



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 02:01 PM UTC

PDB ID : 5MLC / pdb_00005mlc
EMDB ID : EMD-3525
Title : Cryo-EM structure of the spinach chloroplast ribosome reveals the location of plastid-specific ribosomal proteins and extensions
Authors : Graf, M.; Arenz, S.; Huter, P.; Doenhoefer, A.; Novacek, J.; Wilson, D.N.
Deposited on : 2016-12-06
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

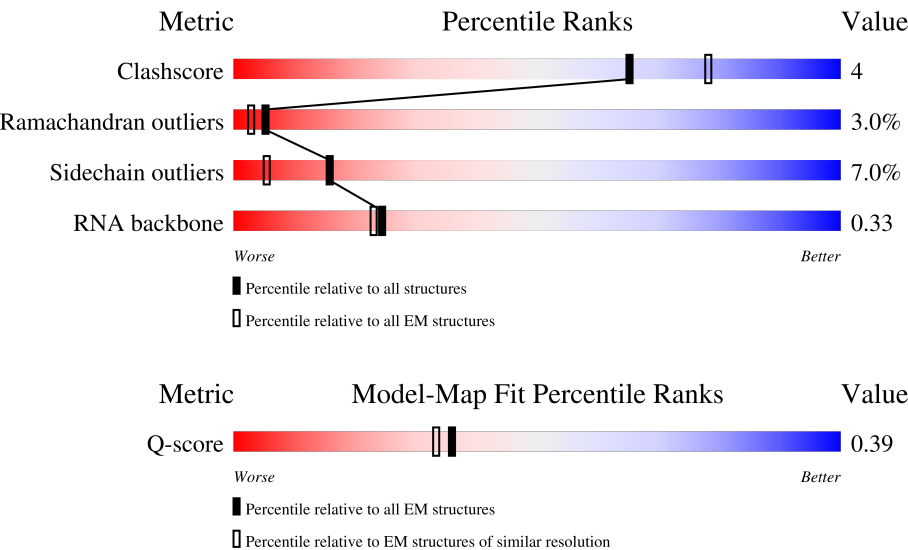
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	A	2811	
2	B	121	
3	C	103	

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Mol	Chain	Length	Quality of chain
4	D	272	
5	E	305	
6	F	293	
7	G	220	
8	H	220	
9	I	196	
10	L	250	
11	M	121	
12	N	271	
13	O	135	
14	P	126	
15	Q	166	
16	R	233	
17	S	128	
18	T	256	
19	U	199	
20	V	198	
21	W	191	
22	X	194	
23	Y	148	
24	Z	168	
25	2	57	
26	3	66	
27	4	152	
28	5	159	

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Mol	Chain	Length	Quality of chain
29	6	37	35% 95% 5%
30	9	271	37% 37% 61%
31	7	142	11% 26% 5% 68%
32	8	116	9% 30% 8% 59%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90647 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 23S ribosomal RNA, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2750	Total	C	N	O	P	0	0
			59074	26351	10944	19029	2750		

- Molecule 2 is a RNA chain called 5S ribosomal RNA, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2564	1145	464	835	120		

- Molecule 3 is a RNA chain called 4.8S ribosomal RNA, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	93	Total	C	N	O	P	0	0
			2001	893	374	641	93		

- Molecule 4 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	246	Total	C	N	O	S	0	0
			1895	1175	388	326	6		

- Molecule 5 is a protein called 50S ribosomal protein L3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	219	Total	C	N	O	S	0	0
			1669	1056	304	298	11		

- Molecule 6 is a protein called 50S ribosomal protein L4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	205	Total	C	N	O	S	0	0
			1617	1024	303	287	3		

- Molecule 7 is a protein called 50S ribosomal protein L5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	179	Total	C	N	O	S	0	0
			1387	883	241	255	8		

- Molecule 8 is a protein called 50S ribosomal protein L6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	178	Total	C	N	O	S	0	0
			1386	874	255	253	4		

- Molecule 9 is a protein called 50S ribosomal protein L9, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	45	Total	C	N	O	0	0
			359	237	65	57		

- Molecule 10 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	196	Total	C	N	O	S	0	0
			1489	942	280	264	3		

- Molecule 11 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	120	Total	C	N	O	S	0	0
			934	582	178	169	5		

- Molecule 12 is a protein called 50S ribosomal protein L15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	182	Total	C	N	O	S	0	0
			1385	864	273	242	6		

- Molecule 13 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	135	Total	C	N	O	S	0	0
			1075	677	218	174	6		

- Molecule 14 is a protein called 50S ribosomal protein L17, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	116	Total	C	N	O	S	0	0
			945	592	193	156	4		

- Molecule 15 is a protein called 50S ribosomal protein L18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	118	Total	C	N	O	S	0	0
			931	579	179	168	5		

- Molecule 16 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	114	Total	C	N	O	S	0	0
			915	586	178	150	1		

- Molecule 17 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	116	Total	C	N	O	S	0	0
			1003	637	209	155	2		

- Molecule 18 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	T	134	Total	C	N	O	0	0
			1017	653	183	181		

- Molecule 19 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	152	Total	C	N	O	S	0	0
			1165	738	212	208	7		

- Molecule 20 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	91	Total	C	N	O	S	0	0
			734	474	127	131	2		

- Molecule 21 is a protein called 50S ribosomal protein L24, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	129	Total	C	N	O	S	0	0
			1018	641	193	182	2		

- Molecule 22 is a protein called 50S ribosomal protein L27, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	108	Total	C	N	O	S	0	0
			866	545	172	149			

- Molecule 23 is a protein called 50S ribosomal protein L28, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	75	Total	C	N	O	S	0	0
			616	391	125	99	1		

- Molecule 24 is a protein called 50S ribosomal protein L29, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	94	Total	C	N	O	S	0	0
			788	492	156	137	3		

- Molecule 25 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2	42	Total	C	N	O	S	0	0
			341	223	65	53			

- Molecule 26 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3	60	Total	C	N	O	S	0	0
			489	304	98	83	4		

- Molecule 27 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4	61	Total	C	N	O	S	0	0
			471	284	108	76	3		

- Molecule 28 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	70	Total	C	N	O	S	0	0
			575	362	121	91	1		

- Molecule 29 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	6	37	Total	C	N	O	S	0	0
			305	186	70	45	4		

- Molecule 30 is a protein called Ribosome-recycling factor, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	9	107	Total	C	N	O	S	0	0
			881	545	158	175	3		

- Molecule 31 is a protein called PSRP5alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	7	46	Total	C	N	O	S	0	0
			378	241	77	56	4		

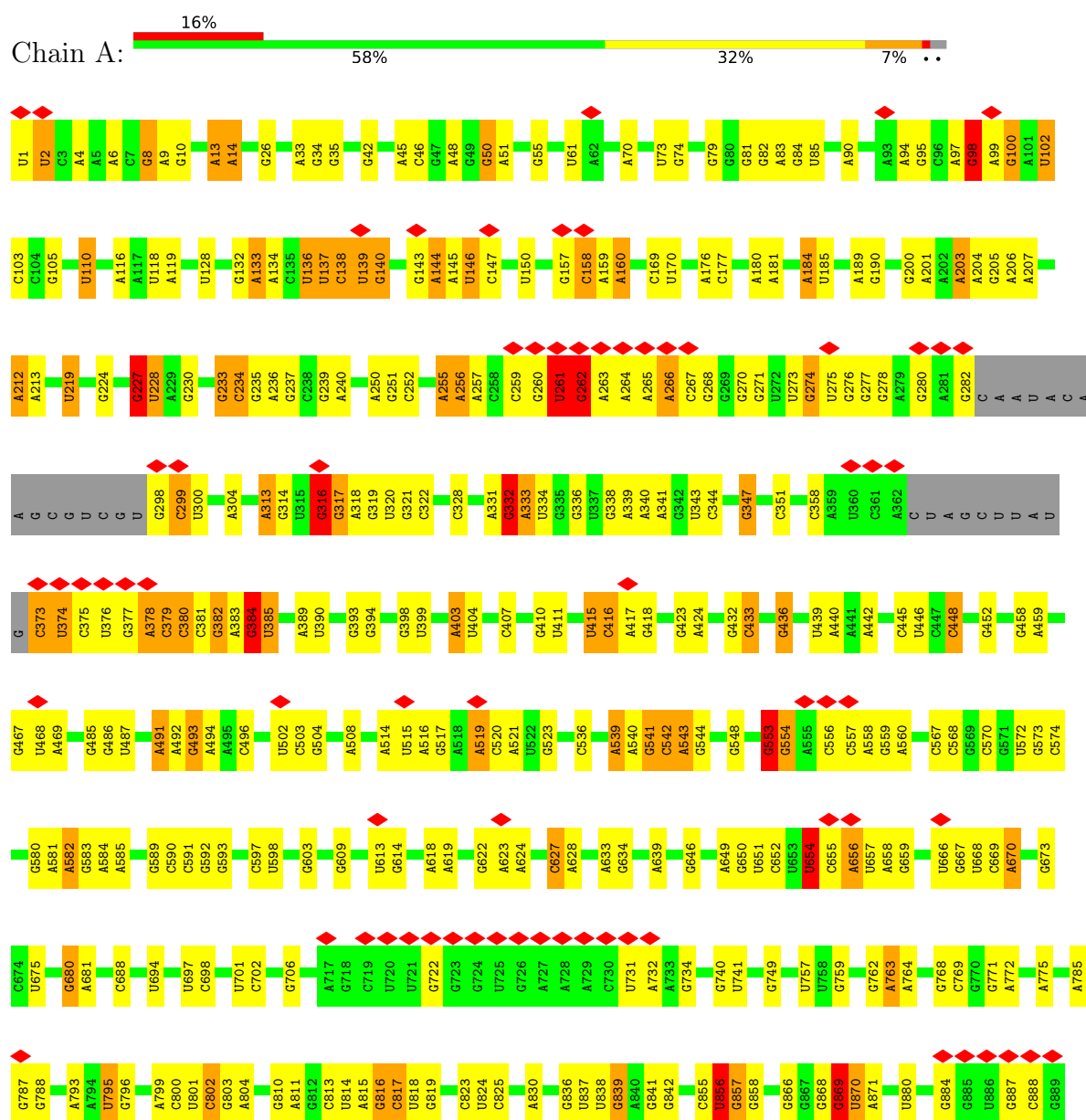
- Molecule 32 is a protein called PSRP6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	8	47	Total	C	N	O	S	0	0
			374	240	72	61	1		

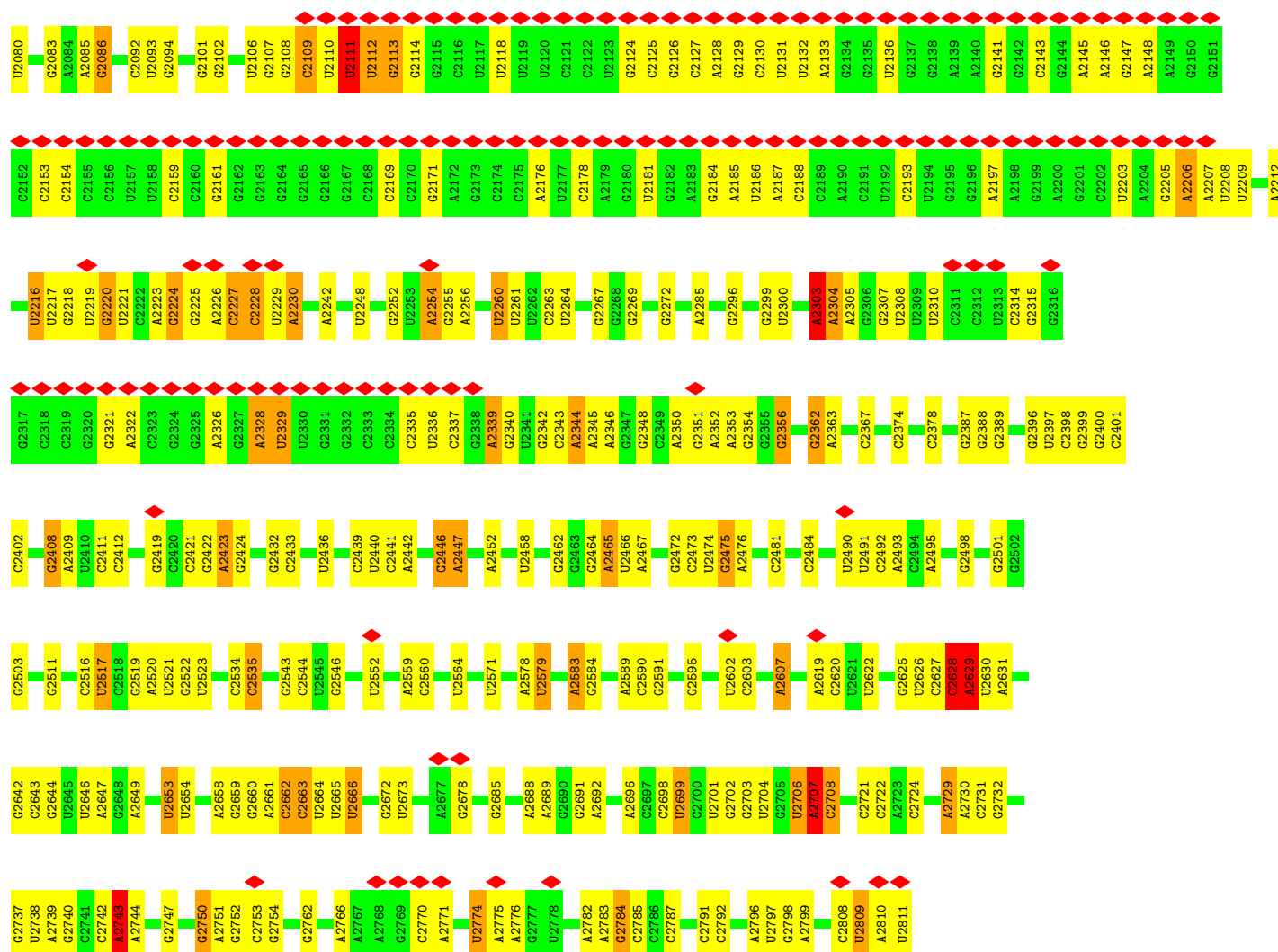
3 Residue-property plots

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.

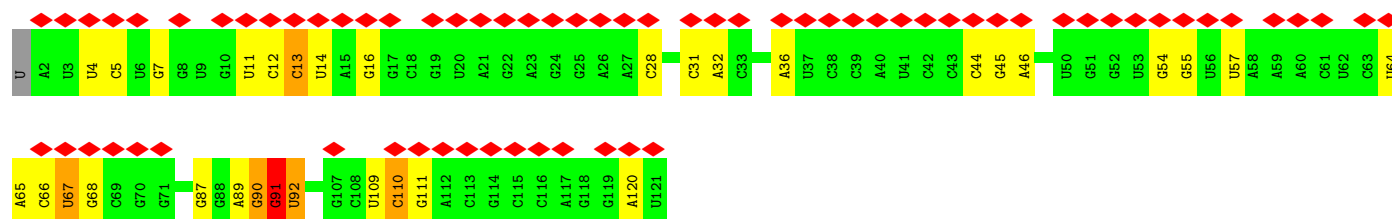
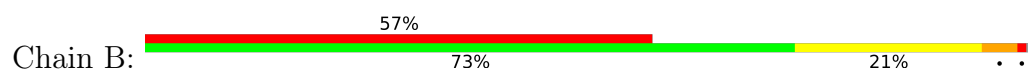
- Molecule 1: 23S ribosomal RNA, chloroplastic



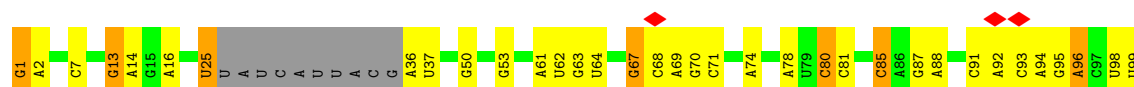




• Molecule 2: 5S ribosomal RNA, chloroplastic

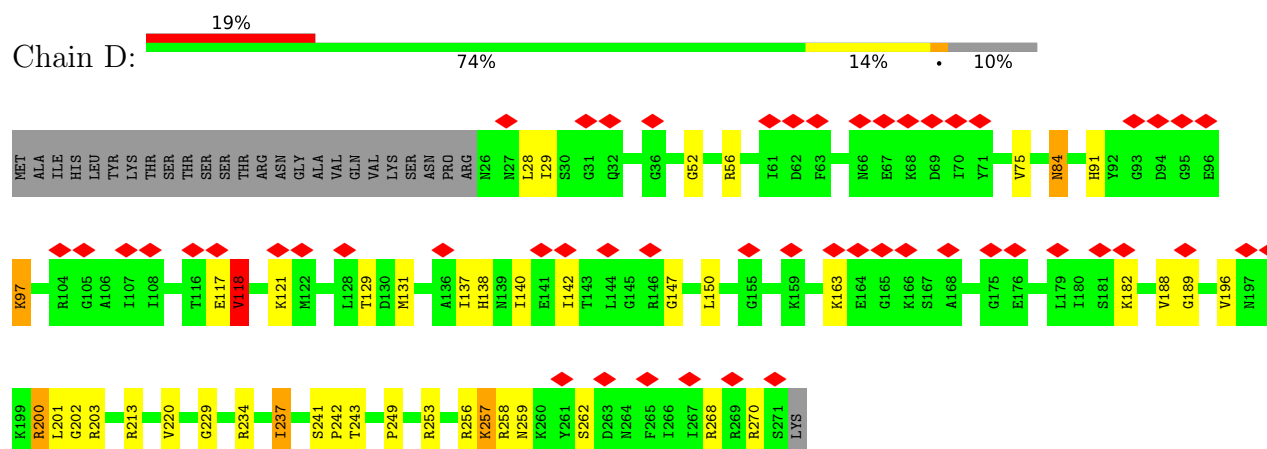


• Molecule 3: 4.8S ribosomal RNA, chloroplastic

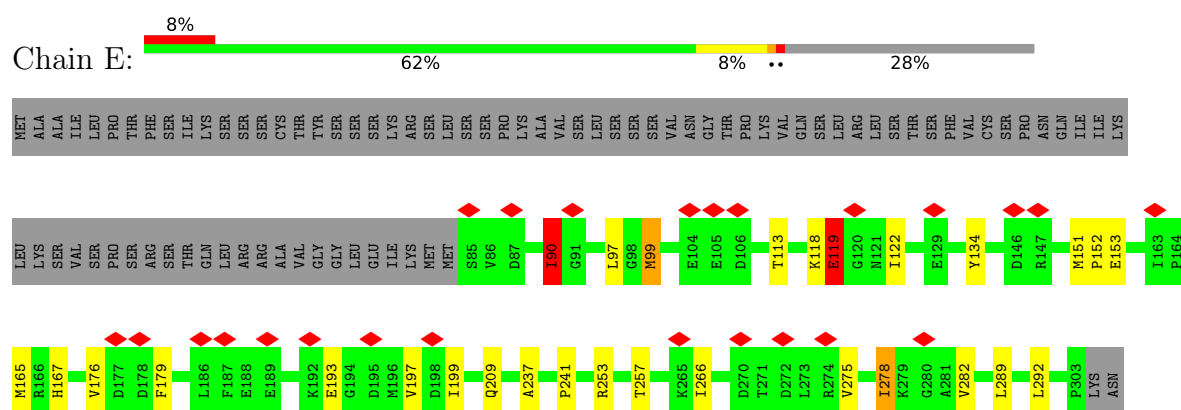




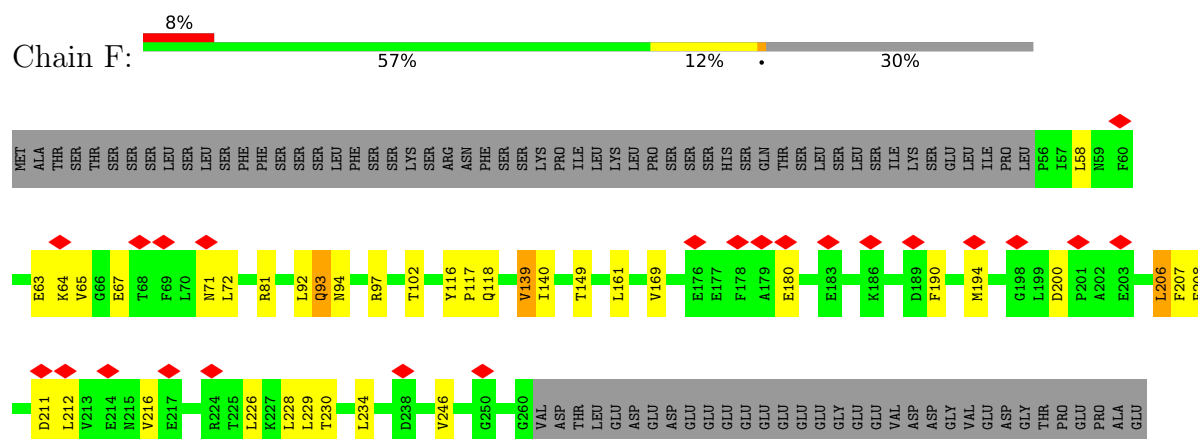
- Molecule 4: 50S ribosomal protein L2, chloroplastic



- Molecule 5: 50S ribosomal protein L3, chloroplastic

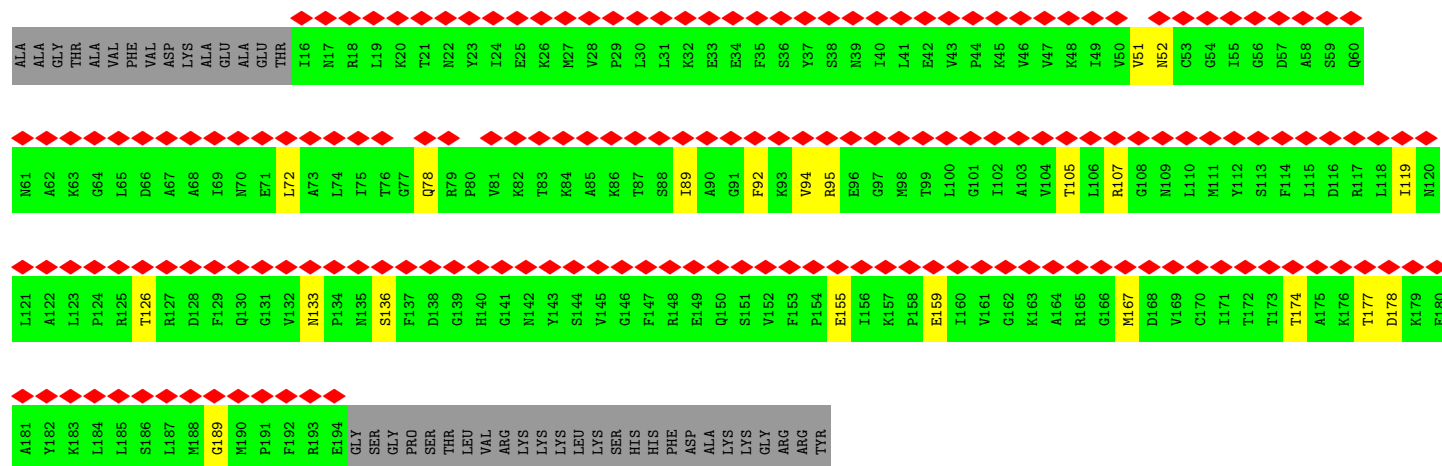


- Molecule 6: 50S ribosomal protein L4, chloroplastic

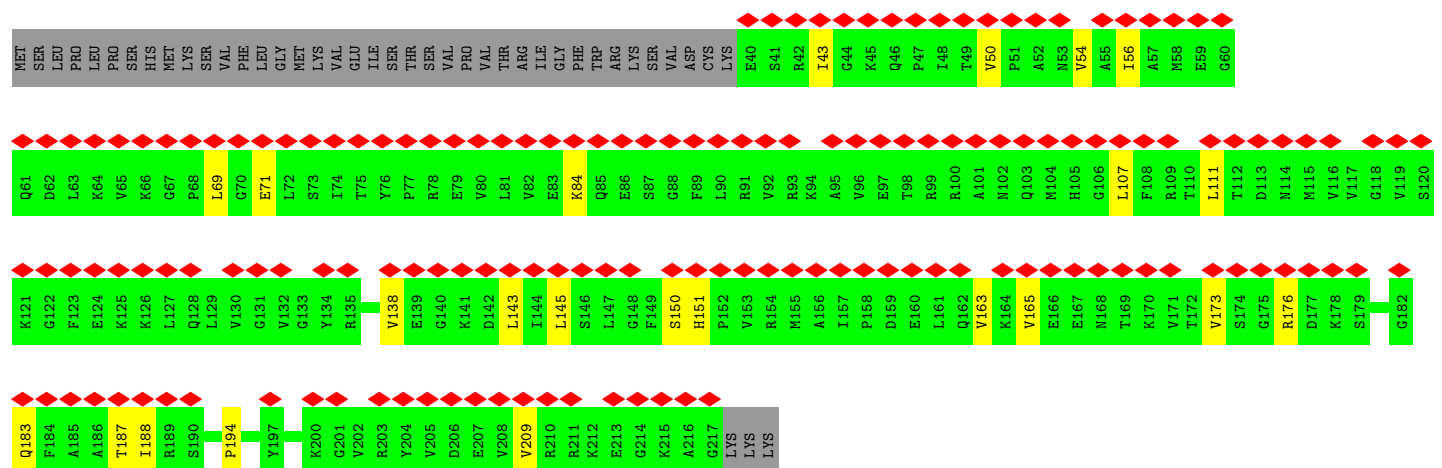


- Molecule 7: 50S ribosomal protein L5, chloroplastic

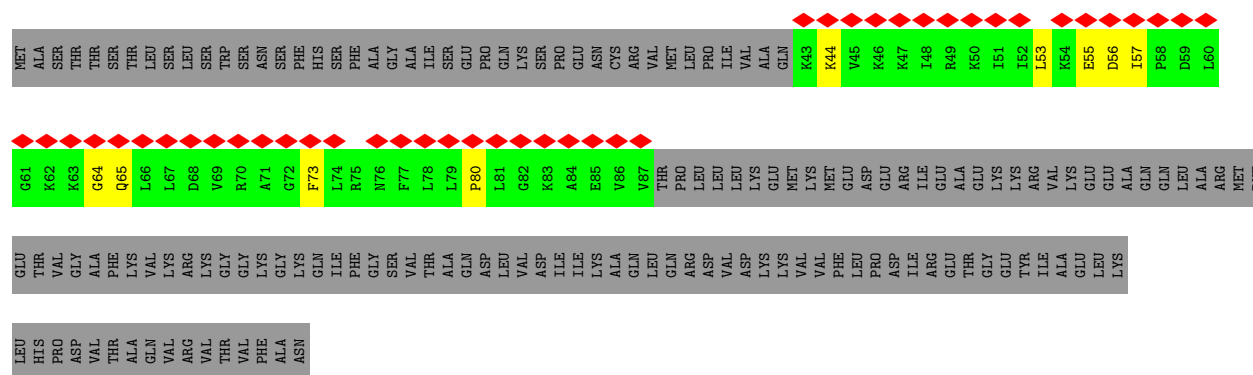




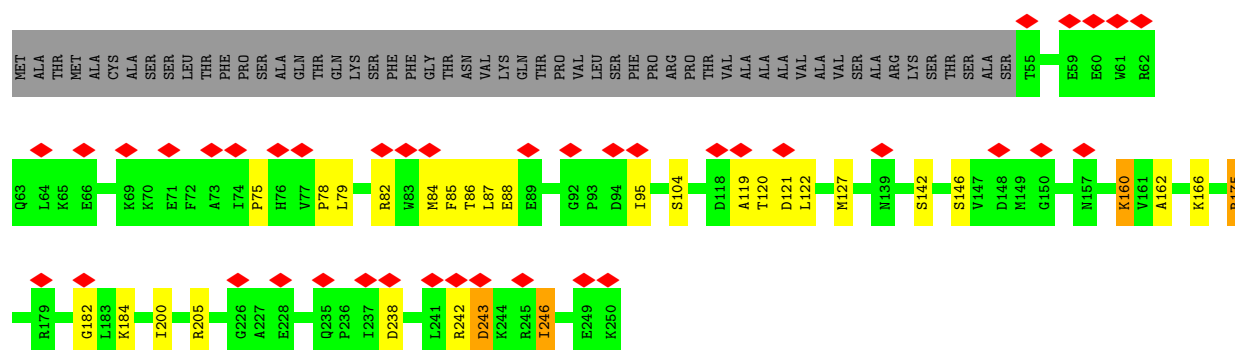
• Molecule 8: 50S ribosomal protein L6, chloroplastic



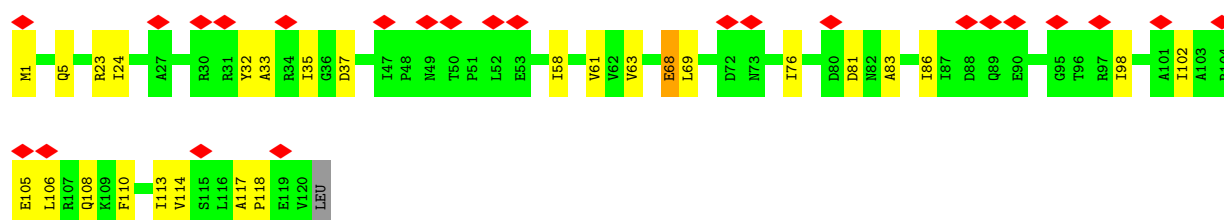
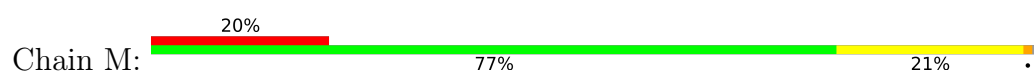
• Molecule 9: 50S ribosomal protein L9, chloroplastic



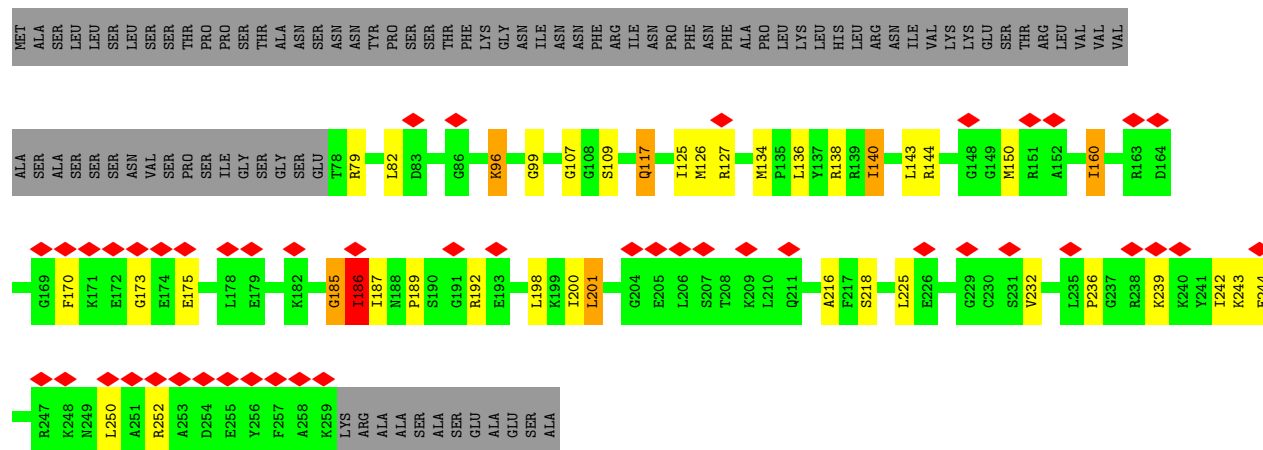
• Molecule 10: 50S ribosomal protein L13, chloroplastic



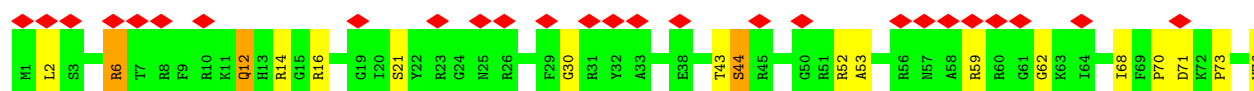
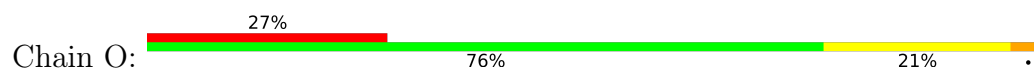
- Molecule 11: 50S ribosomal protein L14, chloroplastic

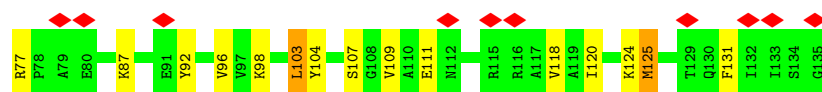


- Molecule 12: 50S ribosomal protein L15, chloroplastic

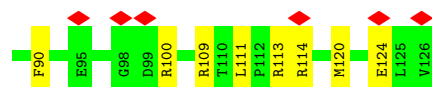
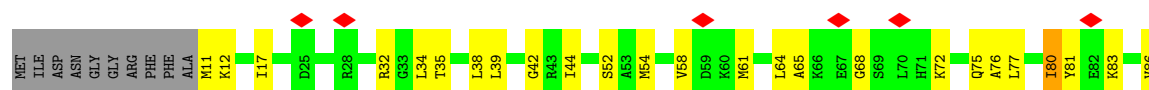


- Molecule 13: 50S ribosomal protein L16, chloroplastic

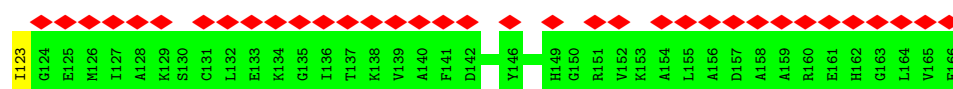
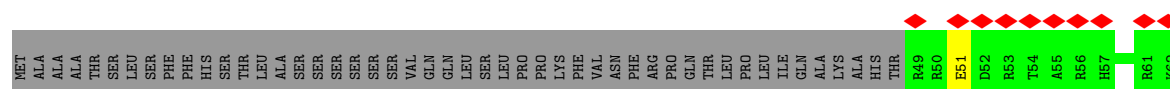




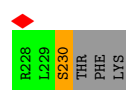
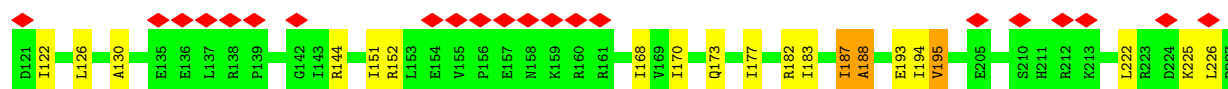
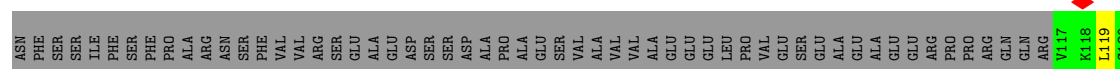
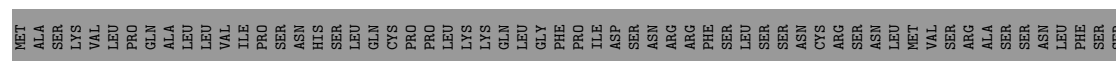
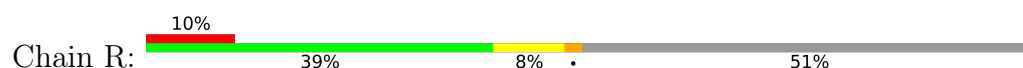
- Molecule 14: 50S ribosomal protein L17, chloroplastic



- Molecule 15: 50S ribosomal protein L18, chloroplastic



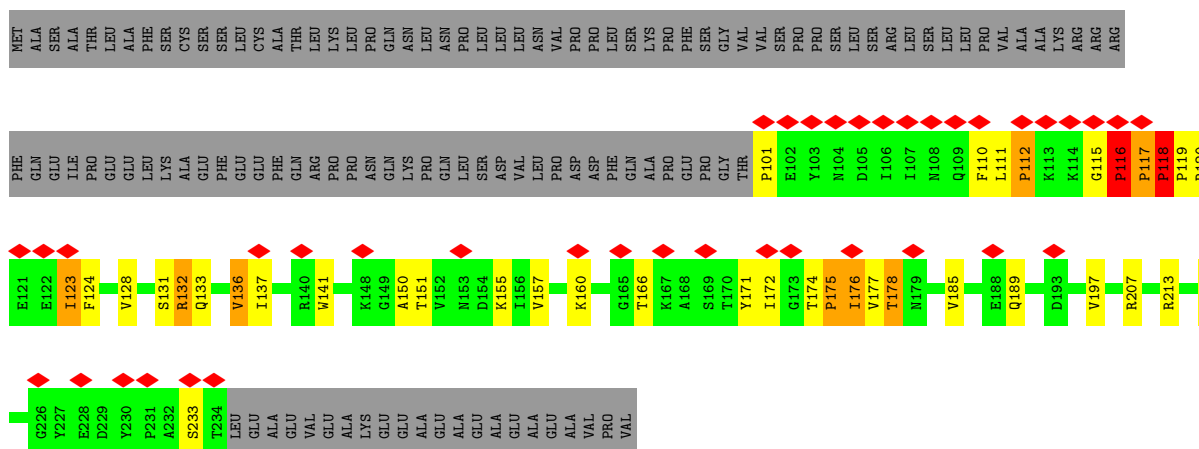
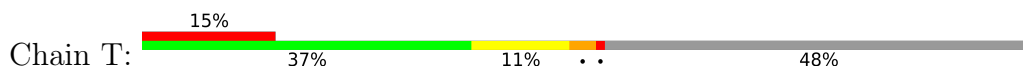
- Molecule 16: 50S ribosomal protein L19, chloroplastic



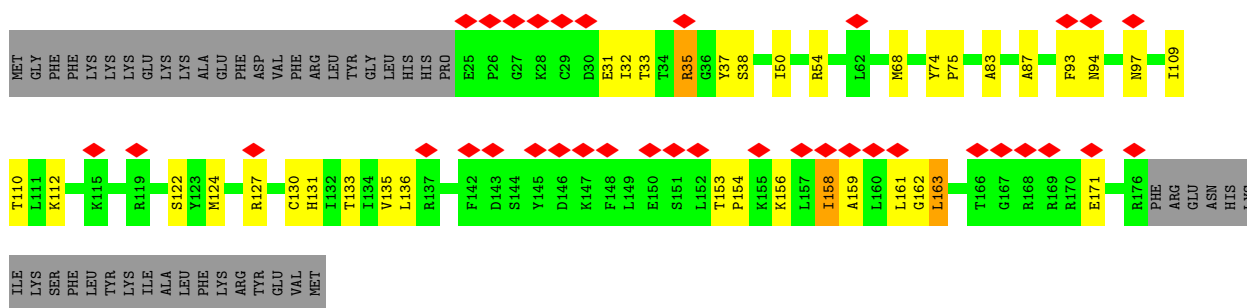
- Molecule 17: 50S ribosomal protein L20, chloroplastic



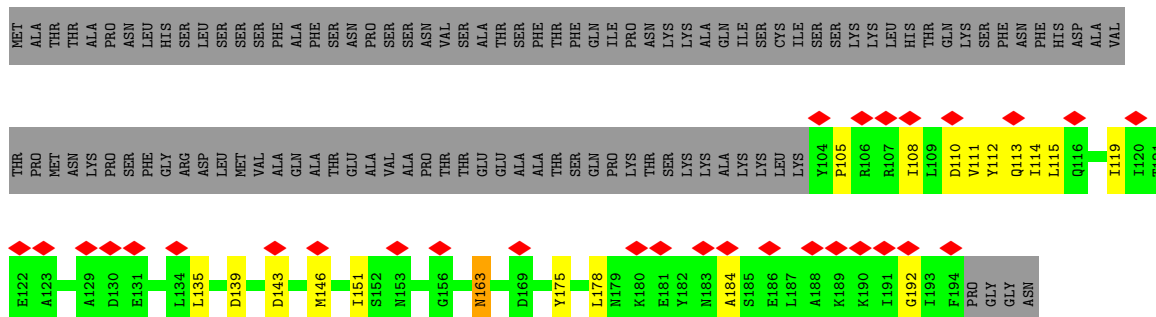
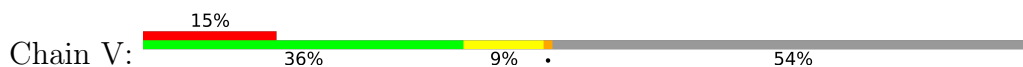
- Molecule 18: 50S ribosomal protein L21, chloroplastic



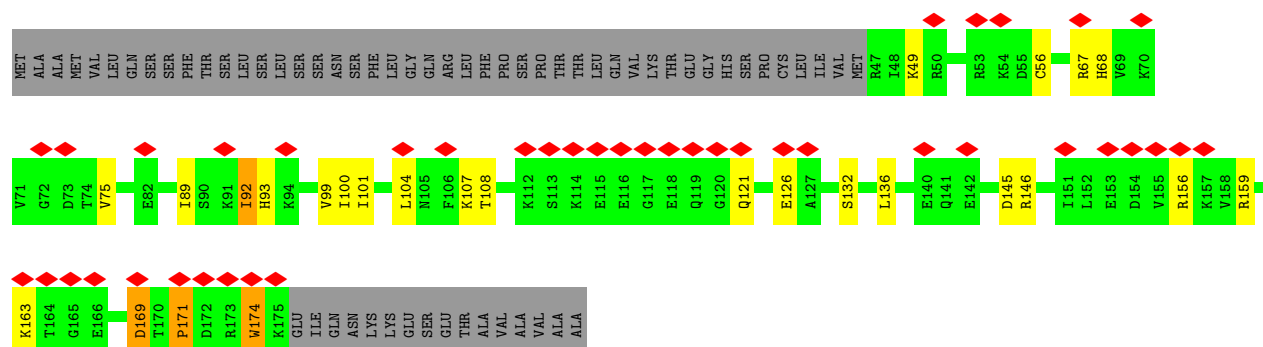
- Molecule 19: 50S ribosomal protein L22, chloroplastic



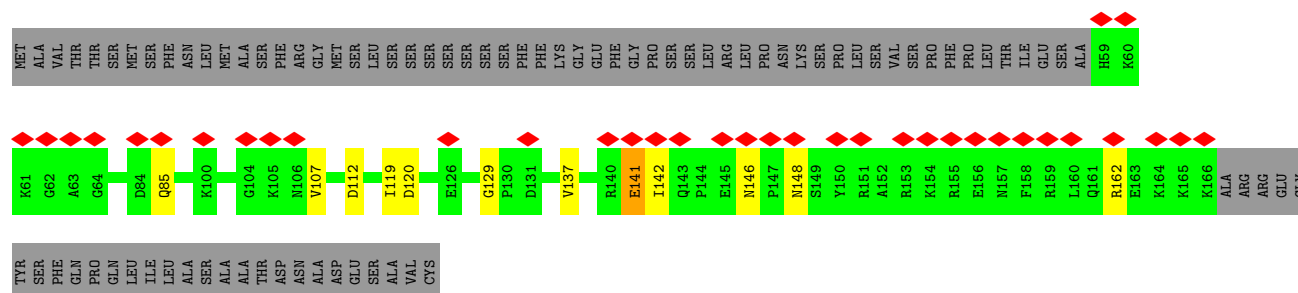
- Molecule 20: 50S ribosomal protein L23, chloroplastic



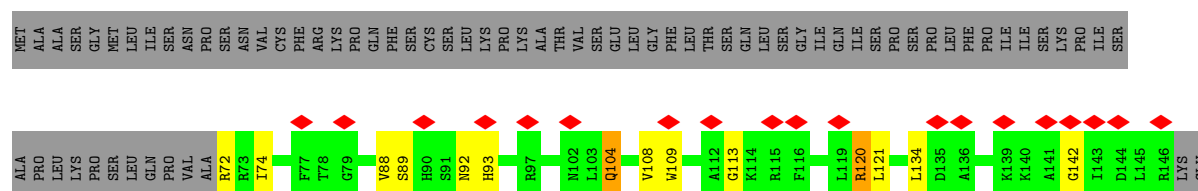
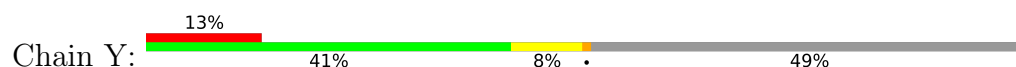
- Molecule 21: 50S ribosomal protein L24, chloroplastic



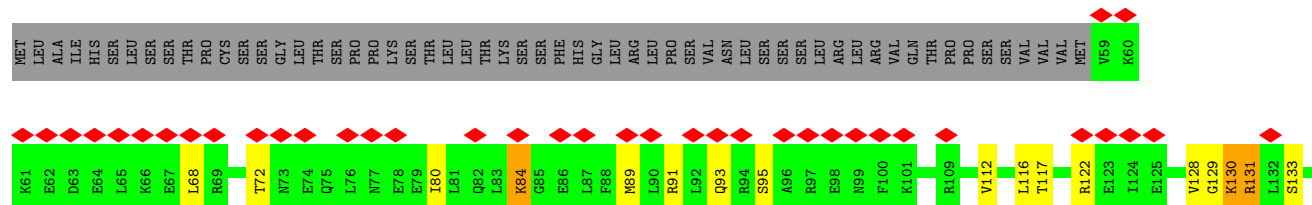
- Molecule 22: 50S ribosomal protein L27, chloroplastic



- Molecule 23: 50S ribosomal protein L28, chloroplastic



- Molecule 24: 50S ribosomal protein L29, chloroplastic





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37636	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	2.218	Depositor
Minimum map value	-1.456	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.068	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	390.448, 390.448, 390.448	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	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	A	0.43	6/66169 (0.0%)	0.79	102/103225 (0.1%)
2	B	0.40	0/2868	0.73	2/4469 (0.0%)
3	C	0.39	0/2241	0.77	2/3492 (0.1%)
4	D	0.60	0/1928	0.89	1/2588 (0.0%)
5	E	0.60	0/1696	0.88	1/2269 (0.0%)
6	F	0.63	2/1648 (0.1%)	0.96	0/2215
7	G	0.68	0/1408	0.83	0/1896
8	H	0.67	1/1407 (0.1%)	0.77	0/1892
9	I	0.72	0/362	0.92	0/480
10	L	0.71	1/1521 (0.1%)	0.97	4/2062 (0.2%)
11	M	0.56	0/943	0.80	0/1271
12	N	0.60	0/1405	1.00	2/1864 (0.1%)
13	O	0.61	0/1097	0.92	1/1471 (0.1%)
14	P	0.65	0/960	0.98	1/1280 (0.1%)
15	Q	0.66	0/946	0.92	0/1268
16	R	0.62	1/928 (0.1%)	0.88	0/1248
17	S	0.62	0/1020	1.06	1/1361 (0.1%)
18	T	0.95	4/1034 (0.4%)	1.13	11/1405 (0.8%)
19	U	1.45	5/1184 (0.4%)	1.01	3/1593 (0.2%)
20	V	0.62	0/744	0.90	0/1000
21	W	0.89	2/1030 (0.2%)	0.93	2/1374 (0.1%)
22	X	0.56	0/882	0.81	0/1172
23	Y	0.57	0/626	0.89	0/833
24	Z	0.62	0/796	1.01	1/1056 (0.1%)
25	2	0.80	0/348	1.01	0/462
26	3	0.63	0/497	0.98	0/664
27	4	0.66	0/474	1.05	0/624
28	5	0.55	0/581	1.01	0/768
29	6	0.57	0/307	0.89	0/403
30	9	0.61	0/883	0.91	1/1169 (0.1%)
31	7	0.67	0/381	0.99	0/498
32	8	0.76	1/388 (0.3%)	0.91	0/528
All	All	0.52	23/98702 (0.0%)	0.83	135/147900 (0.1%)

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
18	T	0	1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	U	158	ILE	C-N	40.64	1.84	1.33
1	A	1554	C	O3'-P	-18.46	1.33	1.61
21	W	169	ASP	C-N	18.41	1.58	1.33
18	T	118	PRO	C-N	16.05	1.71	1.33
1	A	1435	U	O3'-P	-11.18	1.44	1.61
10	L	84	MET	C-N	9.30	1.46	1.33
18	T	110	PHE	CA-C	8.13	1.61	1.53
1	A	1618	C	O3'-P	-8.03	1.49	1.61
8	H	71	GLU	CD-OE2	7.66	1.40	1.25
1	A	1239	C	C3'-O3'	7.23	1.52	1.42
6	F	180	GLU	CD-OE2	7.00	1.38	1.25
16	R	230	SER	C-O	6.71	1.36	1.23
18	T	115	GLY	N-CA	6.37	1.53	1.44
1	A	1239	C	O3'-P	6.07	1.70	1.61
19	U	163	LEU	CA-C	5.71	1.60	1.52
19	U	163	LEU	N-CA	5.57	1.53	1.46
1	A	1608	C	O3'-P	-5.57	1.52	1.61
32	8	83	PRO	CA-C	5.49	1.54	1.51
19	U	171	GLU	CA-C	5.36	1.59	1.52
6	F	211	ASP	CB-CG	5.26	1.65	1.52
18	T	111	LEU	N-CA	5.08	1.52	1.45
19	U	161	LEU	N-CA	5.07	1.52	1.46
21	W	174	TRP	N-CA	5.05	1.52	1.46

All (135) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	763	A	C2'-C3'-O3'	12.81	128.71	109.50
1	A	50	G	C2'-C3'-O3'	11.38	126.57	109.50
1	A	1260	G	C2'-C3'-O3'	-9.97	98.75	113.70
18	T	117	PRO	N-CA-C	9.96	122.86	110.70
1	A	1399	A	C4'-C3'-O3'	9.82	124.13	109.40
10	L	75	PRO	N-CA-CB	9.44	109.73	102.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	98	G	C4'-C3'-O3'	8.81	122.62	109.40
18	T	118	PRO	CA-C-N	-8.79	108.85	119.84
18	T	118	PRO	C-N-CA	-8.79	108.85	119.84
1	A	1618	C	P-O3'-C3'	-8.68	107.17	120.20
1	A	654	U	C2'-C3'-O3'	8.57	122.35	109.50
18	T	118	PRO	O-C-N	8.48	131.47	121.46
1	A	261	U	N1-C1'-C2'	-8.46	99.31	112.00
1	A	1050	G	C2'-C3'-O3'	8.43	122.15	109.50
1	A	2254	A	C4'-C3'-O3'	8.29	125.44	113.00
1	A	1341	C	C4'-C3'-O3'	-8.26	100.61	113.00
1	A	1239	C	C4'-C3'-O3'	8.16	125.25	113.00
1	A	1435	U	O3'-P-O5'	-8.04	91.95	104.00
1	A	261	U	C2'-C3'-O3'	8.03	125.74	113.70
18	T	118	PRO	N-CA-CB	7.99	110.83	103.08
1	A	1198	A	C4'-C3'-O3'	7.90	121.25	109.40
1	A	1411	U	C2'-C3'-O3'	7.88	125.52	113.70
1	A	2583	A	C2'-C3'-O3'	7.76	121.14	109.50
18	T	116	PRO	N-CA-CB	7.65	110.50	103.08
18	T	117	PRO	N-CA-CB	7.61	110.47	103.08
1	A	1608	C	O3'-P-O5'	7.61	115.42	104.00
1	A	1260	G	C4'-C3'-O3'	7.58	124.38	113.00
1	A	1754	A	C4'-C3'-O3'	7.52	120.68	109.40
1	A	553	G	C2'-C3'-O3'	7.44	120.66	109.50
1	A	2408	G	C4'-C3'-O3'	7.44	124.15	113.00
1	A	2707	A	C1'-C2'-O2'	7.36	122.84	111.80
1	A	261	U	C4'-C3'-O3'	7.35	124.03	113.00
1	A	313	A	C2'-C3'-O3'	7.29	124.63	113.70
3	C	13	G	C4'-C3'-O3'	-7.27	102.09	113.00
1	A	1048	C	C2'-C3'-O3'	7.22	120.33	109.50
1	A	1039	A	C4'-C3'-O3'	7.18	120.16	109.40
19	U	171	GLU	N-CA-C	7.14	118.71	111.07
1	A	896	G	C4'-C3'-O3'	7.05	119.98	109.40
1	A	1472	A	C2'-C3'-O3'	6.94	119.91	109.50
21	W	171	PRO	N-CA-CB	6.92	110.52	103.25
1	A	1474	A	C4'-C3'-O3'	6.91	119.76	109.40
1	A	1202	A	C4'-C3'-O3'	-6.88	102.68	113.00
10	L	78	PRO	N-CA-CB	6.87	110.47	103.25
1	A	2465	A	C4'-C3'-O3'	6.86	119.69	109.40
18	T	101	PRO	N-CA-CB	6.81	110.49	103.00
1	A	316	G	C2'-C3'-O3'	6.77	119.65	109.50
1	A	491	A	C4'-C3'-O3'	6.74	119.51	109.40
1	A	1954	U	C2'-C3'-O3'	6.74	119.61	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2628	C	C2'-C3'-O3'	6.68	123.72	113.70
1	A	433	C	C4'-C3'-O3'	-6.66	103.01	113.00
1	A	212	A	C4'-C3'-O3'	-6.66	103.02	113.00
12	N	143	LEU	N-CA-C	6.62	120.31	111.30
1	A	493	G	C4'-C3'-O3'	-6.48	103.28	113.00
1	A	1567	C	C4'-C3'-O3'	-6.48	103.28	113.00
1	A	1493	C	C2'-C3'-O3'	6.44	123.36	113.70
1	A	1194	G	C4'-C3'-O3'	6.43	119.05	109.40
1	A	2216	U	C2'-C3'-O3'	6.43	123.34	113.70
1	A	1536	A	C2'-C3'-O3'	6.42	123.32	113.70
1	A	1439	U	C2'-C3'-O3'	6.39	123.29	113.70
1	A	1048	C	C4'-C3'-O3'	6.33	118.90	109.40
1	A	1228	A	C4'-C3'-O3'	6.29	118.83	109.40
1	A	1569	A	C2'-C3'-O3'	6.26	118.89	109.50
1	A	656	A	C4'-C3'-O3'	6.26	118.79	109.40
1	A	2729	A	C4'-C3'-O3'	-6.18	103.74	113.00
1	A	795	U	C4'-C3'-O3'	-6.17	103.75	113.00
1	A	2737	G	C4'-C3'-O3'	-6.14	103.78	113.00
1	A	2254	A	C2'-C3'-O3'	-6.11	104.54	113.70
1	A	627	C	C4'-C3'-O3'	6.09	122.13	113.00
1	A	986	U	C2'-C3'-O3'	-6.05	104.63	113.70
1	A	1012	G	C2'-C3'-O3'	-5.95	104.77	113.70
3	C	1	G	C4'-C3'-O3'	5.94	118.31	109.40
10	L	246	ILE	N-CA-C	5.94	116.12	110.42
1	A	762	G	C4'-C3'-O3'	-5.92	104.12	113.00
1	A	1098	A	C2'-C3'-O3'	5.91	118.36	109.50
1	A	227	G	C2'-C3'-O3'	5.88	118.31	109.50
1	A	2423	A	C2'-C3'-O3'	-5.85	104.93	113.70
1	A	1050	G	C4'-C3'-O3'	5.81	118.11	109.40
18	T	116	PRO	CA-C-N	5.80	126.36	120.38
18	T	116	PRO	C-N-CA	5.80	126.36	120.38
1	A	1654	A	C2'-C3'-O3'	-5.78	100.83	109.50
1	A	856	U	C2'-C3'-O3'	5.75	122.33	113.70
1	A	262	G	C4'-C3'-O3'	5.74	121.61	113.00
1	A	2109	C	C4'-C3'-O3'	-5.65	104.53	113.00
1	A	332	G	C2'-C3'-O3'	5.64	117.96	109.50
1	A	261	U	C4'-C3'-C2'	-5.61	96.99	102.60
1	A	1349	G	C4'-C3'-O3'	-5.60	104.60	113.00
1	A	2111	U	C2'-C3'-O3'	5.60	117.90	109.50
1	A	2629	A	C4'-C3'-O3'	-5.57	104.65	113.00
1	A	1612	A	C4'-C3'-O3'	5.55	121.32	113.00
1	A	1610	C	C2'-C3'-O3'	5.53	122.00	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2113	G	C2'-C3'-O3'	5.48	117.72	109.50
30	9	96	LYS	N-CA-C	5.42	116.88	110.97
4	D	118	VAL	N-CA-C	5.41	120.56	108.88
1	A	1866	G	C4'-C3'-O3'	-5.41	104.89	113.00
1	A	869	G	C3'-C2'-O2'	5.40	118.80	110.70
1	A	1448	A	C4'-C3'-O3'	5.39	117.48	109.40
12	N	200	ILE	CB-CA-C	5.38	116.74	110.88
1	A	2743	A	C4'-C3'-O3'	-5.38	104.94	113.00
10	L	79	LEU	N-CA-C	5.35	117.06	107.80
1	A	2628	C	C3'-C2'-O2'	5.34	118.71	110.70
1	A	1228	A	C1'-C2'-O2'	5.34	119.81	111.80
1	A	384	G	C3'-C2'-O2'	5.32	118.68	110.70
2	B	67	U	C4'-C3'-O3'	5.32	120.98	113.00
19	U	158	ILE	CA-C-N	5.31	131.53	121.81
19	U	158	ILE	C-N-CA	5.31	131.53	121.81
21	W	169	ASP	O-C-N	-5.28	115.98	122.05
2	B	91	G	C3'-C2'-O2'	5.25	118.58	110.70
1	A	2583	A	C4'-C3'-O3'	5.24	117.26	109.40
24	Z	131	ARG	N-CA-C	-5.24	104.57	111.96
14	P	80	ILE	N-CA-C	5.21	119.40	111.89
1	A	203	A	C4'-C3'-O3'	-5.20	105.19	113.00
1	A	1139	A	C2'-C3'-O3'	5.19	121.49	113.70
1	A	138	C	N1-C1'-C2'	5.19	119.78	112.00
1	A	694	U	C4'-C3'-O3'	-5.19	105.22	113.00
1	A	2363	A	C4'-C3'-O3'	5.18	117.17	109.40
17	S	102	ILE	N-CA-C	5.18	115.28	110.42
1	A	2774	U	C4'-C3'-O3'	5.17	117.15	109.40
1	A	1954	U	C4'-C3'-O3'	5.16	117.14	109.40
1	A	2706	U	C4'-C3'-O3'	-5.16	105.25	113.00
1	A	1885	C	C4'-C3'-O3'	5.15	117.13	109.40
1	A	972	G	C4'-C3'-O3'	-5.13	105.31	113.00
1	A	1047	U	C4'-C3'-O3'	-5.12	105.32	113.00
1	A	1496	A	C3'-C2'-O2'	5.11	118.36	110.70
1	A	1885	C	C2'-C3'-O3'	5.09	117.13	109.50
1	A	1239	C	C2'-C3'-O3'	5.08	121.32	113.70
1	A	2498	G	C4'-C3'-O3'	-5.08	105.38	113.00
18	T	112	PRO	N-CA-CB	5.08	108.58	103.25
1	A	2303	A	C2'-C3'-O3'	-5.06	101.91	109.50
1	A	274	G	C2'-C3'-O3'	5.06	117.08	109.50
1	A	1683	G	C2'-C3'-O3'	5.05	117.07	109.50
1	A	1445	G	C3'-C2'-O2'	5.03	118.24	110.70
13	O	12	GLN	N-CA-C	5.03	116.45	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	90	ILE	N-CA-CB	5.02	116.19	110.72
1	A	2353	A	C2'-C3'-O3'	5.01	117.02	109.50
1	A	180	A	C4'-C3'-O3'	-5.00	105.49	113.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	T	116	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	59074	0	29746	385	0
2	B	2564	0	1295	8	0
3	C	2001	0	1008	11	0
4	D	1895	0	1977	18	0
5	E	1669	0	1753	13	0
6	F	1617	0	1677	12	0
7	G	1387	0	1443	9	0
8	H	1386	0	1448	12	0
9	I	359	0	415	3	0
10	L	1489	0	1434	10	0
11	M	934	0	985	12	0
12	N	1385	0	1464	14	0
13	O	1075	0	1134	14	0
14	P	945	0	1004	15	0
15	Q	931	0	952	3	0
16	R	915	0	1008	8	0
17	S	1003	0	1069	6	0
18	T	1017	0	1017	15	0
19	U	1165	0	1175	12	0
20	V	734	0	780	10	0
21	W	1018	0	1072	7	0
22	X	866	0	909	7	0
23	Y	616	0	665	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	Z	788	0	849	24	0
25	2	341	0	379	6	0
26	3	489	0	511	5	0
27	4	471	0	529	2	0
28	5	575	0	642	3	0
29	6	305	0	344	0	0
30	9	881	0	932	4	0
31	7	378	0	445	6	0
32	8	374	0	391	5	0
All	All	90647	0	60452	596	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 4.

All (596) 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:A:133:A:C6	24:Z:131:ARG:NH1	1.78	1.50
18:T:118:PRO:C	18:T:119:PRO:N	1.71	1.46
1:A:133:A:C2	24:Z:131:ARG:NH2	1.80	1.45
1:A:133:A:C5	24:Z:131:ARG:NH1	1.78	1.36
19:U:158:ILE:C	19:U:159:ALA:N	1.84	1.31
1:A:137:U:N3	1:A:160:A:N1	1.85	1.24
1:A:81:G:N2	1:A:102:U:O4	1.71	1.21
1:A:1049:A:N1	1:A:1168:U:O4	1.71	1.20
1:A:133:A:C6	24:Z:131:ARG:CZ	2.33	1.11
1:A:137:U:O2	1:A:160:A:H2	1.32	1.11
1:A:133:A:N1	24:Z:131:ARG:CZ	2.21	1.03
1:A:219:U:H3	1:A:442:A:N6	1.58	1.02
1:A:1524:G:N3	31:7:102:GLN:NE2	2.06	1.02
1:A:1239:C:H2'	1:A:1240:G:H5''	1.37	1.00
1:A:262:G:C8	1:A:262:G:H5''	1.99	0.98
1:A:2666:U:N3	1:A:2688:A:C2	2.31	0.98
1:A:2227:C:O2	1:A:2230:A:N6	1.97	0.97
1:A:1242:G:H5'	1:A:1242:G:H8	1.26	0.97
1:A:1529:A:N1	1:A:1537:U:N3	2.14	0.95
1:A:133:A:C2	24:Z:131:ARG:CZ	2.51	0.93
1:A:1524:G:C2	31:7:102:GLN:NE2	2.38	0.92
1:A:2666:U:O4	1:A:2688:A:N1	2.03	0.91
1:A:137:U:O2	1:A:160:A:C2	2.23	0.90
1:A:2517:U:O2	1:A:2521:U:O4	1.90	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:940:C:O2	1:A:956:G:N2	2.06	0.88
1:A:219:U:H2'	1:A:219:U:O2	1.75	0.86
1:A:1239:C:C5	1:A:1240:G:N2	2.44	0.85
1:A:2666:U:H3	1:A:2688:A:H2	0.86	0.85
1:A:2666:U:N3	1:A:2688:A:H2	1.67	0.85
1:A:110:U:OP2	24:Z:130:LYS:NZ	2.11	0.84
1:A:1239:C:C2'	1:A:1240:G:H5''	2.05	0.84
1:A:133:A:N1	24:Z:131:ARG:NH2	2.24	0.83
1:A:1242:G:H5'	1:A:1242:G:C8	2.14	0.83
1:A:1535:A:O2'	4:D:97:LYS:NZ	2.12	0.83
1:A:137:U:C2	1:A:160:A:C2	2.67	0.82
1:A:2321:G:H22	1:A:2329:U:H3	1.24	0.82
19:U:33:THR:HG22	19:U:135:VAL:HG22	1.58	0.82
1:A:1047:U:N3	1:A:1169:A:N6	2.29	0.81
1:A:227:G:O2'	1:A:228:U:OP2	1.99	0.81
1:A:137:U:N3	1:A:160:A:C2	2.46	0.80
1:A:98:G:N2	1:A:100:G:H22	1.78	0.80
1:A:2663:C:C4	1:A:2750:G:C2	2.71	0.78
1:A:2663:C:C5	1:A:2750:G:C2	2.71	0.78
4:D:142:ILE:HD11	4:D:150:LEU:HD21	1.65	0.78
1:A:1434:G:O6	1:A:1623:A:N6	2.16	0.78
1:A:137:U:C2	1:A:160:A:H2	2.01	0.77
1:A:219:U:H3	1:A:442:A:H61	0.80	0.77
1:A:2666:U:C4	1:A:2688:A:N1	2.53	0.77
11:M:102:ILE:HD11	11:M:117:ALA:HB2	1.67	0.77
18:T:118:PRO:C	18:T:119:PRO:CA	2.59	0.75
5:E:199:ILE:HD11	5:E:278:ILE:HD13	1.67	0.75
1:A:1438:G:C2'	1:A:1623:A:HO2'	1.98	0.74
1:A:2328:A:HO2'	1:A:2329:U:H6	1.34	0.74
1:A:941:C:O2	1:A:955:G:N2	2.18	0.74
1:A:98:G:C2	1:A:100:G:N2	2.56	0.74
1:A:541:G:O6	1:A:2037:G:OP1	2.06	0.73
1:A:1749:U:O4	1:A:1755:A:N1	2.20	0.73
1:A:98:G:N2	1:A:100:G:N2	2.36	0.73
1:A:1242:G:H8	1:A:1242:G:C5'	2.03	0.72
14:P:34:LEU:HD13	14:P:54:MET:HE2	1.72	0.71
1:A:158:C:N4	24:Z:129:GLY:O	2.23	0.71
1:A:1950:A:N1	1:A:1957:U:O4	2.24	0.71
16:R:130:ALA:HB1	16:R:177:ILE:HD12	1.73	0.71
1:A:1530:G:H22	1:A:1536:A:H2	1.37	0.71
1:A:2663:C:C5	1:A:2750:G:N2	2.58	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1049:A:N1	1:A:1168:U:C4	2.58	0.70
1:A:2521:U:H2'	1:A:2521:U:O2	1.92	0.69
1:A:2128:A:C6	1:A:2131:U:C4	2.79	0.69
1:A:1004:G:O6	1:A:1016:G:N2	2.26	0.69
20:V:178:LEU:HD12	20:V:184:ALA:HB2	1.75	0.68
1:A:1438:G:O2'	1:A:1623:A:O2'	1.69	0.68
1:A:2329:U:O2	1:A:2329:U:H2'	1.92	0.68
1:A:2665:U:H2'	1:A:2666:U:C6	2.29	0.68
1:A:1663:G:N7	31:7:142:VAL:HB	2.10	0.67
1:A:219:U:O2	1:A:219:U:C2'	2.43	0.67
1:A:2328:A:O2'	1:A:2329:U:H6	1.78	0.66
1:A:1524:G:N2	31:7:102:GLN:NE2	2.44	0.66
1:A:133:A:C4	24:Z:131:ARG:NH1	2.44	0.66
13:O:68:ILE:HD13	13:O:103:LEU:HD23	1.78	0.66
18:T:123:ILE:HG22	18:T:166:THR:HB	1.78	0.65
1:A:1227:U:N3	1:A:1261:A:N6	2.43	0.65
10:L:127:MET:HE1	10:L:200:ILE:HD12	1.77	0.65
1:A:234:C:O2	28:5:100:LYS:NZ	2.30	0.65
1:A:2128:A:C6	1:A:2131:U:O4	2.50	0.65
15:Q:100:THR:HG23	15:Q:123:ILE:HD11	1.78	0.65
1:A:102:U:C5	1:A:103:C:C5	2.86	0.64
1:A:446:U:O2	1:A:448:C:C4	2.49	0.64
30:9:225:TYR:CE1	30:9:242:LEU:HD13	2.33	0.64
1:A:2224:G:O6	1:A:2228:C:N4	2.31	0.64
14:P:61:MET:HE1	14:P:80:ILE:HD11	1.79	0.64
1:A:2663:C:C4	1:A:2750:G:N2	2.66	0.64
1:A:2128:A:N6	1:A:2131:U:C4	2.66	0.64
5:E:90:ILE:HD11	5:E:179:PHE:CE1	2.33	0.63
1:A:1439:U:H2'	1:A:1440:C:O4'	1.98	0.63
1:A:609:G:C2	1:A:670:A:C2	2.87	0.63
1:A:1047:U:C4	1:A:1169:A:N6	2.67	0.63
1:A:1530:G:N2	1:A:1536:A:H2	1.97	0.63
20:V:119:ILE:HD12	20:V:135:LEU:HG	1.81	0.63
1:A:1049:A:C2	1:A:1168:U:O4	2.51	0.62
1:A:1476:G:O6	1:A:2721:C:N3	2.32	0.62
10:L:119:ALA:HA	10:L:122:LEU:HD12	1.80	0.61
14:P:38:LEU:HD23	14:P:58:VAL:HG21	1.82	0.61
18:T:160:LYS:HD2	18:T:176:ILE:HD11	1.81	0.61
1:A:133:A:N6	24:Z:131:ARG:NH1	2.44	0.61
16:R:119:LEU:HD23	16:R:122:ILE:HD12	1.83	0.61
2:B:66:C:C5	2:B:110:C:C4	2.89	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:U:C2	1:A:448:C:N4	2.69	0.60
1:A:1228:A:O2'	1:A:1229:G:O5'	2.18	0.60
1:A:26:G:C2	1:A:523:G:N3	2.69	0.60
1:A:932:A:O2'	22:X:85:GLN:NE2	2.27	0.60
13:O:118:VAL:HG21	13:O:131:PHE:CD1	2.37	0.60
5:E:237:ALA:HB3	5:E:241:PRO:HG3	1.82	0.60
1:A:261:U:H3	1:A:266:A:H2	1.47	0.59
1:A:1880:G:N7	12:N:252:ARG:NH1	2.49	0.59
1:A:2784:G:N3	1:A:2784:G:H2'	2.17	0.59
1:A:1475:U:O2'	1:A:1476:G:N2	2.35	0.59
1:A:2339:A:H2'	1:A:2340:G:O4'	2.03	0.59
1:A:651:U:H2'	1:A:652:C:C6	2.38	0.58
1:A:966:G:OP1	28:5:157:ARG:NH2	2.37	0.58
1:A:2472:G:H2'	1:A:2473:C:H6	1.68	0.58
1:A:1870:U:H3	1:A:1896:G:H1	1.51	0.58
18:T:118:PRO:CA	18:T:119:PRO:N	2.62	0.58
1:A:1227:U:N3	1:A:1261:A:C6	2.70	0.58
1:A:2218:G:C2	1:A:2220:G:C5	2.92	0.58
1:A:6:A:C2	3:C:98:U:C2	2.92	0.57
1:A:227:G:HO2'	1:A:228:U:P	2.22	0.57
27:4:120:THR:HG23	27:4:123:GLY:HA3	1.86	0.57
24:Z:68:LEU:O	24:Z:122:ARG:NH2	2.36	0.57
1:A:956:G:C6	1:A:957:U:O4	2.57	0.57
1:A:2344:A:H2'	1:A:2345:A:C8	2.40	0.57
6:F:212:LEU:HD11	6:F:228:LEU:HD23	1.87	0.57
1:A:1047:U:C2	1:A:1171:G:N2	2.73	0.57
5:E:167:HIS:CG	5:E:289:LEU:HD11	2.40	0.57
1:A:1239:C:C6	1:A:1240:G:N2	2.72	0.57
1:A:1230:G:O2'	1:A:1258:A:N1	2.35	0.56
1:A:26:G:N2	1:A:523:G:H1'	2.21	0.56
1:A:255:A:O2'	1:A:256:A:O4'	2.22	0.56
12:N:160:ILE:HD11	12:N:198:LEU:HD13	1.88	0.56
1:A:2472:G:H2'	1:A:2473:C:C6	2.40	0.56
4:D:129:THR:HG22	4:D:182:LYS:HD2	1.87	0.56
1:A:379:C:H2'	1:A:380:C:H6	1.71	0.56
1:A:446:U:O2	1:A:448:C:N4	2.38	0.56
5:E:97:LEU:HD11	16:R:119:LEU:HD22	1.88	0.56
14:P:77:LEU:HD13	14:P:86:VAL:HG11	1.87	0.56
1:A:1:U:H2'	1:A:2:U:C5	2.40	0.56
1:A:389:A:C6	1:A:390:U:C4	2.94	0.56
1:A:378:A:C8	1:A:379:C:C5	2.94	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:839:G:H4'	1:A:842:G:N1	2.21	0.56
1:A:298:G:C2	1:A:299:C:C6	2.94	0.55
1:A:981:G:OP2	13:O:16:ARG:NH1	2.38	0.55
1:A:2328:A:C2'	1:A:2329:U:H6	2.19	0.55
32:8:82:LEU:HD23	32:8:83:PRO:HD2	1.88	0.55
1:A:2703:G:H2'	1:A:2704:U:O4'	2.07	0.55
1:A:2688:A:H2'	1:A:2689:A:C8	2.41	0.55
18:T:136:VAL:HG23	18:T:221:ILE:HG13	1.86	0.55
12:N:225:LEU:HD13	12:N:232:VAL:HG21	1.89	0.55
26:3:15:CYS:HB3	26:3:17:GLY:O	2.07	0.55
1:A:2108:G:H1	1:A:2209:U:H3	1.55	0.55
12:N:185:GLY:C	12:N:186:ILE:HD12	2.31	0.55
1:A:262:G:C8	1:A:262:G:C5'	2.85	0.55
1:A:856:U:O2'	1:A:857:G:OP1	2.16	0.55
1:A:1238:G:N2	1:A:1253:G:H22	2.05	0.55
1:A:1238:G:N2	1:A:1253:G:N2	2.55	0.54
1:A:446:U:O2	1:A:448:C:C5	2.60	0.54
3:C:85:C:O4'	3:C:85:C:O2	2.23	0.54
10:L:122:LEU:O	10:L:162:ALA:HB3	2.07	0.54
1:A:494:A:O2'	1:A:508:A:N1	2.36	0.54
1:A:769:C:H2'	1:A:769:C:O2	2.07	0.54
11:M:24:ILE:HD12	11:M:33:ALA:HB2	1.88	0.54
1:A:102:U:C4	1:A:103:C:C5	2.95	0.54
15:Q:100:THR:CG2	15:Q:123:ILE:HD11	2.37	0.54
1:A:1056:A:N3	1:A:2503:G:O2'	2.33	0.54
31:7:110:LYS:HG2	31:7:114:LEU:HD12	1.90	0.54
1:A:1047:U:N3	1:A:1169:A:C6	2.72	0.54
26:3:18:CYS:HG	26:3:55:CYS:HG	1.50	0.54
12:N:99:GLY:HA2	12:N:107:GLY:HA2	1.90	0.53
1:A:1500:U:H2'	1:A:1500:U:O2	2.07	0.53
1:A:2362:G:N3	1:A:2398:C:H2'	2.24	0.53
7:G:72:LEU:HD21	7:G:167:MET:HE1	1.90	0.53
30:9:109:ASN:HB3	30:9:206:LEU:HD22	1.90	0.53
1:A:1559:A:H2'	1:A:1559:A:N3	2.23	0.53
25:2:34:LEU:HD13	25:2:34:LEU:O	2.09	0.53
1:A:2345:A:H2'	1:A:2346:A:C8	2.43	0.53
1:A:2472:G:C4	1:A:2473:C:C5	2.97	0.53
21:W:75:VAL:HG21	21:W:89:ILE:HD11	1.91	0.53
1:A:13:A:H2'	1:A:14:A:C8	2.43	0.53
14:P:113:ARG:NH1	14:P:120:MET:HE1	2.23	0.53
21:W:101:ILE:HG21	21:W:104:LEU:HD22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2644:G:O2'	1:A:2799:A:N1	2.32	0.53
1:A:975:A:O2'	1:A:1012:G:N2	2.39	0.52
1:A:1612:A:H2'	1:A:1613:A:O4'	2.10	0.52
1:A:1004:G:C6	1:A:1016:G:N2	2.78	0.52
1:A:1693:U:H2'	1:A:1694:C:H6	1.75	0.52
1:A:2701:U:OP2	16:R:173:GLN:NE2	2.42	0.52
14:P:65:ALA:HA	14:P:90:PHE:CE1	2.44	0.52
1:A:1438:G:C2'	1:A:1623:A:O2'	2.54	0.52
1:A:2227:C:C2	1:A:2230:A:N6	2.76	0.52
1:A:2517:U:O2	1:A:2521:U:C4	2.61	0.52
21:W:145:ASP:CG	21:W:146:ARG:N	2.68	0.52
24:Z:93:GLN:OE1	24:Z:93:GLN:N	2.43	0.52
1:A:403:A:C4	1:A:404:U:C6	2.98	0.52
1:A:2303:A:H4'	1:A:2304:A:O4'	2.09	0.52
1:A:2329:U:O2	7:G:52:ASN:ND2	2.43	0.52
2:B:13:C:O2	2:B:13:C:O4'	2.25	0.52
1:A:415:U:O2'	1:A:416:C:O2	2.24	0.52
24:Z:130:LYS:NZ	24:Z:130:LYS:CB	2.73	0.52
1:A:138:C:H2'	1:A:138:C:O2	2.09	0.51
1:A:204:A:H2	1:A:219:U:O2	1.93	0.51
1:A:956:G:C4	1:A:957:U:C5	2.99	0.51
1:A:133:A:C4	24:Z:131:ARG:NH2	2.73	0.51
1:A:1410:G:N2	1:A:1420:C:C2	2.79	0.51
1:A:333:A:N6	1:A:347:G:O2'	2.43	0.51
1:A:1024:A:OP1	18:T:132:ARG:HD2	2.10	0.51
1:A:1227:U:H2'	1:A:1228:A:O5'	2.10	0.51
1:A:2033:A:N7	25:2:6:LYS:NZ	2.52	0.51
1:A:138:C:O2	1:A:138:C:C2'	2.58	0.51
1:A:2329:U:O2	1:A:2329:U:C2'	2.58	0.51
16:R:187:ILE:HG23	16:R:188:ALA:N	2.24	0.51
1:A:2707:A:HO2'	1:A:2708:C:H6	1.57	0.51
1:A:2535:C:H2'	1:A:2535:C:O2	2.11	0.51
1:A:1213:G:OP2	12:N:96:LYS:NZ	2.44	0.51
13:O:21:SER:HB2	13:O:98:LYS:HB2	1.93	0.51
17:S:14:ARG:HD2	17:S:32:THR:HG23	1.93	0.51
1:A:771:G:H2'	1:A:772:A:O4'	2.11	0.51
1:A:1242:G:C8	1:A:1242:G:C5'	2.87	0.51
1:A:1819:A:H2'	1:A:1820:A:C8	2.45	0.50
1:A:133:A:N3	24:Z:131:ARG:NH2	2.17	0.50
1:A:384:G:O2'	1:A:385:U:OP2	2.29	0.50
1:A:1693:U:H2'	1:A:1694:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:740:G:OP2	4:D:203:ARG:NH2	2.45	0.50
1:A:2307:G:H2'	1:A:2308:U:C6	2.46	0.50
19:U:130:CYS:SG	19:U:131:HIS:N	2.85	0.50
1:A:416:C:O2	1:A:416:C:O4'	2.29	0.50
1:A:2784:G:C2	1:A:2785:C:C6	3.00	0.50
6:F:190:PHE:CE2	6:F:194:MET:HE3	2.46	0.50
18:T:175:PRO:HG2	32:8:82:LEU:HD21	1.94	0.50
1:A:553:G:O2'	1:A:554:G:C8	2.61	0.50
1:A:2521:U:O2	1:A:2521:U:C2'	2.60	0.50
1:A:956:G:C6	1:A:957:U:C4	2.99	0.49
1:A:570:C:O2'	17:S:52:ARG:NH2	2.41	0.49
1:A:2699:U:C5	5:E:99:MET:HE2	2.47	0.49
1:A:8:G:O2'	3:C:96:A:N6	2.46	0.49
1:A:580:G:H2'	1:A:2044:A:N7	2.27	0.49
1:A:1114:A:N3	1:A:1114:A:H2'	2.26	0.49
1:A:1495:C:C2	1:A:1548:A:N6	2.80	0.49
1:A:1950:A:N1	1:A:1957:U:C4	2.80	0.49
8:H:50:VAL:HG13	8:H:54:VAL:HG11	1.94	0.49
16:R:170:ILE:HD11	16:R:182:ARG:HD3	1.94	0.49
1:A:1228:A:O2'	1:A:1229:G:H8	1.94	0.49
1:A:1547:C:OP1	31:7:106:MET:HE1	2.12	0.49
1:A:818:U:C2	1:A:819:G:C8	3.01	0.49
1:A:1806:U:H2'	1:A:1807:C:H6	1.77	0.49
14:P:61:MET:CE	14:P:80:ILE:HD11	2.42	0.49
1:A:2707:A:O2'	1:A:2708:C:P	2.70	0.49
8:H:138:VAL:HG21	8:H:165:VAL:HG21	1.95	0.49
6:F:102:THR:HB	6:F:139:VAL:HG11	1.95	0.49
6:F:116:TYR:HB2	6:F:117:PRO:HD2	1.95	0.49
22:X:119:ILE:HG23	22:X:120:ASP:O	2.13	0.49
1:A:542:C:O2'	17:S:41:ARG:NH2	2.42	0.48
4:D:131:MET:SD	4:D:137:ILE:HG21	2.53	0.48
14:P:38:LEU:CD2	14:P:58:VAL:HG21	2.42	0.48
4:D:200:ARG:O	4:D:202:GLY:N	2.46	0.48
1:A:1499:G:H2'	1:A:1500:U:C6	2.48	0.48
6:F:94:ASN:ND2	6:F:149:THR:HG23	2.28	0.48
12:N:126:MET:HE3	12:N:127:ARG:O	2.13	0.48
1:A:1194:G:O2'	1:A:1195:U:O5'	2.31	0.48
23:Y:88:VAL:HG13	23:Y:92:ASN:HA	1.95	0.48
1:A:1007:A:H4'	32:8:64:PRO:HG3	1.94	0.48
13:O:104:TYR:CE2	13:O:125:MET:HE3	2.49	0.48
1:A:403:A:C5	1:A:404:U:C5	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2642:G:H2'	1:A:2643:C:O4'	2.13	0.48
24:Z:130:LYS:HZ3	24:Z:130:LYS:HB3	1.78	0.48
1:A:85:U:H3	1:A:95:G:H1	1.62	0.48
1:A:1551:G:C2	1:A:1552:U:C5	3.01	0.48
4:D:256:ARG:O	4:D:257:LYS:C	2.56	0.48
5:E:122:ILE:HD12	5:E:165:MET:CE	2.44	0.48
1:A:2738:U:C2	1:A:2739:A:C8	3.02	0.47
9:I:53:LEU:HD13	9:I:65:GLN:HB2	1.96	0.47
1:A:394:G:H22	1:A:404:U:H3	1.62	0.47
1:A:2809:U:O2	1:A:2809:U:O4'	2.30	0.47
14:P:44:ILE:HD11	14:P:54:MET:HE1	1.97	0.47
1:A:382:G:C6	1:A:436:G:N7	2.82	0.47
6:F:208:PHE:CE1	6:F:234:LEU:HD13	2.50	0.47
1:A:1224:U:O4	1:A:1225:G:C2	2.68	0.47
1:A:373:C:H2'	1:A:374:U:C6	2.50	0.47
1:A:2328:A:C2'	1:A:2329:U:C6	2.97	0.47
4:D:84:ASN:ND2	4:D:196:VAL:HG11	2.29	0.47
27:4:146:SER:O	27:4:150:ALA:HB2	2.14	0.47
1:A:816:G:O4'	12:N:117:GLN:HG3	2.14	0.47
1:A:1220:U:H2'	1:A:1221:C:C6	2.48	0.47
1:A:2663:C:C5	1:A:2750:G:N3	2.82	0.47
1:A:378:A:N3	1:A:378:A:H2'	2.29	0.47
1:A:445:C:H2'	1:A:446:U:C6	2.49	0.47
1:A:589:G:H2'	1:A:590:C:C6	2.49	0.47
1:A:955:G:C6	1:A:956:G:C8	3.02	0.47
19:U:32:ILE:HG21	19:U:87:ALA:HB2	1.95	0.47
1:A:2263:C:H2'	1:A:2264:U:C6	2.50	0.47
14:P:64:LEU:HD23	14:P:76:ALA:HB2	1.96	0.47
1:A:1:U:H2'	1:A:2:U:C6	2.49	0.47
1:A:2310:U:H3	1:A:2356:G:H1	1.63	0.47
1:A:2707:A:C8	1:A:2708:C:C6	3.03	0.47
3:C:100:G:H2'	3:C:101:A:C8	2.49	0.47
4:D:29:ILE:HG23	4:D:29:ILE:O	2.14	0.47
1:A:138:C:N3	1:A:139:U:C5	2.82	0.47
1:A:261:U:O4	1:A:266:A:N1	2.48	0.47
1:A:880:U:OP1	13:O:6:ARG:NH1	2.48	0.47
1:A:1419:C:H2'	1:A:1419:C:O2	2.14	0.47
8:H:183:GLN:O	8:H:187:THR:HG23	2.14	0.47
18:T:124:PHE:CB	18:T:137:ILE:HG22	2.44	0.47
1:A:328:C:N3	1:A:332:G:O6	2.47	0.46
1:A:553:G:O2'	1:A:554:G:O5'	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:932:A:C2'	22:X:85:GLN:HE22	2.27	0.46
1:A:176:A:H2'	1:A:177:C:C6	2.49	0.46
1:A:2658:A:OP2	10:L:175:ARG:NH2	2.49	0.46
11:M:58:ILE:HD13	11:M:86:ILE:HG23	1.98	0.46
12:N:201:LEU:HD23	12:N:218:SER:HB3	1.98	0.46
1:A:824:U:H2'	1:A:825:C:C6	2.50	0.46
1:A:1950:A:C2	1:A:1957:U:N3	2.83	0.46
12:N:160:ILE:HD11	12:N:198:LEU:CD1	2.45	0.46
20:V:112:TYR:CE1	24:Z:146:VAL:HG23	2.51	0.46
22:X:141:GLU:HB3	22:X:142:ILE:HD12	1.96	0.46
1:A:133:A:C4	24:Z:131:ARG:CZ	2.98	0.46
1:A:2707:A:O2'	1:A:2708:C:O5'	2.30	0.46
1:A:1321:A:C2	1:A:1662:A:N6	2.84	0.46
14:P:77:LEU:HD11	14:P:83:LYS:HG2	1.97	0.46
1:A:137:U:C4	1:A:160:A:N1	2.76	0.46
2:B:90:G:O2'	2:B:91:G:O5'	2.31	0.46
5:E:197:VAL:CG2	5:E:266:ILE:HD11	2.46	0.46
11:M:98:ILE:HD13	11:M:113:ILE:HG23	1.98	0.46
18:T:176:ILE:HD13	32:8:86:PRO:HD2	1.98	0.46
1:A:384:G:O2'	1:A:385:U:P	2.73	0.46
20:V:192:GLY:HA3	24:Z:93:GLN:HE21	1.81	0.46
23:Y:104:GLN:O	23:Y:120:ARG:HA	2.16	0.46
1:A:379:C:H2'	1:A:380:C:C6	2.51	0.46
20:V:135:LEU:HD13	20:V:175:TYR:CD1	2.51	0.46
23:Y:88:VAL:HG12	23:Y:89:SER:O	2.16	0.46
8:H:194:PRO:HB2	8:H:209:VAL:HG11	1.97	0.46
8:H:194:PRO:CG	8:H:209:VAL:HG21	2.45	0.46
13:O:53:ALA:HB1	13:O:120:ILE:CG2	2.46	0.46
1:A:138:C:C2	1:A:139:U:C5	3.04	0.46
1:A:299:C:H2'	1:A:300:U:C6	2.51	0.46
1:A:1558:U:H2'	1:A:1559:A:O4'	2.16	0.46
1:A:2043:G:N1	1:A:2047:A:OP2	2.43	0.46
3:C:25:U:O2	3:C:80:C:C4	2.69	0.46
1:A:227:G:C2'	1:A:228:U:OP2	2.64	0.45
1:A:2354:G:H2'	1:A:2354:G:N3	2.31	0.45
24:Z:89:MET:HE1	24:Z:152:LEU:HD23	1.98	0.45
1:A:119:A:C8	1:A:132:G:C5	3.05	0.45
1:A:1239:C:C4	1:A:1240:G:N2	2.84	0.45
6:F:93:GLN:HE21	6:F:93:GLN:HB3	1.64	0.45
1:A:79:G:N2	1:A:105:G:C4	2.84	0.45
1:A:2663:C:C6	1:A:2750:G:N2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:869:G:O2'	1:A:870:U:P	2.75	0.45
1:A:2653:U:O2'	5:E:134:TYR:OH	2.32	0.45
1:A:2722:C:O2'	3:C:53:G:OP1	2.27	0.45
4:D:137:ILE:HG22	4:D:188:VAL:HA	1.97	0.45
1:A:857:G:O2'	1:A:858:G:C8	2.69	0.45
1:A:1957:U:N3	1:A:1959:G:O4'	2.49	0.45
1:A:2092:C:H2'	1:A:2093:U:O4'	2.16	0.45
2:B:44:C:O2	7:G:107:ARG:NH1	2.49	0.45
11:M:35:ILE:HD12	11:M:69:LEU:HD23	1.98	0.45
1:A:144:A:C2	1:A:2224:G:N2	2.85	0.45
1:A:2304:A:O2'	1:A:2305:A:H2'	2.17	0.45
1:A:2663:C:N4	1:A:2750:G:C2	2.85	0.45
20:V:163:ASN:OD1	20:V:163:ASN:N	2.49	0.45
7:G:119:ILE:HD13	7:G:189:GLY:O	2.17	0.45
23:Y:72:ARG:CD	23:Y:74:ILE:HD12	2.46	0.45
1:A:2128:A:N1	1:A:2131:U:O4	2.50	0.45
13:O:53:ALA:HB1	13:O:120:ILE:HG22	1.99	0.45
1:A:603:G:H1	1:A:675:U:H3	1.63	0.45
3:C:36:A:C2	3:C:80:C:C6	3.05	0.45
1:A:869:G:HO2'	1:A:870:U:P	2.40	0.45
1:A:1201:A:H2'	1:A:1202:A:C8	2.50	0.45
1:A:1500:U:H3	1:A:1545:G:H1	1.65	0.45
4:D:75:VAL:HG21	4:D:91:HIS:ND1	2.32	0.45
11:M:81:ASP:OD2	11:M:83:ALA:HB2	2.17	0.45
1:A:1694:C:C2	1:A:1695:U:C5	3.05	0.44
1:A:2102:G:H1	1:A:2248:U:H3	1.66	0.44
1:A:2218:G:C2	1:A:2220:G:N7	2.85	0.44
1:A:701:U:H2'	1:A:702:C:O4'	2.17	0.44
1:A:1701:A:H2'	1:A:1702:G:O4'	2.17	0.44
1:A:1749:U:C4	1:A:1755:A:N1	2.84	0.44
1:A:2770:C:OP2	8:H:43:ILE:HD11	2.18	0.44
19:U:74:TYR:HB3	19:U:75:PRO:HD3	1.99	0.44
26:3:15:CYS:SG	26:3:61:HIS:CE1	3.11	0.44
1:A:404:U:H2'	1:A:404:U:O2	2.16	0.44
1:A:650:G:H2'	1:A:651:U:C6	2.52	0.44
11:M:69:LEU:HD12	11:M:69:LEU:C	2.42	0.44
21:W:92:ILE:HG23	21:W:92:ILE:O	2.18	0.44
1:A:1629:G:H2'	1:A:1630:G:O4'	2.17	0.44
1:A:2421:C:H2'	1:A:2422:G:O4'	2.18	0.44
10:L:243:ASP:HB3	10:L:246:ILE:HB	1.99	0.44
1:A:1605:A:H2'	1:A:1606:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:96:A:H2'	3:C:96:A:N3	2.32	0.44
7:G:78:GLN:NE2	7:G:105:THR:O	2.51	0.44
1:A:1885:C:O2'	1:A:1886:A:O5'	2.35	0.44
1:A:966:G:C6	1:A:967:C:C4	3.06	0.44
1:A:1001:A:O4'	1:A:1209:U:C6	2.71	0.44
1:A:1296:A:N6	1:A:1317:C:H4'	2.33	0.44
1:A:1763:G:C2	1:A:1766:G:C2	3.05	0.44
1:A:2707:A:O2'	1:A:2708:C:H6	2.01	0.44
1:A:2791:C:N3	1:A:2792:C:C5	2.86	0.44
7:G:119:ILE:HG21	7:G:189:GLY:O	2.18	0.44
10:L:242:ARG:O	10:L:243:ASP:HB2	2.18	0.44
1:A:680:G:N3	1:A:680:G:H2'	2.32	0.44
1:A:1250:C:H2'	1:A:1251:G:C8	2.53	0.44
1:A:1261:A:C5	1:A:1262:A:C8	3.06	0.44
1:A:1559:A:C2	1:A:1560:C:C2	3.05	0.44
1:A:2387:G:C6	1:A:2388:G:C6	3.05	0.44
17:S:47:HIS:CE1	18:T:197:VAL:HG13	2.53	0.44
19:U:112:LYS:HB3	19:U:124:MET:HE3	1.99	0.44
22:X:146:ASN:HD22	22:X:148:ASN:HB2	1.83	0.44
1:A:316:G:H1'	1:A:317:G:OP2	2.18	0.43
1:A:856:U:C2'	1:A:857:G:OP1	2.66	0.43
1:A:2474:U:H2'	1:A:2475:G:O4'	2.18	0.43
2:B:91:G:C2'	2:B:92:U:OP2	2.66	0.43
5:E:122:ILE:HD12	5:E:165:MET:HE1	1.99	0.43
7:G:94:VAL:HG23	7:G:95:ARG:HG2	2.00	0.43
1:A:410:G:C6	1:A:411:U:C4	3.06	0.43
1:A:519:A:N6	19:U:38:SER:OG	2.50	0.43
1:A:824:U:H2'	1:A:825:C:H6	1.83	0.43
1:A:1731:G:N2	1:A:1732:G:C8	2.85	0.43
1:A:2085:A:H2'	1:A:2086:G:H8	1.84	0.43
8:H:56:ILE:HG21	8:H:84:LYS:HD3	2.00	0.43
8:H:163:VAL:HG22	8:H:173:VAL:HG13	2.00	0.43
14:P:42:GLY:O	14:P:124:GLU:HB2	2.18	0.43
1:A:1261:A:H3'	1:A:1261:A:C8	2.54	0.43
2:B:66:C:C6	2:B:110:C:N4	2.87	0.43
1:A:1798:C:C5'	4:D:220:VAL:HG21	2.48	0.43
6:F:194:MET:HE1	6:F:207:PHE:CZ	2.53	0.43
14:P:64:LEU:HD12	14:P:72:LYS:HD2	2.01	0.43
25:2:25:TYR:CD2	25:2:25:TYR:C	2.97	0.43
1:A:389:A:C5	1:A:390:U:C5	3.06	0.43
1:A:572:U:C2	1:A:582:A:C8	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:869:G:O2'	1:A:870:U:OP2	2.34	0.43
1:A:1042:A:C6	1:A:1043:C:N4	2.86	0.43
1:A:1344:G:O6	1:A:1345:G:C6	2.72	0.43
1:A:2303:A:C2	26:3:48:LEU:HD11	2.53	0.43
13:O:12:GLN:HE21	13:O:73:PRO:HD2	1.82	0.43
1:A:2085:A:H2'	1:A:2086:G:C8	2.54	0.43
1:A:2663:C:N4	1:A:2750:G:N1	2.66	0.43
16:R:168:ILE:O	16:R:183:ILE:HA	2.19	0.43
1:A:591:C:H2'	1:A:592:G:C8	2.54	0.43
2:B:66:C:C6	2:B:110:C:C4	3.07	0.43
3:C:63:G:H2'	3:C:64:U:O4'	2.19	0.43
19:U:87:ALA:HB1	19:U:93:PHE:HE2	1.83	0.43
4:D:138:HIS:ND1	4:D:189:GLY:O	2.51	0.43
1:A:503:C:H2'	1:A:504:G:O4'	2.18	0.43
1:A:1610:C:H5''	1:A:1610:C:H6	1.83	0.43
1:A:2111:U:O2'	1:A:2112:U:C6	2.59	0.43
1:A:2411:C:H2'	1:A:2412:C:O4'	2.19	0.43
1:A:298:G:H2'	1:A:298:G:N3	2.34	0.43
1:A:618:A:H2'	1:A:619:A:O4'	2.19	0.43
1:A:799:A:OP1	1:A:802:C:N4	2.48	0.43
1:A:1084:G:N2	1:A:1130:C:C5	2.87	0.43
1:A:1440:C:H2'	1:A:1441:C:O4'	2.19	0.43
6:F:207:PHE:CD1	6:F:226:LEU:HD11	2.54	0.43
32:8:81:PRO:O	32:8:82:LEU:HB2	2.19	0.43
1:A:976:C:O2	1:A:1012:G:O2'	2.37	0.42
1:A:1261:A:C8	1:A:1261:A:C3'	3.02	0.42
1:A:1363:A:O2'	1:A:1365:U:OP2	2.28	0.42
1:A:2030:U:O2'	25:2:4:PRO:O	2.35	0.42
6:F:206:LEU:HD11	6:F:229:LEU:HD12	2.00	0.42
12:N:160:ILE:HD11	12:N:198:LEU:HD22	2.00	0.42
12:N:187:ILE:HG22	12:N:189:PRO:HD3	2.02	0.42
21:W:89:ILE:HD12	21:W:99:VAL:HG21	2.01	0.42
1:A:591:C:H2'	1:A:592:G:H8	1.84	0.42
1:A:1026:C:H2'	1:A:1027:U:O4'	2.19	0.42
1:A:1142:G:C6	1:A:1143:C:C4	3.08	0.42
1:A:1171:G:H2'	1:A:1172:C:H6	1.84	0.42
1:A:2396:G:H2'	1:A:2397:U:C6	2.54	0.42
18:T:150:ALA:HB3	18:T:189:GLN:HE22	1.84	0.42
1:A:373:C:H2'	1:A:374:U:H6	1.84	0.42
1:A:1374:A:H2'	1:A:1375:A:C8	2.54	0.42
1:A:1806:U:H2'	1:A:1807:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:133:ASN:HD22	7:G:136:SER:HB2	1.84	0.42
21:W:68:HIS:O	21:W:159:ARG:NH2	2.53	0.42
1:A:668:U:H2'	1:A:669:C:C6	2.54	0.42
7:G:51:VAL:CG1	7:G:167:MET:HE2	2.49	0.42
11:M:1:MET:HE2	11:M:32:TYR:CZ	2.55	0.42
26:3:52:CYS:SG	26:3:55:CYS:SG	3.14	0.42
1:A:227:G:HO2'	1:A:239:G:H1	1.67	0.42
1:A:1743:G:C5	1:A:1744:C:C5	3.07	0.42
1:A:2791:C:C4	1:A:2792:C:C5	3.07	0.42
11:M:76:ILE:HG12	16:R:195:VAL:HG22	2.02	0.42
14:P:34:LEU:HB3	14:P:54:MET:SD	2.60	0.42
18:T:172:ILE:HD12	18:T:175:PRO:HA	2.01	0.42
18:T:155:LYS:HA	18:T:185:VAL:HA	2.01	0.42
21:W:93:HIS:CE1	21:W:100:ILE:HD11	2.55	0.42
1:A:176:A:H2'	1:A:177:C:H6	1.83	0.42
1:A:559:G:O6	18:T:141:TRP:CD1	2.73	0.42
1:A:654:U:O2	1:A:654:U:O4'	2.36	0.42
1:A:836:G:H2'	1:A:837:U:O4'	2.20	0.42
1:A:1671:A:H2'	1:A:1672:U:O4'	2.20	0.42
1:A:2743:A:O2'	1:A:2744:A:C8	2.73	0.42
11:M:63:VAL:HG12	11:M:106:LEU:HD21	2.02	0.42
22:X:107:VAL:CG2	22:X:137:VAL:HG23	2.49	0.42
1:A:2543:G:C5	1:A:2544:C:C5	3.08	0.42
5:E:167:HIS:CD2	5:E:289:LEU:HD11	2.55	0.42
19:U:83:ALA:HB1	19:U:136:LEU:HD11	2.02	0.42
1:A:410:G:C5	1:A:411:U:C5	3.08	0.42
1:A:539:A:C2	1:A:2056:A:H2'	2.55	0.42
1:A:815:A:H2'	1:A:817:C:C4	2.55	0.42
1:A:1202:A:H2'	1:A:1203:C:C6	2.54	0.42
1:A:2607:A:H5''	4:D:234:ARG:HE	1.84	0.42
10:L:95:ILE:O	17:S:99:GLN:NE2	2.53	0.42
12:N:136:LEU:HD22	12:N:140:ILE:CD1	2.49	0.42
13:O:43:THR:HG22	13:O:92:TYR:CD2	2.54	0.42
20:V:115:LEU:HD21	20:V:151:ILE:CG1	2.50	0.42
1:A:1530:G:H1	1:A:1536:A:H2	1.64	0.41
1:A:1634:C:O2	1:A:1634:C:H2'	2.20	0.41
1:A:2472:G:C5	1:A:2473:C:C5	3.08	0.41
1:A:2484:C:O2	13:O:124:LYS:NZ	2.52	0.41
4:D:91:HIS:CD2	4:D:97:LYS:HD3	2.55	0.41
6:F:207:PHE:CE1	6:F:246:VAL:HG11	2.55	0.41
1:A:102:U:C4	1:A:103:C:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1261:A:H8	1:A:1261:A:C5'	2.33	0.41
1:A:1530:G:C2	1:A:1536:A:H2	2.39	0.41
1:A:2307:G:H2'	1:A:2308:U:O4'	2.20	0.41
1:A:2628:C:O2'	1:A:2629:A:O5'	2.31	0.41
5:E:151:MET:N	5:E:152:PRO:HD2	2.36	0.41
13:O:2:LEU:N	13:O:44:SER:OG	2.53	0.41
20:V:110:ASP:HB2	20:V:146:MET:HE1	2.01	0.41
1:A:136:U:C4	1:A:137:U:O4	2.74	0.41
1:A:548:G:N2	1:A:567:C:N4	2.69	0.41
1:A:1137:C:N3	1:A:1138:G:C2	2.88	0.41
1:A:1500:U:O2	1:A:1500:U:C2'	2.68	0.41
1:A:1956:C:O2'	30:9:218:ARG:NH2	2.54	0.41
19:U:153:THR:HB	19:U:154:PRO:HD3	2.02	0.41
24:Z:80:ILE:HG22	24:Z:84:LYS:HD2	2.01	0.41
1:A:233:G:H5'	1:A:235:G:N7	2.35	0.41
1:A:393:G:H2'	1:A:394:G:O4'	2.20	0.41
1:A:2207:A:H2'	1:A:2208:U:O4'	2.21	0.41
4:D:117:GLU:O	4:D:118:VAL:O	2.39	0.41
5:E:118:LYS:O	5:E:119:GLU:C	2.63	0.41
8:H:194:PRO:HG3	8:H:209:VAL:HG21	2.02	0.41
24:Z:112:VAL:HG12	24:Z:116:LEU:HD12	2.02	0.41
1:A:26:G:C4	1:A:523:G:C2	3.08	0.41
1:A:1362:G:N3	20:V:163:ASN:ND2	2.69	0.41
1:A:2205:G:H2'	1:A:2206:A:O4'	2.21	0.41
8:H:138:VAL:HG22	8:H:143:LEU:HD23	2.01	0.41
10:L:85:PHE:O	10:L:86:THR:C	2.64	0.41
1:A:14:A:N3	25:2:15:ILE:HD12	2.35	0.41
1:A:169:C:H2'	1:A:170:U:C6	2.55	0.41
1:A:567:C:O2'	10:L:146:SER:O	2.39	0.41
24:Z:130:LYS:HA	24:Z:133:SER:OG	2.20	0.41
1:A:205:G:C6	1:A:439:U:C5	3.08	0.41
1:A:1169:A:O5'	1:A:1169:A:H8	2.03	0.41
1:A:1601:G:OP1	4:D:56:ARG:NH2	2.53	0.41
1:A:2691:G:H2'	1:A:2692:A:C8	2.56	0.41
4:D:237:ILE:HD11	4:D:242:PRO:HA	2.03	0.41
13:O:30:GLY:HA2	13:O:107:SER:HB2	2.03	0.41
17:S:8:TYR:CZ	17:S:12:ARG:HD3	2.56	0.41
20:V:115:LEU:HD21	20:V:151:ILE:HG12	2.01	0.41
28:5:150:LEU:HA	28:5:151:PRO:HD3	1.87	0.41
1:A:139:U:O2	1:A:140:G:C8	2.74	0.41
1:A:856:U:O4	22:X:162:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1168:U:H4'	1:A:1169:A:O5'	2.21	0.41
1:A:1278:U:H2'	1:A:1279:C:C6	2.55	0.41
1:A:1875:G:H2'	1:A:1889:G:N2	2.36	0.41
8:H:145:LEU:HD21	8:H:188:ILE:HG23	2.03	0.41
9:I:55:GLU:HG3	9:I:56:ASP:N	2.36	0.41
11:M:110:PHE:HB3	11:M:113:ILE:HD12	2.02	0.41
14:P:35:THR:HG22	14:P:61:MET:HE1	2.02	0.41
1:A:145:A:N6	1:A:146:U:O4	2.54	0.41
1:A:185:U:H5'	23:Y:93:HIS:ND1	2.36	0.41
1:A:2446:G:OP2	1:A:2447:A:OP2	2.39	0.41
25:2:8:THR:HG21	25:2:16:ARG:HH12	1.86	0.41
1:A:184:A:H1'	23:Y:93:HIS:CE1	2.56	0.40
1:A:1530:G:N1	1:A:1536:A:H2	2.18	0.40
1:A:2660:G:H2'	1:A:2661:A:O4'	2.20	0.40
19:U:35:ARG:HB3	19:U:133:THR:HG23	2.02	0.40
1:A:79:G:C6	1:A:105:G:C6	3.09	0.40
1:A:618:A:H2'	1:A:619:A:C8	2.56	0.40
1:A:2047:A:O2'	1:A:2049:G:OP2	2.34	0.40
1:A:2543:G:C6	1:A:2544:C:C4	3.09	0.40
10:L:120:THR:HG23	10:L:160:LYS:HB3	2.02	0.40
1:A:2260:U:H2'	1:A:2261:U:C6	2.57	0.40
3:C:70:G:H2'	3:C:71:C:C6	2.56	0.40
1:A:2432:G:H2'	1:A:2433:C:H6	1.86	0.40
1:A:2559:A:H4'	1:A:2560:G:C8	2.56	0.40
1:A:2578:A:C2	1:A:2579:U:H1'	2.56	0.40
1:A:2661:A:H2'	1:A:2662:C:H5''	2.03	0.40
3:C:50:G:N2	3:C:67:G:O2'	2.55	0.40
6:F:58:LEU:HD21	6:F:169:VAL:HG23	2.03	0.40
9:I:80:PRO:HB3	23:Y:109:TRP:CE2	2.57	0.40
11:M:33:ALA:HB1	11:M:37:ASP:HB2	2.03	0.40
12:N:136:LEU:HD22	12:N:140:ILE:HD12	2.04	0.40
13:O:62:GLY:HA3	13:O:109:VAL:HG13	2.03	0.40
1:A:541:G:O2'	1:A:543:A:C8	2.66	0.40
1:A:1169:A:O5'	1:A:1169:A:C8	2.74	0.40
1:A:1337:U:H2'	1:A:1338:C:C6	2.57	0.40
2:B:28:C:OP1	15:Q:81:HIS:NE2	2.54	0.40
8:H:107:LEU:O	8:H:111:LEU:N	2.54	0.40
19:U:94:ASN:HB3	19:U:97:ASN:HD22	1.87	0.40
30:9:95:THR:HG23	30:9:217:ILE:HG22	2.04	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	
4	D	244/272 (90%)	200 (82%)	34 (14%)	10 (4%)	2	19
5	E	217/305 (71%)	191 (88%)	24 (11%)	2 (1%)	14	46
6	F	203/293 (69%)	170 (84%)	28 (14%)	5 (2%)	4	28
7	G	177/220 (80%)	160 (90%)	15 (8%)	2 (1%)	11	43
8	H	176/220 (80%)	152 (86%)	23 (13%)	1 (1%)	21	54
9	I	43/196 (22%)	33 (77%)	7 (16%)	3 (7%)	1	10
10	L	194/250 (78%)	171 (88%)	19 (10%)	4 (2%)	5	31
11	M	118/121 (98%)	101 (86%)	15 (13%)	2 (2%)	7	35
12	N	180/271 (66%)	142 (79%)	26 (14%)	12 (7%)	1	11
13	O	133/135 (98%)	120 (90%)	10 (8%)	3 (2%)	5	30
14	P	114/126 (90%)	102 (90%)	10 (9%)	2 (2%)	6	34
15	Q	116/166 (70%)	103 (89%)	11 (10%)	2 (2%)	7	35
16	R	112/233 (48%)	95 (85%)	16 (14%)	1 (1%)	14	46
17	S	114/128 (89%)	105 (92%)	7 (6%)	2 (2%)	6	34
18	T	132/256 (52%)	99 (75%)	23 (17%)	10 (8%)	1	9
19	U	150/199 (75%)	119 (79%)	29 (19%)	2 (1%)	9	39
20	V	89/198 (45%)	77 (86%)	9 (10%)	3 (3%)	3	23
21	W	127/191 (66%)	102 (80%)	20 (16%)	5 (4%)	2	20
22	X	106/194 (55%)	99 (93%)	5 (5%)	2 (2%)	6	33
23	Y	73/148 (49%)	64 (88%)	6 (8%)	3 (4%)	2	19
24	Z	92/168 (55%)	73 (79%)	14 (15%)	5 (5%)	1	14
25	2	40/57 (70%)	36 (90%)	3 (8%)	1 (2%)	4	28
26	3	58/66 (88%)	43 (74%)	9 (16%)	6 (10%)	0	5
27	4	59/152 (39%)	55 (93%)	2 (3%)	2 (3%)	3	23
28	5	68/159 (43%)	60 (88%)	8 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	6	35/37 (95%)	31 (89%)	3 (9%)	1 (3%)	3	26
30	9	103/271 (38%)	100 (97%)	3 (3%)	0	100	100
31	7	44/142 (31%)	39 (89%)	2 (4%)	3 (7%)	1	11
32	8	45/116 (39%)	32 (71%)	6 (13%)	7 (16%)	0	2
All	All	3362/5290 (64%)	2874 (86%)	387 (12%)	101 (3%)	5	25

All (101) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	118	VAL
4	D	201	LEU
4	D	253	ARG
4	D	257	LYS
12	N	201	LEU
12	N	216	ALA
12	N	236	PRO
12	N	243	LYS
14	P	111	LEU
18	T	118	PRO
18	T	175	PRO
18	T	176	ILE
19	U	163	LEU
20	V	113	GLN
21	W	171	PRO
24	Z	72	THR
26	3	24	ASN
26	3	25	LYS
27	4	139	CYS
31	7	131	TRP
32	8	73	LYS
32	8	88	GLU
4	D	229	GLY
5	E	119	GLU
7	G	89	ILE
7	G	92	PHE
9	I	44	LYS
9	I	64	GLY
10	L	82	ARG
10	L	182	GLY
12	N	109	SER
12	N	144	ARG

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Mol	Chain	Res	Type
12	N	175	GLU
12	N	185	GLY
14	P	68	GLY
16	R	188	ALA
17	S	7	GLY
17	S	72	ARG
18	T	117	PRO
18	T	178	THR
20	V	105	PRO
23	Y	134	LEU
24	Z	84	LYS
24	Z	95	SER
31	7	140	LYS
4	D	52	GLY
4	D	258	ARG
6	F	64	LYS
6	F	139	VAL
11	M	68	GLU
11	M	118	PRO
12	N	239	LYS
15	Q	115	PRO
18	T	120	ARG
21	W	49	LYS
21	W	67	ARG
21	W	174	TRP
22	X	129	GLY
24	Z	91	ARG
26	3	29	GLY
26	3	30	VAL
32	8	74	ARG
32	8	81	PRO
32	8	87	ALA
6	F	200	ASP
8	H	150	SER
9	I	57	ILE
10	L	243	ASP
12	N	173	GLY
13	O	6	ARG
13	O	59	ARG
23	Y	142	GLY
25	2	40	THR
5	E	193	GLU

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Mol	Chain	Res	Type
10	L	142	SER
12	N	150	MET
13	O	70	PRO
15	Q	81	HIS
18	T	233	SER
20	V	114	ILE
29	6	36	GLN
32	8	92	VAL
4	D	249	PRO
6	F	72	LEU
6	F	140	ILE
12	N	186	ILE
18	T	112	PRO
21	W	163	LYS
22	X	141	GLU
27	4	148	LYS
32	8	82	LEU
4	D	237	ILE
23	Y	113	GLY
26	3	26	GLY
19	U	162	GLY
24	Z	128	VAL
4	D	147	GLY
18	T	116	PRO
31	7	133	PRO
18	T	174	THR
26	3	64	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	194/217 (89%)	180 (93%)	14 (7%)	13	40
5	E	180/259 (70%)	167 (93%)	13 (7%)	13	40
6	F	171/254 (67%)	158 (92%)	13 (8%)	12	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	152/183 (83%)	146 (96%)	6 (4%)	28	54
8	H	150/190 (79%)	147 (98%)	3 (2%)	48	66
9	I	39/170 (23%)	38 (97%)	1 (3%)	40	62
10	L	142/213 (67%)	132 (93%)	10 (7%)	14	41
11	M	100/101 (99%)	93 (93%)	7 (7%)	14	41
12	N	139/215 (65%)	124 (89%)	15 (11%)	6	28
13	O	108/108 (100%)	97 (90%)	11 (10%)	7	30
14	P	96/103 (93%)	85 (88%)	11 (12%)	5	25
15	Q	97/139 (70%)	94 (97%)	3 (3%)	35	59
16	R	100/207 (48%)	88 (88%)	12 (12%)	5	24
17	S	103/115 (90%)	91 (88%)	12 (12%)	5	25
18	T	101/223 (45%)	88 (87%)	13 (13%)	4	22
19	U	119/176 (68%)	108 (91%)	11 (9%)	8	33
20	V	80/171 (47%)	75 (94%)	5 (6%)	16	44
21	W	111/171 (65%)	101 (91%)	10 (9%)	9	33
22	X	90/163 (55%)	89 (99%)	1 (1%)	65	74
23	Y	65/130 (50%)	61 (94%)	4 (6%)	16	44
24	Z	87/153 (57%)	82 (94%)	5 (6%)	18	46
25	2	35/50 (70%)	30 (86%)	5 (14%)	3	19
26	3	56/60 (93%)	55 (98%)	1 (2%)	51	68
27	4	50/125 (40%)	45 (90%)	5 (10%)	7	30
28	5	61/140 (44%)	60 (98%)	1 (2%)	55	69
29	6	34/34 (100%)	33 (97%)	1 (3%)	37	60
30	9	101/244 (41%)	101 (100%)	0	100	100
31	7	41/121 (34%)	38 (93%)	3 (7%)	13	40
32	8	41/96 (43%)	38 (93%)	3 (7%)	13	40
All	All	2843/4531 (63%)	2644 (93%)	199 (7%)	16	41

All (199) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	28	LEU
4	D	84	ASN

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Mol	Chain	Res	Type
4	D	97	LYS
4	D	121	LYS
4	D	140	ILE
4	D	163	LYS
4	D	200	ARG
4	D	213	ARG
4	D	241	SER
4	D	243	THR
4	D	259	ASN
4	D	262	SER
4	D	268	ARG
4	D	270	ARG
5	E	90	ILE
5	E	99	MET
5	E	113	THR
5	E	119	GLU
5	E	153	GLU
5	E	176	VAL
5	E	209	GLN
5	E	253	ARG
5	E	257	THR
5	E	275	VAL
5	E	278	ILE
5	E	282	VAL
5	E	292	LEU
6	F	63	GLU
6	F	65	VAL
6	F	67	GLU
6	F	71	ASN
6	F	81	ARG
6	F	92	LEU
6	F	93	GLN
6	F	97	ARG
6	F	118	GLN
6	F	161	LEU
6	F	206	LEU
6	F	216	VAL
6	F	230	THR
7	G	126	THR
7	G	155	GLU
7	G	159	GLU
7	G	174	THR

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Mol	Chain	Res	Type
7	G	177	THR
7	G	178	ASP
8	H	69	LEU
8	H	151	HIS
8	H	176	ARG
9	I	73	PHE
10	L	87	LEU
10	L	88	GLU
10	L	104	SER
10	L	121	ASP
10	L	160	LYS
10	L	166	LYS
10	L	175	ARG
10	L	184	LYS
10	L	205	ARG
10	L	238	ASP
11	M	5	GLN
11	M	23	ARG
11	M	61	VAL
11	M	68	GLU
11	M	105	GLU
11	M	108	GLN
11	M	114	VAL
12	N	79	ARG
12	N	82	LEU
12	N	96	LYS
12	N	117	GLN
12	N	125	ILE
12	N	134	MET
12	N	138	ARG
12	N	140	ILE
12	N	160	ILE
12	N	170	PHE
12	N	186	ILE
12	N	192	ARG
12	N	242	ILE
12	N	244	GLU
12	N	250	LEU
13	O	14	ARG
13	O	44	SER
13	O	52	ARG
13	O	71	ASP

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Mol	Chain	Res	Type
13	O	76	VAL
13	O	77	ARG
13	O	87	LYS
13	O	96	VAL
13	O	103	LEU
13	O	111	GLU
13	O	125	MET
14	P	11	MET
14	P	12	LYS
14	P	17	ILE
14	P	32	ARG
14	P	39	LEU
14	P	52	SER
14	P	75	GLN
14	P	81	TYR
14	P	100	ARG
14	P	109	ARG
14	P	114	ARG
15	Q	51	GLU
15	Q	90	THR
15	Q	102	GLN
16	R	126	LEU
16	R	144	ARG
16	R	151	ILE
16	R	152	ARG
16	R	187	ILE
16	R	193	GLU
16	R	194	ILE
16	R	195	VAL
16	R	222	LEU
16	R	225	LYS
16	R	226	LEU
16	R	230	SER
17	S	3	ARG
17	S	6	ARG
17	S	11	ARG
17	S	18	ARG
17	S	23	SER
17	S	56	ASP
17	S	59	ARG
17	S	83	HIS
17	S	90	LEU

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Mol	Chain	Res	Type
17	S	97	LEU
17	S	107	CYS
17	S	113	ASN
18	T	123	ILE
18	T	128	VAL
18	T	131	SER
18	T	132	ARG
18	T	133	GLN
18	T	136	VAL
18	T	151	THR
18	T	157	VAL
18	T	171	TYR
18	T	177	VAL
18	T	178	THR
18	T	207	ARG
18	T	213	ARG
19	U	31	GLU
19	U	35	ARG
19	U	37	TYR
19	U	50	ILE
19	U	54	ARG
19	U	68	MET
19	U	109	ILE
19	U	110	THR
19	U	122	SER
19	U	127	ARG
19	U	156	LYS
20	V	108	ILE
20	V	111	VAL
20	V	139	ASP
20	V	143	ASP
20	V	163	ASN
21	W	56	CYS
21	W	92	ILE
21	W	107	LYS
21	W	108	THR
21	W	121	GLN
21	W	126	GLU
21	W	132	SER
21	W	136	LEU
21	W	156	ARG
21	W	169	ASP

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Mol	Chain	Res	Type
22	X	112	ASP
23	Y	104	GLN
23	Y	108	VAL
23	Y	120	ARG
23	Y	121	LEU
24	Z	117	THR
24	Z	130	LYS
24	Z	136	LEU
24	Z	137	ASP
24	Z	145	VAL
25	2	5	LYS
25	2	9	SER
25	2	11	TYR
25	2	16	ARG
25	2	29	LEU
26	3	30	VAL
27	4	96	LEU
27	4	98	LEU
27	4	104	SER
27	4	141	LYS
27	4	143	ASN
28	5	155	VAL
29	6	7	VAL
31	7	140	LYS
31	7	141	ASN
31	7	142	VAL
32	8	50	ARG
32	8	54	LYS
32	8	82	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (57) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	84	ASN
4	D	102	HIS
4	D	149	GLN
5	E	167	HIS
5	E	209	GLN
5	E	301	ASN
6	F	93	GLN
6	F	215	ASN
6	F	241	ASN

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Mol	Chain	Res	Type
7	G	22	ASN
7	G	133	ASN
8	H	102	ASN
8	H	114	ASN
9	I	76	ASN
10	L	97	ASN
10	L	157	ASN
11	M	5	GLN
11	M	13	ASN
12	N	88	GLN
12	N	102	HIS
12	N	106	GLN
12	N	211	GLN
12	N	249	ASN
13	O	12	GLN
13	O	35	GLN
14	P	18	HIS
14	P	26	GLN
14	P	101	ASN
16	R	173	GLN
16	R	174	ASN
16	R	202	ASN
17	S	47	HIS
17	S	53	GLN
17	S	99	GLN
18	T	159	ASN
18	T	205	ASN
18	T	209	ASN
20	V	153	ASN
21	W	93	HIS
21	W	119	GLN
21	W	133	ASN
22	X	59	HIS
22	X	68	ASN
22	X	85	GLN
22	X	161	GLN
24	Z	73	ASN
24	Z	75	GLN
24	Z	99	ASN
26	3	24	ASN
26	3	58	HIS
26	3	61	HIS

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Mol	Chain	Res	Type
27	4	143	ASN
28	5	118	GLN
28	5	145	ASN
30	9	216	ASN
31	7	102	GLN
31	7	141	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2745/2811 (97%)	837 (30%)	128 (4%)
2	B	119/121 (98%)	29 (24%)	3 (2%)
3	C	92/103 (89%)	28 (30%)	2 (2%)
All	All	2956/3035 (97%)	894 (30%)	133 (4%)

All (894) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	U
1	A	4	A
1	A	8	G
1	A	9	A
1	A	10	G
1	A	13	A
1	A	14	A
1	A	33	A
1	A	34	G
1	A	35	G
1	A	42	G
1	A	45	A
1	A	46	C
1	A	48	A
1	A	50	G
1	A	51	A
1	A	55	G
1	A	61	U
1	A	70	A
1	A	73	U
1	A	74	G
1	A	82	G
1	A	83	A

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Mol	Chain	Res	Type
1	A	84	G
1	A	90	A
1	A	94	A
1	A	97	A
1	A	98	G
1	A	99	A
1	A	100	G
1	A	102	U
1	A	110	U
1	A	116	A
1	A	118	U
1	A	128	U
1	A	133	A
1	A	134	A
1	A	136	U
1	A	137	U
1	A	139	U
1	A	140	G
1	A	144	A
1	A	146	U
1	A	147	C
1	A	150	U
1	A	157	G
1	A	158	C
1	A	159	A
1	A	160	A
1	A	181	A
1	A	184	A
1	A	189	A
1	A	200	G
1	A	201	A
1	A	203	A
1	A	206	A
1	A	207	A
1	A	212	A
1	A	213	A
1	A	219	U
1	A	224	G
1	A	227	G
1	A	228	U
1	A	230	G
1	A	233	G

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Mol	Chain	Res	Type
1	A	234	C
1	A	236	A
1	A	237	G
1	A	240	A
1	A	250	A
1	A	251	G
1	A	252	C
1	A	255	A
1	A	256	A
1	A	257	A
1	A	259	C
1	A	260	G
1	A	261	U
1	A	262	G
1	A	264	A
1	A	265	A
1	A	266	A
1	A	267	C
1	A	268	G
1	A	270	G
1	A	271	G
1	A	273	U
1	A	274	G
1	A	275	U
1	A	276	G
1	A	277	G
1	A	278	G
1	A	280	G
1	A	282	G
1	A	299	C
1	A	304	A
1	A	313	A
1	A	314	G
1	A	316	G
1	A	317	G
1	A	318	A
1	A	319	G
1	A	320	U
1	A	321	G
1	A	322	C
1	A	331	A
1	A	332	G

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Mol	Chain	Res	Type
1	A	333	A
1	A	334	U
1	A	336	G
1	A	338	G
1	A	339	A
1	A	340	A
1	A	341	A
1	A	343	U
1	A	344	C
1	A	347	G
1	A	351	C
1	A	358	C
1	A	374	U
1	A	375	C
1	A	376	U
1	A	377	G
1	A	378	A
1	A	379	C
1	A	380	C
1	A	381	C
1	A	382	G
1	A	383	A
1	A	384	G
1	A	385	U
1	A	398	G
1	A	399	U
1	A	403	A
1	A	407	C
1	A	415	U
1	A	416	C
1	A	417	A
1	A	418	G
1	A	423	G
1	A	424	A
1	A	432	G
1	A	433	C
1	A	436	G
1	A	440	A
1	A	448	C
1	A	452	G
1	A	467	G
1	A	468	U

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Mol	Chain	Res	Type
1	A	469	A
1	A	485	G
1	A	486	G
1	A	487	U
1	A	491	A
1	A	492	A
1	A	493	G
1	A	496	C
1	A	502	U
1	A	514	A
1	A	515	U
1	A	516	A
1	A	517	G
1	A	519	A
1	A	520	C
1	A	521	A
1	A	536	C
1	A	539	A
1	A	540	A
1	A	541	G
1	A	542	C
1	A	543	A
1	A	544	G
1	A	553	G
1	A	554	G
1	A	556	C
1	A	557	C
1	A	558	A
1	A	560	A
1	A	568	C
1	A	573	G
1	A	574	C
1	A	581	A
1	A	582	A
1	A	583	G
1	A	584	A
1	A	585	A
1	A	593	G
1	A	597	C
1	A	598	U
1	A	613	U
1	A	614	G

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Mol	Chain	Res	Type
1	A	622	G
1	A	623	A
1	A	624	A
1	A	628	A
1	A	633	A
1	A	634	G
1	A	639	A
1	A	646	G
1	A	649	A
1	A	654	U
1	A	655	C
1	A	656	A
1	A	657	U
1	A	658	A
1	A	659	G
1	A	667	G
1	A	670	A
1	A	673	G
1	A	680	G
1	A	681	A
1	A	688	C
1	A	697	U
1	A	698	C
1	A	706	G
1	A	722	G
1	A	731	U
1	A	732	A
1	A	734	G
1	A	741	U
1	A	749	G
1	A	759	G
1	A	763	A
1	A	764	A
1	A	768	G
1	A	775	A
1	A	785	A
1	A	786	G
1	A	787	G
1	A	788	G
1	A	793	A
1	A	795	U
1	A	796	G

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Mol	Chain	Res	Type
1	A	800	C
1	A	801	U
1	A	802	C
1	A	803	G
1	A	804	A
1	A	810	G
1	A	811	A
1	A	813	C
1	A	814	U
1	A	816	G
1	A	817	C
1	A	823	C
1	A	830	A
1	A	838	U
1	A	839	G
1	A	841	G
1	A	855	C
1	A	856	U
1	A	857	G
1	A	866	G
1	A	869	G
1	A	870	U
1	A	871	A
1	A	884	G
1	A	887	G
1	A	888	C
1	A	890	G
1	A	891	G
1	A	893	C
1	A	896	G
1	A	897	A
1	A	898	G
1	A	901	C
1	A	903	G
1	A	905	A
1	A	906	C
1	A	907	C
1	A	908	A
1	A	916	G
1	A	919	A
1	A	923	C
1	A	924	U

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Mol	Chain	Res	Type
1	A	937	U
1	A	938	G
1	A	939	A
1	A	940	C
1	A	956	G
1	A	969	A
1	A	974	G
1	A	981	G
1	A	985	A
1	A	986	U
1	A	987	A
1	A	989	G
1	A	995	U
1	A	996	C
1	A	997	G
1	A	1002	G
1	A	1003	A
1	A	1007	A
1	A	1009	A
1	A	1011	A
1	A	1012	G
1	A	1013	C
1	A	1017	G
1	A	1018	A
1	A	1023	C
1	A	1024	A
1	A	1027	U
1	A	1036	U
1	A	1040	U
1	A	1041	G
1	A	1048	C
1	A	1049	A
1	A	1050	G
1	A	1051	U
1	A	1053	A
1	A	1055	A
1	A	1060	A
1	A	1061	G
1	A	1062	G
1	A	1070	G
1	A	1074	A
1	A	1081	C

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Mol	Chain	Res	Type
1	A	1082	A
1	A	1085	A
1	A	1086	G
1	A	1088	U
1	A	1089	U
1	A	1090	U
1	A	1093	C
1	A	1094	U
1	A	1096	G
1	A	1097	A
1	A	1098	A
1	A	1099	G
1	A	1100	C
1	A	1103	C
1	A	1104	C
1	A	1107	C
1	A	1112	A
1	A	1115	G
1	A	1116	A
1	A	1119	G
1	A	1120	C
1	A	1125	U
1	A	1132	C
1	A	1134	G
1	A	1137	C
1	A	1139	A
1	A	1140	G
1	A	1141	C
1	A	1142	G
1	A	1143	C
1	A	1147	U
1	A	1158	U
1	A	1159	G
1	A	1160	A
1	A	1161	A
1	A	1162	C
1	A	1166	G
1	A	1169	A
1	A	1170	A
1	A	1177	U
1	A	1182	A
1	A	1189	G

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Mol	Chain	Res	Type
1	A	1194	G
1	A	1195	U
1	A	1196	A
1	A	1199	A
1	A	1200	A
1	A	1202	A
1	A	1203	C
1	A	1218	G
1	A	1227	U
1	A	1229	G
1	A	1232	A
1	A	1233	G
1	A	1236	A
1	A	1240	G
1	A	1241	U
1	A	1242	G
1	A	1243	C
1	A	1251	G
1	A	1253	G
1	A	1254	U
1	A	1258	A
1	A	1259	C
1	A	1260	G
1	A	1261	A
1	A	1262	A
1	A	1265	G
1	A	1268	A
1	A	1269	G
1	A	1270	C
1	A	1272	A
1	A	1273	G
1	A	1274	A
1	A	1277	G
1	A	1281	G
1	A	1283	U
1	A	1289	A
1	A	1292	G
1	A	1293	C
1	A	1294	A
1	A	1295	A
1	A	1296	A
1	A	1310	C

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Mol	Chain	Res	Type
1	A	1315	G
1	A	1321	A
1	A	1322	A
1	A	1327	U
1	A	1332	G
1	A	1333	U
1	A	1339	C
1	A	1342	A
1	A	1346	U
1	A	1351	C
1	A	1359	G
1	A	1362	G
1	A	1366	C
1	A	1368	G
1	A	1371	C
1	A	1373	U
1	A	1385	G
1	A	1386	A
1	A	1389	G
1	A	1395	G
1	A	1399	A
1	A	1400	U
1	A	1402	G
1	A	1404	C
1	A	1405	A
1	A	1411	U
1	A	1412	G
1	A	1416	A
1	A	1417	U
1	A	1418	U
1	A	1426	U
1	A	1429	C
1	A	1432	U
1	A	1434	G
1	A	1436	U
1	A	1437	G
1	A	1438	G
1	A	1439	U
1	A	1440	C
1	A	1441	C
1	A	1443	G
1	A	1445	G

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Mol	Chain	Res	Type
1	A	1449	C
1	A	1472	A
1	A	1473	G
1	A	1474	A
1	A	1475	U
1	A	1476	G
1	A	1478	U
1	A	1479	U
1	A	1480	A
1	A	1494	G
1	A	1495	C
1	A	1496	A
1	A	1497	A
1	A	1498	G
1	A	1500	U
1	A	1501	G
1	A	1524	G
1	A	1527	G
1	A	1528	U
1	A	1529	A
1	A	1530	G
1	A	1531	A
1	A	1532	G
1	A	1533	A
1	A	1534	A
1	A	1535	A
1	A	1536	A
1	A	1537	U
1	A	1540	C
1	A	1542	C
1	A	1543	G
1	A	1544	A
1	A	1545	G
1	A	1549	A
1	A	1550	U
1	A	1558	U
1	A	1559	A
1	A	1567	C
1	A	1568	U
1	A	1569	A
1	A	1570	C
1	A	1572	G

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Mol	Chain	Res	Type
1	A	1573	C
1	A	1574	G
1	A	1580	G
1	A	1589	G
1	A	1591	C
1	A	1592	A
1	A	1593	U
1	A	1594	A
1	A	1595	C
1	A	1600	A
1	A	1603	A
1	A	1610	C
1	A	1611	G
1	A	1612	A
1	A	1615	G
1	A	1616	A
1	A	1617	C
1	A	1618	C
1	A	1619	U
1	A	1620	U
1	A	1621	C
1	A	1622	A
1	A	1623	A
1	A	1624	C
1	A	1628	A
1	A	1630	G
1	A	1634	C
1	A	1643	G
1	A	1644	A
1	A	1645	A
1	A	1647	C
1	A	1653	C
1	A	1662	A
1	A	1663	G
1	A	1682	C
1	A	1683	G
1	A	1684	C
1	A	1687	G
1	A	1690	A
1	A	1696	C
1	A	1698	C
1	A	1710	G

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Mol	Chain	Res	Type
1	A	1713	A
1	A	1730	C
1	A	1731	G
1	A	1734	A
1	A	1736	A
1	A	1742	U
1	A	1748	C
1	A	1749	U
1	A	1750	C
1	A	1751	A
1	A	1752	C
1	A	1753	A
1	A	1754	A
1	A	1755	A
1	A	1756	G
1	A	1759	G
1	A	1760	G
1	A	1767	U
1	A	1768	G
1	A	1774	G
1	A	1783	A
1	A	1786	G
1	A	1790	A
1	A	1791	C
1	A	1792	C
1	A	1796	A
1	A	1801	A
1	A	1810	C
1	A	1811	A
1	A	1812	A
1	A	1821	G
1	A	1822	A
1	A	1825	A
1	A	1826	U
1	A	1828	U
1	A	1830	U
1	A	1843	C
1	A	1866	G
1	A	1867	A
1	A	1870	U
1	A	1876	A
1	A	1881	A

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Mol	Chain	Res	Type
1	A	1882	U
1	A	1883	G
1	A	1884	A
1	A	1885	C
1	A	1886	A
1	A	1888	G
1	A	1898	G
1	A	1899	A
1	A	1910	G
1	A	1912	U
1	A	1914	A
1	A	1915	A
1	A	1919	C
1	A	1920	G
1	A	1921	G
1	A	1924	G
1	A	1935	G
1	A	1939	C
1	A	1943	G
1	A	1944	G
1	A	1945	U
1	A	1950	A
1	A	1951	A
1	A	1952	A
1	A	1953	U
1	A	1954	U
1	A	1955	C
1	A	1965	U
1	A	1969	U
1	A	1975	C
1	A	1979	C
1	A	1981	C
1	A	1984	A
1	A	1985	A
1	A	1986	G
1	A	1999	G
1	A	2001	G
1	A	2005	U
1	A	2007	U
1	A	2018	G
1	A	2026	G
1	A	2034	C

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Mol	Chain	Res	Type
1	A	2036	U
1	A	2037	G
1	A	2045	A
1	A	2046	G
1	A	2047	A
1	A	2053	A
1	A	2056	A
1	A	2057	C
1	A	2065	U
1	A	2066	G
1	A	2069	C
1	A	2070	A
1	A	2074	A
1	A	2075	G
1	A	2076	A
1	A	2080	U
1	A	2083	G
1	A	2086	G
1	A	2094	G
1	A	2101	G
1	A	2107	G
1	A	2109	C
1	A	2110	U
1	A	2111	U
1	A	2112	U
1	A	2113	G
1	A	2114	G
1	A	2118	U
1	A	2124	G
1	A	2125	C
1	A	2126	G
1	A	2127	C
1	A	2129	G
1	A	2130	C
1	A	2132	U
1	A	2133	A
1	A	2136	U
1	A	2141	G
1	A	2143	C
1	A	2145	A
1	A	2146	A
1	A	2147	G

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Mol	Chain	Res	Type
1	A	2148	A
1	A	2153	C
1	A	2154	C
1	A	2159	C
1	A	2161	G
1	A	2169	C
1	A	2171	G
1	A	2176	A
1	A	2178	C
1	A	2181	U
1	A	2184	G
1	A	2185	A
1	A	2186	U
1	A	2187	A
1	A	2188	C
1	A	2193	C
1	A	2197	A
1	A	2203	U
1	A	2206	A
1	A	2212	A
1	A	2216	U
1	A	2217	U
1	A	2219	U
1	A	2220	G
1	A	2221	U
1	A	2223	A
1	A	2224	G
1	A	2225	G
1	A	2226	A
1	A	2227	C
1	A	2228	C
1	A	2229	U
1	A	2230	A
1	A	2242	A
1	A	2252	G
1	A	2254	A
1	A	2255	G
1	A	2256	A
1	A	2260	U
1	A	2267	G
1	A	2269	G
1	A	2272	G

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Mol	Chain	Res	Type
1	A	2285	A
1	A	2296	G
1	A	2300	U
1	A	2303	A
1	A	2304	A
1	A	2314	C
1	A	2315	G
1	A	2322	A
1	A	2326	A
1	A	2328	A
1	A	2329	U
1	A	2335	C
1	A	2336	U
1	A	2337	C
1	A	2339	A
1	A	2342	G
1	A	2343	C
1	A	2344	A
1	A	2348	G
1	A	2350	A
1	A	2351	G
1	A	2352	A
1	A	2356	G
1	A	2362	G
1	A	2367	C
1	A	2374	C
1	A	2378	C
1	A	2389	G
1	A	2399	G
1	A	2400	G
1	A	2401	C
1	A	2402	C
1	A	2409	A
1	A	2419	G
1	A	2423	A
1	A	2424	G
1	A	2436	U
1	A	2439	C
1	A	2440	U
1	A	2441	C
1	A	2442	A
1	A	2446	G

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Mol	Chain	Res	Type
1	A	2447	A
1	A	2452	A
1	A	2458	U
1	A	2462	G
1	A	2464	G
1	A	2465	A
1	A	2466	U
1	A	2467	A
1	A	2475	G
1	A	2476	A
1	A	2481	C
1	A	2490	U
1	A	2491	U
1	A	2492	C
1	A	2493	A
1	A	2495	A
1	A	2501	G
1	A	2511	G
1	A	2516	C
1	A	2517	U
1	A	2519	G
1	A	2520	A
1	A	2522	G
1	A	2523	U
1	A	2534	C
1	A	2535	C
1	A	2546	G
1	A	2552	U
1	A	2564	U
1	A	2571	U
1	A	2579	U
1	A	2583	A
1	A	2584	G
1	A	2589	A
1	A	2590	C
1	A	2591	G
1	A	2595	G
1	A	2602	U
1	A	2603	C
1	A	2607	A
1	A	2619	A
1	A	2620	G

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Mol	Chain	Res	Type
1	A	2622	U
1	A	2625	G
1	A	2626	U
1	A	2627	C
1	A	2628	C
1	A	2629	A
1	A	2630	U
1	A	2631	A
1	A	2646	U
1	A	2647	A
1	A	2649	A
1	A	2653	U
1	A	2654	U
1	A	2659	G
1	A	2662	C
1	A	2663	C
1	A	2664	U
1	A	2666	U
1	A	2672	G
1	A	2673	U
1	A	2678	G
1	A	2685	G
1	A	2696	A
1	A	2699	U
1	A	2702	G
1	A	2706	U
1	A	2707	A
1	A	2708	C
1	A	2724	C
1	A	2729	A
1	A	2730	A
1	A	2731	C
1	A	2732	G
1	A	2740	G
1	A	2742	C
1	A	2743	A
1	A	2747	G
1	A	2750	G
1	A	2751	A
1	A	2752	G
1	A	2753	C
1	A	2754	G

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Mol	Chain	Res	Type
1	A	2762	G
1	A	2766	A
1	A	2771	A
1	A	2775	A
1	A	2776	A
1	A	2782	A
1	A	2783	A
1	A	2784	G
1	A	2787	C
1	A	2796	A
1	A	2797	U
1	A	2798	G
1	A	2808	C
1	A	2809	U
1	A	2810	A
1	A	2811	U
2	B	4	U
2	B	5	C
2	B	7	G
2	B	11	U
2	B	12	C
2	B	13	C
2	B	14	U
2	B	16	G
2	B	31	C
2	B	32	A
2	B	36	A
2	B	45	G
2	B	46	A
2	B	54	G
2	B	55	G
2	B	57	U
2	B	64	U
2	B	65	A
2	B	67	U
2	B	68	G
2	B	87	G
2	B	89	A
2	B	90	G
2	B	91	G
2	B	92	U
2	B	109	U

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Mol	Chain	Res	Type
2	B	110	C
2	B	111	G
2	B	120	A
3	C	2	A
3	C	7	C
3	C	13	G
3	C	14	A
3	C	16	A
3	C	25	U
3	C	37	U
3	C	61	A
3	C	62	U
3	C	67	G
3	C	68	C
3	C	69	A
3	C	74	A
3	C	78	A
3	C	80	C
3	C	81	C
3	C	85	C
3	C	87	G
3	C	88	A
3	C	91	C
3	C	92	A
3	C	93	C
3	C	94	A
3	C	95	G
3	C	96	A
3	C	99	U
3	C	101	A
3	C	103	C

All (133) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	45	A
1	A	50	G
1	A	73	U
1	A	98	G
1	A	133	A
1	A	143	G

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Mol	Chain	Res	Type
1	A	190	G
1	A	212	A
1	A	227	G
1	A	234	C
1	A	255	A
1	A	261	U
1	A	262	G
1	A	263	A
1	A	265	A
1	A	274	G
1	A	313	A
1	A	316	G
1	A	317	G
1	A	332	G
1	A	373	C
1	A	374	U
1	A	379	C
1	A	384	G
1	A	415	U
1	A	416	C
1	A	458	G
1	A	459	A
1	A	486	G
1	A	491	A
1	A	514	A
1	A	539	A
1	A	543	A
1	A	553	G
1	A	581	A
1	A	597	C
1	A	613	U
1	A	627	C
1	A	654	U
1	A	656	A
1	A	666	U
1	A	757	U
1	A	763	A
1	A	775	A
1	A	785	A
1	A	787	G
1	A	800	C
1	A	838	U

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Mol	Chain	Res	Type
1	A	856	U
1	A	868	G
1	A	869	G
1	A	896	G
1	A	985	A
1	A	1012	G
1	A	1039	A
1	A	1048	C
1	A	1050	G
1	A	1098	A
1	A	1139	A
1	A	1158	U
1	A	1169	A
1	A	1194	G
1	A	1198	A
1	A	1228	A
1	A	1241	U
1	A	1242	G
1	A	1257	G
1	A	1272	A
1	A	1332	G
1	A	1399	A
1	A	1411	U
1	A	1417	U
1	A	1437	G
1	A	1439	U
1	A	1448	A
1	A	1471	A
1	A	1472	A
1	A	1474	A
1	A	1480	A
1	A	1493	C
1	A	1495	C
1	A	1496	A
1	A	1529	A
1	A	1534	A
1	A	1536	A
1	A	1543	G
1	A	1569	A
1	A	1600	A
1	A	1617	C
1	A	1644	A

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Mol	Chain	Res	Type
1	A	1662	A
1	A	1754	A
1	A	1755	A
1	A	1778	G
1	A	1796	A
1	A	1825	A
1	A	1882	U
1	A	1885	C
1	A	1898	G
1	A	1914	A
1	A	1944	G
1	A	1950	A
1	A	1953	U
1	A	1954	U
1	A	2106	U
1	A	2111	U
1	A	2113	G
1	A	2216	U
1	A	2219	U
1	A	2229	U
1	A	2254	A
1	A	2299	G
1	A	2303	A
1	A	2343	C
1	A	2408	G
1	A	2439	C
1	A	2465	A
1	A	2475	G
1	A	2534	C
1	A	2583	A
1	A	2626	U
1	A	2628	C
1	A	2646	U
1	A	2662	C
1	A	2672	G
1	A	2698	C
1	A	2774	U
2	B	45	G
2	B	67	U
2	B	89	A
3	C	1	G
3	C	80	C

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
19	U	1
18	T	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U	158:ILE	C	159:ALA	N	1.84
1	T	118:PRO	C	119:PRO	N	1.71
1	A	1554:C	O3'	1555:G	P	1.33

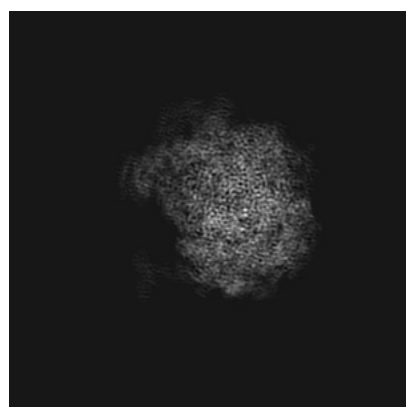
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3525. These allow visual inspection of the internal detail of the map and identification of artifacts.

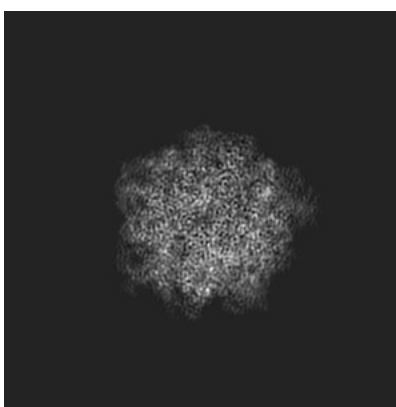
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

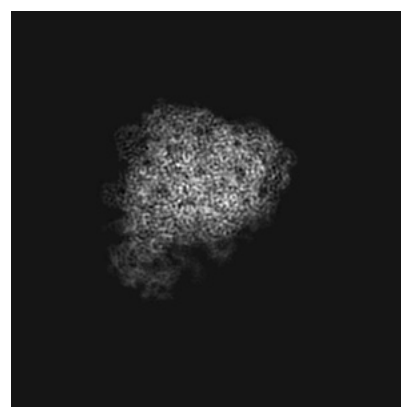
6.1.1 Primary map



X



Y

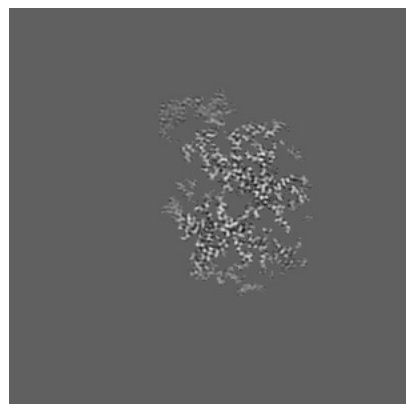


Z

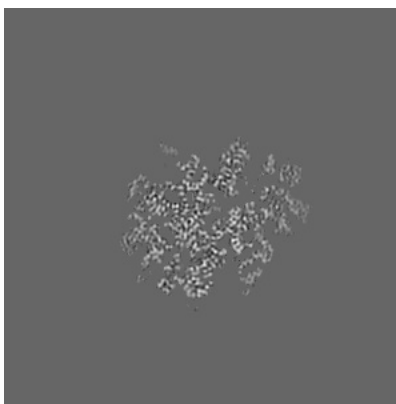
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 184



Y Index: 184

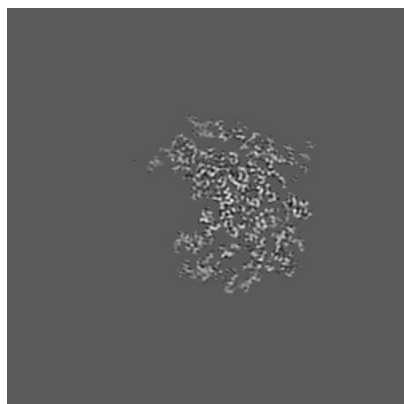


Z Index: 184

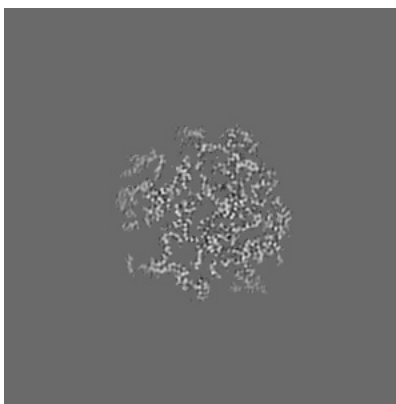
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 163



Y Index: 214

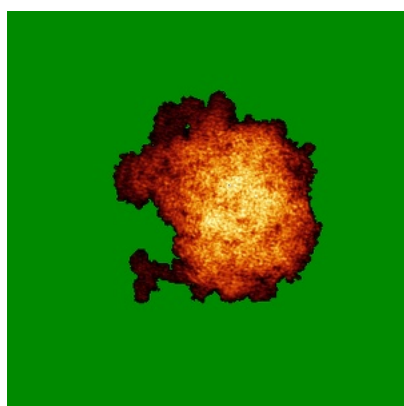


Z Index: 184

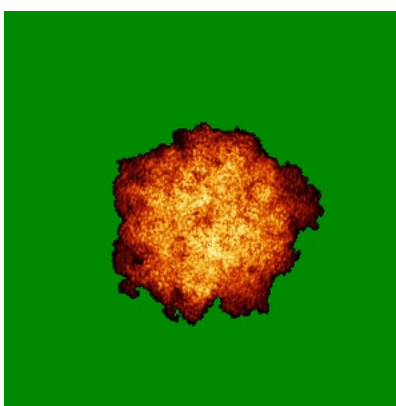
The images above show the largest variance slices of the map in three orthogonal directions.

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

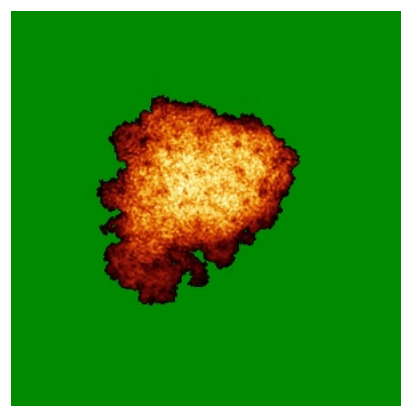
6.4.1 Primary map



X



Y

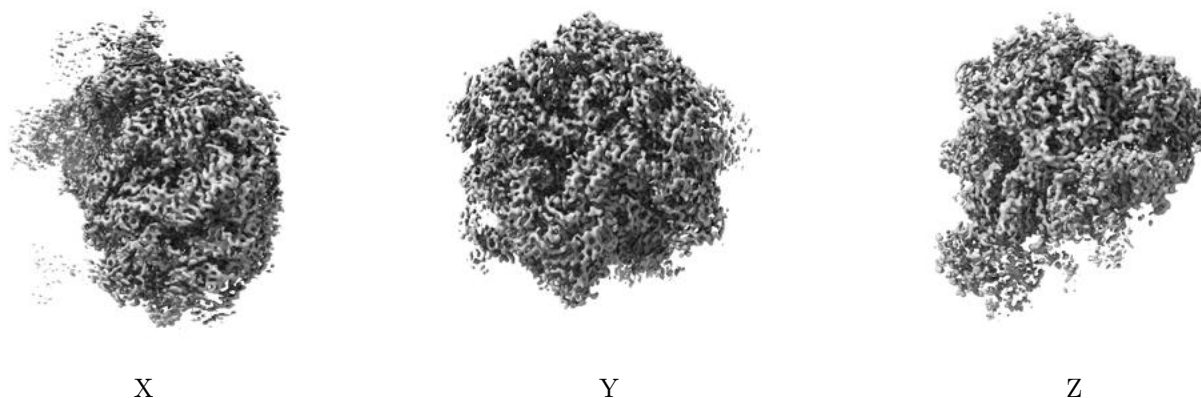


Z

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 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

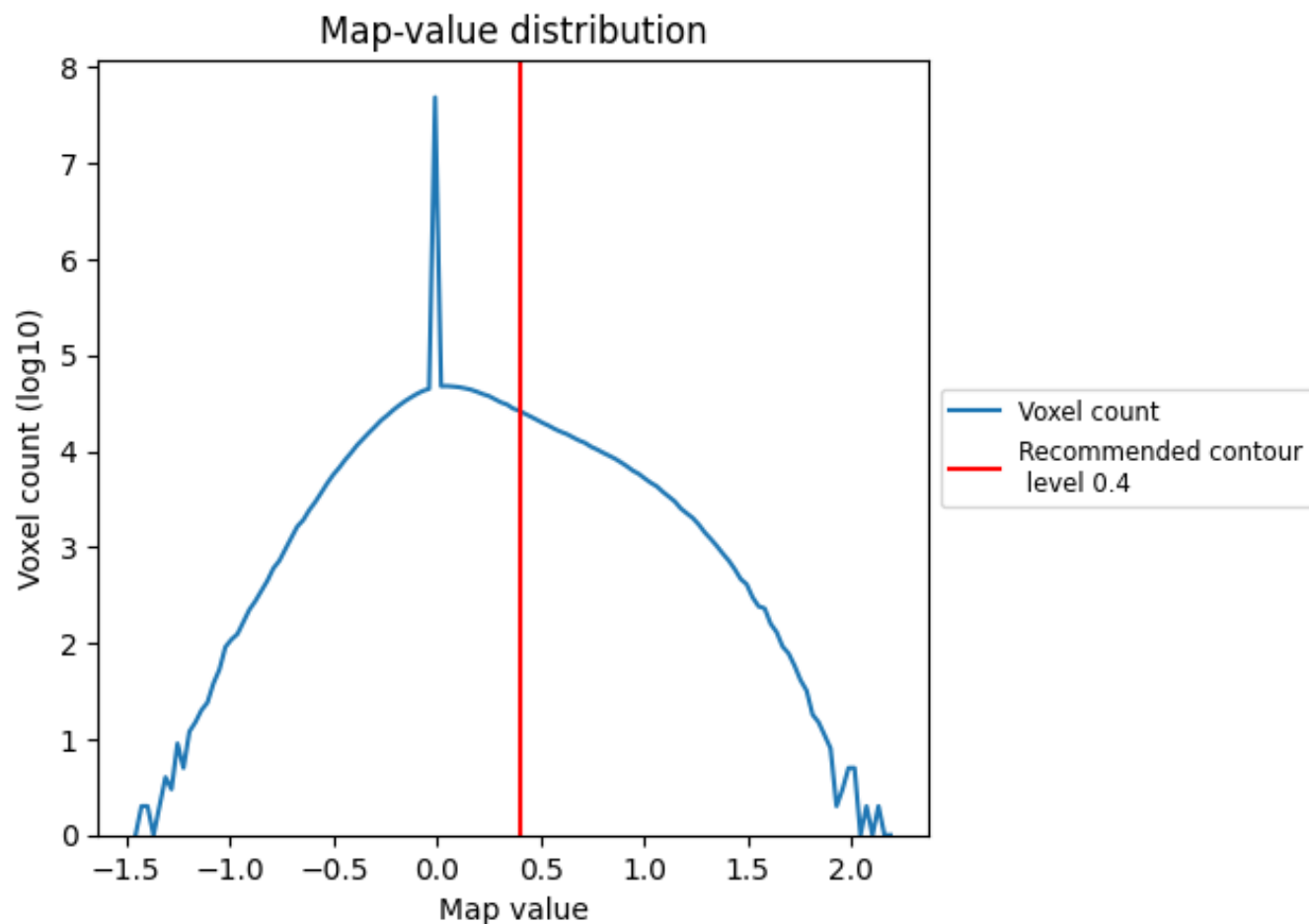
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

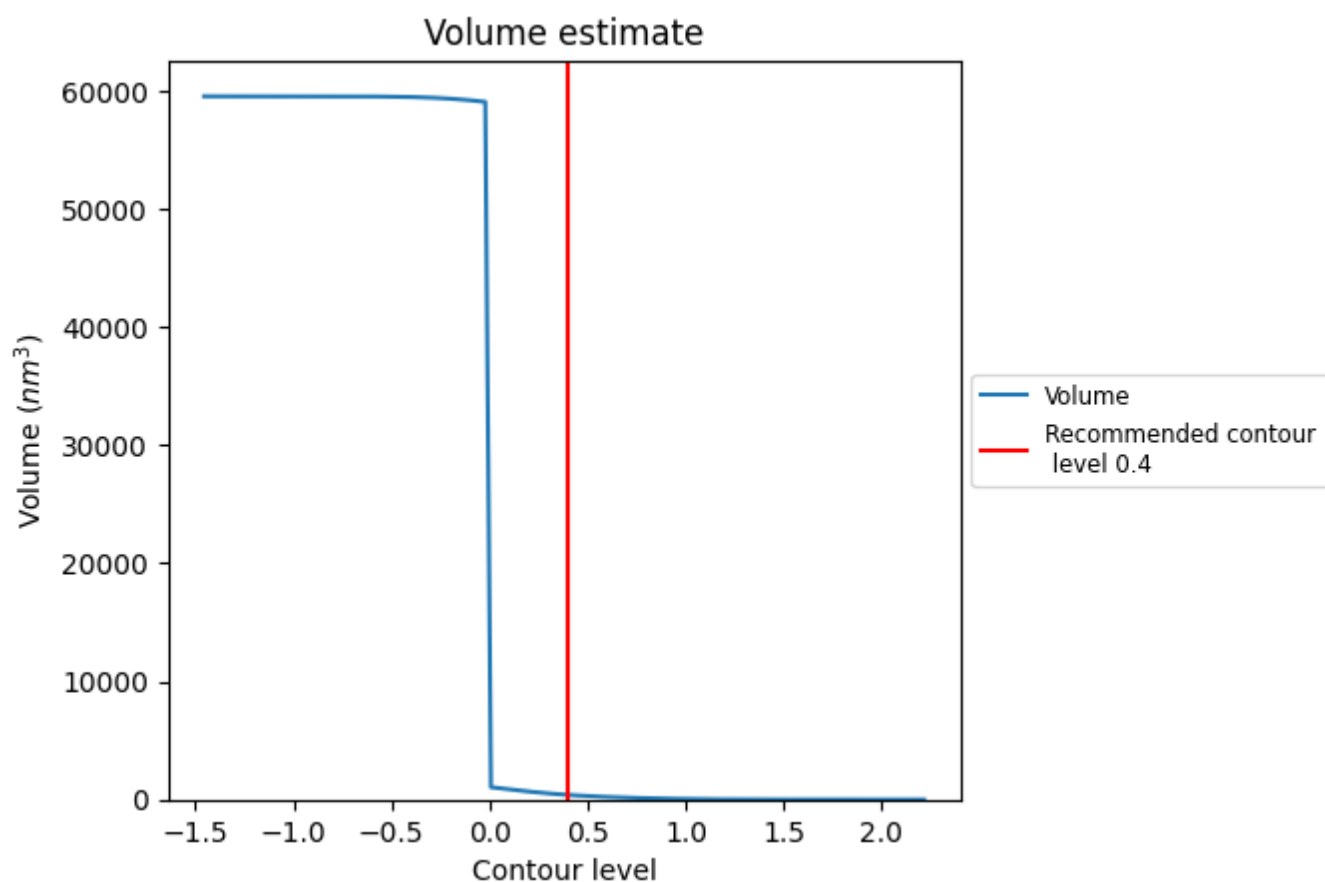
This section contains the results of statistical analysis of the map.

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.

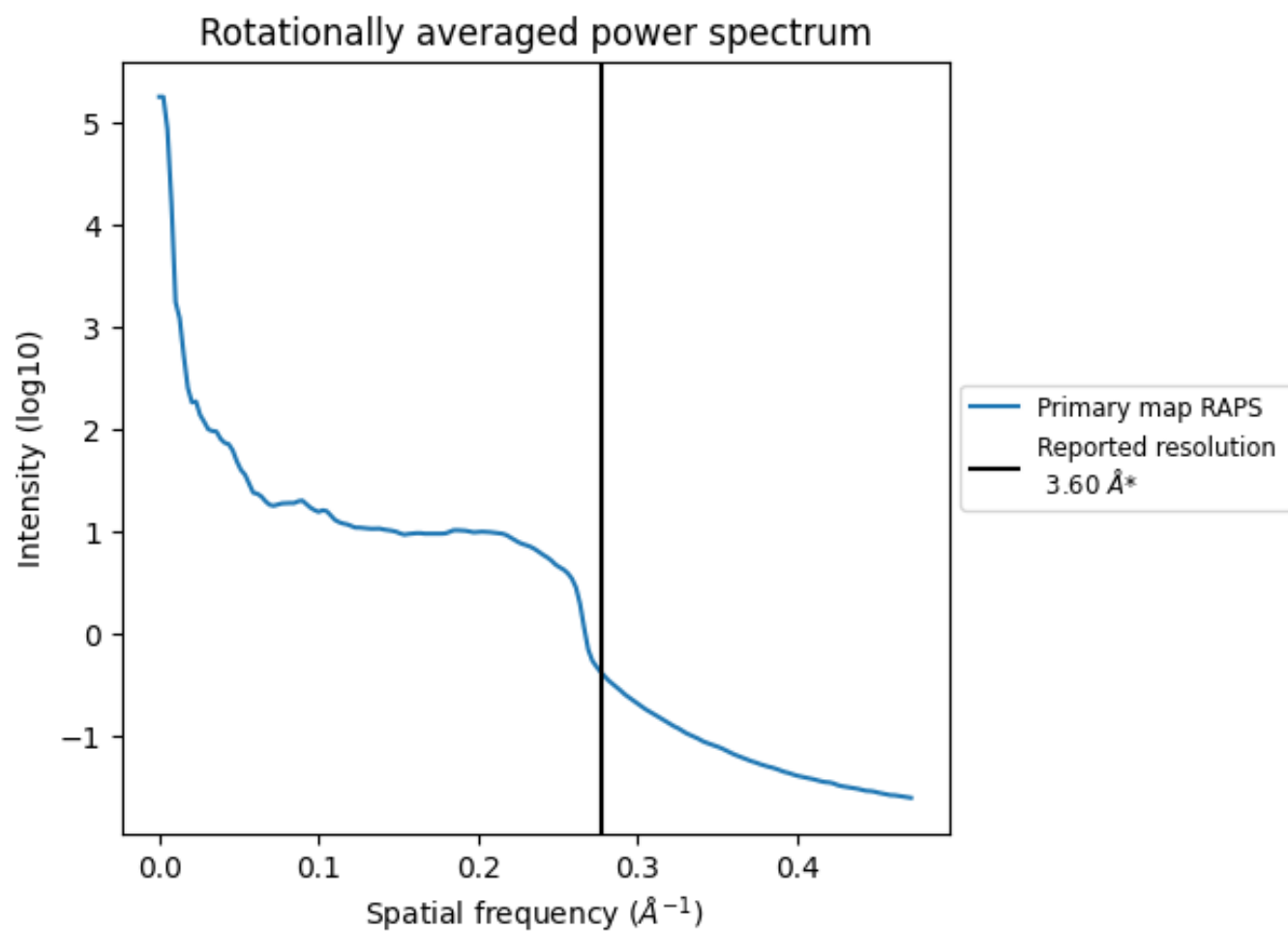
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 396 nm^3 ; this corresponds to an approximate mass of 358 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 0.278 Å⁻¹

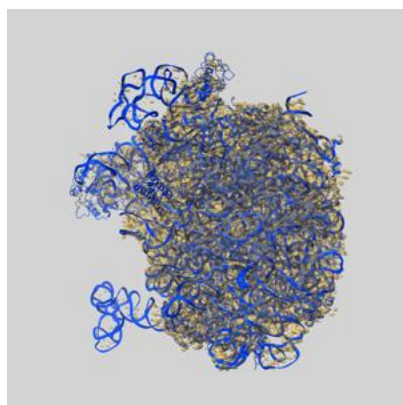
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

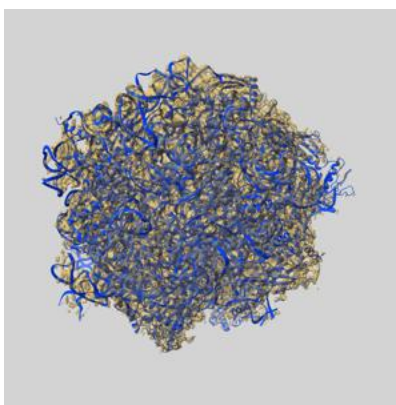
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3525 and PDB model 5MLC. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

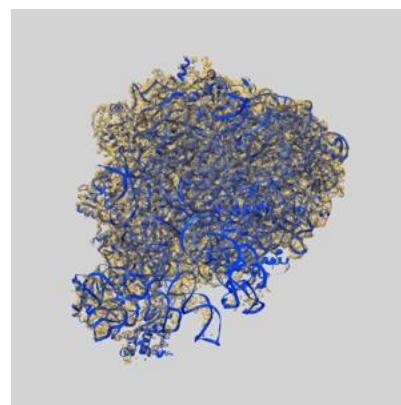
9.1 Map-model overlay [i](#)



X



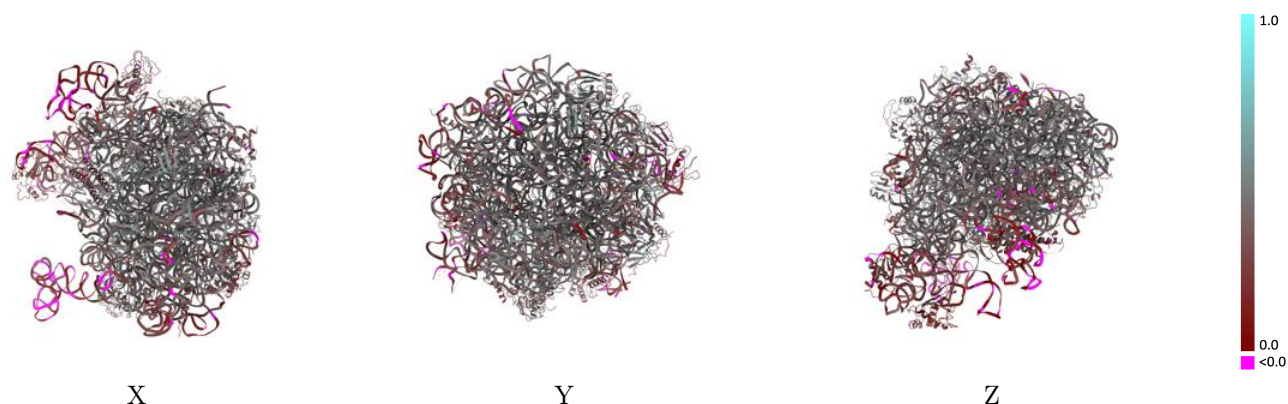
Y



Z

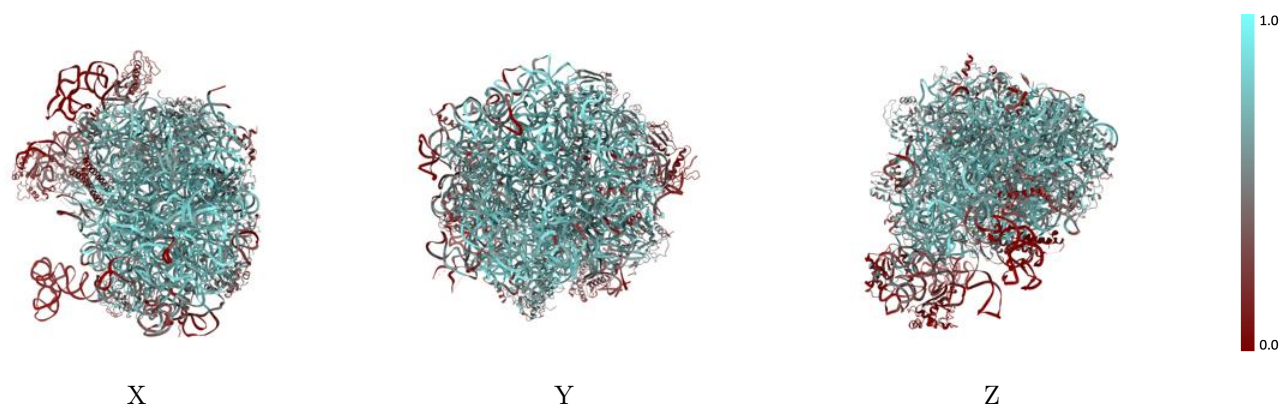
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



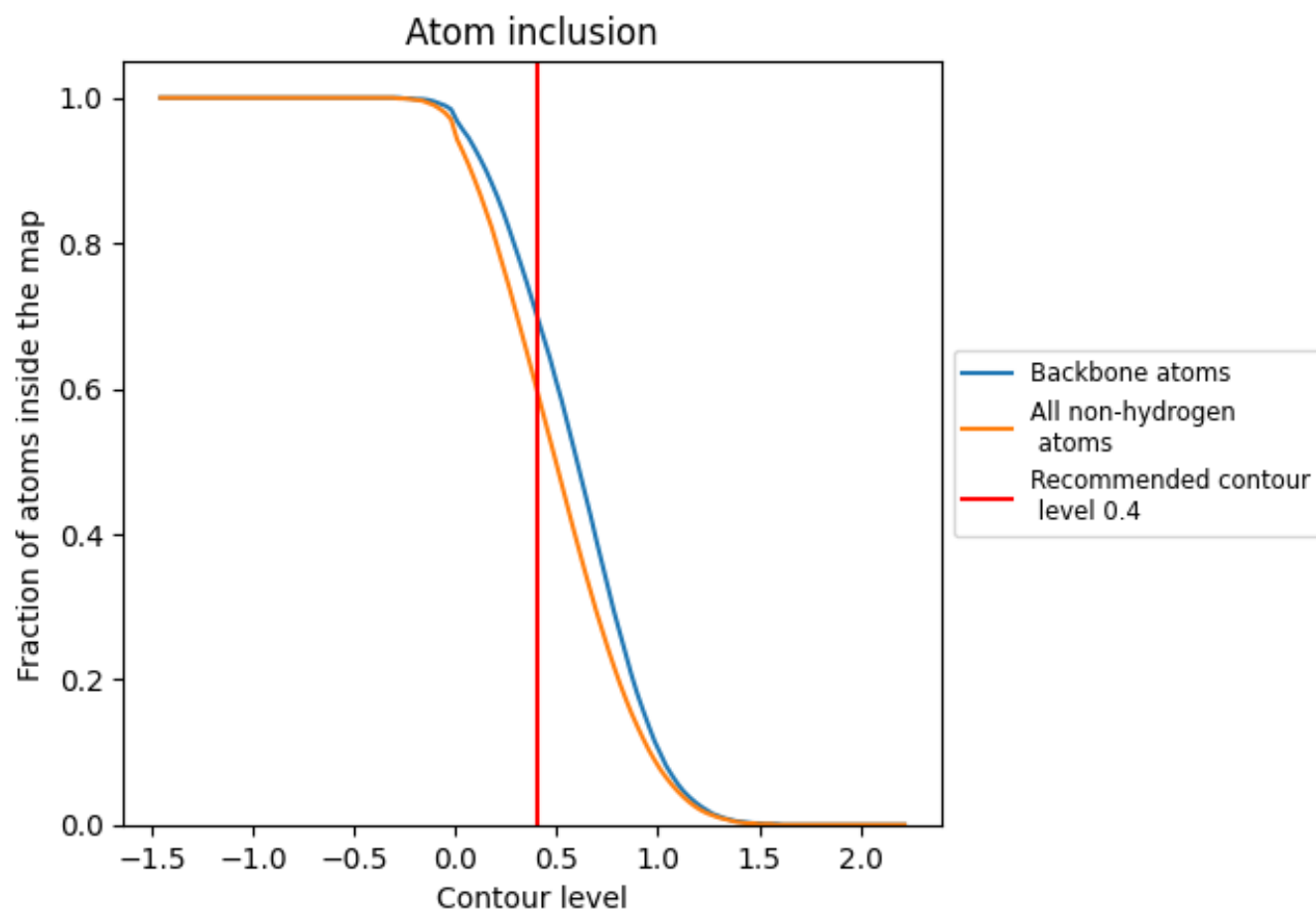
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 60% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6010	 0.3900
2	 0.5620	 0.3790
3	 0.5170	 0.4100
4	 0.6640	 0.4670
5	 0.6570	 0.4830
6	 0.5050	 0.4420
7	 0.4820	 0.3950
8	 0.5620	 0.4360
9	 0.1320	 0.3000
A	 0.6590	 0.3890
B	 0.3700	 0.2550
C	 0.7310	 0.4280
D	 0.5850	 0.4550
E	 0.6100	 0.4630
F	 0.6090	 0.4520
G	 0.0630	 0.2180
H	 0.1700	 0.2890
I	 0.1810	 0.2880
L	 0.6000	 0.4440
M	 0.5540	 0.4480
N	 0.5620	 0.4130
O	 0.5410	 0.4420
P	 0.6540	 0.4610
Q	 0.1710	 0.2770
R	 0.5650	 0.4460
S	 0.6200	 0.4510
T	 0.5330	 0.4180
U	 0.5460	 0.4420
V	 0.4890	 0.3990
W	 0.5020	 0.4220
X	 0.4710	 0.3950
Y	 0.5280	 0.4050
Z	 0.4190	 0.3330

