D	177	LEU
5	D	181	VAL
5	D	184	ILE
5	D	210	ILE
6	E	227	VAL
7	F	33	ILE
7	F	79	HIS
7	F	89	THR
7	F	168	THR
7	F	197	GLU
8	G	18	VAL
8	G	34	THR
8	G	46	LYS
8	G	133	LEU
8	G	200	LYS
9	H	21	SER
9	H	40	LEU
9	H	51	ILE
9	H	60	ILE
9	H	75	ILE
9	H	166	VAL
9	H	172	THR
9	H	184	ASP
10	I	73	THR
10	I	86	SER
10	I	116	HIS
10	I	159	SER
11	J	67	ASP
11	J	159	PHE

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Mol	Chain	Res	Type
12	K	90	VAL
13	L	66	VAL
13	L	76	VAL
14	M	24	THR
14	M	49	LEU
14	M	52	LEU
15	N	28	LEU
15	N	30	SER
15	N	143	SER
16	O	39	ASP
16	O	52	THR
16	O	90	ILE
16	O	113	GLN
16	O	122	SER
16	O	133	THR
17	P	45	LEU
17	P	76	VAL
17	P	86	LEU
17	P	93	MET
17	P	107	ILE
18	Q	68	ILE
18	Q	116	ASP
18	Q	121	VAL
19	R	9	VAL
19	R	98	VAL
19	R	102	THR
19	R	124	VAL
20	S	3	LEU
20	S	30	ILE
20	S	39	ARG
20	S	53	THR
20	S	60	THR
20	S	71	MET
20	S	98	VAL
20	S	99	LEU
20	S	127	TRP
20	S	131	VAL
20	S	139	THR
21	T	9	VAL
21	T	27	LYS
21	T	48	TYR
21	T	64	LEU

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Mol	Chain	Res	Type
21	T	66	LEU
21	T	67	ARG
21	T	94	ARG
21	T	103	VAL
22	U	22	ILE
23	V	39	VAL
24	W	26	LEU
24	W	57	ARG
24	W	74	VAL
24	W	80	ASP
25	X	57	VAL
25	X	72	VAL
25	X	82	THR
25	X	102	VAL
26	Y	35	VAL
26	Y	84	LYS
26	Y	102	THR
27	Z	104	ARG
28	a	2	THR
28	a	30	VAL
28	a	55	GLU
28	a	59	PHE
28	a	63	VAL
29	b	3	LEU
29	b	26	GLN
29	b	44	THR
29	b	45	THR
29	b	53	VAL
30	c	60	GLU
31	d	14	PHE
31	d	30	LEU
32	e	29	THR
32	e	58	ASN
33	f	86	THR
33	f	108	VAL
34	g	14	HIS
34	g	35	SER
34	g	40	ILE
34	g	41	ILE
34	g	52	TYR
34	g	59	LEU
34	g	60	ARG

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Mol	Chain	Res	Type
34	g	69	VAL
34	g	96	THR
34	g	97	THR
34	g	102	VAL
34	g	194	TYR
34	g	199	THR
34	g	229	THR
34	g	289	LEU
34	g	297	THR
34	g	303	THR
34	g	307	VAL
34	g	310	TRP
36	n	169	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	101	HIS
3	B	159	GLN
3	B	202	GLN
5	D	101	GLN
5	D	145	GLN
5	D	165	ASN
6	E	98	ASN
6	E	142	HIS
8	G	81	HIS
8	G	105	ASN
9	H	39	GLN
9	H	76	GLN
10	I	155	ASN
11	J	143	ASN
12	K	44	HIS
12	K	66	HIS
13	L	19	ASN
14	M	19	GLN
14	M	72	HIS
15	N	13	GLN
15	N	58	HIS
15	N	90	HIS
15	N	105	ASN
16	O	83	GLN
17	P	53	GLN

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Mol	Chain	Res	Type
17	P	98	ASN
18	Q	11	GLN
18	Q	35	ASN
18	Q	48	GLN
18	Q	142	GLN
19	R	31	ASN
20	S	72	GLN
20	S	87	GLN
20	S	97	GLN
21	T	63	HIS
21	T	126	GLN
22	U	85	HIS
22	U	100	GLN
26	Y	22	GLN
26	Y	63	HIS
27	Z	106	GLN
28	a	19	GLN
31	d	26	ASN
34	g	62	HIS
34	g	147	HIS
34	g	159	ASN
34	g	215	GLN
34	g	296	GLN
36	n	178	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1653/1869 (88%)	615 (37%)	24 (1%)

All (615) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	15	U
1	2	17	C
1	2	26	U
1	2	33	G
1	2	41	G
1	2	42	A

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Mol	Chain	Res	Type
1	2	44	U
1	2	45	A
1	2	46	A
1	2	56	G
1	2	67	C
1	2	68	A
1	2	71	G
1	2	73	C
1	2	74	G
1	2	76	U
1	2	84	A
1	2	102	A
1	2	103	A
1	2	113	G
1	2	114	G
1	2	115	U
1	2	124	U
1	2	125	C
1	2	126	G
1	2	127	C
1	2	128	U
1	2	129	C
1	2	130	G
1	2	141	A
1	2	142	C
1	2	143	U
1	2	147	A
1	2	150	A
1	2	155	G
1	2	160	U
1	2	168	C
1	2	170	A
1	2	173	A
1	2	174	C
1	2	175	A
1	2	176	U
1	2	177	G
1	2	178	C
1	2	179	C
1	2	180	G
1	2	181	A
1	2	183	G

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Mol	Chain	Res	Type
1	2	184	G
1	2	189	U
1	2	190	G
1	2	193	C
1	2	194	C
1	2	195	C
1	2	197	U
1	2	199	C
1	2	200	G
1	2	202	G
1	2	204	G
1	2	205	G
1	2	211	G
1	2	212	C
1	2	213	G
1	2	215	G
1	2	216	C
1	2	217	A
1	2	218	U
1	2	219	U
1	2	221	A
1	2	222	U
1	2	224	A
1	2	225	G
1	2	305	U
1	2	306	C
1	2	308	G
1	2	309	G
1	2	310	C
1	2	311	C
1	2	314	U
1	2	315	C
1	2	316	G
1	2	317	C
1	2	318	A
1	2	319	C
1	2	320	G
1	2	330	G
1	2	331	C
1	2	332	G
1	2	335	G
1	2	339	A

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Mol	Chain	Res	Type
1	2	340	C
1	2	343	A
1	2	344	U
1	2	352	U
1	2	353	C
1	2	362	C
1	2	364	A
1	2	368	U
1	2	369	C
1	2	370	G
1	2	381	C
1	2	385	G
1	2	386	C
1	2	398	A
1	2	400	C
1	2	407	G
1	2	408	A
1	2	409	C
1	2	413	G
1	2	415	A
1	2	416	U
1	2	417	C
1	2	418	A
1	2	438	G
1	2	448	A
1	2	449	A
1	2	450	C
1	2	464	A
1	2	466	G
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	478	G
1	2	482	G
1	2	487	U
1	2	488	U
1	2	492	C
1	2	501	C
1	2	513	G

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Mol	Chain	Res	Type
1	2	514	U
1	2	515	G
1	2	525	A
1	2	532	C
1	2	533	A
1	2	534	G
1	2	537	C
1	2	538	U
1	2	539	C
1	2	540	U
1	2	541	U
1	2	544	G
1	2	545	A
1	2	546	G
1	2	547	G
1	2	550	C
1	2	552	G
1	2	554	A
1	2	555	A
1	2	556	U
1	2	557	U
1	2	559	G
1	2	564	A
1	2	570	C
1	2	576	A
1	2	579	C
1	2	584	A
1	2	587	A
1	2	589	G
1	2	590	A
1	2	591	U
1	2	597	G
1	2	604	A
1	2	605	A
1	2	607	U
1	2	608	C
1	2	614	C
1	2	617	G
1	2	627	U
1	2	632	C
1	2	640	A
1	2	643	A

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Mol	Chain	Res	Type
1	2	644	G
1	2	645	C
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
1	2	688	U
1	2	747	U
1	2	748	C
1	2	752	G
1	2	793	G
1	2	794	A
1	2	795	A
1	2	797	C
1	2	799	U
1	2	803	C
1	2	809	A
1	2	811	A
1	2	820	U
1	2	821	G
1	2	822	U
1	2	823	U
1	2	824	C
1	2	827	A
1	2	832	G
1	2	834	C
1	2	842	C
1	2	843	C
1	2	844	U
1	2	847	A
1	2	848	U
1	2	860	G
1	2	862	A
1	2	864	A
1	2	868	G
1	2	869	A
1	2	870	A
1	2	871	U
1	2	874	G

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Mol	Chain	Res	Type
1	2	875	A
1	2	876	C
1	2	877	C
1	2	878	G
1	2	879	C
1	2	880	G
1	2	881	G
1	2	884	C
1	2	885	U
1	2	888	U
1	2	889	U
1	2	890	U
1	2	892	U
1	2	893	U
1	2	894	G
1	2	897	U
1	2	898	U
1	2	900	C
1	2	901	G
1	2	902	G
1	2	904	A
1	2	906	U
1	2	907	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	952	G
1	2	953	C
1	2	955	A
1	2	957	A
1	2	959	G
1	2	960	U
1	2	961	G
1	2	964	A
1	2	969	U
1	2	970	G
1	2	977	C

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Mol	Chain	Res	Type
1	2	978	G
1	2	982	G
1	2	990	A
1	2	991	G
1	2	992	A
1	2	999	G
1	2	1001	A
1	2	1002	U
1	2	1017	U
1	2	1021	U
1	2	1023	A
1	2	1026	C
1	2	1027	A
1	2	1028	A
1	2	1045	U
1	2	1049	A
1	2	1050	A
1	2	1056	U
1	2	1060	A
1	2	1062	A
1	2	1070	A
1	2	1080	A
1	2	1083	A
1	2	1085	C
1	2	1088	U
1	2	1096	G
1	2	1100	A
1	2	1109	C
1	2	1113	A
1	2	1114	U
1	2	1115	U
1	2	1116	C
1	2	1133	A
1	2	1136	U
1	2	1137	U
1	2	1138	C
1	2	1139	C
1	2	1140	G
1	2	1143	A
1	2	1148	A
1	2	1154	U
1	2	1156	U

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Mol	Chain	Res	Type
1	2	1157	G
1	2	1171	G
1	2	1195	A
1	2	1201	U
1	2	1207	G
1	2	1209	A
1	2	1215	C
1	2	1216	C
1	2	1220	A
1	2	1221	G
1	2	1222	G
1	2	1225	U
1	2	1226	G
1	2	1227	G
1	2	1229	G
1	2	1230	C
1	2	1231	C
1	2	1234	C
1	2	1237	C
1	2	1238	U
1	2	1240	A
1	2	1241	A
1	2	1242	U
1	2	1243	U
1	2	1244	U
1	2	1245	G
1	2	1247	C
1	2	1248	U
1	2	1249	C
1	2	1251	A
1	2	1253	A
1	2	1254	C
1	2	1255	G
1	2	1256	G
1	2	1257	G
1	2	1259	A
1	2	1260	A
1	2	1262	C
1	2	1263	U
1	2	1264	C
1	2	1266	C
1	2	1267	C

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Mol	Chain	Res	Type
1	2	1268	C
1	2	1269	G
1	2	1271	C
1	2	1275	G
1	2	1276	A
1	2	1277	C
1	2	1279	C
1	2	1282	A
1	2	1283	C
1	2	1284	A
1	2	1288	U
1	2	1289	U
1	2	1290	G
1	2	1291	A
1	2	1293	A
1	2	1294	G
1	2	1295	A
1	2	1297	U
1	2	1298	G
1	2	1299	A
1	2	1300	U
1	2	1302	G
1	2	1303	C
1	2	1304	U
1	2	1306	U
1	2	1308	U
1	2	1309	C
1	2	1311	C
1	2	1313	A
1	2	1315	U
1	2	1319	U
1	2	1321	G
1	2	1322	G
1	2	1323	U
1	2	1324	G
1	2	1325	G
1	2	1326	U
1	2	1331	C
1	2	1337	C
1	2	1340	U
1	2	1341	C
1	2	1345	G

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Mol	Chain	Res	Type
1	2	1358	U
1	2	1364	U
1	2	1371	U
1	2	1372	U
1	2	1373	C
1	2	1378	A
1	2	1382	A
1	2	1387	G
1	2	1394	G
1	2	1396	A
1	2	1397	U
1	2	1398	G
1	2	1403	C
1	2	1404	U
1	2	1405	A
1	2	1406	G
1	2	1407	U
1	2	1410	C
1	2	1411	G
1	2	1414	A
1	2	1415	C
1	2	1416	C
1	2	1439	A
1	2	1440	C
1	2	1441	U
1	2	1443	C
1	2	1444	U
1	2	1447	G
1	2	1448	A
1	2	1449	G
1	2	1454	A
1	2	1462	U
1	2	1463	U
1	2	1466	G
1	2	1471	C
1	2	1475	G
1	2	1477	U
1	2	1478	U
1	2	1479	G
1	2	1485	U
1	2	1486	A
1	2	1488	C

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Mol	Chain	Res	Type
1	2	1489	A
1	2	1490	G
1	2	1494	U
1	2	1495	G
1	2	1496	U
1	2	1497	G
1	2	1498	A
1	2	1500	G
1	2	1508	A
1	2	1509	U
1	2	1512	C
1	2	1513	C
1	2	1514	G
1	2	1515	G
1	2	1517	G
1	2	1519	U
1	2	1520	G
1	2	1521	C
1	2	1523	C
1	2	1524	G
1	2	1530	U
1	2	1531	A
1	2	1532	C
1	2	1533	A
1	2	1534	C
1	2	1535	U
1	2	1537	A
1	2	1539	U
1	2	1540	G
1	2	1541	G
1	2	1543	U
1	2	1544	C
1	2	1546	G
1	2	1547	C
1	2	1552	G
1	2	1554	C
1	2	1560	U
1	2	1561	A
1	2	1562	C
1	2	1564	C
1	2	1565	C
1	2	1566	G

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Mol	Chain	Res	Type
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	1573	G
1	2	1575	G
1	2	1578	U
1	2	1580	A
1	2	1581	C
1	2	1584	G
1	2	1586	U
1	2	1587	G
1	2	1588	A
1	2	1589	A
1	2	1590	C
1	2	1591	C
1	2	1592	C
1	2	1594	A
1	2	1595	U
1	2	1596	U
1	2	1598	G
1	2	1599	U
1	2	1600	G
1	2	1601	A
1	2	1603	G
1	2	1604	G
1	2	1607	A
1	2	1608	U
1	2	1609	C
1	2	1611	G
1	2	1612	G
1	2	1614	A
1	2	1615	U
1	2	1616	U
1	2	1617	G
1	2	1618	C
1	2	1619	A
1	2	1621	U
1	2	1622	U
1	2	1623	A

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Mol	Chain	Res	Type
1	2	1624	U
1	2	1626	C
1	2	1627	C
1	2	1630	A
1	2	1631	U
1	2	1632	G
1	2	1634	A
1	2	1635	C
1	2	1636	G
1	2	1637	A
1	2	1638	G
1	2	1639	G
1	2	1640	A
1	2	1642	U
1	2	1643	U
1	2	1649	U
1	2	1654	G
1	2	1657	G
1	2	1660	C
1	2	1661	A
1	2	1662	U
1	2	1663	A
1	2	1665	G
1	2	1671	G
1	2	1677	U
1	2	1686	G
1	2	1690	U
1	2	1698	C
1	2	1707	U
1	2	1709	G
1	2	1710	C
1	2	1711	U
1	2	1712	A
1	2	1713	C
1	2	1714	U
1	2	1715	A
1	2	1718	G
1	2	1719	A
1	2	1720	U
1	2	1721	U
1	2	1723	G
1	2	1724	A

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Mol	Chain	Res	Type
1	2	1725	U
1	2	1726	G
1	2	1728	U
1	2	1729	U
1	2	1736	G
1	2	1737	G
1	2	1739	C
1	2	1740	C
1	2	1741	U
1	2	1742	C
1	2	1743	G
1	2	1745	A
1	2	1746	U
1	2	1750	C
1	2	1752	C
1	2	1754	G
1	2	1760	G
1	2	1761	U
1	2	1773	C
1	2	1774	C
1	2	1776	G
1	2	1777	G
1	2	1778	C
1	2	1779	G
1	2	1780	G
1	2	1783	C
1	2	1784	G
1	2	1788	A
1	2	1790	A
1	2	1791	A
1	2	1793	A
1	2	1794	C
1	2	1795	G
1	2	1796	G
1	2	1800	A
1	2	1801	A
1	2	1803	U
1	2	1804	U
1	2	1806	A
1	2	1809	A
1	2	1811	C
1	2	1812	U

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Mol	Chain	Res	Type
1	2	1816	G
1	2	1825	A
1	2	1826	G
1	2	1828	C
1	2	1829	G
1	2	1830	U
1	2	1835	A
1	2	1838	U
1	2	1840	U
1	2	1846	G
1	2	1849	G
1	2	1850	A
1	2	1851	A
1	2	1861	G
1	2	1862	G
1	2	1863	A
1	2	1864	U
1	2	1865	C
1	2	1869	A

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	180	G
1	2	578	C
1	2	604	A
1	2	808	A
1	2	819	G
1	2	880	G
1	2	900	C
1	2	958	G
1	2	1138	C
1	2	1200	A
1	2	1230	C
1	2	1339	U
1	2	1344	A
1	2	1487	A
1	2	1546	G
1	2	1588	A
1	2	1589	A
1	2	1590	C
1	2	1591	C

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Mol	Chain	Res	Type
1	2	1597	C
1	2	1608	U
1	2	1642	U
1	2	1712	A
1	2	1718	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.

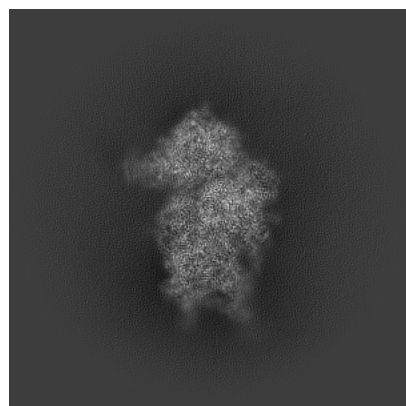
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62446. These allow visual inspection of the internal detail of the map and identification of artifacts.

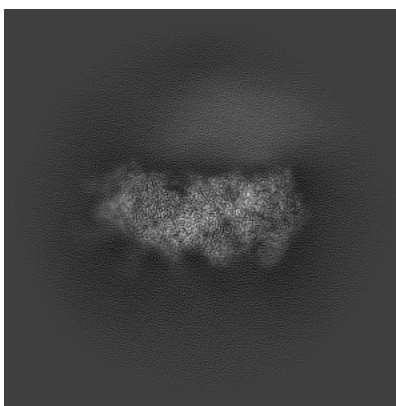
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

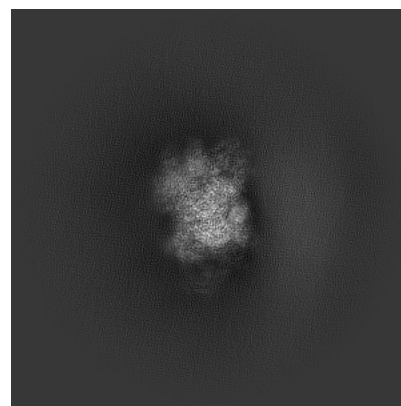
6.1.1 Primary map



X

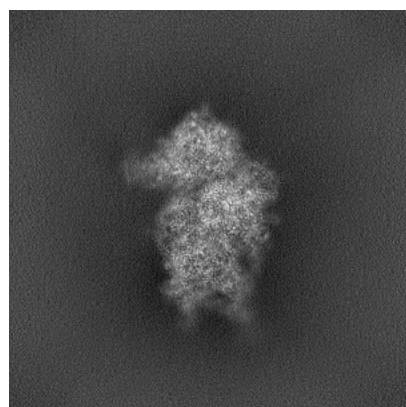


Y

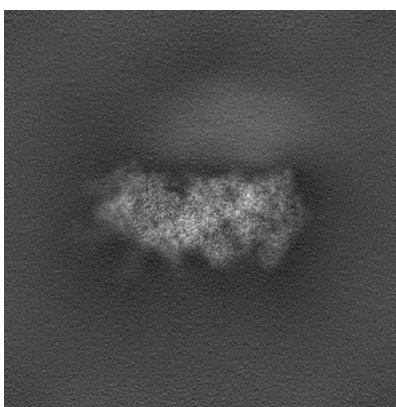


Z

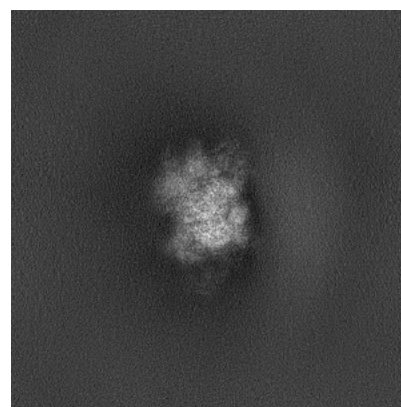
6.1.2 Raw map



X



Y

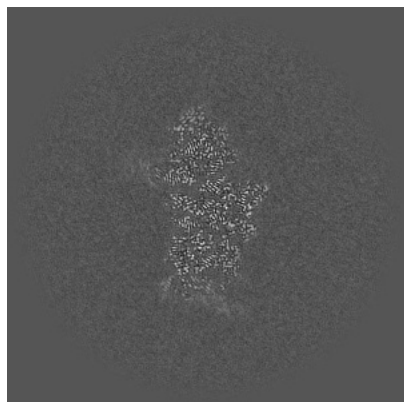


Z

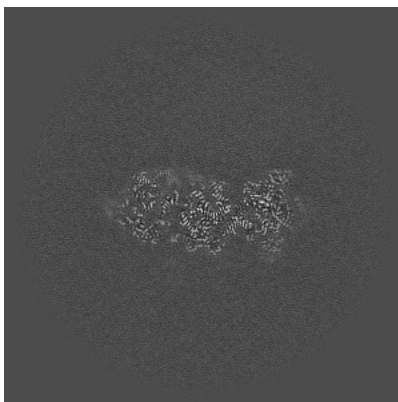
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

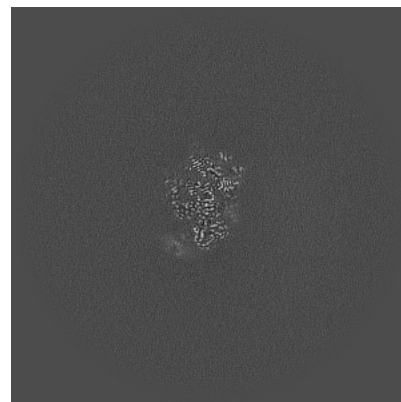
6.2.1 Primary map



X Index: 256

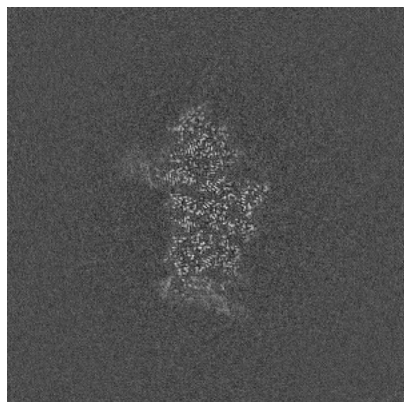


Y Index: 256

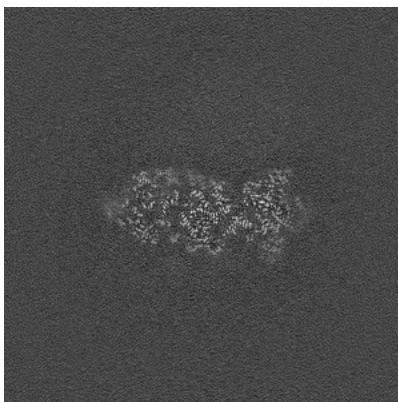


Z Index: 256

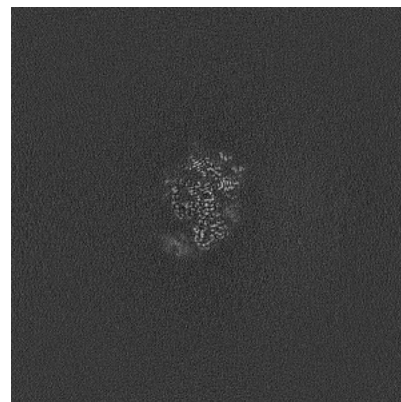
6.2.2 Raw map



X Index: 256



Y Index: 256

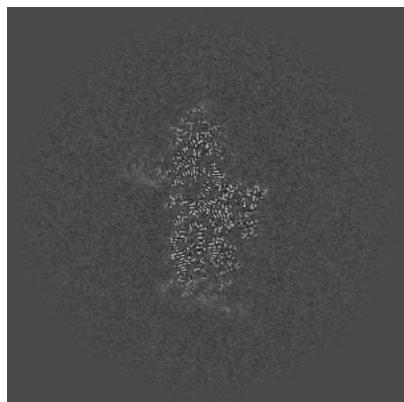


Z Index: 256

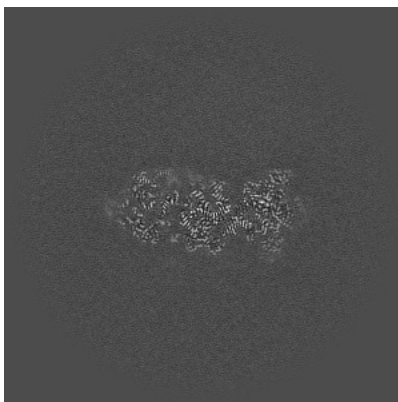
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

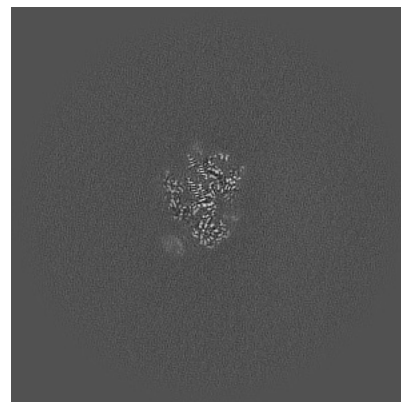
6.3.1 Primary map



X Index: 252

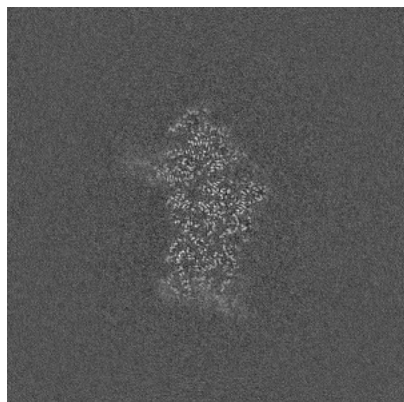


Y Index: 256

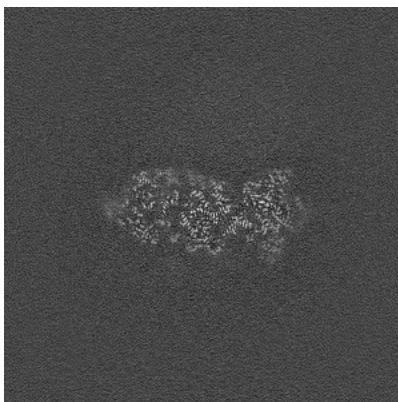


Z Index: 260

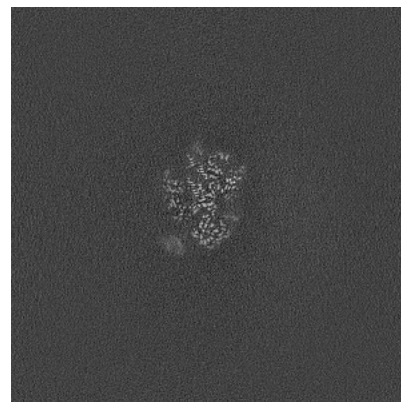
6.3.2 Raw map



X Index: 258



Y Index: 256

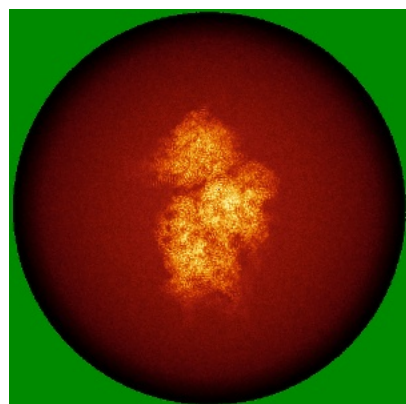


Z Index: 260

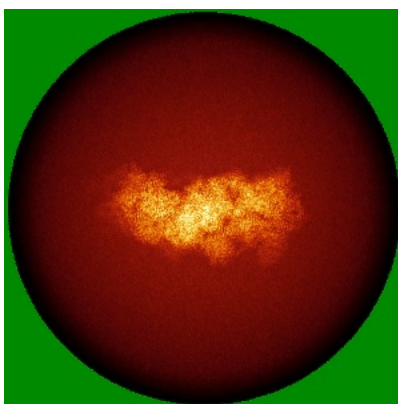
The images above show the largest variance slices of the map in three orthogonal directions.

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

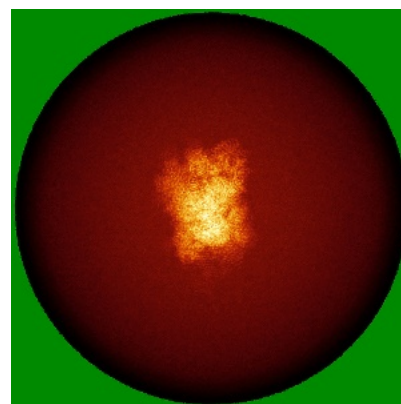
6.4.1 Primary map



X

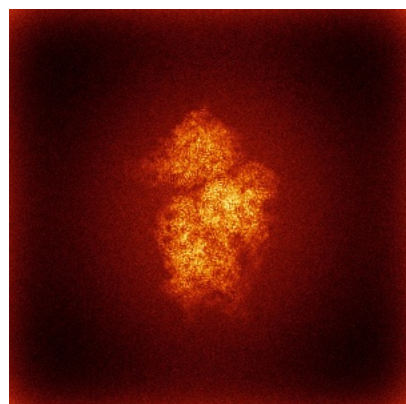


Y

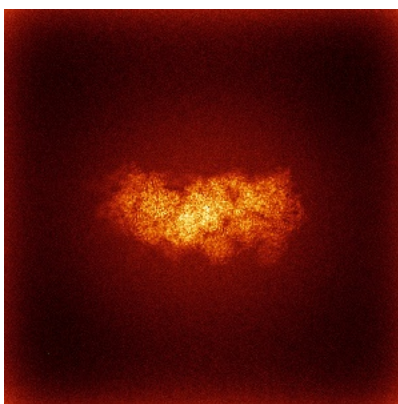


Z

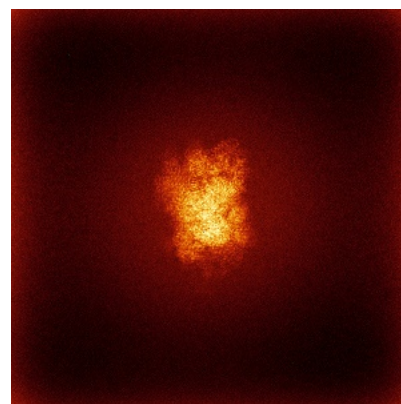
6.4.2 Raw map



X



Y

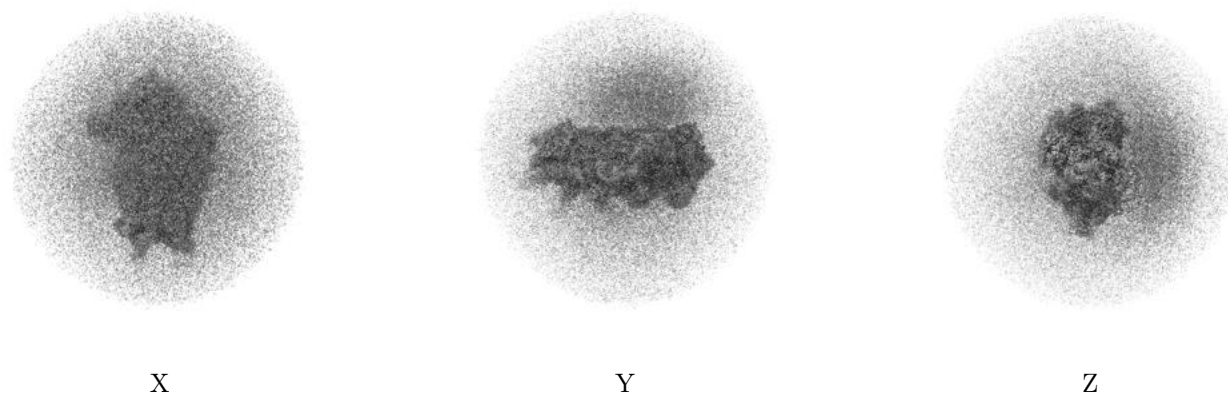


Z

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.

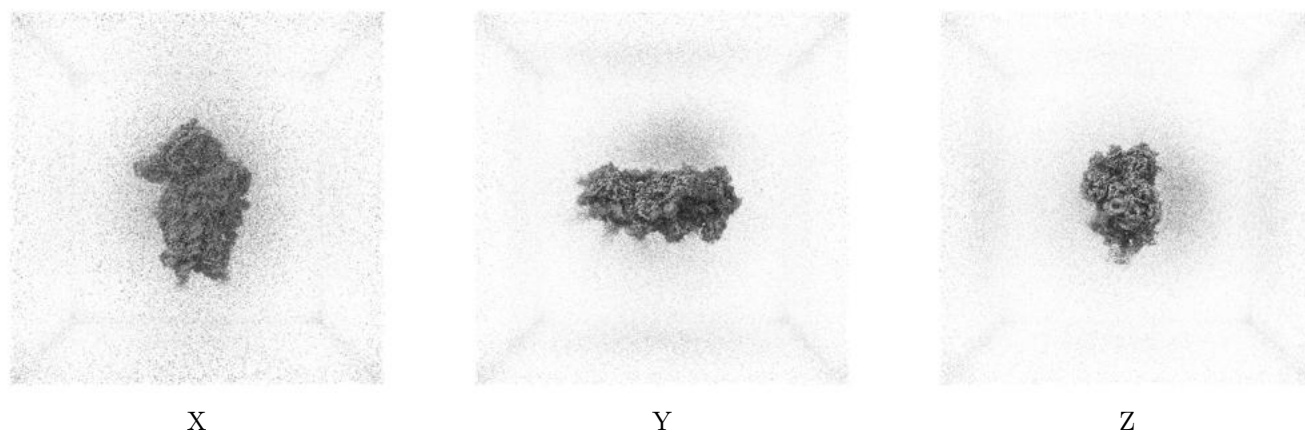
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

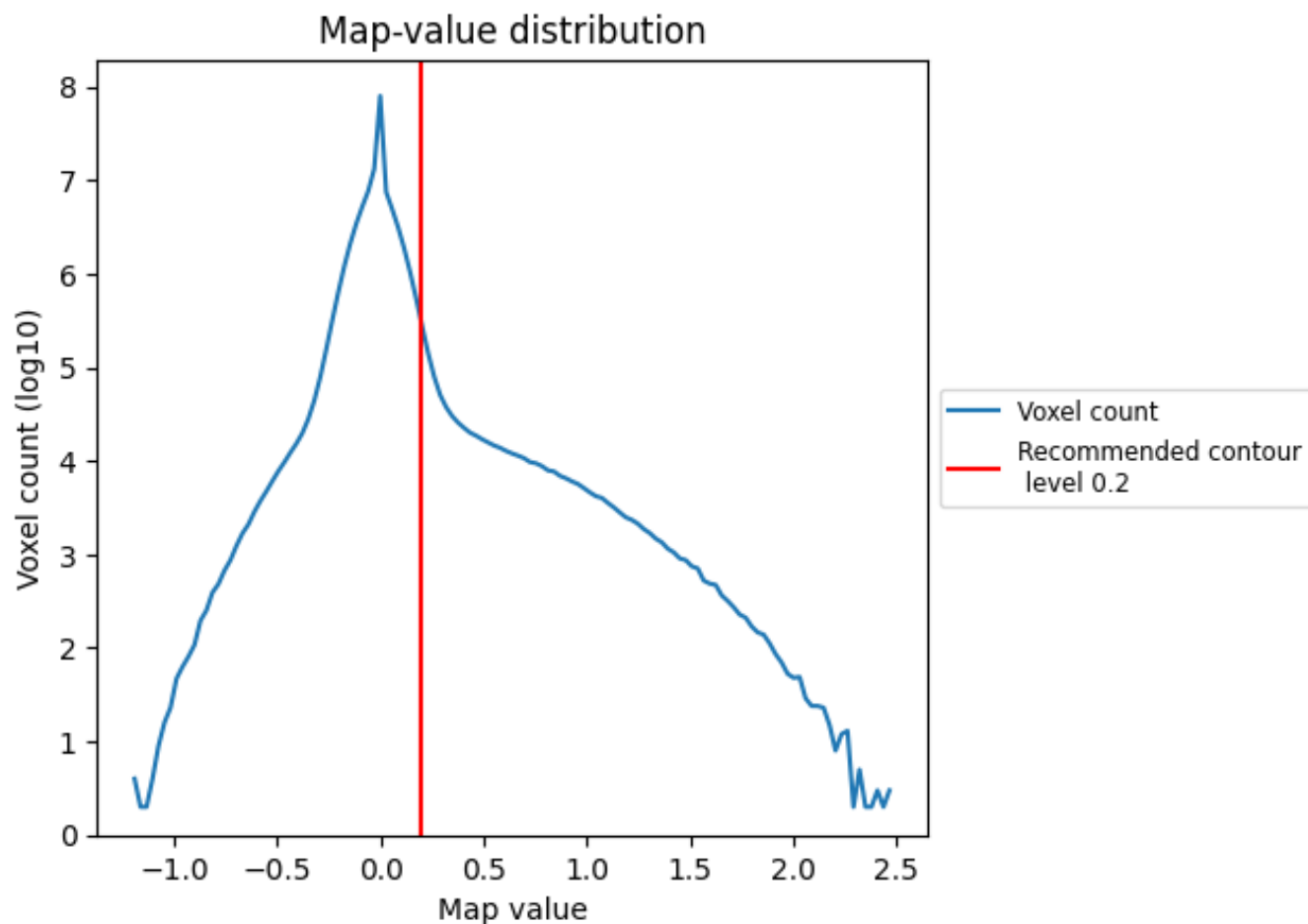
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

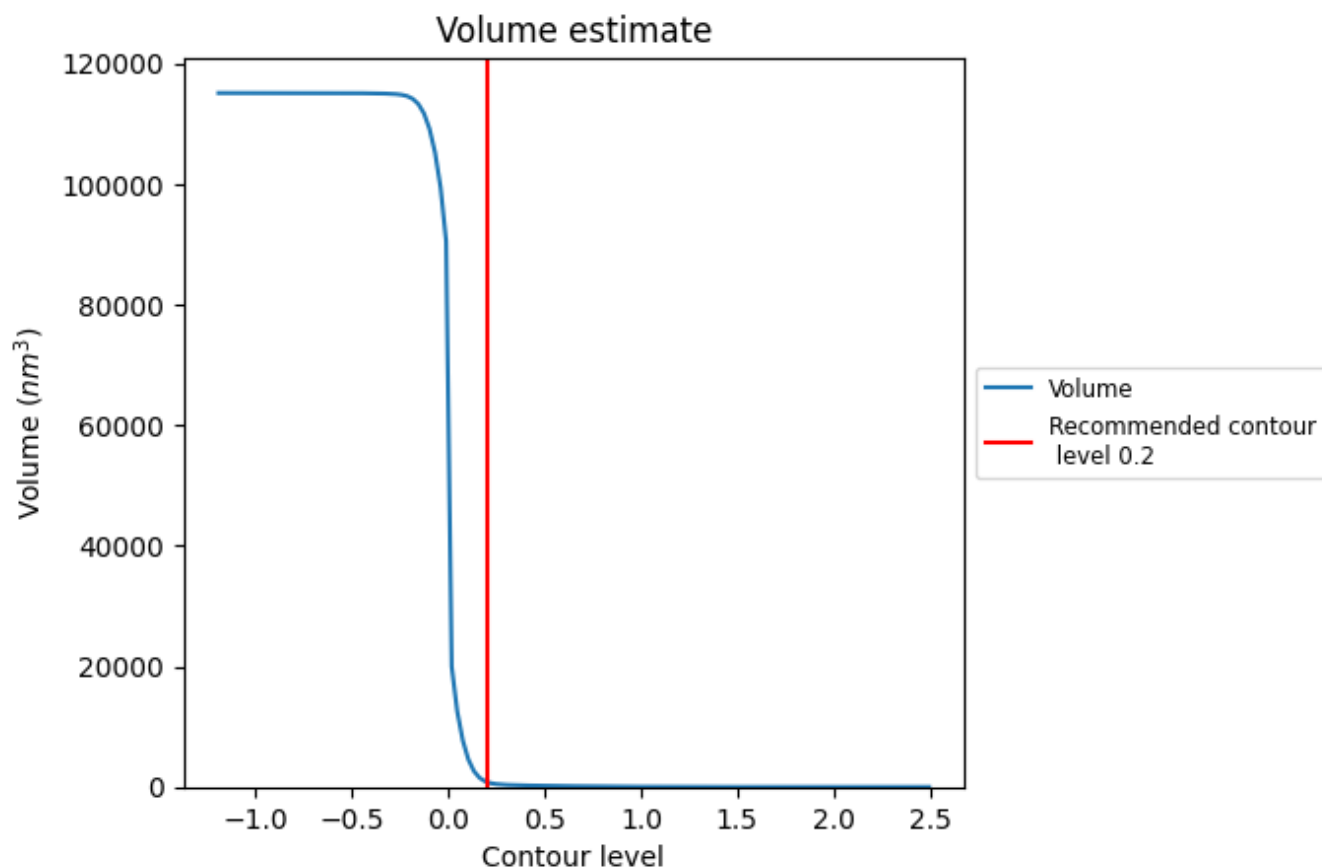
This section contains the results of statistical analysis of the map.

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.

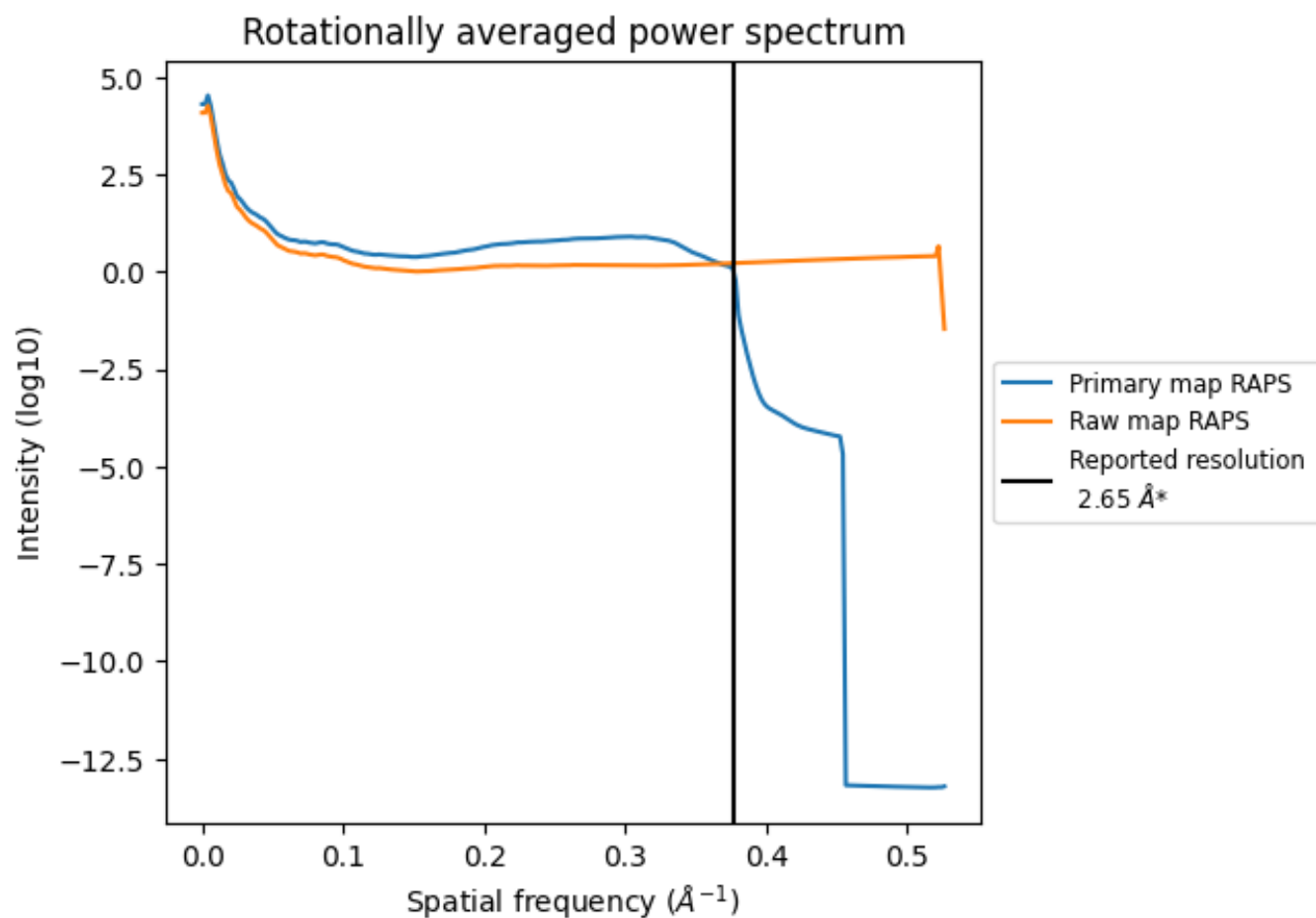
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 846 nm^3 ; this corresponds to an approximate mass of 764 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 ⓘ

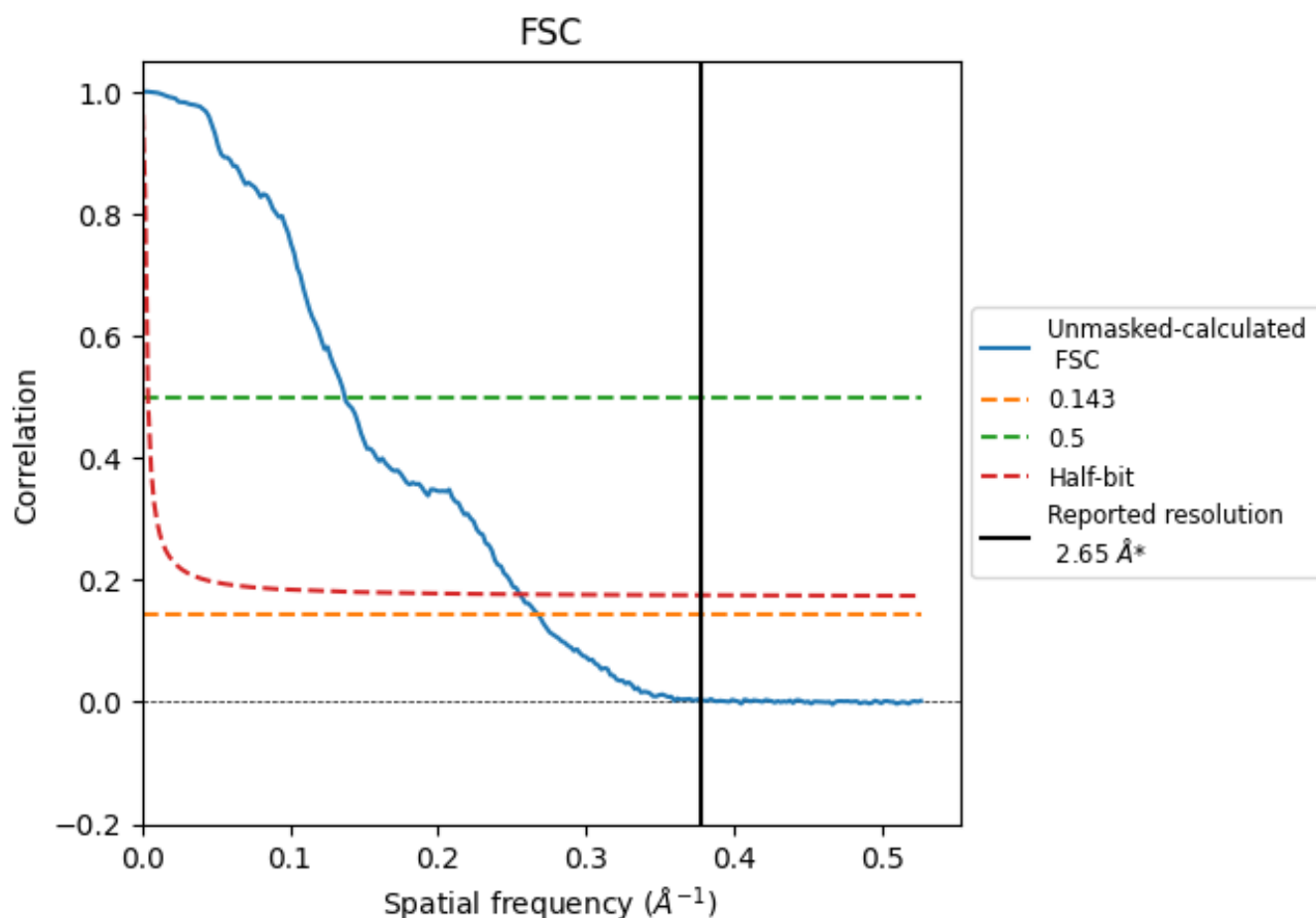


*Reported resolution corresponds to spatial frequency of 0.377 Å⁻¹

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 $0.377 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

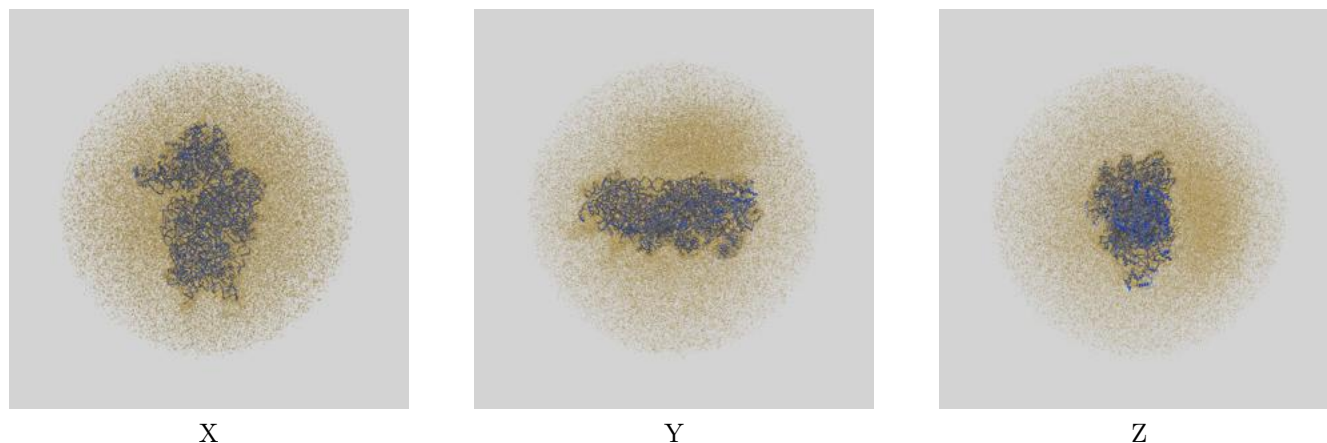
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.65	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.74	7.30	3.92

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 2.65 by more than 10 %

9 Map-model fit [i](#)

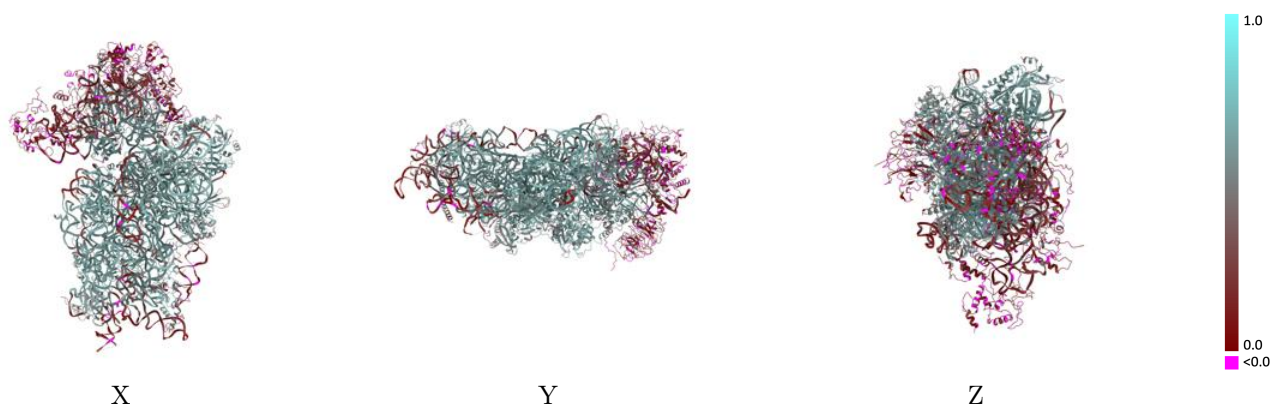
This section contains information regarding the fit between EMDB map EMD-62446 and PDB model 9KMV. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



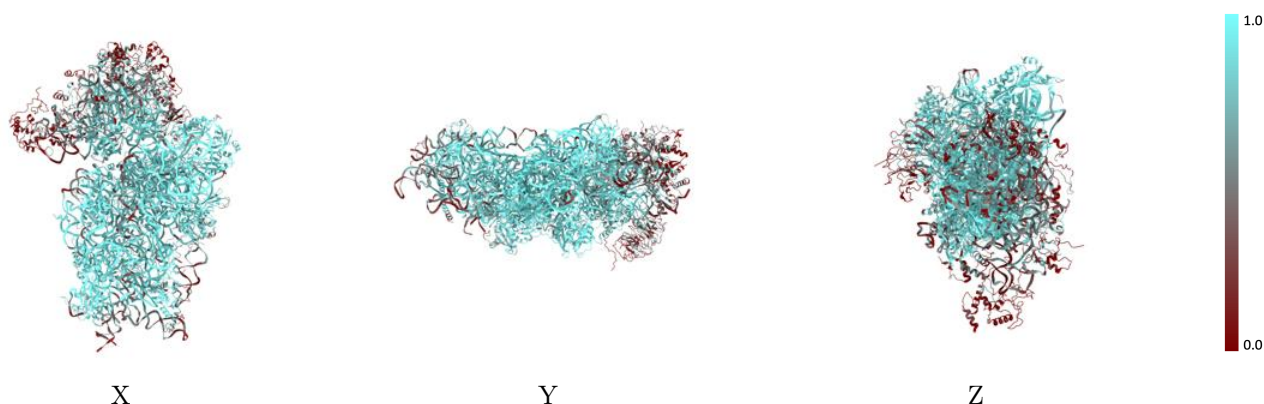
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



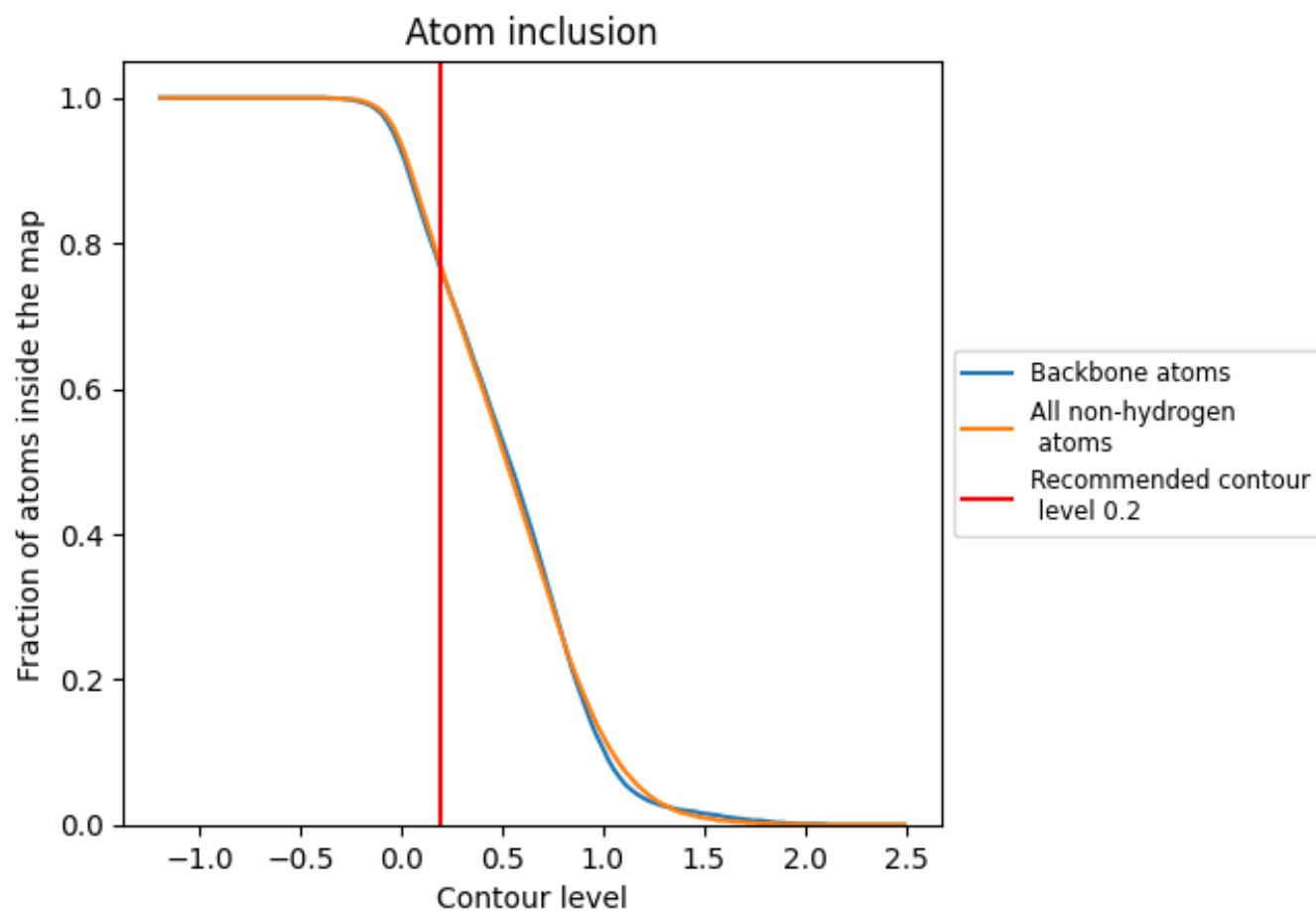
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 77% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7660	 0.4750
2	 0.8070	 0.4850
A	 0.9550	 0.6250
B	 0.9320	 0.6070
C	 0.9510	 0.6320
D	 0.7780	 0.5010
E	 0.9520	 0.6290
F	 0.3580	 0.1900
G	 0.8540	 0.5430
H	 0.7640	 0.5100
I	 0.8290	 0.5420
J	 0.9560	 0.6300
K	 0.4120	 0.2010
L	 0.8900	 0.6010
M	 0.1540	 0.0940
N	 0.9400	 0.6120
O	 0.9200	 0.5980
P	 0.3380	 0.2060
Q	 0.5670	 0.2950
R	 0.8600	 0.5650
S	 0.3710	 0.2050
T	 0.4600	 0.2050
U	 0.7580	 0.5000
V	 0.9490	 0.6220
W	 0.9710	 0.6430
X	 0.9540	 0.6320
Y	 0.9430	 0.6170
Z	 0.1910	 0.1440
a	 0.9520	 0.6260
b	 0.8600	 0.5600
c	 0.4030	 0.2500
d	 0.7890	 0.5140
e	 0.8220	 0.5440
f	 0.0740	 0.1400
g	 0.3030	 0.1600



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Chain	Atom inclusion	Q-score
h	 0.8710	 0.5700
n	 0.9180	 0.6190