



Full wwPDB EM Validation Report ⓘ

Dec 10, 2022 – 08:44 am GMT

PDB ID : 5ANC
EMDB ID : EMD-3147
Title : Mechanism of eIF6 release from the nascent 60S ribosomal subunit
Authors : Weis, F.; Giudice, E.; Churcher, M.; Jin, L.; Hilcenko, C.; Wong, C.C.;
Traynor, D.; Kay, R.R.; Warren, A.J.
Deposited on : 2015-09-06
Resolution : 4.20 Å(reported)

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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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

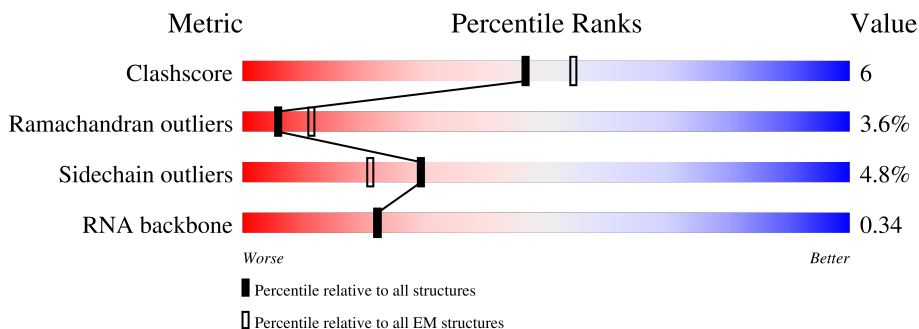
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.




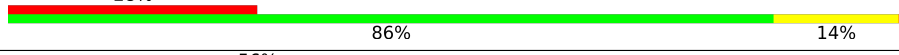

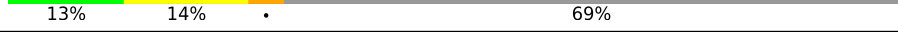
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	398	 5% 70% 26%
2	B	188	 5% 75% 24%
3	C	205	 55% 95% 5%
4	D	166	 41% 90% 10%
5	E	136	 5% 79% 18%
6	F	217	 5% 77% 20%
7	G	69	 5% 80% 19%

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Mol	Chain	Length	Quality of chain
8	H	52	 77% 19%
9	J	250	 28% 86% 14%
10	K	1120	 56% 90% 9%
11	N	3741	 13% 14% 69%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 46807 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 protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	398	3176	2018	599	547	12	0	0

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	188	1491	944	264	277	6	0	0

- Molecule 3 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	205	1571	998	271	294	8	0	0

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	166	1245	790	220	228	7	0	0

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	136	1017	640	188	181	8	0	0

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	217	1721	1079	332	297	13	0	0

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	69	586	378	105	99	4	0	0

- Molecule 8 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	52	427	269	88	64	6	0	0

- Molecule 9 is a protein called RIBOSOME MATURATION PROTEIN SBDS.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	250	2015	1272	352	380	11	0	0

- Molecule 10 is a protein called ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	1120	8800	5547	1518	1682	53	0	0

- Molecule 11 is a RNA chain called 26S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	N	1162	24758	11082	4431	8087	1158	0	0

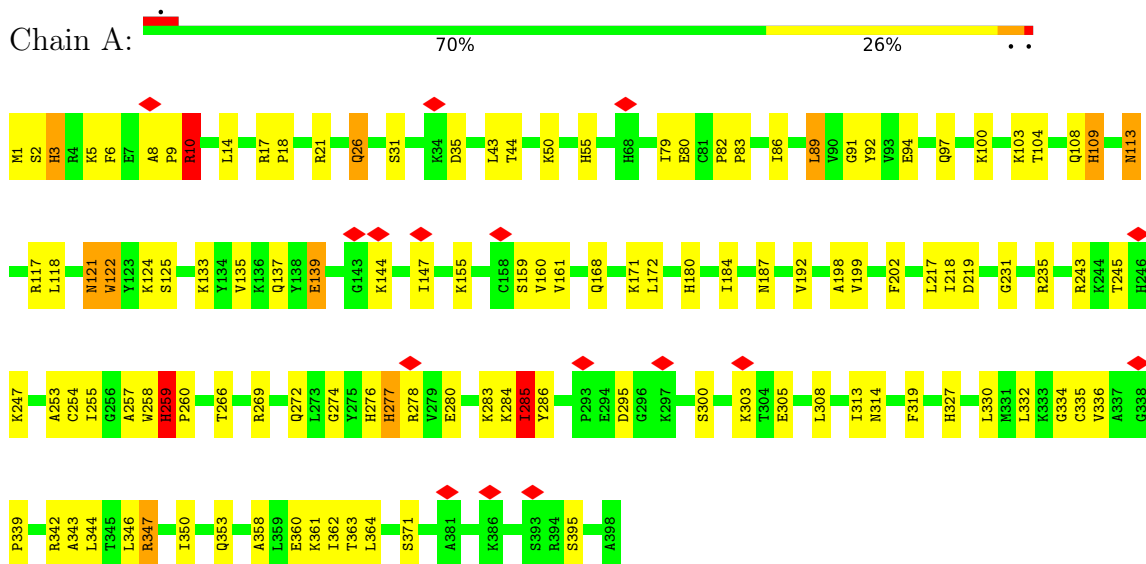
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	3119	C	G	conflict	GB FR733594.

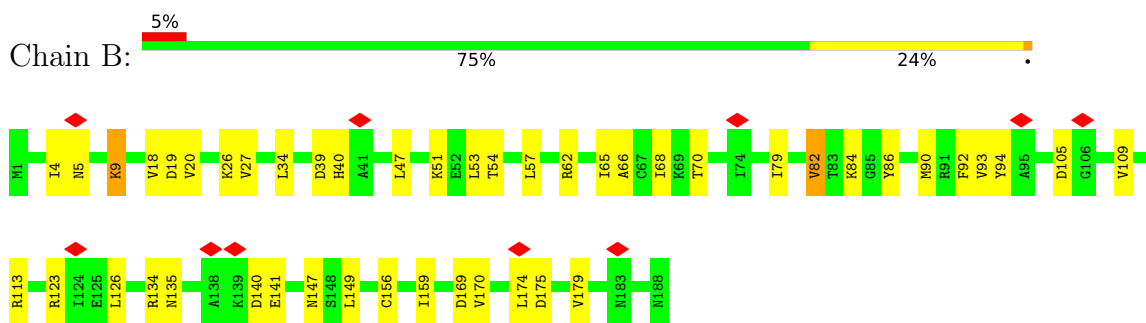
3 Residue-property plots

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.

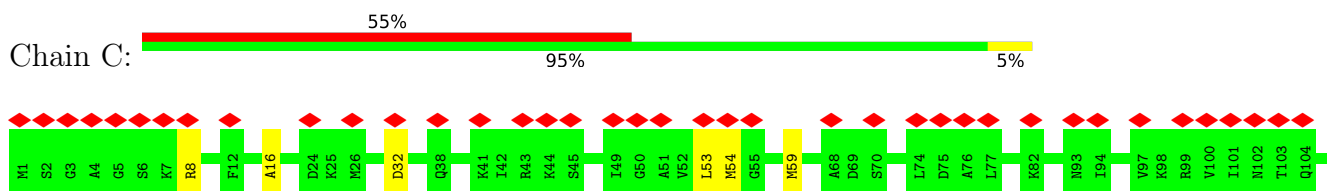
- Molecule 1: 60S RIBOSOMAL PROTEIN L3

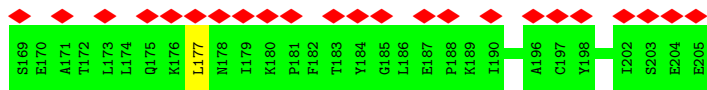
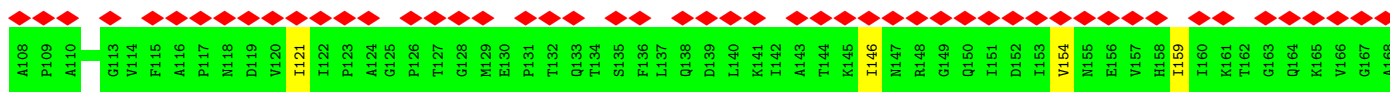


- Molecule 2: 60S RIBOSOMAL PROTEIN L9

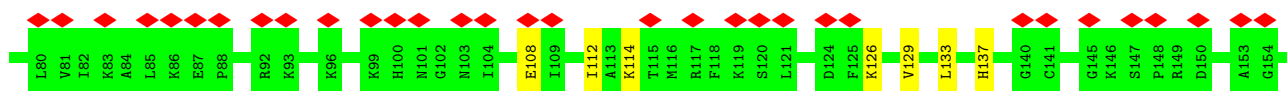
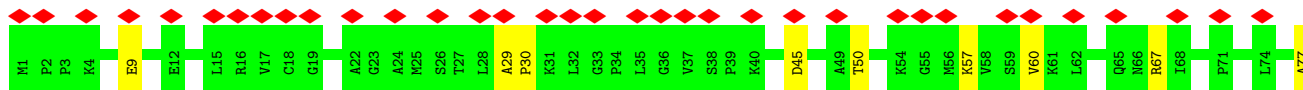
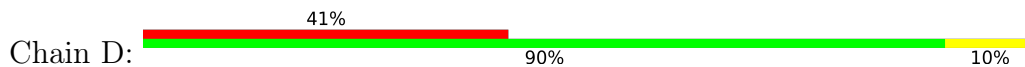


- Molecule 3: 60S ACIDIC RIBOSOMAL PROTEIN P0

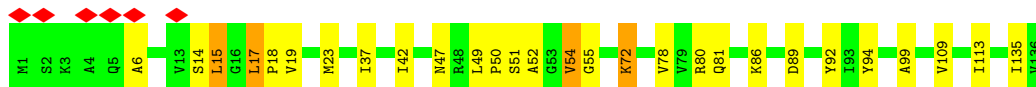
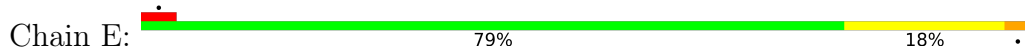




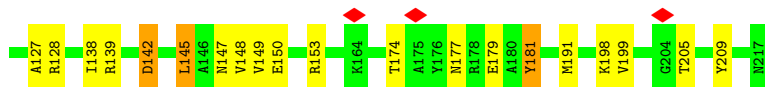
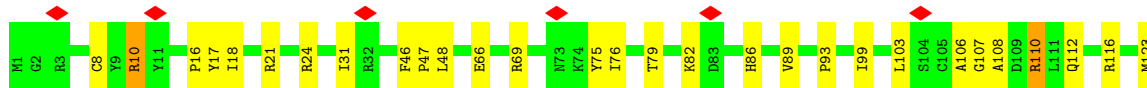
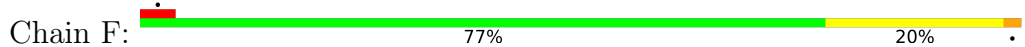
- Molecule 4: 60S RIBOSOMAL PROTEIN L12



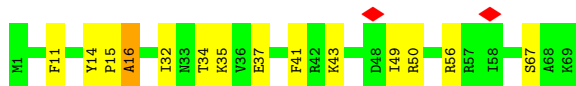
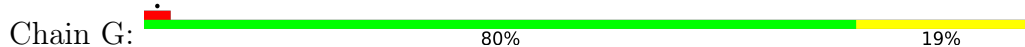
- Molecule 5: 60S RIBOSOMAL PROTEIN L23



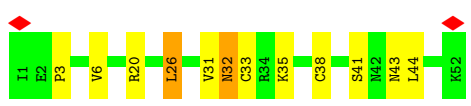
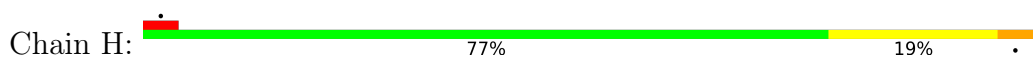
- Molecule 6: 60S RIBOSOMAL PROTEIN L10



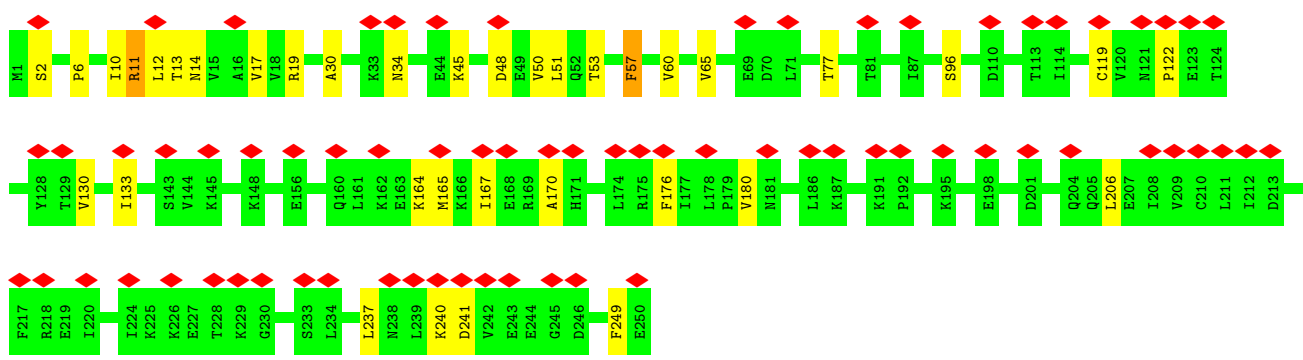
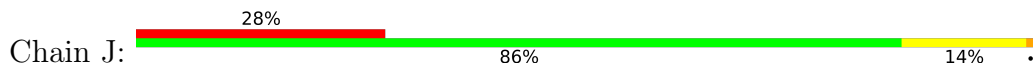
- Molecule 7: 60S RIBOSOMAL PROTEIN L24



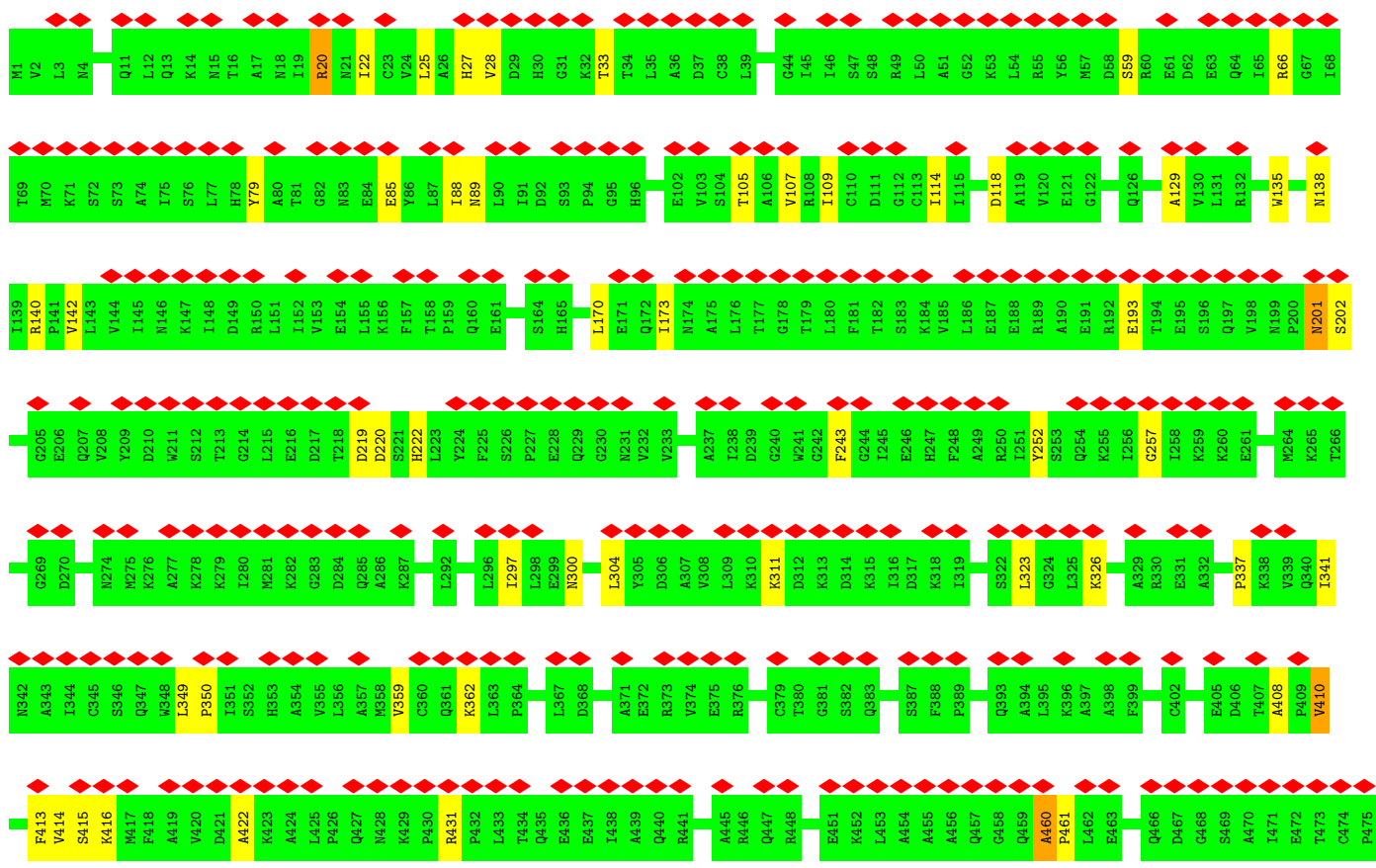
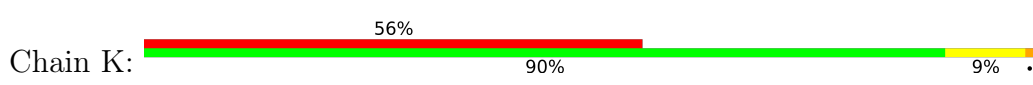
- Molecule 8: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

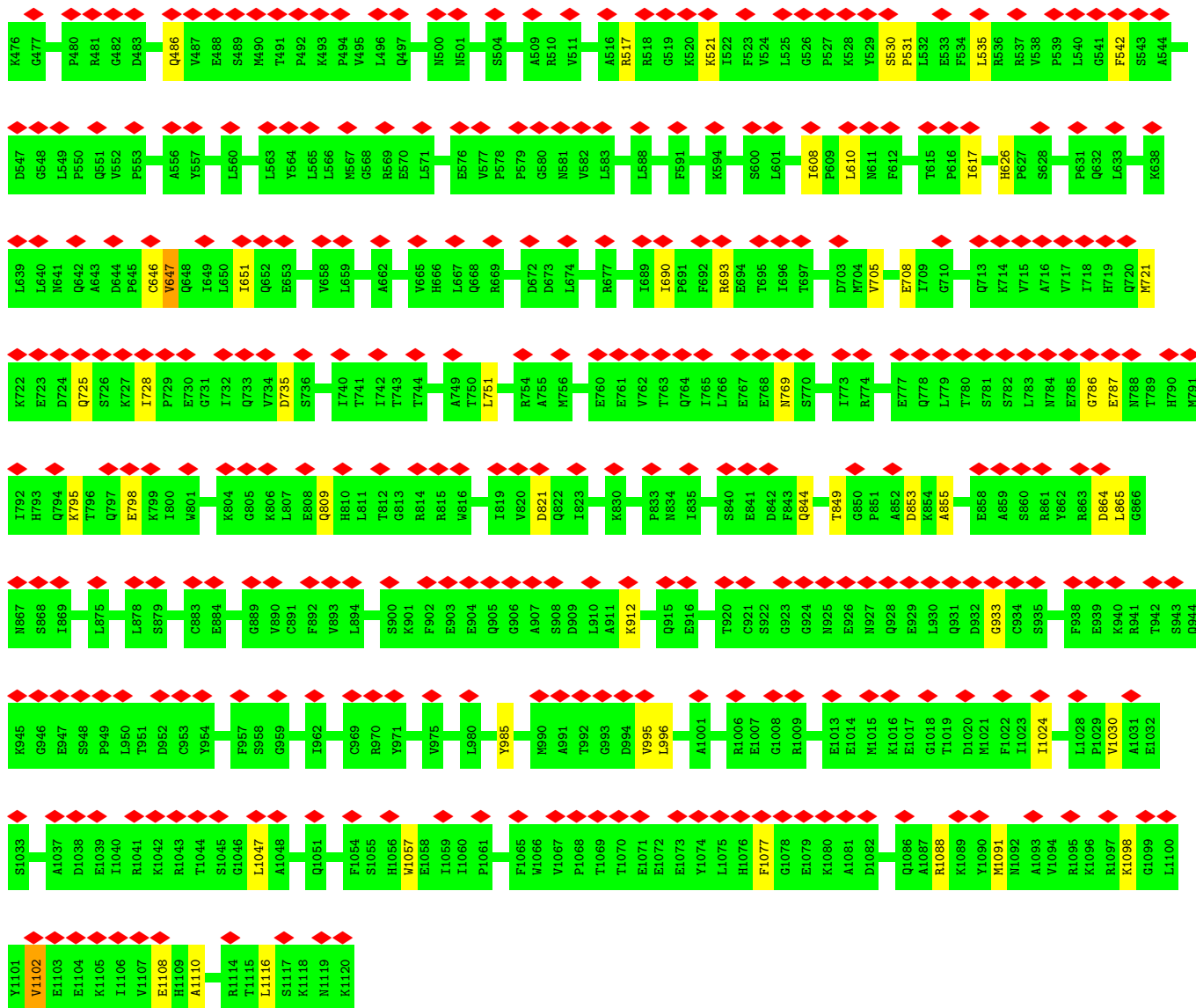


• Molecule 9: RIBOSOME MATURATION PROTEIN SBDS

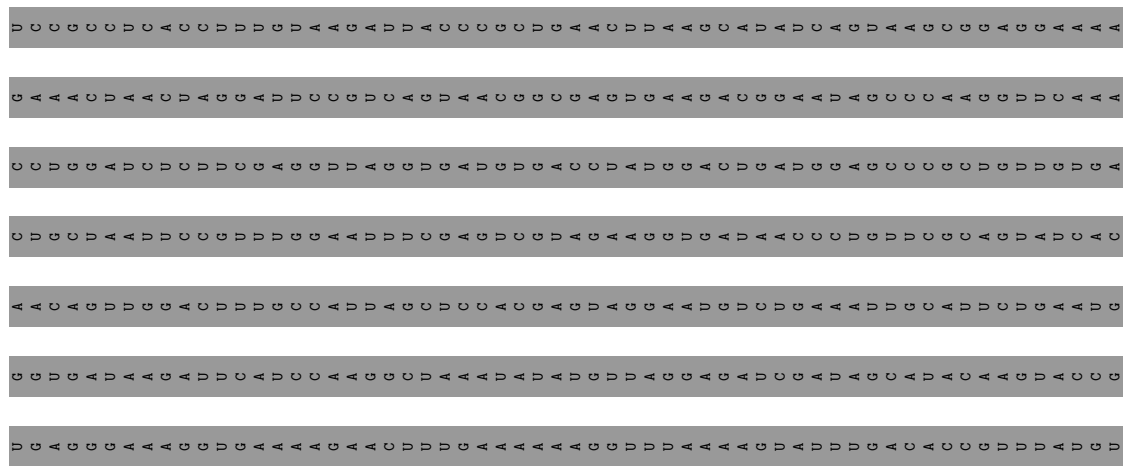


• Molecule 10: ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1





● Molecule 11: 26S RIBOSOMAL RNA



U3014	U3099	G3186	G3262	A3330	C3423	C	U	G	U
C3019	A3102	C3187	A3263	U3331	U3426	U	A	A	A
G3020	G3190	U3188	G3264	U3332	A3427	A	A	A	A
U3021	U3105	G3189	C3190	U3335	C3428	A	A	A	A
A3022	U3109	U3191	A3267	U3336	U3435	A	A	A	A
G3023	A3110	U3192	C3268	G3337	G3436	U	U	U	U
A3024	A3111	U3193	A3269	C3338	C3429	U	U	U	U
G3025	A3112	U3194	A3270	G3339	U3438	U	U	U	U
U3026	U3113	U3195	G3271	U3340	G3437	G	A	A	A
A3027	A3114	U3201	G3272	A3341	A3438	U	U	U	U
A3028	A3115	A3202	A3273	A3342	U3440	U	U	U	U
A3029	U3116	G3204	A3274	G3348	A3441	U	U	U	U
A3030	U3117	A3205	C3275	C3349	A3442	U	U	U	U
G3031	A3118	U3206	G3276	U3350	U3443	A	A	A	A
G3032	C3119	G3207	A3277	U3355	G3444	G	A	A	A
C3033	U3127	U3208	G3278	U3356	G3445	C	U	U	U
C3034	U3128	C3209	A3279	A3357	C3446	U	C	G	U
A3035	G3129	G3210	C3280	A3357	U3447	U	C	U	U
A3036	U3133	G3211	C3281	G3362	A3448	C	U	U	U
A3037	A3134	G3212	U3282	A3363	A3449	C	C	G	G
A3038	A3135	C3215	G3283	G3364	G3452	G	G	G	G
G3039	A3136	U3216	G3284	A3365	U3453	U	U	U	U
C3040	G3143	U3219	G3285	U3376	C3454	A	U	U	U
C3041	A3137	A3220	U3286	G3377	U3457	U	C	U	U
U3042	G3138	U3221	U3287	G3378	A3458	A	C	A	A
G3047	U3139	C3222	U3288	C3379	U3459	G	C	U	U
U3050	U3140	A3223	A3289	A3379	A3460	C	U	U	U
C3051	G3143	U3224	G3290	U3383	U3463	U	U	U	U
U3055	A3146	U3225	A3291	C3384	A3465	U	U	U	U
C3059	G3149	U3226	C3292	A3385	U3467	U	U	U	U
A3060	U3151	U3227	U3298	A3386	A3470	C	U	U	U
G3061	A3152	A3230	G3299	U3387	U3474	A	A	A	A
U3062	U3159	G3231	A3304	C3388	G3475	G	U	U	U
U3065	U3160	C3232	G3305	U3389	A3476	G	U	U	U
A3067	G3164	U3237	G3306	G3392	A3477	G	U	U	U
G3070	C3165	A3242	U3307	U3393	A3478	U	U	U	U
G3077	A3166	A3243	G3310	G3394	C3479	U	U	U	U
G3078	G3167	A3244	U3311	U3395	A3480	A	A	A	A
A3079	C3168	G3245	U3312	A3396	G	C	U	U	U
G3085	C3169	U3246	U3313	G3397	A	A	A	A	A
G3086	U3172	U3248	A3315	U3400	C	C	U	U	U
G3086	C3173	U3249	C3316	A3405	U	U	U	U	U
C3089	G3174	G3250	G3317	A3406	A	A	A	A	A
U3090	C3175	G3251	C3318	G3414	U	U	U	U	U
A3091	U3176	A3252	U3319	U3415	A	A	A	A	A
U3092	U3177	U3253	A3320	G3416	C	C	U	U	U
C3093	C3177	U3254	U3321	A3417	U	U	U	U	U
A3094	A3178	G3255	G3323	C3418	A	A	A	A	A
A3095	U3179	U3256	U3324	C3419	U	U	U	U	U
	A3180	U3257	C3325	U3420	A	A	A	A	A
		A3259	A3328	C3422	U	U	U	U	U

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9794	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	105263	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.676	Depositor
Minimum map value	-0.416	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.06	Depositor
Map size (\AA)	399.0, 399.0, 399.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.33, 1.33, 1.33	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.57	0/3241	0.86	1/4339 (0.0%)
2	B	0.42	0/1510	0.73	0/2030
3	C	0.39	0/1592	0.55	0/2142
4	D	0.40	0/1265	0.57	0/1702
5	E	0.48	0/1032	0.81	1/1386 (0.1%)
6	F	0.51	0/1752	0.79	1/2345 (0.0%)
7	G	0.53	0/600	0.79	0/801
8	H	0.46	0/433	0.84	0/571
9	J	0.45	0/2038	0.74	1/2727 (0.0%)
10	K	0.40	0/8969	0.63	0/12124
11	N	0.41	2/27702 (0.0%)	0.80	14/43160 (0.0%)
All	All	0.43	2/50134 (0.0%)	0.76	18/73327 (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
1	A	0	5
6	F	0	1
9	J	0	1
11	N	0	1
All	All	0	8

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	N	1550	U	O3'-P	5.07	1.67	1.61
11	N	2405	A	O3'-P	5.07	1.67	1.61

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	N	1221	A	C5'-C4'-O4'	7.66	118.29	109.10
11	N	2625	C	C2'-C3'-O3'	7.09	125.10	109.50
11	N	1221	A	C5'-C4'-C3'	6.37	126.19	116.00
11	N	2515	G	C2'-C3'-O3'	6.20	123.62	113.70
11	N	3421	G	C2'-C3'-O3'	6.18	123.59	113.70
11	N	1550	U	C2'-C3'-O3'	6.10	123.46	113.70
11	N	2625	C	C1'-O4'-C4'	-5.92	105.17	109.90
11	N	3477	A	C2'-C3'-O3'	-5.73	96.90	109.50
6	F	10	ARG	NE-CZ-NH1	5.54	123.07	120.30
11	N	2944	U	C5'-C4'-O4'	5.46	115.65	109.10
11	N	3205	A	N9-C1'-C2'	5.45	121.09	114.00
11	N	3065	U	C2'-C3'-O3'	5.35	122.26	113.70
11	N	2398	A	C2'-C3'-O3'	5.32	122.21	113.70
11	N	1550	U	P-O3'-C3'	5.29	126.04	119.70
5	E	17	LEU	CA-CB-CG	5.21	127.28	115.30
1	A	259	HIS	C-N-CD	5.20	139.32	128.40
9	J	11	ARG	NE-CZ-NH1	5.13	122.86	120.30
11	N	3231	G	C4'-C3'-O3'	-5.04	98.82	109.40

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	GLN	Peptide
1	A	122	TRP	Peptide
1	A	277	HIS	Peptide
1	A	5	LYS	Peptide
1	A	9	PRO	Peptide
6	F	181	TYR	Peptide
9	J	57	PHE	Peptide
11	N	3379	C	Sidechain

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	3176	0	3319	56	0
2	B	1491	0	1555	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1571	0	1657	1	0
4	D	1245	0	1338	4	0
5	E	1017	0	1076	14	0
6	F	1721	0	1778	22	0
7	G	586	0	601	5	0
8	H	427	0	483	6	0
9	J	2015	0	2112	15	0
10	K	8800	0	8840	27	0
11	N	24758	0	12487	382	0
All	All	46807	0	35246	522	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 6.

All (522) 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)
11:N:3224:U:N3	11:N:3466:A:C6	2.39	0.90
11:N:3224:U:C4	11:N:3466:A:N6	2.42	0.88
11:N:3224:U:N3	11:N:3466:A:N6	2.23	0.87
11:N:1598:U:H2'	11:N:1599:U:C6	2.13	0.84
1:A:79:ILE:HG21	1:A:344:LEU:HD12	1.63	0.81
8:H:26:LEU:HD23	8:H:44:LEU:HD23	1.66	0.77
5:E:92:TYR:OH	11:N:3386:C:O2	2.01	0.77
1:A:218:ILE:HG21	1:A:346:LEU:HD22	1.67	0.76
1:A:199:VAL:HA	1:A:202:PHE:CE2	2.24	0.73
11:N:2437:G:N2	11:N:2438:C:C2	2.58	0.71
1:A:50:LYS:HA	1:A:79:ILE:HG22	1.73	0.70
11:N:1438:A:OP2	11:N:1536:A:N6	2.24	0.70
6:F:8:CYS:SG	11:N:1365:U:O2'	2.43	0.70
6:F:107:GLY:HA3	9:J:12:LEU:HD23	1.74	0.69
6:F:106:ALA:HB3	9:J:14:ASN:HD22	1.56	0.69
11:N:1599:U:H2'	11:N:1600:A:O4'	1.92	0.69
11:N:1568:G:N2	11:N:1569:C:C2	2.62	0.67
11:N:1385:G:N2	11:N:1393:C:C2	2.62	0.67
11:N:2479:A:H2'	11:N:2480:A:C8	2.30	0.67
1:A:217:LEU:HD11	1:A:358:ALA:HB1	1.76	0.67
1:A:335:CYS:SG	11:N:3383:U:H1'	2.34	0.67
9:J:57:PHE:CD2	9:J:60:VAL:HG12	2.30	0.67
1:A:300:SER:HB3	1:A:313:ILE:HG23	1.77	0.67
11:N:3287:U:O2'	11:N:3288:U:OP2	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:821:ASP:HB2	10:K:855:ALA:HB2	1.78	0.66
1:A:283:LYS:NZ	1:A:335:CYS:O	2.29	0.65
11:N:3019:C:H2'	11:N:3020:G:O4'	1.95	0.65
11:N:3167:G:N2	11:N:3168:C:C2	2.66	0.64
2:B:66:ALA:O	11:N:3449:A:O2'	2.16	0.64
11:N:2618:A:H3'	11:N:2620:C:H42	1.62	0.64
11:N:3242:A:H2'	11:N:3243:A:O4'	1.97	0.63
11:N:1598:U:H2'	11:N:1599:U:H6	1.63	0.63
11:N:2601:G:N2	11:N:2604:C:N3	2.45	0.63
11:N:1553:C:H2'	11:N:1553:C:O2	1.99	0.63
10:K:996:LEU:HD22	10:K:1024:ILE:HD11	1.81	0.62
11:N:2980:A:H2'	11:N:2981:A:O4'	1.98	0.62
11:N:1579:A:H2'	11:N:1580:A:C8	2.34	0.62
1:A:10:ARG:HG3	1:A:14:LEU:HD21	1.81	0.62
9:J:17:VAL:HG22	9:J:60:VAL:HG21	1.82	0.61
1:A:91:GLY:HA2	1:A:161:VAL:HG12	1.83	0.61
4:D:60:VAL:HG21	4:D:77:ALA:HB2	1.83	0.61
11:N:3031:G:H2'	11:N:3032:G:O4'	2.01	0.60
5:E:17:LEU:O	5:E:52:ALA:HB2	2.00	0.60
11:N:2437:G:N1	11:N:2438:C:C4	2.70	0.60
1:A:6:PHE:O	11:N:3249:U:OP1	2.18	0.60
11:N:2416:A:N1	11:N:2454:A:O4'	2.34	0.60
11:N:1371:G:O2'	11:N:2975:A:N3	2.34	0.59
11:N:1374:C:H2'	11:N:1375:U:O4'	2.02	0.59
11:N:3189:G:N2	11:N:3190:C:C2	2.70	0.59
11:N:3215:U:H2'	11:N:3216:U:O4'	2.02	0.59
11:N:3230:A:C8	11:N:3232:C:N3	2.70	0.59
1:A:155:LYS:HG3	1:A:192:VAL:HG22	1.84	0.59
11:N:2671:C:C5	11:N:2672:C:C5	2.90	0.59
11:N:3478:A:H4'	11:N:3479:A:C5'	2.33	0.58
11:N:3267:A:H2'	11:N:3268:C:O4'	2.03	0.58
11:N:3445:G:C2	11:N:3462:C:C2	2.92	0.58
6:F:209:TYR:CG	6:F:209:TYR:O	2.57	0.58
1:A:285:ILE:HD11	1:A:330:LEU:HD13	1.86	0.58
11:N:1418:A:H2'	11:N:1419:U:O4'	2.04	0.58
11:N:3378:C:C4	11:N:3379:C:C5	2.92	0.58
2:B:9:LYS:HB3	2:B:54:THR:HG22	1.85	0.58
11:N:3172:G:N2	11:N:3173:C:C2	2.72	0.58
11:N:3027:A:H2'	11:N:3028:A:C8	2.39	0.58
11:N:3337:G:H2'	11:N:3338:C:C6	2.39	0.58
11:N:2416:A:C2	11:N:2454:A:O4'	2.57	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:2438:C:H2'	11:N:2439:U:C6	2.39	0.57
11:N:2562:A:C2	11:N:3252:A:O4'	2.58	0.57
11:N:1439:A:H2'	11:N:1440:A:O4'	2.04	0.57
11:N:3255:G:C6	11:N:3256:U:C4	2.93	0.56
11:N:2547:A:C2	11:N:3292:C:H1'	2.40	0.56
11:N:3194:U:H2'	11:N:3195:U:O4'	2.04	0.56
11:N:3251:G:N2	11:N:3262:C:C2	2.73	0.56
1:A:55:HIS:CE1	7:G:16:ALA:HB1	2.41	0.56
1:A:259:HIS:CG	1:A:260:PRO:HD3	2.40	0.56
1:A:286:TYR:CD1	1:A:362:ILE:HG21	2.41	0.56
10:K:460:ALA:HB3	10:K:461:PRO:HD3	1.87	0.56
11:N:2984:G:C2	11:N:3129:G:C4	2.94	0.56
11:N:3378:C:H2'	11:N:3379:C:O4'	2.05	0.56
11:N:2975:A:H2'	11:N:2976:A:C8	2.41	0.56
2:B:90:MET:HG2	2:B:179:VAL:HG22	1.87	0.56
2:B:62:ARG:O	2:B:65:ILE:HG22	2.06	0.56
5:E:80:ARG:HG3	5:E:99:ALA:HB3	1.87	0.56
6:F:99:ILE:HD12	6:F:123:MET:HB3	1.87	0.56
11:N:3269:A:H2'	11:N:3270:A:H8	1.71	0.56
6:F:79:THR:HG23	6:F:147:ASN:CB	2.36	0.55
1:A:26:GLN:HA	1:A:343:ALA:HB3	1.88	0.55
11:N:2500:G:C6	11:N:2501:C:C4	2.95	0.55
11:N:1553:C:C6	11:N:1555:G:C8	2.95	0.55
11:N:3415:U:O2	11:N:3415:U:O4'	2.24	0.55
11:N:2625:C:HO2'	11:N:2626:C:C4'	2.18	0.55
11:N:2993:C:H2'	11:N:2994:A:C8	2.42	0.55
11:N:2497:C:O4'	11:N:2497:C:O2	2.25	0.55
11:N:2686:C:H2'	11:N:2687:U:O4'	2.07	0.55
2:B:86:TYR:CD1	2:B:149:LEU:HD13	2.42	0.55
6:F:79:THR:HG23	6:F:147:ASN:HB2	1.88	0.55
11:N:2999:C:H2'	11:N:2999:C:O2	2.06	0.54
9:J:130:VAL:HA	9:J:133:ILE:HD12	1.90	0.54
1:A:89:LEU:HG	1:A:198:ALA:HB1	1.88	0.54
10:K:304:LEU:HD21	10:K:341:ILE:HD12	1.90	0.54
11:N:1385:G:C2	11:N:1393:C:C2	2.95	0.54
11:N:3377:G:C6	11:N:3378:C:C4	2.96	0.54
11:N:3000:A:H2'	11:N:3001:G:O4'	2.07	0.54
11:N:2939:G:H2'	11:N:2939:G:N3	2.22	0.54
11:N:2544:C:C2	11:N:2573:G:C2	2.96	0.54
11:N:3348:G:C2	11:N:3379:C:O2	2.60	0.53
2:B:93:VAL:HG13	2:B:175:ASP:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:31:VAL:HG23	8:H:32:ASN:ND2	2.23	0.53
11:N:2500:G:C2	11:N:2501:C:C2	2.96	0.53
2:B:18:VAL:HG22	2:B:27:VAL:HG12	1.91	0.53
11:N:1239:G:C8	11:N:1242:A:C2	2.96	0.53
9:J:30:ALA:HB3	9:J:53:THR:HB	1.91	0.53
11:N:2534:U:H2'	11:N:2535:U:H2'	1.90	0.53
11:N:3442:A:H2'	11:N:3443:U:O4'	2.08	0.53
11:N:3059:C:C5	11:N:3061:G:C4	2.97	0.53
11:N:2680:G:C6	11:N:2681:C:C4	2.96	0.53
1:A:254:CYS:SG	11:N:3276:G:N2	2.82	0.53
2:B:156:CYS:HA	2:B:159:ILE:HD12	1.90	0.53
1:A:118:LEU:HD23	1:A:121:ASN:HD21	1.73	0.52
10:K:1098:LYS:HB2	10:K:1102:VAL:HG12	1.90	0.52
11:N:1269:A:N7	11:N:2970:A:C8	2.77	0.52
11:N:1571:C:C2	11:N:1572:A:C8	2.97	0.52
11:N:3246:U:C2	11:N:3247:G:C8	2.97	0.52
11:N:2429:G:N1	11:N:2430:C:C2	2.78	0.52
11:N:3167:G:N1	11:N:3168:C:C4	2.78	0.52
11:N:3093:C:O4'	11:N:3093:C:O2	2.28	0.52
1:A:276:HIS:ND1	1:A:277:HIS:O	2.43	0.52
9:J:50:VAL:HG23	9:J:51:LEU:HD13	1.92	0.52
6:F:46:PHE:HB3	6:F:139:ARG:HG2	1.92	0.52
11:N:1251:G:N2	11:N:1252:C:C2	2.77	0.52
11:N:2944:U:C2	11:N:2945:U:C6	2.98	0.52
11:N:3441:A:C8	11:N:3464:G:N2	2.78	0.52
6:F:93:PRO:HA	6:F:127:ALA:HB2	1.92	0.51
11:N:1553:C:C2	11:N:1555:G:N7	2.78	0.51
11:N:3164:G:C6	11:N:3165:C:C4	2.98	0.51
11:N:3417:A:C6	11:N:3418:C:C4	2.99	0.51
4:D:29:ALA:HB1	4:D:30:PRO:HD2	1.91	0.51
9:J:19:ARG:NE	11:N:2574:C:O2'	2.43	0.51
11:N:1406:A:H2'	11:N:1407:A:C8	2.46	0.51
11:N:1553:C:C2	11:N:1555:G:C5	2.99	0.51
11:N:2618:A:C2	11:N:2620:C:C2	2.99	0.51
11:N:3224:U:C2	11:N:3466:A:N6	2.79	0.51
11:N:3437:G:H2'	11:N:3438:G:C8	2.44	0.51
11:N:1433:C:H3'	11:N:1434:C:H2'	1.92	0.51
11:N:2951:G:N2	11:N:2977:C:O2'	2.44	0.51
11:N:3224:U:C2	11:N:3466:A:C6	2.99	0.51
11:N:1557:G:H2'	11:N:1558:G:O4'	2.11	0.51
11:N:3364:G:H2'	11:N:3365:A:C8	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:164:LYS:N	9:J:165:MET:HA	2.26	0.51
11:N:1438:A:N3	11:N:3188:U:O2'	2.35	0.51
11:N:3164:G:C2	11:N:3165:C:C2	2.99	0.51
11:N:3178:A:C2	11:N:3179:U:C6	2.99	0.51
11:N:3377:G:C2	11:N:3378:C:C2	2.98	0.51
11:N:1564:C:H2'	11:N:1565:G:O4'	2.10	0.51
1:A:109:HIS:ND1	1:A:202:PHE:O	2.44	0.51
11:N:2699:U:C5	11:N:2700:U:H2'	2.46	0.51
11:N:3047:G:H5''	11:N:3047:G:N3	2.26	0.51
11:N:1474:C:C2	11:N:1485:G:C2	2.99	0.50
11:N:1568:G:N1	11:N:1569:C:C4	2.79	0.50
11:N:2395:C:H2'	11:N:2396:C:O4'	2.10	0.50
11:N:2400:U:C5	11:N:2401:G:C8	2.98	0.50
11:N:2477:U:O4'	11:N:2477:U:O2	2.29	0.50
11:N:3230:A:C8	11:N:3232:C:C2	3.00	0.50
7:G:35:LYS:HB3	11:N:3420:U:O3'	2.11	0.50
11:N:2442:U:H2'	11:N:2442:U:O2	2.11	0.50
11:N:2993:C:O2'	11:N:3077:G:N3	2.44	0.50
11:N:3279:A:C6	11:N:3315:A:C2	2.99	0.50
11:N:3287:U:O2'	11:N:3288:U:P	2.70	0.50
11:N:3304:A:OP2	11:N:3305:G:H5''	2.11	0.50
11:N:1472:G:C6	11:N:1473:C:C4	2.99	0.50
11:N:1553:C:O2	11:N:1553:C:C2'	2.59	0.50
11:N:2685:A:C4	11:N:2686:C:C5	3.00	0.50
11:N:3258:C:C5	11:N:3259:A:C8	3.00	0.50
1:A:82:PRO:HB2	1:A:83:PRO:CD	2.41	0.50
2:B:5:ASN:HD22	2:B:5:ASN:N	2.10	0.50
11:N:1429:G:H2'	11:N:1430:A:C8	2.46	0.50
5:E:42:ILE:HG21	5:E:50:PRO:HA	1.94	0.50
6:F:8:CYS:SG	11:N:1365:U:H1'	2.52	0.50
11:N:1530:G:C6	11:N:1531:C:C4	3.00	0.50
11:N:2524:U:O2	11:N:2524:U:O4'	2.28	0.50
11:N:2635:G:H2'	11:N:2636:G:C8	2.46	0.50
11:N:2969:A:H3'	11:N:2969:A:N3	2.27	0.50
11:N:1548:G:C2	11:N:1549:C:C2	3.00	0.50
11:N:2564:U:C5	11:N:3254:U:H1'	2.46	0.50
7:G:37:GLU:HG2	7:G:41:PHE:CE2	2.47	0.49
11:N:1240:U:O2	11:N:1240:U:O4'	2.29	0.49
11:N:1526:A:H2'	11:N:1527:C:O4'	2.12	0.49
11:N:3255:G:H2'	11:N:3256:U:O4'	2.12	0.49
11:N:2620:C:H3'	11:N:2620:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:SER:N	11:N:3272:G:OP2	2.45	0.49
11:N:2480:A:H2'	11:N:2481:A:O4'	2.12	0.49
11:N:2987:C:O4'	11:N:2990:A:C2	2.65	0.49
11:N:3172:G:N1	11:N:3173:C:C4	2.81	0.49
1:A:313:ILE:HD12	1:A:314:ASN:N	2.27	0.49
1:A:336:VAL:HG21	1:A:344:LEU:HD11	1.94	0.49
11:N:1531:C:C4	11:N:1532:C:C5	3.01	0.49
11:N:3439:A:H2'	11:N:3440:U:O4'	2.13	0.49
5:E:15:LEU:HD13	5:E:15:LEU:N	2.27	0.49
9:J:65:VAL:N	11:N:2955:C:O2	2.38	0.49
1:A:257:ALA:HB2	11:N:3276:G:N3	2.28	0.48
11:N:2568:G:H2'	11:N:2569:A:O4'	2.13	0.48
11:N:3435:U:O2'	11:N:3436:U:H5'	2.13	0.48
1:A:14:LEU:O	1:A:17:ARG:HB2	2.13	0.48
11:N:2544:C:C5	11:N:2571:G:C6	3.01	0.48
11:N:3150:A:OP2	11:N:3201:U:OP2	2.31	0.48
5:E:86:LYS:HB2	5:E:92:TYR:CE2	2.49	0.48
11:N:2680:G:C2	11:N:2681:C:C2	3.01	0.48
11:N:2686:C:C4	11:N:2687:U:C5	3.01	0.48
11:N:2996:G:C6	11:N:2997:C:C4	3.00	0.48
6:F:48:LEU:HD21	6:F:145:LEU:HB3	1.94	0.48
6:F:48:LEU:HD22	6:F:142:ASP:HA	1.95	0.48
10:K:138:ASN:HD22	10:K:222:HIS:CE1	2.32	0.48
11:N:2689:U:C4	11:N:2938:G:C2	3.02	0.48
11:N:3032:G:C2	11:N:3089:C:C2	3.01	0.48
11:N:3169:C:O2	11:N:3169:C:O4'	2.31	0.48
1:A:303:LYS:O	1:A:308:LEU:N	2.46	0.48
11:N:1223:U:C2	11:N:1258:C:C2	3.01	0.48
11:N:2437:G:C2	11:N:2438:C:C4	3.01	0.48
1:A:113:ASN:N	1:A:113:ASN:HD22	2.12	0.48
2:B:126:LEU:HD21	2:B:159:ILE:HD11	1.96	0.48
11:N:2544:C:C2	11:N:2573:G:N2	2.82	0.48
11:N:2546:A:C4	11:N:2548:U:C5	3.02	0.48
5:E:15:LEU:CB	5:E:52:ALA:HB3	2.43	0.48
8:H:20:ARG:NH1	11:N:3180:A:OP2	2.47	0.48
11:N:2619:G:OP2	11:N:2620:C:N4	2.47	0.48
11:N:2985:U:C4	11:N:2986:C:C5	3.01	0.48
11:N:2994:A:O2'	11:N:3078:G:H4'	2.14	0.48
11:N:1472:G:C2	11:N:1473:C:C2	3.02	0.48
11:N:3445:G:C6	11:N:3446:C:C4	3.02	0.47
2:B:86:TYR:CE1	2:B:149:LEU:HD13	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:2546:A:C5	11:N:2548:U:C6	3.02	0.47
11:N:3207:G:H3'	11:N:3278:G:H22	1.80	0.47
11:N:3287:U:HO2'	11:N:3288:U:P	2.35	0.47
2:B:109:VAL:HG11	2:B:123:ARG:CZ	2.45	0.47
1:A:92:TYR:HB2	1:A:160:VAL:O	2.13	0.47
1:A:155:LYS:CG	1:A:192:VAL:HG22	2.44	0.47
10:K:985:TYR:CE2	10:K:1030:VAL:HG13	2.49	0.47
11:N:1548:G:C6	11:N:1549:C:C4	3.01	0.47
11:N:2441:U:O2	11:N:2441:U:O4'	2.31	0.47
11:N:2630:G:H22	11:N:2662:G:H1'	1.78	0.47
11:N:3139:U:H2'	11:N:3140:U:C6	2.49	0.47
11:N:3209:C:C2	11:N:3285:G:C2	3.02	0.47
11:N:1382:G:C5	11:N:1383:U:C5	3.02	0.47
11:N:3377:G:H2'	11:N:3378:C:O4'	2.13	0.47
1:A:80:GLU:OE1	1:A:172:LEU:HD22	2.15	0.47
11:N:1536:A:H4'	11:N:1537:A:O5'	2.14	0.47
5:E:18:PRO:HB2	5:E:49:LEU:HD13	1.96	0.47
10:K:995:VAL:HG11	10:K:1047:LEU:HB2	1.96	0.47
11:N:2487:G:C4	11:N:2489:G:OP2	2.67	0.47
11:N:2541:A:H2'	11:N:2542:G:O4'	2.14	0.47
11:N:2613:U:O4'	11:N:2613:U:O2	2.33	0.47
11:N:2615:U:C5	11:N:2616:A:C6	3.02	0.47
11:N:2996:G:C2	11:N:2997:C:C2	3.03	0.47
11:N:3024:A:H2'	11:N:3025:G:O4'	2.14	0.47
11:N:3039:G:N2	11:N:3040:C:C2	2.83	0.47
11:N:3221:U:C4	11:N:3244:A:C5	3.02	0.47
11:N:1500:U:H2'	11:N:1501:G:O4'	2.15	0.47
11:N:2623:A:H2'	11:N:2624:A:H5'	1.96	0.47
11:N:3348:G:C2	11:N:3379:C:C2	3.02	0.47
11:N:3387:U:C2	11:N:3388:G:C8	3.02	0.47
1:A:21:ARG:N	11:N:3324:U:OP1	2.36	0.47
11:N:2415:A:H2'	11:N:2416:A:C5	2.49	0.47
11:N:2957:G:C6	11:N:2958:C:C4	3.03	0.47
11:N:3189:G:C6	11:N:3190:C:N4	2.83	0.47
11:N:3417:A:C5	11:N:3418:C:C5	3.03	0.47
11:N:3446:C:H2'	11:N:3447:U:C6	2.50	0.47
6:F:110:ARG:HD2	9:J:11:ARG:HH22	1.80	0.47
11:N:3118:A:H2'	11:N:3119:C:O4'	2.15	0.47
11:N:3457:U:H4'	11:N:3458:A:OP1	2.14	0.47
9:J:50:VAL:HG23	9:J:51:LEU:CD1	2.44	0.46
10:K:530:SER:N	10:K:531:PRO:CD	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:1599:U:H2'	11:N:1600:A:C8	2.49	0.46
11:N:2415:A:H2'	11:N:2416:A:C4	2.50	0.46
11:N:2626:C:O2	11:N:2626:C:O4'	2.32	0.46
11:N:2655:C:H2'	11:N:2656:A:C8	2.50	0.46
11:N:3189:G:N1	11:N:3190:C:C4	2.83	0.46
11:N:3289:A:N6	11:N:3310:G:O2'	2.46	0.46
9:J:119:CYS:CB	9:J:133:ILE:HD11	2.45	0.46
11:N:2956:G:C6	11:N:2957:G:C5	3.03	0.46
11:N:3022:A:H4'	11:N:3023:G:C4	2.51	0.46
11:N:1267:U:H2'	11:N:1268:G:O4'	2.16	0.46
11:N:3039:G:C6	11:N:3040:C:C4	3.04	0.46
11:N:3319:U:H2'	11:N:3319:U:O2	2.15	0.46
11:N:3445:G:N2	11:N:3446:C:C2	2.83	0.46
11:N:2506:G:C6	11:N:2507:U:C4	3.03	0.46
11:N:2665:A:H2'	11:N:2666:G:O4'	2.16	0.46
11:N:3175:C:C5	11:N:3176:U:C5	3.04	0.46
11:N:3226:G:H2'	11:N:3227:U:O4'	2.16	0.46
11:N:2625:C:O2'	11:N:2626:C:O4'	2.29	0.46
11:N:2978:G:C2	11:N:2979:C:C2	3.04	0.46
11:N:3376:U:O2	11:N:3377:G:C8	2.69	0.46
11:N:3394:U:O4'	11:N:3394:U:O2	2.33	0.46
6:F:145:LEU:HA	6:F:148:VAL:HG22	1.98	0.46
11:N:2483:U:C2	11:N:2484:G:C8	3.04	0.46
11:N:2664:A:C6	11:N:3279:A:C5	3.03	0.46
11:N:3220:A:H2'	11:N:3220:A:N3	2.30	0.46
11:N:1461:G:C2	11:N:1462:C:C2	3.04	0.46
11:N:1542:G:H1'	11:N:1543:A:C8	2.51	0.46
11:N:2978:G:N2	11:N:2979:C:C2	2.84	0.46
8:H:3:PRO:HA	8:H:6:VAL:HG12	1.97	0.46
11:N:3306:G:C5	11:N:3307:U:C5	3.04	0.46
1:A:6:PHE:HB2	11:N:3249:U:OP1	2.16	0.46
11:N:1385:G:C2	11:N:1393:C:N3	2.83	0.46
11:N:2425:A:H61	11:N:2442:U:H3	1.61	0.46
10:K:170:LEU:O	10:K:173:ILE:HG22	2.16	0.46
11:N:1476:U:O2	11:N:1476:U:O4'	2.33	0.46
11:N:1547:C:H2'	11:N:1548:G:O4'	2.16	0.45
1:A:113:ASN:OD1	1:A:117:ARG:NH2	2.50	0.45
11:N:3281:C:H2'	11:N:3282:U:C6	2.51	0.45
11:N:2462:C:C2	11:N:2513:G:C2	3.04	0.45
11:N:2546:A:C5	11:N:2548:U:C5	3.04	0.45
11:N:3159:U:H2'	11:N:3160:U:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:3441:A:H2'	11:N:3442:A:C8	2.52	0.45
11:N:2579:A:H1'	11:N:2581:G:C8	2.52	0.45
11:N:2673:C:H2'	11:N:2674:U:H6	1.82	0.45
11:N:2978:G:C6	11:N:2979:C:C4	3.04	0.45
11:N:3027:A:C2	11:N:3028:A:C2	3.05	0.45
11:N:3318:C:H2'	11:N:3319:U:O4'	2.16	0.45
11:N:1580:A:N1	11:N:1581:A:C5	2.85	0.45
1:A:43:LEU:O	1:A:184:ILE:HG22	2.17	0.45
1:A:255:ILE:HG12	11:N:2660:G:O5'	2.17	0.45
11:N:3188:U:H2'	11:N:3189:G:O4'	2.17	0.45
11:N:3355:U:H2'	11:N:3356:U:O4'	2.17	0.45
6:F:103:LEU:HB2	6:F:110:ARG:HD3	1.99	0.45
11:N:3189:G:C2	11:N:3190:C:C2	3.05	0.45
11:N:2509:A:O4'	11:N:2579:A:H5''	2.18	0.44
11:N:2673:C:C2	11:N:2674:U:C5	3.05	0.44
11:N:2989:A:C5	11:N:2991:G:C8	3.04	0.44
11:N:3208:U:C6	11:N:3287:U:O4	2.70	0.44
1:A:243:ARG:HD2	1:A:245:THR:CG2	2.48	0.44
5:E:18:PRO:HB3	5:E:51:SER:HA	1.98	0.44
10:K:79:TYR:CE1	10:K:88:ILE:HD12	2.52	0.44
10:K:798:GLU:HA	10:K:809:GLN:HE22	1.82	0.44
11:N:2412:A:C6	11:N:2413:C:C4	3.06	0.44
11:N:2671:C:C6	11:N:2672:C:C5	3.05	0.44
11:N:3245:G:C6	11:N:3246:U:C4	3.05	0.44
11:N:3397:G:N2	11:N:3419:C:C2	2.85	0.44
5:E:109:VAL:HG21	5:E:113:ILE:HD11	2.00	0.44
9:J:30:ALA:HB3	9:J:53:THR:CB	2.47	0.44
11:N:3225:U:O4'	11:N:3466:A:N7	2.51	0.44
1:A:10:ARG:HA	11:N:3215:U:OP1	2.18	0.44
10:K:140:ARG:NH1	10:K:362:LYS:O	2.50	0.44
11:N:1479:A:C2	11:N:1483:C:C6	3.05	0.44
11:N:1530:G:C2	11:N:1531:C:C2	3.05	0.44
5:E:54:VAL:O	5:E:81:GLN:NE2	2.50	0.44
11:N:1502:U:H2'	11:N:1503:G:O4'	2.18	0.44
11:N:2957:G:N2	11:N:2958:C:C2	2.86	0.44
11:N:3245:G:N3	11:N:3466:A:O2'	2.45	0.44
11:N:3458:A:C2	11:N:3459:A:C8	3.06	0.44
11:N:1251:G:C6	11:N:1252:C:C4	3.06	0.44
11:N:2436:A:C2	11:N:2437:G:C8	3.06	0.44
11:N:3209:C:H2'	11:N:3210:G:O4'	2.17	0.44
11:N:3341:A:C4	11:N:3476:G:N2	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:GLU:N	1:A:139:GLU:CD	2.70	0.44
2:B:57:LEU:HB2	2:B:68:ILE:HD11	2.00	0.44
11:N:3172:G:C6	11:N:3173:C:C4	3.06	0.44
11:N:3348:G:C6	11:N:3349:C:C4	3.06	0.44
6:F:116:ARG:NH2	11:N:2977:C:N3	2.62	0.44
7:G:50:ARG:HG2	7:G:56:ARG:NE	2.33	0.44
11:N:2544:C:C4	11:N:2571:G:C5	3.06	0.44
11:N:2547:A:N1	11:N:3292:C:H1'	2.32	0.44
11:N:3029:A:H2'	11:N:3030:A:C8	2.52	0.44
11:N:3186:G:C2	11:N:3187:C:C2	3.06	0.44
1:A:243:ARG:HB3	1:A:245:THR:HG22	1.99	0.43
6:F:86:HIS:O	6:F:138:ILE:HG23	2.18	0.43
10:K:25:LEU:HD11	10:K:107:VAL:HG23	2.00	0.43
11:N:2552:U:N3	11:N:2554:G:O4'	2.51	0.43
11:N:2578:A:O2'	11:N:2581:G:N3	2.50	0.43
11:N:3211:G:C6	11:N:3212:C:C4	3.06	0.43
3:C:159:ILE:HG23	3:C:177:LEU:HD11	2.00	0.43
10:K:105:THR:HG22	10:K:415:SER:HA	1.99	0.43
11:N:1251:G:N1	11:N:1252:C:C4	2.86	0.43
11:N:1568:G:C2	11:N:1569:C:C6	3.06	0.43
11:N:2624:A:C2'	11:N:2625:C:H5'	2.48	0.43
11:N:3039:G:C2	11:N:3040:C:C2	3.06	0.43
11:N:3114:C:C5	11:N:3115:U:C5	3.06	0.43
11:N:3186:G:C6	11:N:3187:C:C4	3.06	0.43
1:A:144:LYS:HD2	1:A:147:ILE:HD12	2.00	0.43
11:N:3209:C:C2	11:N:3285:G:N1	2.86	0.43
11:N:3348:G:C2	11:N:3349:C:C2	3.07	0.43
5:E:15:LEU:HB3	5:E:52:ALA:HB3	2.01	0.43
11:N:2416:A:N6	11:N:2453:G:O2'	2.51	0.43
11:N:2450:U:H2'	11:N:2451:G:O4'	2.19	0.43
11:N:2536:A:H2'	11:N:2537:A:C8	2.53	0.43
11:N:2620:C:C6	11:N:2620:C:C3'	3.01	0.43
11:N:2675:G:C2	11:N:3146:A:C2	3.07	0.43
1:A:231:GLY:O	1:A:235:ARG:N	2.51	0.43
11:N:2619:G:H2'	11:N:2620:C:C2	2.53	0.43
11:N:3167:G:C2	11:N:3168:C:C2	3.06	0.43
11:N:2618:A:N3	11:N:2620:C:N3	2.67	0.43
11:N:2957:G:C2	11:N:2958:C:C2	3.06	0.43
11:N:3067:A:H4'	11:N:3090:U:OP1	2.19	0.43
1:A:243:ARG:NH2	11:N:3281:C:O2'	2.50	0.43
11:N:2470:C:C2	11:N:2505:G:N1	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:2580:U:O2	11:N:2580:U:O4'	2.36	0.43
11:N:2973:A:N7	11:N:2974:U:C5	2.86	0.43
11:N:2948:G:C6	11:N:2949:C:C4	3.07	0.43
11:N:3295:U:H2'	11:N:3296:C:O4'	2.19	0.43
11:N:3467:U:O2	11:N:3467:U:H2'	2.18	0.43
11:N:1579:A:C2	11:N:1599:U:N3	2.87	0.42
11:N:3189:G:C2	11:N:3190:C:C4	3.07	0.42
11:N:3418:C:C2	11:N:3419:C:C5	3.07	0.42
11:N:2411:A:C4	11:N:2547:A:N6	2.87	0.42
11:N:3445:G:C2	11:N:3446:C:C2	3.07	0.42
11:N:1254:G:H2'	11:N:1255:A:H8	1.84	0.42
11:N:1461:G:C6	11:N:1462:C:C4	3.07	0.42
11:N:3167:G:C6	11:N:3168:C:C4	3.07	0.42
10:K:201:ASN:HD22	10:K:202:SER:N	2.18	0.42
11:N:2944:U:N3	11:N:2945:U:C5	2.87	0.42
11:N:3221:U:C6	11:N:3244:A:N6	2.87	0.42
11:N:3245:G:C5	11:N:3246:U:C5	3.07	0.42
11:N:3328:C:O2	11:N:3328:C:O4'	2.36	0.42
6:F:16:PRO:HG3	6:F:128:ARG:CZ	2.50	0.42
11:N:2404:U:C5	11:N:2408:U:C5	3.08	0.42
11:N:2419:A:O4'	11:N:2509:A:C2	2.72	0.42
11:N:2680:G:N1	11:N:2681:C:C2	2.87	0.42
1:A:199:VAL:HA	1:A:202:PHE:CD2	2.54	0.42
2:B:70:THR:OG1	11:N:3448:G:O2'	2.36	0.42
11:N:2411:A:C4	11:N:2547:A:C6	3.07	0.42
11:N:2576:U:H2'	11:N:2577:G:C8	2.54	0.42
11:N:2620:C:H3'	11:N:2620:C:H6	1.84	0.42
11:N:3189:G:C6	11:N:3190:C:C4	3.08	0.42
2:B:174:LEU:HD13	8:H:6:VAL:CG2	2.50	0.42
10:K:414:VAL:HG13	10:K:610:LEU:HD22	2.01	0.42
11:N:2948:G:C2	11:N:2949:C:C2	3.08	0.42
11:N:3251:G:C2	11:N:3262:C:N3	2.88	0.42
11:N:1550:U:O2	11:N:1550:U:O4'	2.35	0.42
11:N:2600:U:O2	11:N:2600:U:O4'	2.37	0.42
11:N:3059:C:O2	11:N:3059:C:O4'	2.37	0.42
1:A:218:ILE:HG22	1:A:219:ASP:N	2.35	0.42
6:F:145:LEU:O	6:F:149:VAL:HG13	2.20	0.42
11:N:2589:G:C2	11:N:2591:G:C5	3.08	0.42
11:N:2993:C:H2'	11:N:2994:A:H8	1.81	0.42
11:N:3041:C:H2'	11:N:3042:U:H6	1.85	0.42
11:N:3205:A:H5''	11:N:3206:U:OP2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:3328:C:H3'	11:N:3331:U:C5	2.55	0.42
11:N:3459:A:H2'	11:N:3460:G:H5'	2.02	0.42
6:F:150:GLU:O	6:F:153:ARG:HB3	2.19	0.42
10:K:1110:ALA:HB3	10:K:1116:LEU:HD12	2.01	0.42
11:N:3416:G:C6	11:N:3417:A:C5	3.08	0.42
6:F:191:MET:HB2	6:F:198:LYS:HB3	2.02	0.41
10:K:22:ILE:HD11	10:K:359:VAL:HG13	2.02	0.41
11:N:1243:U:O2	11:N:1243:U:O4'	2.38	0.41
11:N:2672:C:C2	11:N:2673:C:C5	3.07	0.41
11:N:2933:C:C2	11:N:2934:A:C8	3.07	0.41
1:A:168:GLN:HG3	1:A:171:LYS:HB2	2.02	0.41
5:E:55:GLY:HA2	5:E:78:VAL:HG13	2.02	0.41
11:N:1385:G:N1	11:N:1393:C:C4	2.88	0.41
11:N:2514:C:H2'	11:N:2539:G:C8	2.55	0.41
11:N:2608:A:C8	11:N:2609:C:C4	3.08	0.41
1:A:347:ARG:NH1	1:A:350:ILE:HD11	2.35	0.41
11:N:1543:A:N1	11:N:2647:U:O2'	2.45	0.41
11:N:2607:A:C4	11:N:2608:A:C2	3.08	0.41
11:N:3385:A:C5	11:N:3386:C:C5	3.08	0.41
2:B:169:ASP:OD1	2:B:170:VAL:N	2.53	0.41
10:K:33:THR:HG23	10:K:59:SER:HB3	2.01	0.41
11:N:1251:G:C2	11:N:1252:C:C2	3.08	0.41
11:N:1465:G:C2	11:N:1515:C:C2	3.09	0.41
11:N:3172:G:C2	11:N:3173:C:C2	3.09	0.41
11:N:3400:U:C2	11:N:3401:A:C8	3.08	0.41
4:D:114:LYS:HG2	4:D:129:VAL:HG22	2.01	0.41
8:H:33:CYS:O	8:H:35:LYS:HG2	2.21	0.41
11:N:1388:U:C5	11:N:1389:G:C6	3.07	0.41
11:N:1442:G:C2	11:N:1533:C:C2	3.07	0.41
11:N:1517:G:C6	11:N:1518:C:C4	3.08	0.41
11:N:1517:G:C2	11:N:1518:C:C2	3.09	0.41
11:N:3033:G:C6	11:N:3034:C:C4	3.08	0.41
11:N:3050:U:H2'	11:N:3051:C:C6	2.56	0.41
11:N:3105:U:O2	11:N:3105:U:O4'	2.38	0.41
11:N:3226:G:C2	11:N:3242:A:C2	3.08	0.41
1:A:172:LEU:HD23	1:A:327:HIS:CE1	2.55	0.41
2:B:47:LEU:HD13	2:B:53:LEU:HD13	2.02	0.41
7:G:14:TYR:O	7:G:16:ALA:N	2.53	0.41
11:N:1225:G:C5	11:N:1226:C:C5	3.09	0.41
11:N:2412:A:C4	11:N:2413:C:C5	3.09	0.41
1:A:3:HIS:CE1	1:A:8:ALA:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:37:ILE:HG23	11:N:2561:A:C5	2.56	0.41
6:F:31:ILE:HG23	6:F:66:GLU:HB2	2.02	0.41
10:K:300:ASN:HB2	10:K:323:LEU:HD13	2.03	0.41
11:N:2404:U:C6	11:N:2408:U:C5	3.08	0.41
11:N:2945:U:O2	11:N:2945:U:H2'	2.21	0.41
11:N:3251:G:C2	11:N:3262:C:C2	3.08	0.41
11:N:3465:A:C8	11:N:3467:U:C5	3.09	0.41
1:A:17:ARG:N	1:A:18:PRO:CD	2.83	0.41
1:A:217:LEU:HD23	1:A:284:LYS:HA	2.01	0.41
1:A:259:HIS:CD2	1:A:260:PRO:HD3	2.55	0.41
2:B:79:ILE:O	2:B:82:VAL:HG12	2.21	0.41
10:K:996:LEU:CD2	10:K:1024:ILE:HD11	2.50	0.41
11:N:1411:G:C6	11:N:1554:A:C2	3.09	0.41
11:N:1473:C:C2'	11:N:1474:C:OP1	2.68	0.41
11:N:2464:A:H1'	11:N:2536:A:C8	2.56	0.41
11:N:3127:G:H1'	11:N:3128:U:C6	2.55	0.41
11:N:3342:A:C2	11:N:3477:A:C4	3.08	0.41
2:B:34:LEU:HD11	2:B:147:ASN:HB3	2.02	0.41
11:N:1399:U:C4	11:N:1400:U:C5	3.09	0.41
11:N:2515:G:C8	11:N:2538:G:C8	3.09	0.41
11:N:2667:A:N3	11:N:2667:A:O4'	2.54	0.41
11:N:2672:C:H1'	11:N:3152:A:C6	2.56	0.41
11:N:3032:G:N2	11:N:3089:C:C2	2.89	0.41
11:N:3422:C:H2'	11:N:3423:C:O4'	2.20	0.41
10:K:114:ILE:HG22	10:K:142:VAL:HG12	2.03	0.41
11:N:1450:U:H2'	11:N:1451:C:C6	2.56	0.41
11:N:2615:U:C4	11:N:2616:A:N1	2.89	0.41
9:J:240:LYS:HD2	11:N:2524:U:C6	2.56	0.40
11:N:1562:G:N2	11:N:1563:U:H1'	2.35	0.40
11:N:3172:G:C2	11:N:3173:C:C6	3.09	0.40
11:N:3363:A:H2'	11:N:3364:G:O4'	2.21	0.40
11:N:1568:G:C6	11:N:1569:C:C4	3.09	0.40
11:N:1583:G:O2'	11:N:1587:U:O4	2.39	0.40
11:N:3478:A:H4'	11:N:3479:A:H5'	2.02	0.40
10:K:535:LEU:HD21	10:K:542:PHE:CD1	2.57	0.40
11:N:3013:A:H3'	11:N:3014:U:H6	1.86	0.40
11:N:3319:U:C2	11:N:3320:A:C8	3.09	0.40
1:A:259:HIS:HA	11:N:3273:A:O2'	2.22	0.40
4:D:114:LYS:HB2	4:D:133:LEU:HD22	2.04	0.40
10:K:27:HIS:CD2	10:K:28:VAL:HG22	2.57	0.40
11:N:2697:U:H2'	11:N:2698:A:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:TRP:CD1	11:N:2661:G:H5'	2.56	0.40
10:K:413:PHE:CE1	10:K:608:ILE:HG21	2.57	0.40
10:K:646:CYS:O	10:K:647:VAL:HG13	2.21	0.40
11:N:2446:G:C6	11:N:2447:C:N4	2.90	0.40
11:N:2592:A:C6	11:N:2593:U:C4	3.10	0.40
11:N:3445:G:N1	11:N:3446:C:C4	2.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	396/398 (100%)	313 (79%)	61 (15%)	22 (6%)	2	21
2	B	186/188 (99%)	159 (86%)	20 (11%)	7 (4%)	3	27
3	C	203/205 (99%)	168 (83%)	30 (15%)	5 (2%)	5	35
4	D	164/166 (99%)	131 (80%)	29 (18%)	4 (2%)	6	36
5	E	134/136 (98%)	113 (84%)	15 (11%)	6 (4%)	2	25
6	F	215/217 (99%)	171 (80%)	35 (16%)	9 (4%)	3	26
7	G	67/69 (97%)	52 (78%)	11 (16%)	4 (6%)	1	20
8	H	50/52 (96%)	41 (82%)	8 (16%)	1 (2%)	7	40
9	J	248/250 (99%)	214 (86%)	26 (10%)	8 (3%)	4	31
10	K	1118/1120 (100%)	939 (84%)	144 (13%)	35 (3%)	4	31
All	All	2781/2801 (99%)	2301 (83%)	379 (14%)	101 (4%)	6	28

All (101) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	THR

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Mol	Chain	Res	Type
1	A	137	GLN
1	A	253	ALA
1	A	259	HIS
1	A	395	SER
6	F	47	PRO
7	G	67	SER
9	J	2	SER
9	J	180	VAL
10	K	337	PRO
10	K	410	VAL
1	A	3	HIS
1	A	10	ARG
1	A	109	HIS
1	A	274	GLY
1	A	285	ILE
1	A	305	GLU
1	A	339	PRO
1	A	360	GLU
2	B	39	ASP
2	B	40	HIS
2	B	51	LYS
3	C	54	MET
5	E	47	ASN
5	E	89	ASP
6	F	108	ALA
6	F	199	VAL
7	G	16	ALA
7	G	43	LYS
9	J	45	LYS
9	J	167	ILE
9	J	170	ALA
10	K	66	ARG
10	K	416	LYS
10	K	769	ASN
10	K	786	GLY
10	K	864	ASP
10	K	1091	MET
1	A	31	SER
1	A	103	LYS
1	A	124	LYS
1	A	319	PHE
1	A	334	GLY

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Mol	Chain	Res	Type
1	A	371	SER
2	B	4	ILE
2	B	20	VAL
4	D	9	GLU
4	D	126	LYS
5	E	72	LYS
6	F	24	ARG
6	F	110	ARG
6	F	177	ASN
8	H	41	SER
9	J	122	PRO
10	K	89	ASN
10	K	129	ALA
10	K	219	ASP
10	K	795	LYS
10	K	844	GLN
10	K	849	THR
10	K	1102	VAL
10	K	1108	GLU
1	A	295	ASP
1	A	361	LYS
3	C	8	ARG
4	D	67	ARG
5	E	19	VAL
6	F	112	GLN
9	J	10	ILE
10	K	118	ASP
10	K	350	PRO
10	K	422	ALA
10	K	626	HIS
10	K	735	ASP
1	A	125	SER
2	B	113	ARG
3	C	146	ILE
4	D	108	GLU
5	E	6	ALA
10	K	257	GLY
10	K	297	ILE
10	K	408	ALA
10	K	651	ILE
10	K	705	VAL
10	K	728	ILE

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Mol	Chain	Res	Type
10	K	1077	PHE
2	B	141	GLU
3	C	16	ALA
10	K	20	ARG
10	K	311	LYS
10	K	617	ILE
10	K	933	GLY
10	K	109	ILE
3	C	154	VAL
5	E	135	ILE
6	F	89	VAL
7	G	15	PRO
10	K	690	ILE
10	K	460	ALA
6	F	76	ILE
9	J	6	PRO

5.3.2 Protein sidechains [i](#)

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	
1	A	337/337 (100%)	305 (90%)	32 (10%)	8	30
2	B	168/168 (100%)	157 (94%)	11 (6%)	17	44
3	C	172/172 (100%)	168 (98%)	4 (2%)	50	70
4	D	139/139 (100%)	134 (96%)	5 (4%)	35	60
5	E	108/108 (100%)	102 (94%)	6 (6%)	21	48
6	F	180/180 (100%)	167 (93%)	13 (7%)	14	41
7	G	65/65 (100%)	61 (94%)	4 (6%)	18	46
8	H	48/48 (100%)	44 (92%)	4 (8%)	11	37
9	J	228/228 (100%)	218 (96%)	10 (4%)	28	54
10	K	975/975 (100%)	948 (97%)	27 (3%)	43	65
All	All	2420/2420 (100%)	2304 (95%)	116 (5%)	29	52

All (116) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	10	ARG
1	A	26	GLN
1	A	35	ASP
1	A	86	ILE
1	A	89	LEU
1	A	94	GLU
1	A	97	GLN
1	A	100	LYS
1	A	104	THR
1	A	113	ASN
1	A	121	ASN
1	A	122	TRP
1	A	133	LYS
1	A	135	VAL
1	A	139	GLU
1	A	159	SER
1	A	180	HIS
1	A	187	ASN
1	A	247	LYS
1	A	266	THR
1	A	269	ARG
1	A	272	GLN
1	A	278	ARG
1	A	280	GLU
1	A	285	ILE
1	A	332	LEU
1	A	342	ARG
1	A	347	ARG
1	A	353	GLN
1	A	363	THR
1	A	364	LEU
2	B	9	LYS
2	B	19	ASP
2	B	26	LYS
2	B	82	VAL
2	B	84	LYS
2	B	92	PHE
2	B	94	TYR
2	B	105	ASP
2	B	134	ARG
2	B	135	ASN

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Mol	Chain	Res	Type
2	B	140	ASP
3	C	32	ASP
3	C	53	LEU
3	C	59	MET
3	C	121	ILE
4	D	45	ASP
4	D	50	THR
4	D	57	LYS
4	D	112	ILE
4	D	137	HIS
5	E	14	SER
5	E	15	LEU
5	E	23	MET
5	E	54	VAL
5	E	72	LYS
5	E	94	TYR
6	F	10	ARG
6	F	17	TYR
6	F	18	ILE
6	F	21	ARG
6	F	69	ARG
6	F	75	TYR
6	F	82	LYS
6	F	142	ASP
6	F	145	LEU
6	F	174	THR
6	F	179	GLU
6	F	181	TYR
6	F	205	THR
7	G	11	PHE
7	G	32	ILE
7	G	34	THR
7	G	49	ILE
8	H	26	LEU
8	H	32	ASN
8	H	38	CYS
8	H	43	ASN
9	J	13	THR
9	J	34	ASN
9	J	48	ASP
9	J	77	THR
9	J	96	SER

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Mol	Chain	Res	Type
9	J	176	PHE
9	J	206	LEU
9	J	237	LEU
9	J	241	ASP
9	J	249	PHE
10	K	20	ARG
10	K	85	GLU
10	K	135	TRP
10	K	193	GLU
10	K	201	ASN
10	K	220	ASP
10	K	243	PHE
10	K	252	TYR
10	K	326	LYS
10	K	349	LEU
10	K	410	VAL
10	K	431	ARG
10	K	486	GLN
10	K	517	ARG
10	K	521	LYS
10	K	647	VAL
10	K	693	ARG
10	K	708	GLU
10	K	721	MET
10	K	725	GLN
10	K	751	LEU
10	K	787	GLU
10	K	853	ASP
10	K	865	LEU
10	K	912	LYS
10	K	1057	TRP
10	K	1088	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	55	HIS
1	A	108	GLN
1	A	121	ASN
1	A	170	HIS
1	A	207	ASN

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Mol	Chain	Res	Type
1	A	246	HIS
2	B	40	HIS
2	B	135	ASN
2	B	183	ASN
5	E	33	ASN
6	F	73	ASN
6	F	143	ASN
6	F	217	ASN
9	J	52	GLN
9	J	103	GLN
9	J	147	ASN
10	K	30	HIS
10	K	64	GLN
10	K	160	GLN
10	K	172	GLN
10	K	201	ASN
10	K	222	HIS
10	K	486	GLN
10	K	500	ASN
10	K	632	GLN
10	K	657	HIS
10	K	793	HIS
10	K	809	GLN
10	K	845	ASN
10	K	925	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	N	1159/3741 (30%)	362 (31%)	46 (3%)

All (362) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	N	1223	U
11	N	1225	G
11	N	1229	U
11	N	1231	U
11	N	1232	C
11	N	1233	G
11	N	1237	G

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Mol	Chain	Res	Type
11	N	1241	A
11	N	1242	A
11	N	1244	G
11	N	1245	C
11	N	1260	C
11	N	1262	A
11	N	1268	G
11	N	1360	U
11	N	1366	A
11	N	1367	A
11	N	1368	G
11	N	1369	C
11	N	1377	G
11	N	1378	C
11	N	1379	G
11	N	1381	U
11	N	1382	G
11	N	1383	U
11	N	1386	G
11	N	1388	U
11	N	1389	G
11	N	1390	A
11	N	1396	A
11	N	1397	U
11	N	1398	A
11	N	1405	U
11	N	1414	U
11	N	1415	A
11	N	1417	C
11	N	1426	A
11	N	1427	U
11	N	1430	A
11	N	1431	U
11	N	1436	C
11	N	1437	A
11	N	1443	U
11	N	1444	G
11	N	1455	A
11	N	1456	A
11	N	1457	G
11	N	1458	A
11	N	1467	C

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Mol	Chain	Res	Type
11	N	1470	U
11	N	1472	G
11	N	1474	C
11	N	1476	U
11	N	1477	G
11	N	1478	G
11	N	1480	A
11	N	1481	G
11	N	1489	C
11	N	1491	G
11	N	1493	U
11	N	1497	G
11	N	1498	A
11	N	1499	G
11	N	1500	U
11	N	1501	G
11	N	1505	A
11	N	1506	A
11	N	1508	A
11	N	1515	C
11	N	1522	A
11	N	1527	C
11	N	1530	G
11	N	1531	C
11	N	1536	A
11	N	1538	A
11	N	1540	U
11	N	1542	G
11	N	1544	U
11	N	1545	G
11	N	1550	U
11	N	1551	A
11	N	1552	G
11	N	1553	C
11	N	1554	A
11	N	1562	G
11	N	1566	A
11	N	1567	U
11	N	1576	G
11	N	1584	A
11	N	1585	A
11	N	1587	U

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Mol	Chain	Res	Type
11	N	1588	G
11	N	1589	A
11	N	1590	U
11	N	1593	U
11	N	1594	A
11	N	1595	C
11	N	1597	U
11	N	1601	A
11	N	1602	C
11	N	2393	A
11	N	2398	A
11	N	2401	G
11	N	2405	A
11	N	2406	A
11	N	2409	A
11	N	2425	A
11	N	2426	U
11	N	2430	C
11	N	2433	A
11	N	2436	A
11	N	2437	G
11	N	2440	U
11	N	2441	U
11	N	2442	U
11	N	2444	A
11	N	2445	C
11	N	2446	G
11	N	2452	U
11	N	2454	A
11	N	2457	U
11	N	2458	C
11	N	2459	U
11	N	2460	G
11	N	2467	G
11	N	2471	U
11	N	2473	A
11	N	2474	A
11	N	2475	U
11	N	2479	A
11	N	2488	A
11	N	2489	G
11	N	2495	A

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Mol	Chain	Res	Type
11	N	2505	G
11	N	2509	A
11	N	2510	A
11	N	2512	G
11	N	2515	G
11	N	2516	G
11	N	2519	G
11	N	2521	A
11	N	2522	A
11	N	2524	U
11	N	2525	A
11	N	2526	U
11	N	2535	U
11	N	2536	A
11	N	2538	G
11	N	2539	G
11	N	2540	U
11	N	2547	A
11	N	2551	C
11	N	2554	G
11	N	2564	U
11	N	2569	A
11	N	2571	G
11	N	2572	C
11	N	2573	G
11	N	2574	C
11	N	2575	A
11	N	2576	U
11	N	2579	A
11	N	2581	G
11	N	2585	C
11	N	2592	A
11	N	2597	C
11	N	2598	A
11	N	2600	U
11	N	2601	G
11	N	2611	A
11	N	2612	C
11	N	2613	U
11	N	2618	A
11	N	2619	G
11	N	2621	G

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Mol	Chain	Res	Type
11	N	2623	A
11	N	2624	A
11	N	2629	U
11	N	2630	G
11	N	2633	A
11	N	2634	G
11	N	2637	G
11	N	2638	A
11	N	2639	A
11	N	2640	C
11	N	2641	G
11	N	2642	G
11	N	2649	C
11	N	2652	A
11	N	2654	A
11	N	2659	G
11	N	2660	G
11	N	2661	G
11	N	2663	A
11	N	2664	A
11	N	2668	A
11	N	2669	G
11	N	2670	A
11	N	2676	U
11	N	2677	U
11	N	2678	G
11	N	2685	A
11	N	2687	U
11	N	2688	C
11	N	2700	U
11	N	2926	A
11	N	2927	C
11	N	2928	A
11	N	2929	G
11	N	2931	U
11	N	2939	G
11	N	2940	G
11	N	2941	G
11	N	2945	U
11	N	2947	G
11	N	2951	G
11	N	2954	G

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Mol	Chain	Res	Type
11	N	2959	A
11	N	2968	A
11	N	2970	A
11	N	2971	A
11	N	2975	A
11	N	2977	C
11	N	2978	G
11	N	2981	A
11	N	2985	U
11	N	2987	C
11	N	2988	A
11	N	2989	A
11	N	2990	A
11	N	3000	A
11	N	3005	G
11	N	3007	A
11	N	3010	G
11	N	3021	U
11	N	3022	A
11	N	3023	G
11	N	3024	A
11	N	3027	A
11	N	3029	A
11	N	3035	A
11	N	3037	A
11	N	3038	A
11	N	3047	G
11	N	3055	U
11	N	3060	A
11	N	3061	G
11	N	3062	U
11	N	3078	G
11	N	3079	A
11	N	3085	G
11	N	3086	G
11	N	3091	A
11	N	3093	C
11	N	3095	A
11	N	3099	U
11	N	3102	A
11	N	3105	U
11	N	3109	U

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Mol	Chain	Res	Type
11	N	3110	A
11	N	3111	A
11	N	3112	A
11	N	3113	U
11	N	3114	C
11	N	3116	U
11	N	3117	A
11	N	3129	G
11	N	3133	G
11	N	3135	A
11	N	3137	A
11	N	3138	G
11	N	3143	C
11	N	3149	G
11	N	3151	U
11	N	3178	A
11	N	3180	A
11	N	3189	G
11	N	3192	U
11	N	3193	U
11	N	3194	U
11	N	3204	G
11	N	3205	A
11	N	3206	U
11	N	3208	U
11	N	3215	U
11	N	3220	A
11	N	3221	U
11	N	3222	C
11	N	3230	A
11	N	3231	G
11	N	3232	C
11	N	3237	U
11	N	3245	G
11	N	3250	G
11	N	3255	G
11	N	3258	C
11	N	3264	C
11	N	3268	C
11	N	3269	A
11	N	3271	G
11	N	3274	A

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Mol	Chain	Res	Type
11	N	3275	C
11	N	3276	G
11	N	3279	A
11	N	3280	G
11	N	3283	G
11	N	3284	G
11	N	3285	G
11	N	3286	U
11	N	3287	U
11	N	3288	U
11	N	3291	A
11	N	3298	U
11	N	3299	G
11	N	3304	A
11	N	3305	G
11	N	3311	U
11	N	3312	U
11	N	3313	U
11	N	3316	C
11	N	3319	U
11	N	3323	G
11	N	3329	A
11	N	3330	A
11	N	3332	U
11	N	3335	U
11	N	3336	U
11	N	3339	G
11	N	3348	G
11	N	3357	A
11	N	3362	G
11	N	3364	G
11	N	3385	A
11	N	3392	U
11	N	3393	G
11	N	3395	A
11	N	3397	G
11	N	3405	G
11	N	3406	A
11	N	3414	G
11	N	3415	U
11	N	3420	U
11	N	3426	U

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Mol	Chain	Res	Type
11	N	3428	C
11	N	3435	U
11	N	3437	G
11	N	3440	U
11	N	3445	G
11	N	3446	C
11	N	3452	G
11	N	3454	C
11	N	3458	A
11	N	3463	A
11	N	3465	A
11	N	3466	A
11	N	3467	U
11	N	3470	A
11	N	3474	U
11	N	3477	A
11	N	3478	A
11	N	3479	A
11	N	3480	C

All (46) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	N	1221	A
11	N	1259	U
11	N	1381	U
11	N	1397	U
11	N	1457	G
11	N	1473	C
11	N	1550	U
11	N	1565	G
11	N	1588	G
11	N	2400	U
11	N	2441	U
11	N	2444	A
11	N	2445	C
11	N	2470	C
11	N	2475	U
11	N	2515	G
11	N	2538	G
11	N	2571	G
11	N	2600	U

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Mol	Chain	Res	Type
11	N	2618	A
11	N	2625	C
11	N	2638	A
11	N	2669	G
11	N	2676	U
11	N	2955	C
11	N	2968	A
11	N	2970	A
11	N	3060	A
11	N	3070	G
11	N	3115	U
11	N	3150	A
11	N	3193	U
11	N	3205	A
11	N	3219	U
11	N	3283	G
11	N	3287	U
11	N	3304	A
11	N	3316	C
11	N	3328	C
11	N	3384	C
11	N	3391	C
11	N	3429	C
11	N	3457	U
11	N	3466	A
11	N	3476	G
11	N	3477	A

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 monosaccharides 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.

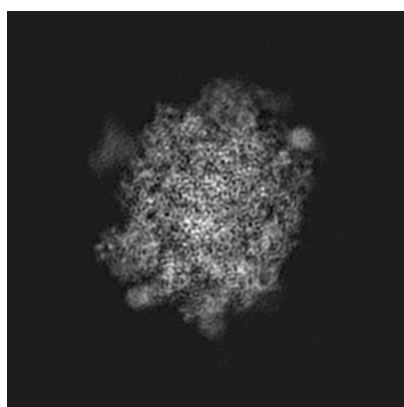
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3147. These allow visual inspection of the internal detail of the map and identification of artifacts.

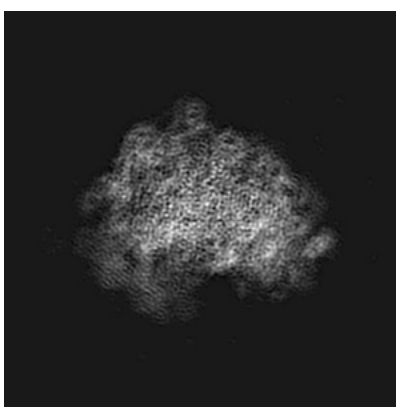
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

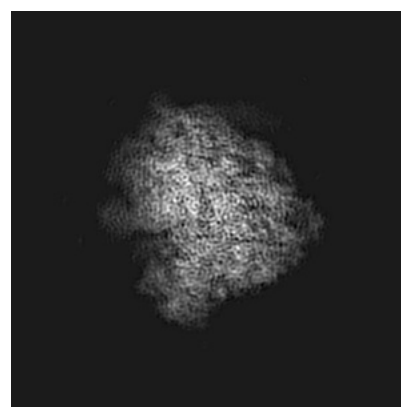
6.1.1 Primary map



X



Y

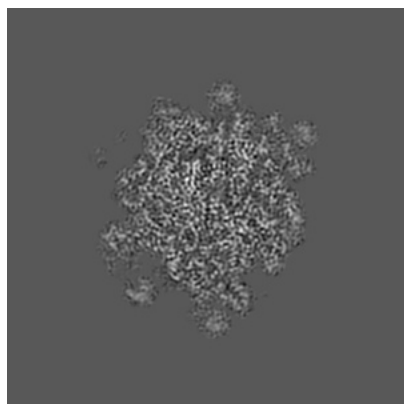


Z

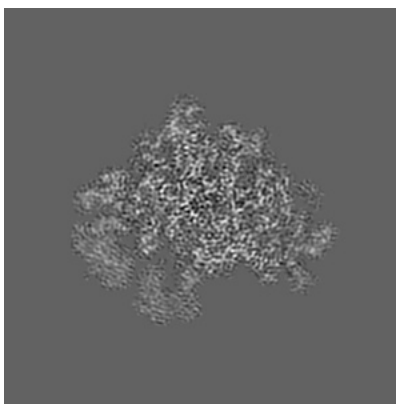
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

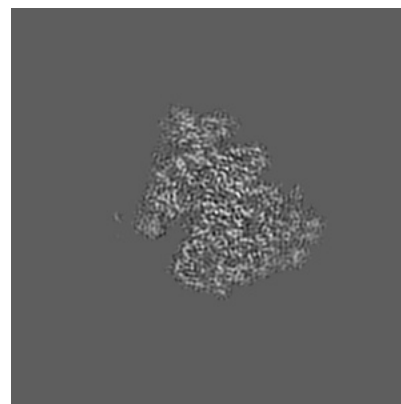
6.2.1 Primary map



X Index: 150



Y Index: 150

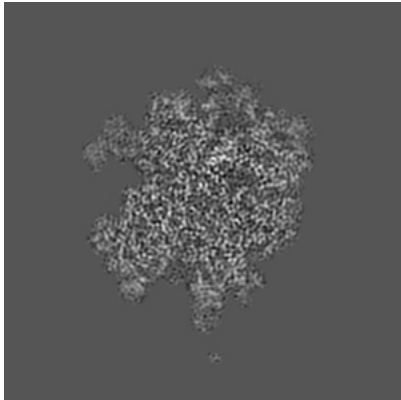


Z Index: 150

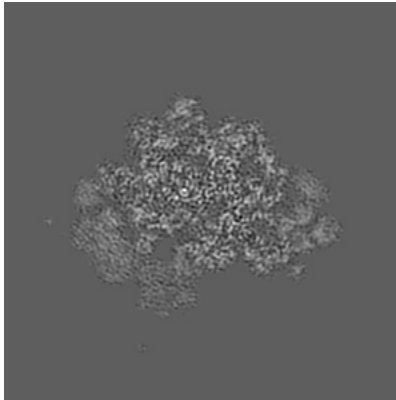
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

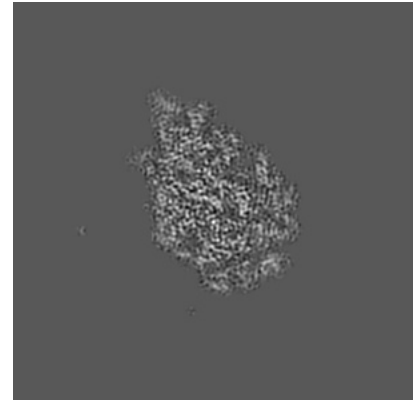
6.3.1 Primary map



X Index: 136



Y Index: 155



Z Index: 171

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

6.4 Orthogonal surface views [i](#)

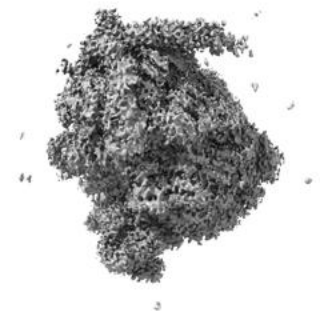
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

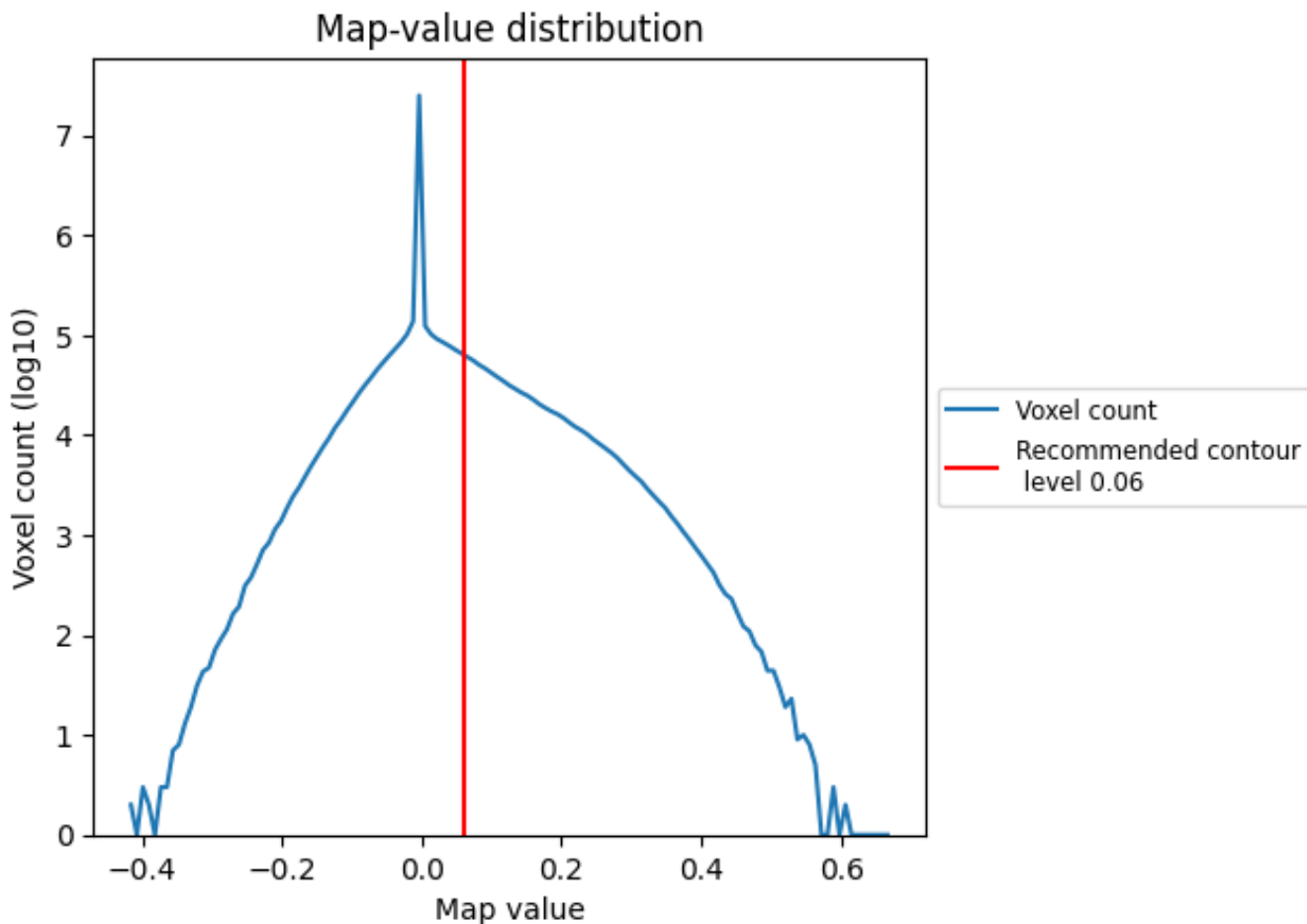
6.5 Mask visualisation

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

7 Map analysis [i](#)

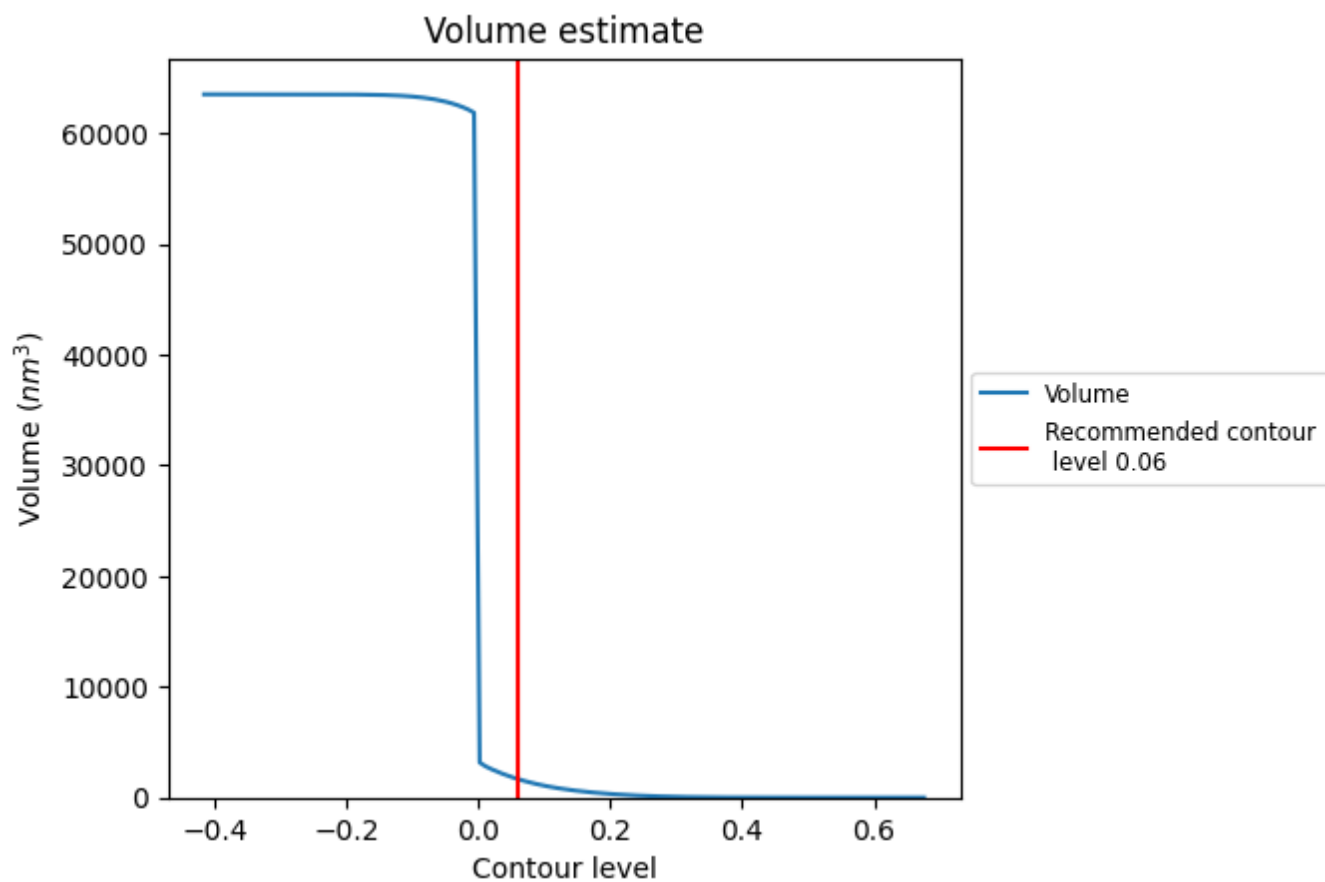
This section contains the results of statistical analysis of the map.

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.

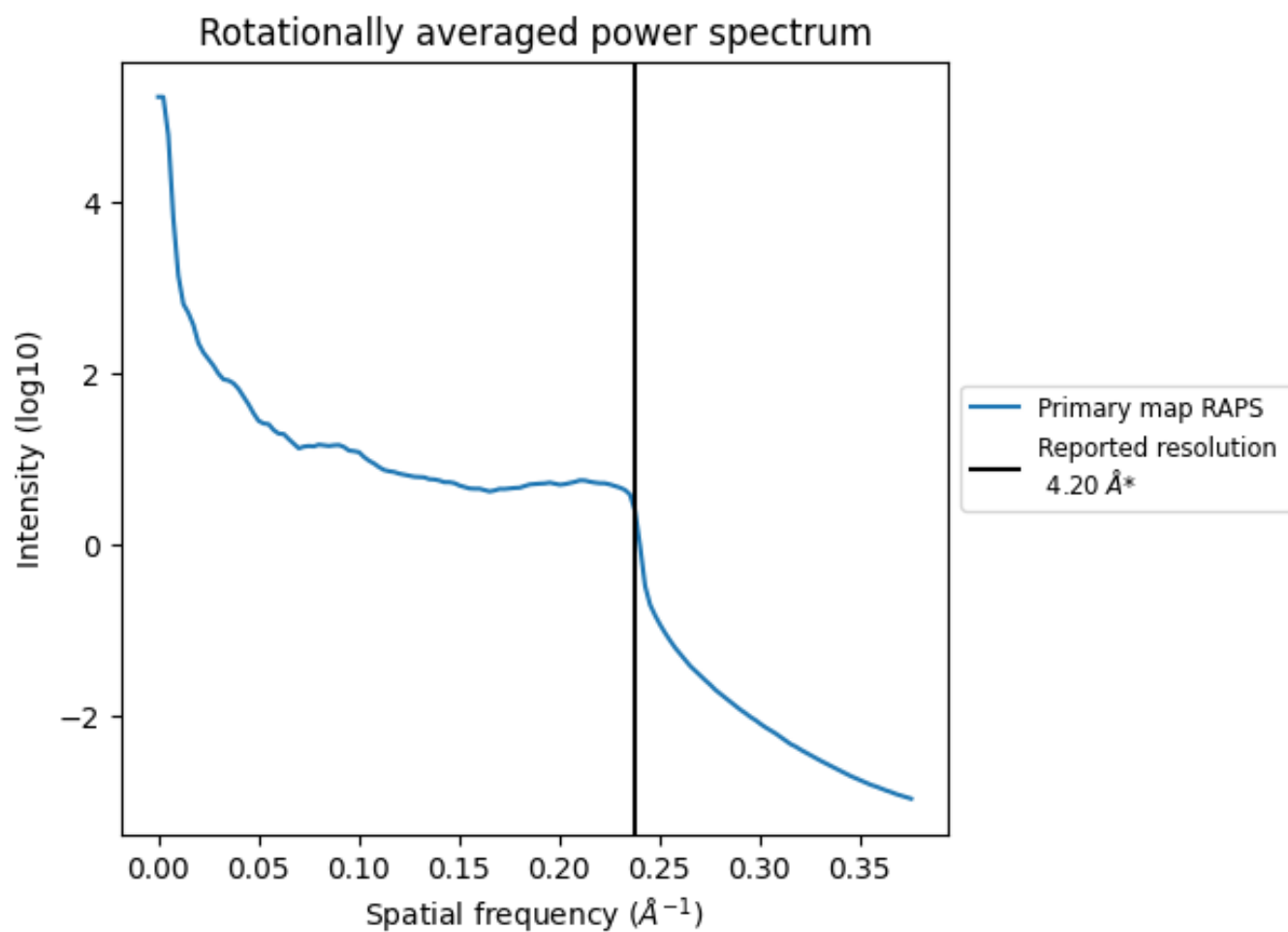
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1667 nm³; this corresponds to an approximate mass of 1506 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.238\AA^{-1}

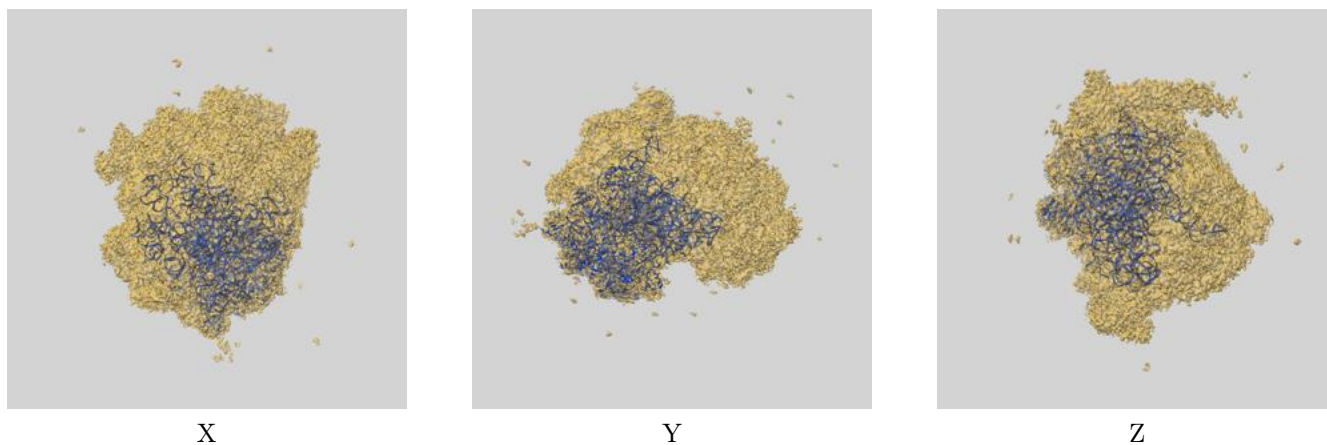
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

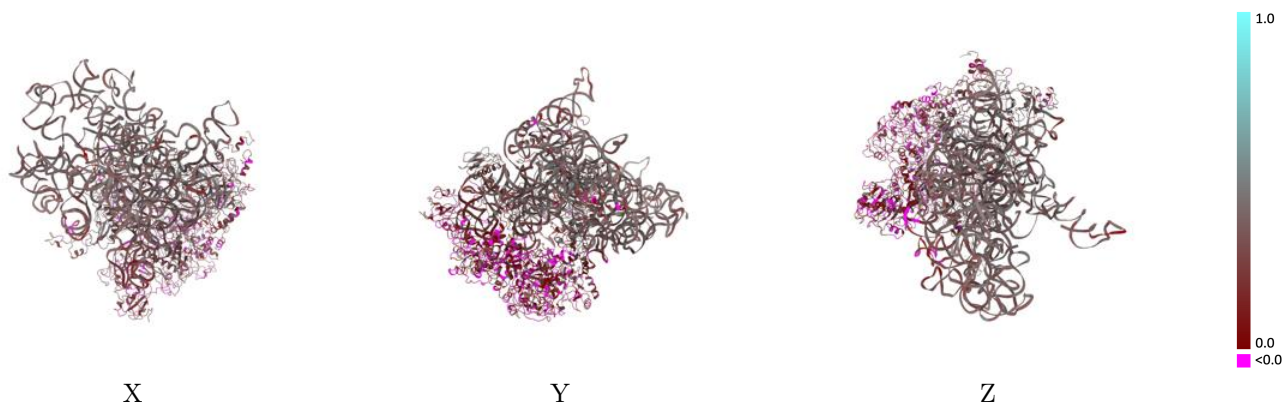
This section contains information regarding the fit between EMDB map EMD-3147 and PDB model 5ANC. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



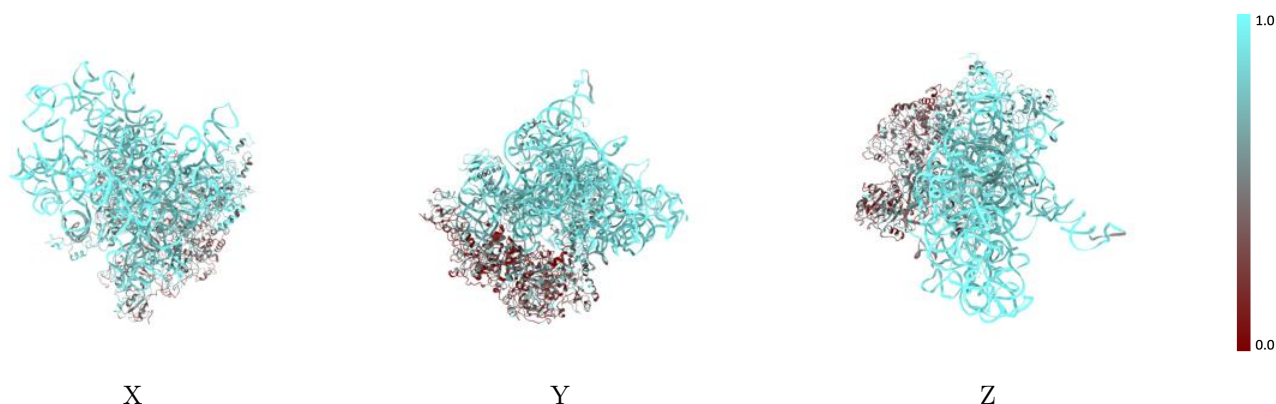
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



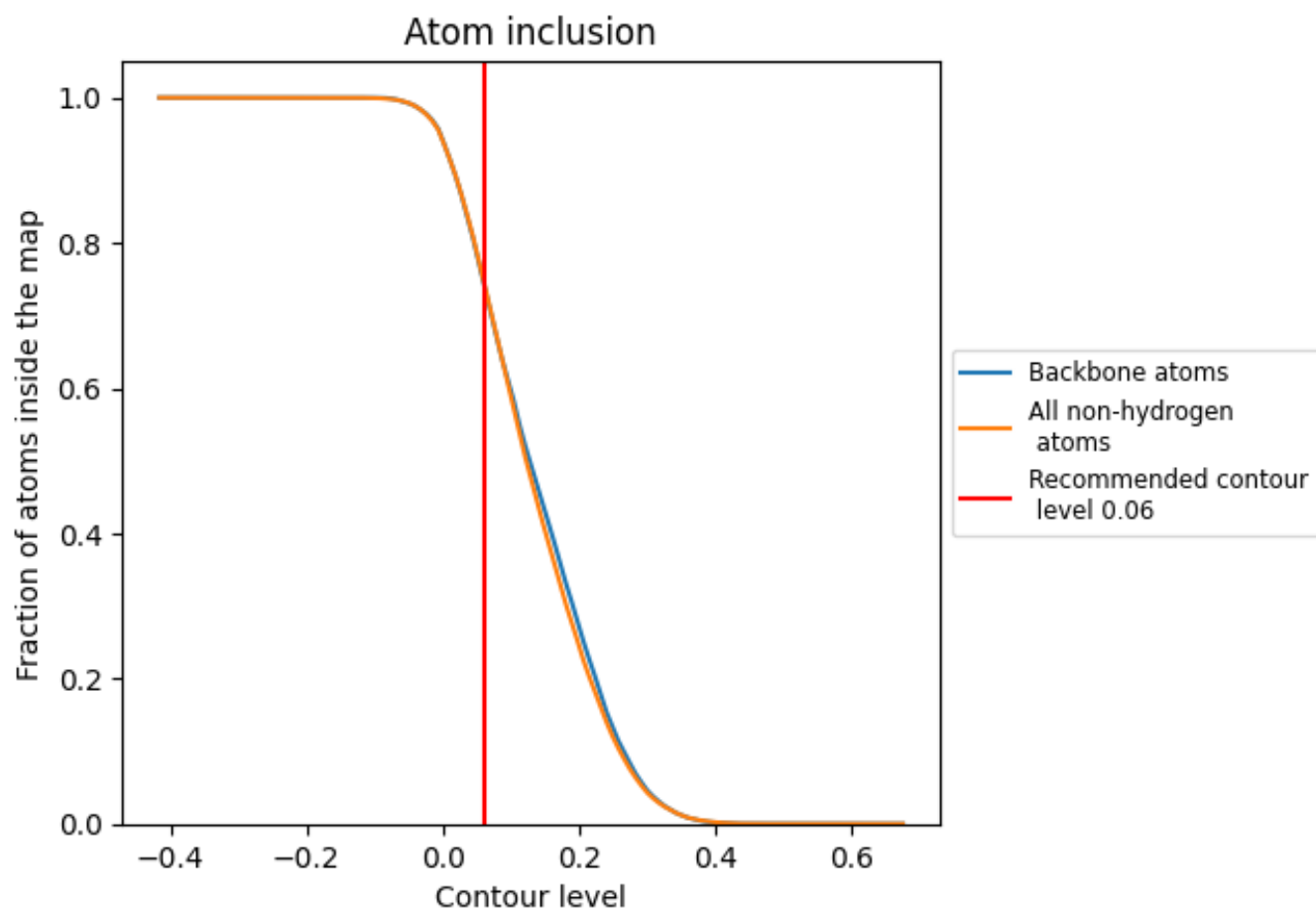
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

























9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7475	 0.2870
A	 0.8236	 0.3410
B	 0.7874	 0.3300
C	 0.3742	 0.1340
D	 0.4773	 0.1360
E	 0.8245	 0.3670
F	 0.8037	 0.3540
G	 0.8060	 0.2920
H	 0.8378	 0.3570
J	 0.5685	 0.2110
K	 0.3674	 0.1140
N	 0.9100	 0.3540

