



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:48 AM UTC

PDB ID : 7OF1 / pdb_00007of1
EMDB ID : EMD-12866
Title : Nog1-TAP associated immature ribosomal particle population A from *S. cerevisiae*
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-04
Resolution : 3.10 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:

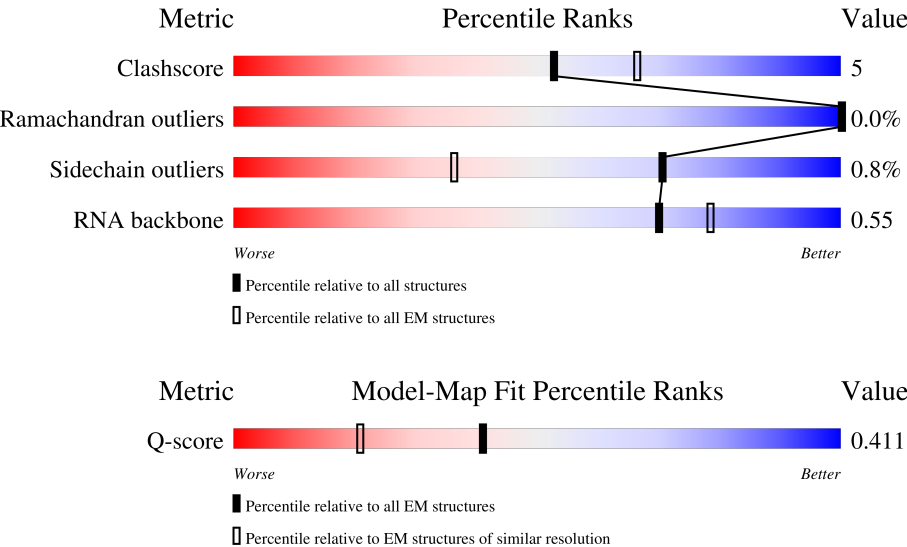
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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	14724 (2.60 - 3.60)

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	1	3396	52% 25% 5% 18%
2	2	158	58% 38%
3	3	121	25% 10% 64%

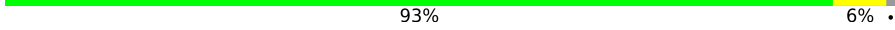
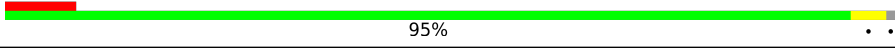
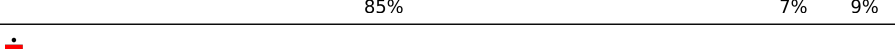
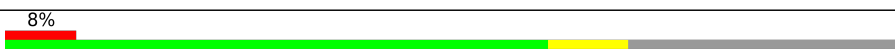
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Mol	Chain	Length	Quality of chain
4	A	254	
5	B	387	
6	C	362	
7	E	176	
8	F	244	
9	G	256	
10	H	191	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	121	
21	V	137	
22	W	236	
23	X	142	
24	Y	127	
25	Z	136	
26	a	149	
27	b	647	
28	c	105	

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Mol	Chain	Length	Quality of chain
29	d	113	 87% 8%
30	e	130	 90% 7%
31	f	107	 86% 12%
32	g	121	 77% 7% 17%
33	h	120	 93% 6%
34	i	100	 88% 8%
35	j	88	 80% 17%
36	k	78	 8% 95%
37	l	51	 86% 12%
38	m	486	 18% 40% 7% 53%
39	p	92	 11% 85% 7% 9%
40	r	261	 34% 62%
41	u	199	 8% 61% 9% 31%
42	y	245	 72% 19% 9%

2 Entry composition [i](#)

There are 43 unique types of molecules in this entry. The entry contains 199300 atoms, of which 84914 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 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	2787	Total	C	H	N	O	P	0	0
			89635	26644	29972	10797	19435	2787		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	158	Total	C	H	N	O	P	0	0
			5048	1500	1695	586	1109	158		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	3	43	Total	C	H	N	O	P	0	0
			1388	412	464	170	299	43		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	A	208	Total	C	H	N	O	S	0	0
			3268	1006	1663	319	279	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	B	386	Total	C	H	N	O	S	0	0
			6247	1956	3166	584	533	8		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	C	361	Total	C	H	N	O	S	0	0
			5613	1730	2864	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	E	160	Total	C	H	N	O	S	0	0
			2637	820	1363	230	223	1		

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	F	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	G	225	Total	C	H	N	O	S	0	0
			3612	1127	1853	313	316	3		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	H	188	Total	C	H	N	O	S	0	0
			3059	948	1566	271	270	4		

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	L	178	Total	C	H	N	O		0	0
			2895	885	1473	296	241			

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	M	137	Total	C	H	N	O	S	0	0
			2214	678	1155	200	179	2		

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	N	203	Total	C	H	N	O	S	0	0
			3500	1077	1780	361	281	1		

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	O	197	Total	C	H	N	O	S	0	0
			3216	1003	1661	289	262	1		

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	176	Total	C	H	N	O		0	0
			2823	865	1430	278	250			

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	Q	146	Total	C	H	N	O	S	0	0
			2335	713	1206	218	197	1		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	R	154	Total	C	H	N	O		0	0
			2572	772	1331	262	207			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	170	Total	C	H	N	O	S	0	0
			2892	916	1467	265	241	3		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	61	Total	C	H	N	O	S	0	0
			976	295	500	95	85	1		

- Molecule 20 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	U	102	Total	C	H	N	O		0	0
			1631	524	823	132	152			

- Molecule 21 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	136	Total	C	H	N	O	S	0	0
			2052	628	1049	189	179	7		

- Molecule 22 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	227	Total	C	H	N	O	S	0	0
			3648	1149	1834	310	350	5		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	X	120	Total	C	H	N	O	S	0	0
			1984	617	1025	168	172	2		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Y	126	Total	C	H	N	O		0	0
			2075	625	1082	192	176			

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	135	Total	C	H	N	O		0	0
			2248	710	1156	202	180			

- Molecule 26 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	a	94	Total	C	H	N	O	S	0	0
			1528	484	786	131	126	1		

- Molecule 27 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	b	497	Total	C	H	N	O	S	0	0
			8098	2554	4075	698	752	19		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	c	97	Total	C	H	N	O	S	0	0
			1541	479	798	124	139	1		

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	d	104	Total	C	H	N	O	S	0	0
			1746	539	899	162	145	1		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	e	126	Total	C	H	N	O	S	0	0
			2093	641	1081	204	166	1		

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	g	101	Total	C	H	N	O	S	0	0
			1652	493	856	164	135	4		

- Molecule 33 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	h	119	Total	C	H	N	O	S	0	0
			2048	615	1079	186	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	i	96	Total	C	H	N	O	S	0	0
			1566	465	823	148	128	2		

- Molecule 35 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	j	85	Total	C	H	N	O	S	0	0
			1348	408	678	146	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	k	77	Total	C	H	N	O		0	0
			1295	391	683	115	106			

- Molecule 37 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	l	50	Total	C	H	N	O	S	0	0
			912	272	476	97	65	2		

- Molecule 38 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	m	229	Total	C	H	N	O	S	0	0
			3669	1162	1855	325	322	5		

- Molecule 39 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	p	84	Total	C	H	N	O	S	0	0
			1329	397	687	130	110	5		

- Molecule 40 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	r	99	Total	C	H	N	O	S	0	0
			1769	531	918	181	136	3		

- Molecule 41 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	u	138	Total	C	H	N	O	S	0	0
			2379	732	1212	235	191	9		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	y	224	Total	C	H	N	O	S	0	0
			3379	1051	1686	294	342	6		

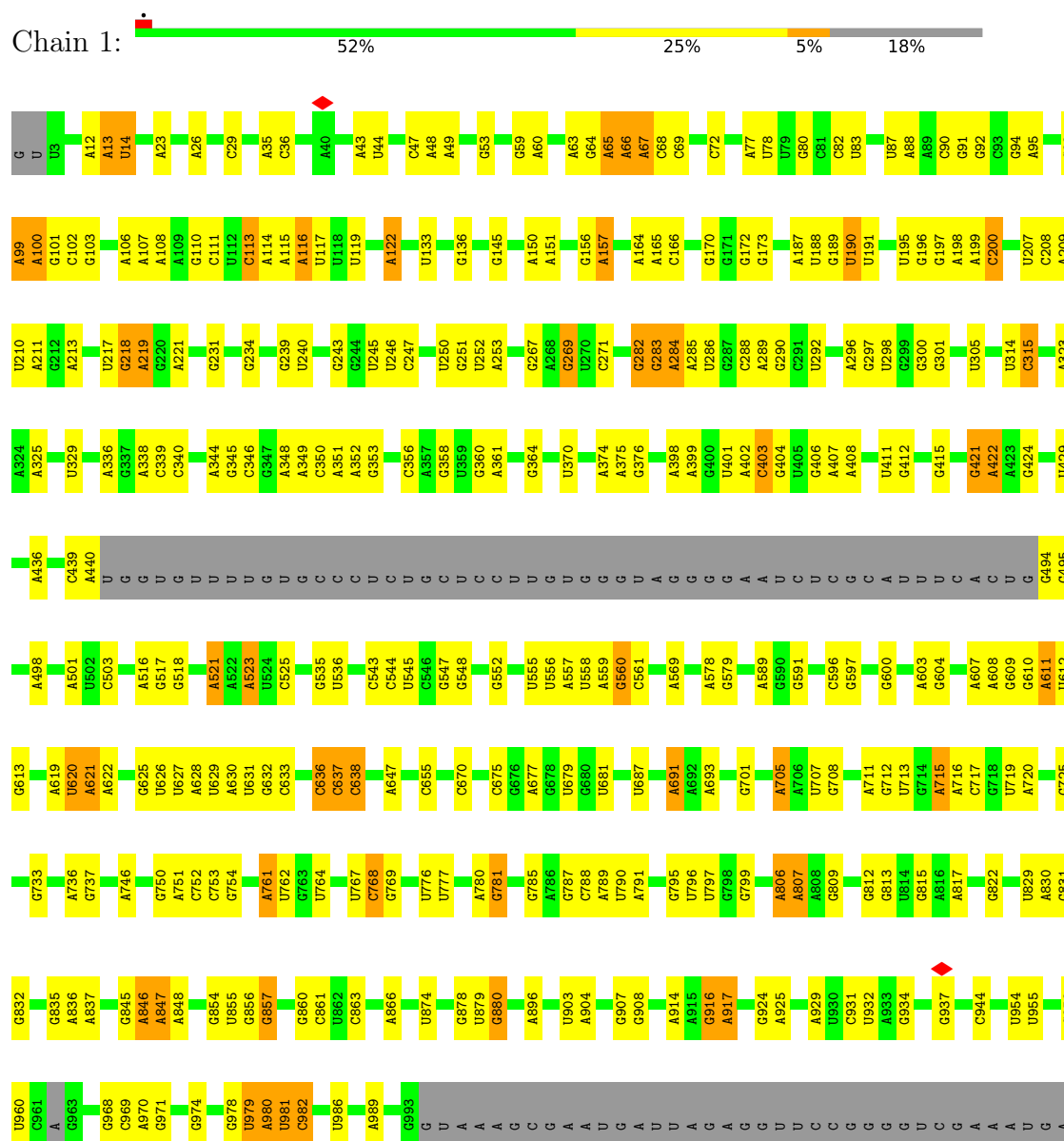
- Molecule 43 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
43	b	1	Total	Mg	0
			1	1	
43	m	1	Total	Mg	0
			1	1	

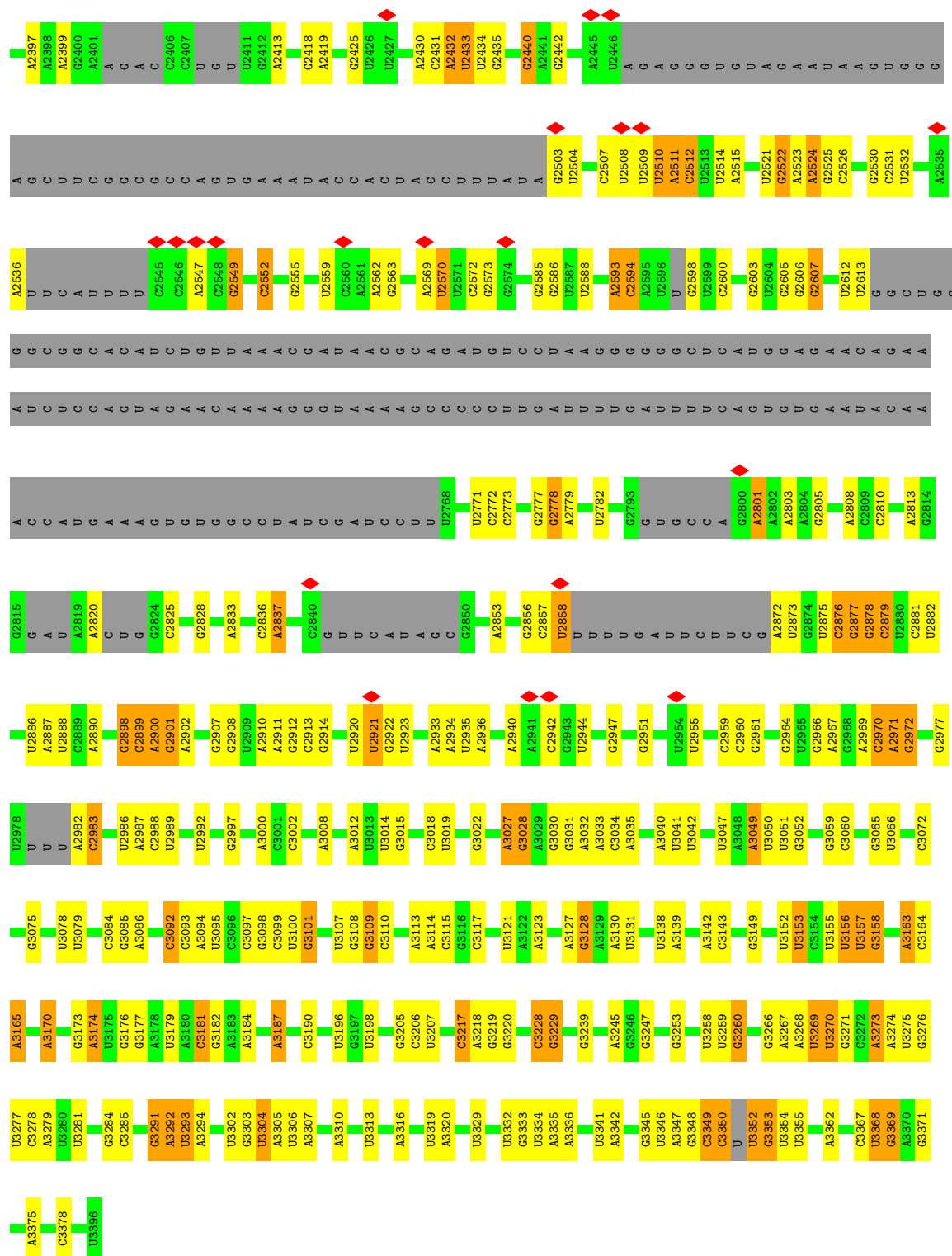
3 Residue-property plots

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

• Molecule 1: 25S rRNA

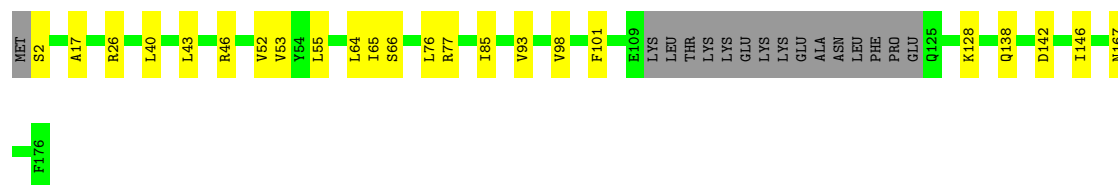






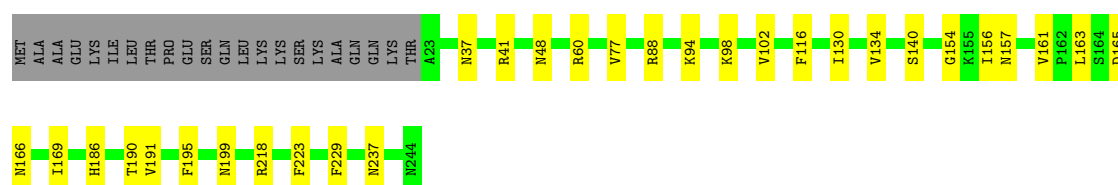
- Molecule 7: 60S ribosomal protein L6-A

Chain E:  78% 13% 9%



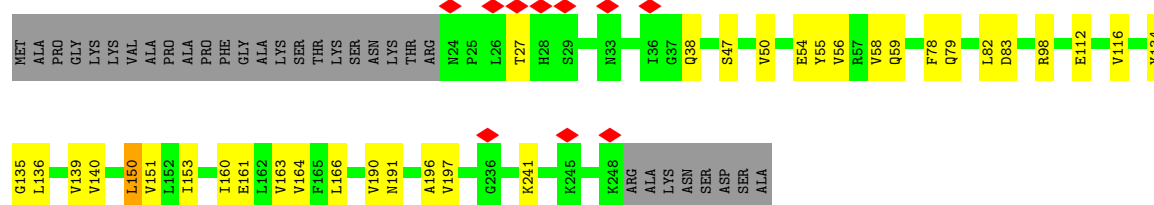
- Molecule 8: 60S ribosomal protein L7-A

Chain F:  79% 12% 9%



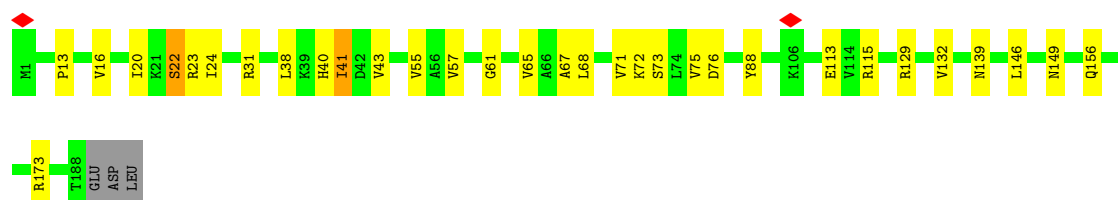
- Molecule 9: 60S ribosomal protein L8-A

Chain G:  75% 13% 12%



- Molecule 10: 60S ribosomal protein L9-A

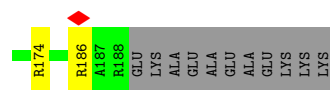
Chain H:  81% 16% ..



- Molecule 11: 60S ribosomal protein L13-A

Chain L:  76% 14% 11%

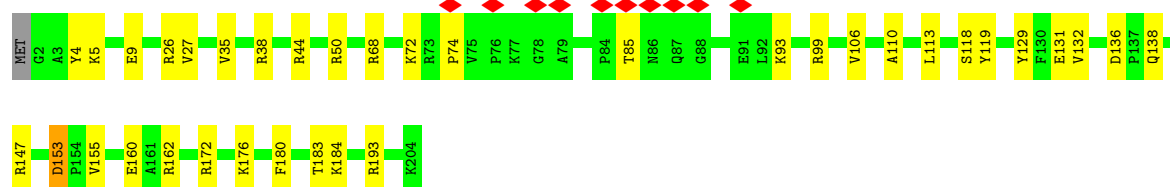
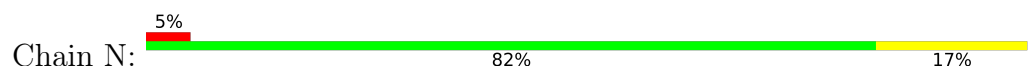




- Molecule 12: 60S ribosomal protein L14-A



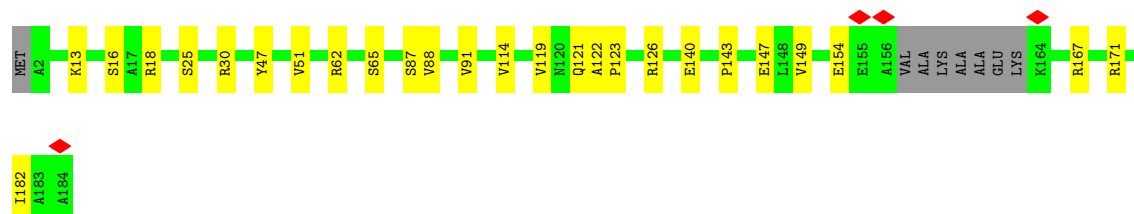
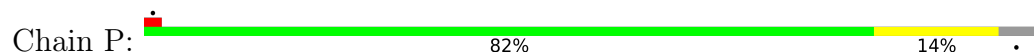
- Molecule 13: 60S ribosomal protein L15-A



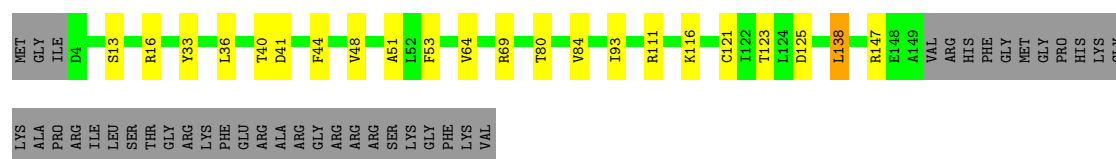
- Molecule 14: 60S ribosomal protein L16-A



- Molecule 15: 60S ribosomal protein L17-A

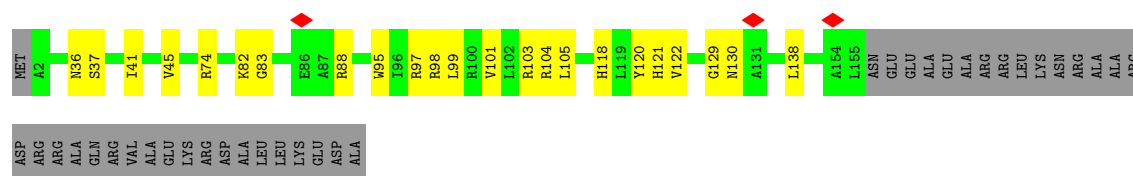


- Molecule 16: 60S ribosomal protein L18-A



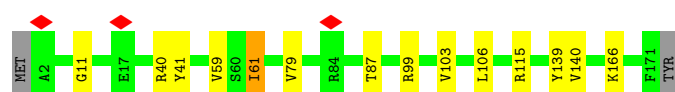
- Molecule 17: 60S ribosomal protein L19-A

Chain R: 



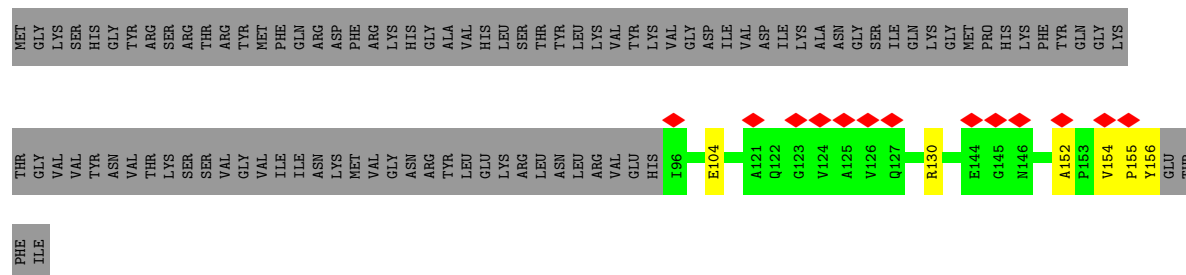
- Molecule 18: 60S ribosomal protein L20-A

Chain S: 



- Molecule 19: 60S ribosomal protein L21-A

Chain T: 



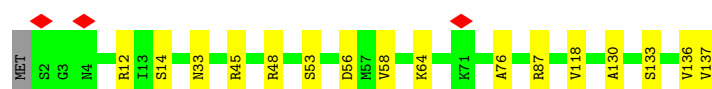
- Molecule 20: 60S ribosomal protein L22-A

Chain U: 



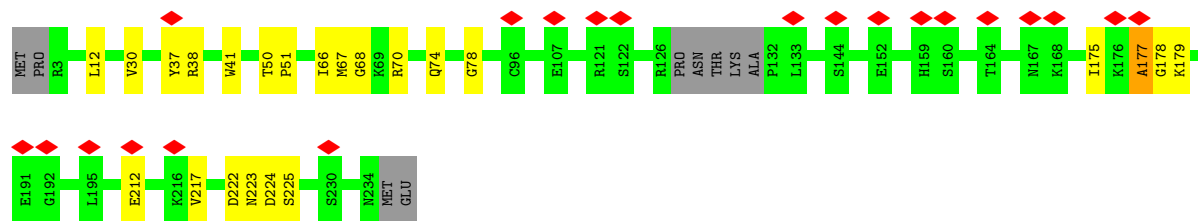
- Molecule 21: 60S ribosomal protein L23-A

Chain V: 

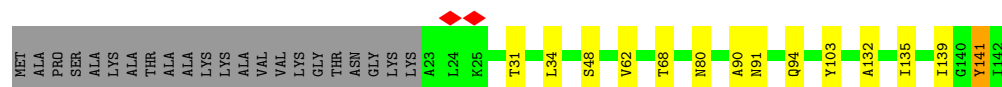
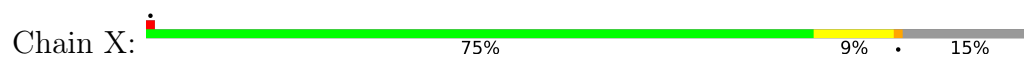


- Molecule 22: Ribosome assembly factor MRT4

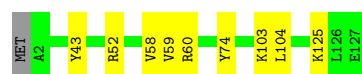
Chain W: 



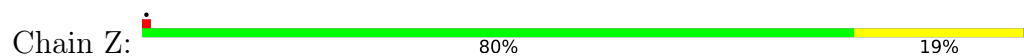
- Molecule 23: 60S ribosomal protein L25



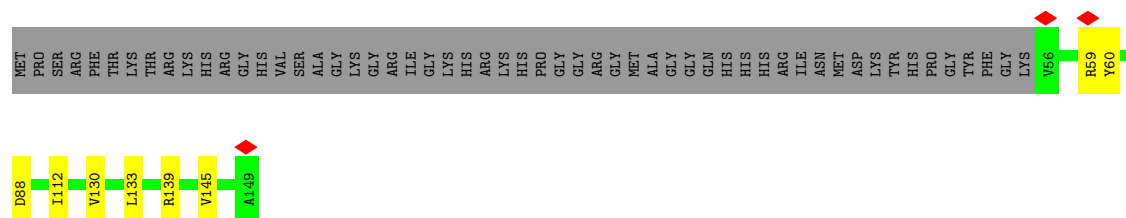
- Molecule 24: 60S ribosomal protein L26-A



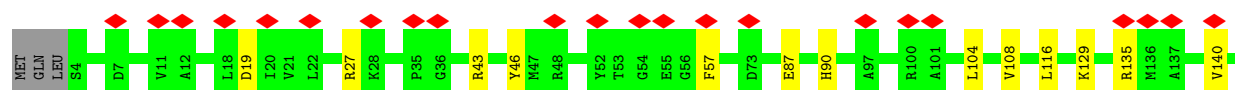
- Molecule 25: 60S ribosomal protein L27-A

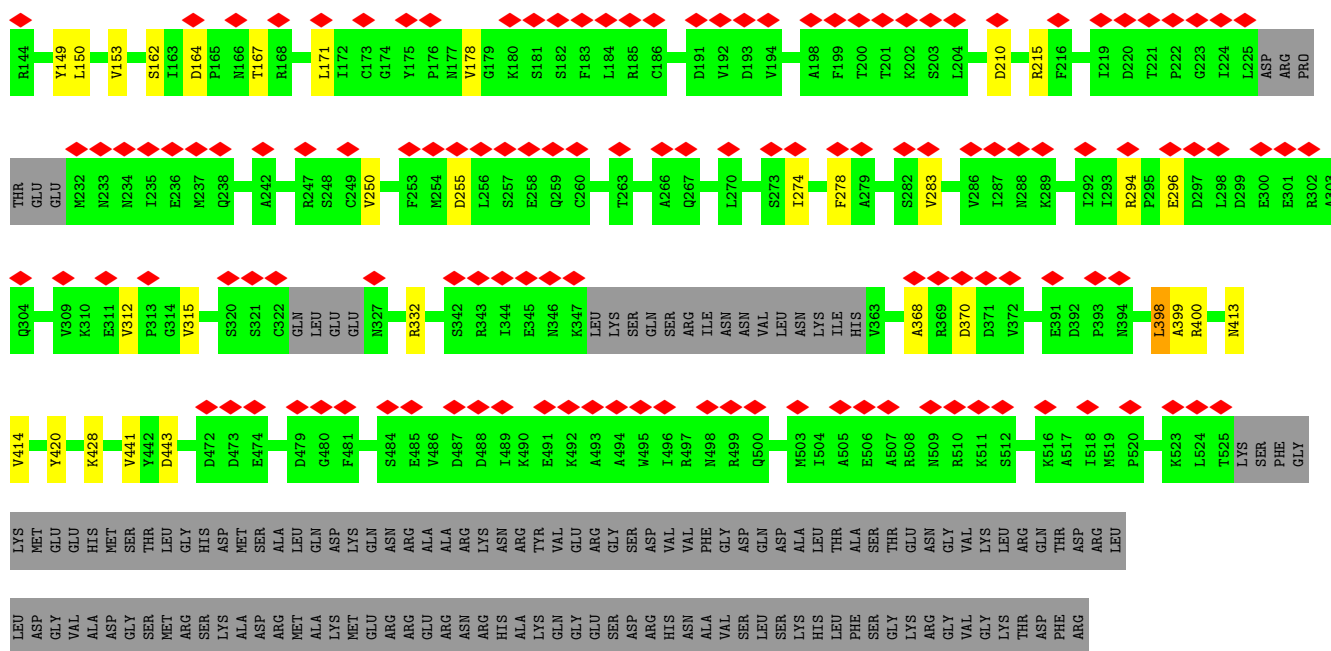


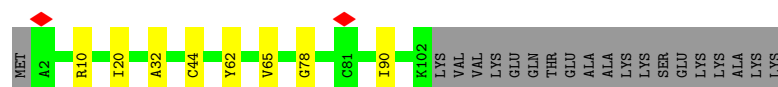
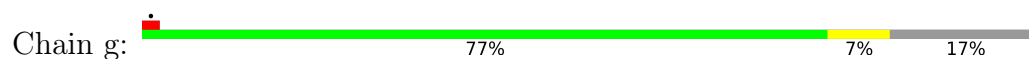
- Molecule 26: 60S ribosomal protein L28



- Molecule 27: Nucleolar GTP-binding protein 1



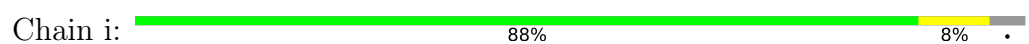




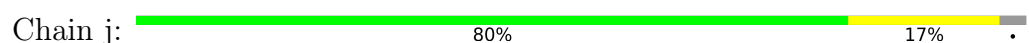
- Molecule 33: 60S ribosomal protein L35-A



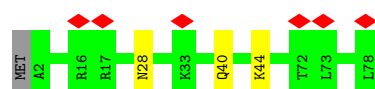
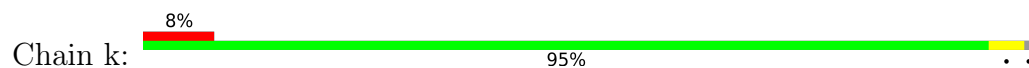
- Molecule 34: 60S ribosomal protein L36-A



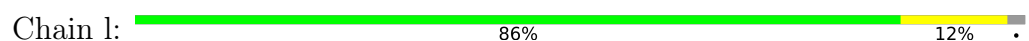
- Molecule 35: 60S ribosomal protein L37-A



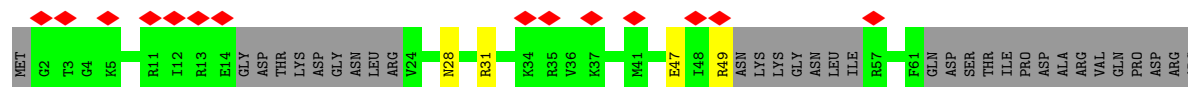
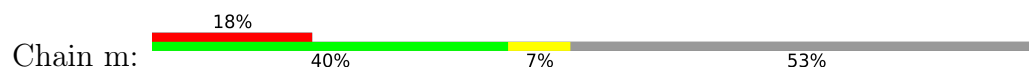
- Molecule 36: 60S ribosomal protein L38

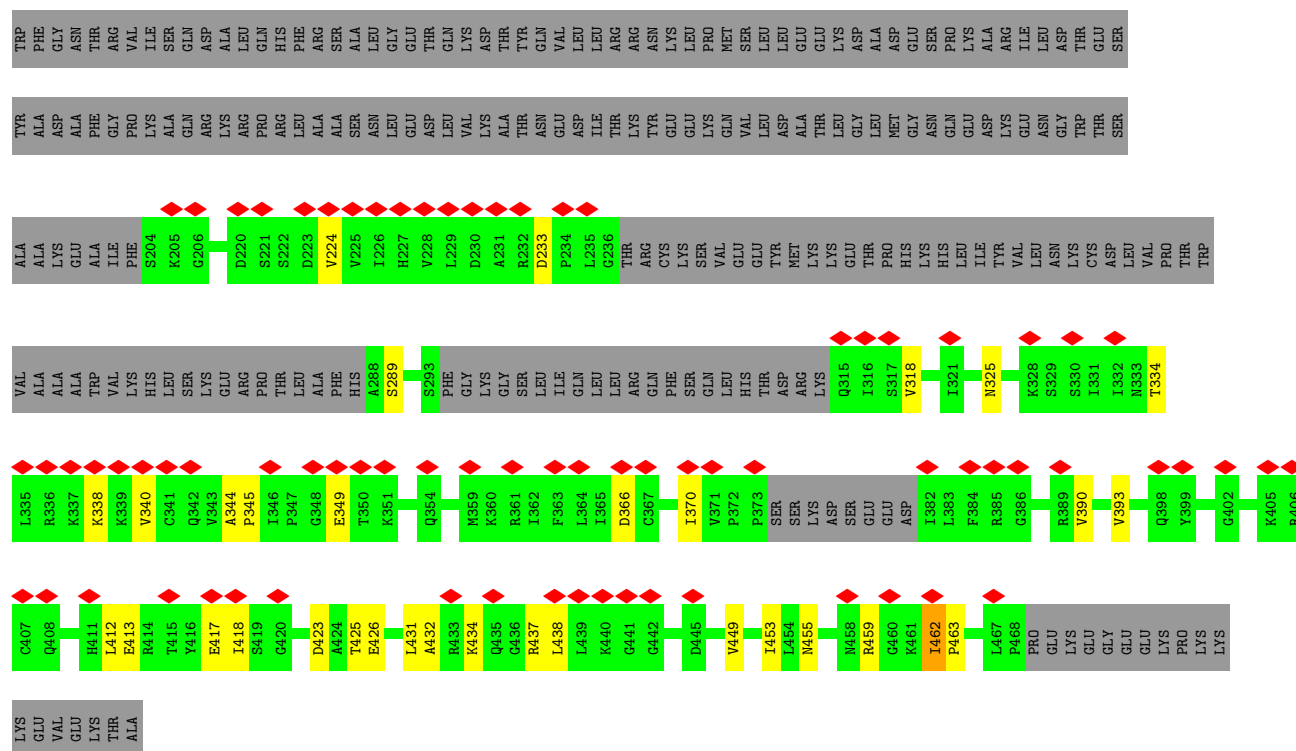


- Molecule 37: 60S ribosomal protein L39

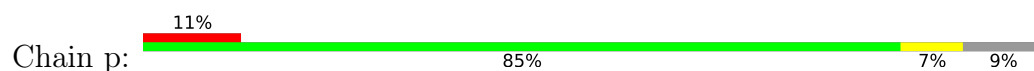


- Molecule 38: Nucleolar GTP-binding protein 2

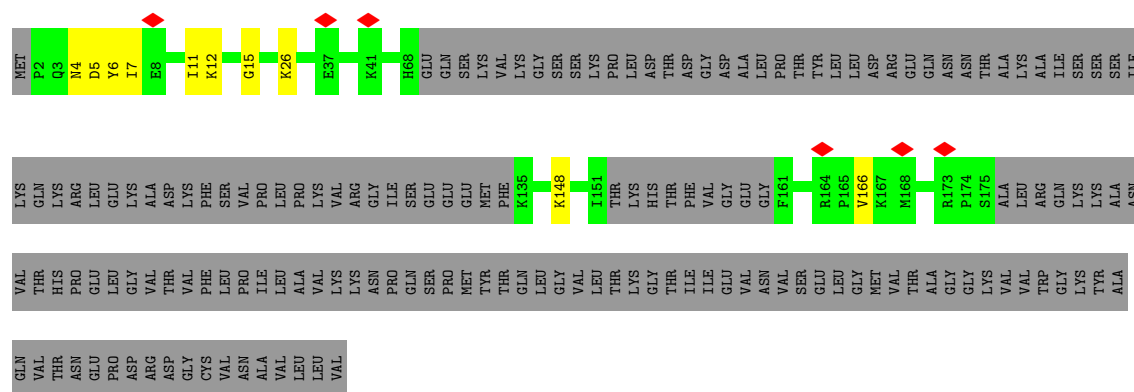




• Molecule 39: 60S ribosomal protein L43-A

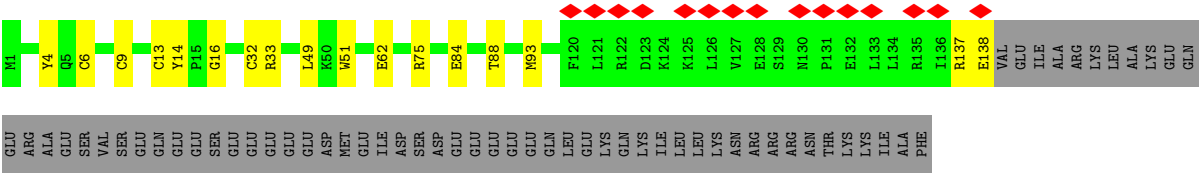


• Molecule 40: Ribosome biogenesis protein NSA2

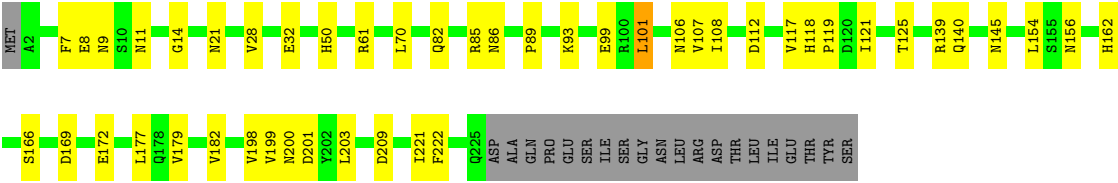


• Molecule 41: Ribosome biogenesis protein RLP24





● Molecule 42: Eukaryotic translation initiation factor 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	95319	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 ($e^-/\text{\AA}^2$)	84.67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.113	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.016	Depositor
Map size ($\text{\AA}$)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	1	0.07	0/66772	0.22	0/104061
2	2	0.08	0/3746	0.21	0/5832
3	3	0.06	0/1034	0.19	0/1611
4	A	0.12	0/1635	0.25	0/2199
5	B	0.12	0/3152	0.28	0/4239
6	C	0.10	0/2801	0.27	0/3792
7	E	0.11	0/1295	0.25	0/1740
8	F	0.10	0/1821	0.24	0/2451
9	G	0.10	0/1791	0.24	0/2418
10	H	0.10	0/1514	0.28	0/2039
11	L	0.12	0/1446	0.29	0/1943
12	M	0.11	0/1074	0.23	0/1446
13	N	0.12	0/1757	0.25	0/2354
14	O	0.11	0/1585	0.22	0/2128
15	P	0.10	0/1415	0.25	0/1900
16	Q	0.10	0/1146	0.22	0/1546
17	R	0.11	0/1258	0.27	0/1679
18	S	0.10	0/1460	0.24	0/1962
19	T	0.15	0/483	0.34	0/650
20	U	0.11	0/825	0.26	0/1120
21	V	0.14	0/1018	0.25	0/1369
22	W	0.11	0/1843	0.26	0/2483
23	X	0.10	0/974	0.22	0/1314
24	Y	0.11	0/1004	0.26	0/1341
25	Z	0.10	0/1118	0.22	0/1497
26	a	0.10	0/758	0.21	0/1023
27	b	0.09	0/4094	0.26	0/5515
28	c	0.10	0/751	0.20	0/1008
29	d	0.11	0/861	0.25	0/1156
30	e	0.11	0/1033	0.22	0/1383
31	f	0.12	0/868	0.26	0/1168
32	g	0.12	0/806	0.28	0/1078

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.11	0/978	0.22	0/1301
34	i	0.12	0/749	0.23	0/995
35	j	0.14	0/685	0.26	0/908
36	k	0.10	0/618	0.24	0/826
37	l	0.15	0/443	0.31	0/588
38	m	0.10	0/1847	0.24	0/2483
39	p	0.12	0/649	0.24	0/865
40	r	0.12	0/864	0.29	0/1133
41	u	0.10	0/1189	0.28	0/1581
42	y	0.09	0/1714	0.23	0/2333
All	All	0.09	0/122874	0.23	0/180458

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
10	H	0	1
22	W	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	H	22	SER	Peptide
22	W	177	ALA	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	1	59663	29972	29997	614	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	2	3353	1695	1695	45	0
3	3	924	464	465	8	0
4	A	1605	1663	1662	19	0
5	B	3081	3166	3165	41	0
6	C	2749	2864	2863	35	0
7	E	1274	1363	1361	16	0
8	F	1784	1863	1862	23	0
9	G	1759	1853	1852	24	0
10	H	1493	1566	1566	26	0
11	L	1422	1473	1472	22	0
12	M	1059	1155	1154	10	0
13	N	1720	1780	1779	29	0
14	O	1555	1661	1659	9	0
15	P	1393	1430	1428	19	0
16	Q	1129	1206	1205	14	0
17	R	1241	1331	1330	18	0
18	S	1425	1467	1466	10	0
19	T	476	500	499	8	0
20	U	808	823	822	9	0
21	V	1003	1049	1048	9	0
22	W	1814	1834	1833	13	0
23	X	959	1025	1023	11	0
24	Y	993	1082	1081	6	0
25	Z	1092	1156	1155	16	0
26	a	742	786	785	7	0
27	b	4023	4075	4071	31	0
28	c	743	798	797	14	0
29	d	847	899	898	4	0
30	e	1012	1081	1079	7	0
31	f	850	881	880	12	0
32	g	796	856	855	4	0
33	h	969	1079	1078	4	0
34	i	743	823	822	6	0
35	j	670	678	677	13	0
36	k	612	683	682	3	0
37	l	436	476	475	8	0
38	m	1814	1855	1848	25	0
39	p	642	687	685	5	0
40	r	851	918	916	10	0
41	u	1167	1212	1212	11	0
42	y	1693	1686	1685	30	0
43	b	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	m	1	0	0	0	0
All	All	114386	84914	84887	1016	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 5.

All (1016) 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)
2:2:13:A:O2'	15:P:121:GLN:O	1.83	0.94
1:1:3149:G:O2'	5:B:129:ALA:O	1.86	0.92
1:1:2234:G:HO2'	1:1:2603:G:HO2'	1.09	0.91
1:1:1268:G:O2'	1:1:1269:U:OP1	1.90	0.90
1:1:408:A:N3	1:1:655:C:O2'	2.06	0.88
1:1:979:U:O2'	1:1:980:A:OP2	1.92	0.88
1:1:2964:G:N2	1:1:2967:A:OP2	2.06	0.86
1:1:518:G:OP2	1:1:518:G:N2	2.09	0.86
1:1:1152:G:OP2	1:1:1152:G:N2	2.09	0.85
1:1:68:C:OP2	1:1:301:G:N2	2.10	0.84
1:1:399:A:O2'	1:1:403:C:O2'	1.95	0.84
1:1:108:A:OP1	11:L:42:ARG:NE	2.10	0.84
1:1:1477:A:OP1	1:1:3075:G:O2'	1.95	0.83
1:1:518:G:O2'	1:1:521:A:O2'	1.96	0.83
1:1:3109:G:N2	10:H:156:GLN:OE1	2.11	0.83
1:1:1188:U:OP1	1:1:1210:U:O2'	1.97	0.83
1:1:200:C:N4	1:1:218:G:OP1	2.12	0.83
1:1:806:A:O2'	1:1:807:A:OP1	1.96	0.82
1:1:2890:A:O2'	1:1:2933:A:N3	2.12	0.82
8:F:186:HIS:O	8:F:190:THR:OG1	1.98	0.82
1:1:1712:G:N2	1:1:1733:G:O6	2.13	0.81
1:1:1543:G:O2'	1:1:2168:A:O2'	1.98	0.81
1:1:63:A:N3	1:1:78:U:O2'	2.13	0.81
1:1:2992:U:OP1	1:1:3310:A:O2'	1.97	0.81
1:1:102:C:O2'	11:L:62:THR:OG1	1.99	0.81
1:1:2165:G:N2	1:1:2168:A:OP2	2.13	0.80
1:1:1176:C:OP2	1:1:1177:G:O2'	2.00	0.80
1:1:3353:G:O2'	1:1:3354:U:O4'	2.00	0.80
1:1:3018:C:OP1	42:y:9:ASN:ND2	2.15	0.80
1:1:3284:G:O2'	1:1:3285:C:O4'	1.97	0.80
1:1:3291:G:O2'	1:1:3292:A:O5'	1.99	0.80
1:1:1394:A:N6	1:1:1416:C:O2	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2858:U:O2'	27:b:135:ARG:NH1	2.15	0.80
1:1:3305:A:O2'	1:1:3306:U:O4'	2.01	0.79
1:1:3352:U:O2'	1:1:3353:G:OP2	2.00	0.78
1:1:931:C:OP2	1:1:932:U:O2'	2.00	0.78
1:1:188:U:O2'	1:1:207:U:O2	2.00	0.78
4:A:180:LEU:HD11	39:p:26:VAL:HG21	1.65	0.78
17:R:98:ARG:NH2	17:R:130:ASN:OD1	2.16	0.77
1:1:1480:G:O4'	1:1:1483:G:N2	2.17	0.77
22:W:67:MET:SD	22:W:68:GLY:N	2.58	0.77
1:1:1643:A:O2'	1:1:1644:C:O4'	2.01	0.77
1:1:1114:U:O2'	1:1:1115:G:O4'	2.04	0.76
1:1:1225:A:N6	1:1:1284:C:O2	2.18	0.76
1:1:3153:U:OP2	1:1:3293:U:O2'	2.03	0.76
1:1:3187:A:OP1	10:H:23:ARG:NE	2.19	0.76
1:1:1113:G:O2'	1:1:1114:U:O5'	2.02	0.76
1:1:1635:G:N2	1:1:1638:A:OP2	2.18	0.76
1:1:3092:C:O2'	1:1:3094:A:OP2	2.03	0.76
1:1:3268:A:OP1	7:E:46:ARG:NH2	2.19	0.76
1:1:2440:G:N1	1:1:2508:U:O4	2.19	0.75
1:1:101:G:OP2	1:1:101:G:N2	2.17	0.75
1:1:348:A:N3	1:1:352:A:O2'	2.20	0.75
1:1:2349:U:O2'	1:1:3307:A:N3	2.20	0.75
1:1:1693:C:O2'	1:1:1772:U:O3'	2.04	0.75
1:1:3274:A:OP2	15:P:171:ARG:NE	2.19	0.75
2:2:103:G:OP2	2:2:105:A:O2'	2.05	0.74
1:1:1942:U:OP2	17:R:74:ARG:NH1	2.21	0.74
1:1:1052:U:O2'	3:3:103:A:O2'	2.05	0.74
10:H:31:ARG:O	10:H:149:ASN:ND2	2.20	0.74
16:Q:111:ARG:NH1	16:Q:121:CYS:SG	2.60	0.74
1:1:3313:U:OP1	5:B:173:GLN:NE2	2.20	0.74
1:1:1064:A:OP2	1:1:1097:G:N2	2.21	0.74
1:1:1191:U:OP2	14:O:49:ARG:NH1	2.21	0.74
42:y:119:PRO:O	42:y:139:ARG:NH2	2.21	0.74
1:1:66:A:OP2	1:1:77:A:O2'	2.05	0.73
1:1:1493:G:OP2	1:1:1493:G:N2	2.16	0.73
1:1:1618:G:O2'	2:2:126:A:N1	2.21	0.73
38:m:432:ALA:HB2	38:m:449:VAL:HG21	1.70	0.73
1:1:2876:C:O2'	1:1:2877:G:OP2	2.04	0.73
1:1:1562:C:O2'	1:1:1563:C:O5'	2.06	0.73
1:1:2521:U:O2'	1:1:2524:A:OP1	2.02	0.73
1:1:3050:U:O2'	41:u:16:GLY:O	2.06	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1868:G:O2'	1:1:2118:C:O2'	1.99	0.73
1:1:845:G:N2	1:1:848:A:OP2	2.22	0.72
1:1:1198:C:OP2	1:1:1199:C:O2'	2.07	0.72
1:1:3028:G:N2	27:b:162:SER:OG	2.23	0.72
1:1:3228:C:O2'	1:1:3229:G:OP2	2.07	0.72
6:C:328:ASN:OD1	8:F:48:ASN:ND2	2.22	0.72
35:j:54:LYS:O	35:j:58:THR:OG1	2.07	0.72
1:1:1619:A:O2'	2:2:125:U:O4	2.07	0.72
1:1:3367:C:OP2	1:1:3368:U:O2'	2.00	0.72
1:1:2964:G:O2'	38:m:31:ARG:NH2	2.22	0.71
3:3:89:G:N2	3:3:92:A:OP2	2.23	0.71
1:1:1259:A:N3	1:1:1280:C:O2'	2.23	0.71
1:1:1508:C:HO2'	1:1:2353:G:HO2'	1.38	0.71
11:L:136:GLU:OE1	33:h:119:LYS:NZ	2.18	0.71
23:X:103:TYR:HB3	23:X:135:ILE:HD11	1.72	0.71
38:m:344:ALA:N	38:m:349:GLU:OE2	2.23	0.71
2:2:110:C:O2'	2:2:112:U:OP2	2.05	0.71
1:1:47:C:OP2	1:1:48:A:O2'	2.05	0.70
1:1:2393:G:O2'	1:1:2982:A:N6	2.25	0.70
40:r:148:LYS:NZ	40:r:166:VAL:O	2.22	0.70
1:1:1779:C:N4	17:R:88:ARG:O	2.24	0.70
1:1:69:C:O2'	1:1:101:G:O2'	2.05	0.70
1:1:625:G:N2	1:1:1401:A:OP1	2.23	0.70
1:1:3275:U:O2'	31:f:99:ARG:NH1	2.25	0.70
1:1:3292:A:O2'	1:1:3293:U:O4'	2.09	0.69
1:1:713:U:O2'	1:1:754:G:OP1	2.09	0.69
1:1:2940:A:O2'	5:B:256:HIS:O	2.08	0.69
1:1:297:G:N2	1:1:297:G:OP2	2.25	0.69
1:1:609:G:OP2	6:C:315:LYS:NZ	2.26	0.69
1:1:412:G:OP1	15:P:62:ARG:NH1	2.24	0.69
1:1:2100:A:O2'	1:1:2101:C:O5'	2.10	0.69
1:1:1390:A:N6	1:1:1418:A:O2'	2.25	0.69
38:m:325:ASN:ND2	38:m:345:PRO:O	2.25	0.69
1:1:2335:G:N2	1:1:2339:C:O2'	2.26	0.69
1:1:3041:U:OP1	21:V:12:ARG:NH1	2.25	0.69
1:1:197:G:O2'	1:1:218:G:N2	2.26	0.69
1:1:3174:A:OP1	31:f:97:SER:OG	2.05	0.68
1:1:1303:A:O2'	1:1:1304:A:O4'	2.10	0.68
1:1:282:G:O2'	1:1:283:G:OP2	2.07	0.68
1:1:3349:C:O2'	1:1:3350:C:OP1	2.10	0.68
1:1:35:A:O2'	1:1:809:G:N3	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1497:C:O2'	1:1:1602:A:O2'	2.11	0.68
1:1:2167:A:O2'	1:1:2168:A:O4'	2.11	0.68
1:1:3060:C:O3'	1:1:3371:G:N2	2.26	0.68
1:1:2215:A:O2'	1:1:2430:A:O2'	2.11	0.68
1:1:68:C:N4	1:1:314:U:O2'	2.26	0.68
1:1:439:C:O2'	1:1:494:G:O2'	2.10	0.68
1:1:717:C:OP1	1:1:751:A:O2'	2.11	0.68
1:1:2419:A:OP2	38:m:28:ASN:ND2	2.25	0.68
1:1:1831:U:O2'	2:2:114:G:OP1	2.07	0.68
11:L:100:ARG:O	11:L:102:GLN:NE2	2.27	0.68
28:c:99:ASP:O	28:c:103:THR:OG1	2.10	0.68
1:1:1447:G:N2	1:1:2356:A:OP2	2.27	0.67
1:1:2099:A:O2'	1:1:2100:A:O5'	2.12	0.67
1:1:1713:G:O2'	1:1:1730:G:N2	2.27	0.67
25:Z:10:VAL:HG22	25:Z:24:VAL:HG12	1.76	0.67
42:y:200:ASN:OD1	42:y:203:LEU:N	2.26	0.67
1:1:3113:A:OP1	10:H:73:SER:OG	2.12	0.67
1:1:799:G:O2'	11:L:18:TRP:NE1	2.26	0.67
1:1:1388:U:O2'	30:e:99:ASN:ND2	2.26	0.67
1:1:1508:C:O2'	1:1:2353:G:O2'	2.12	0.67
1:1:2612:U:HO2'	1:1:2803:A:HO2'	1.41	0.67
1:1:1884:A:OP1	29:d:31:ARG:NH2	2.28	0.67
18:S:61:ILE:HD12	18:S:61:ILE:O	1.95	0.67
27:b:210:ASP:O	27:b:332:ARG:NH1	2.28	0.67
1:1:733:G:N2	1:1:736:A:OP2	2.27	0.67
8:F:130:ILE:O	8:F:134:VAL:HG22	1.95	0.67
1:1:283:G:OP1	1:1:285:A:O2'	2.13	0.66
1:1:358:G:N2	1:1:361:A:OP2	2.26	0.66
1:1:854:G:O2'	17:R:129:GLY:O	2.13	0.66
22:W:37:TYR:O	22:W:223:ASN:ND2	2.28	0.66
10:H:22:SER:O	10:H:24:ILE:N	2.29	0.66
1:1:691:A:N1	2:2:28:C:O2'	2.28	0.65
1:1:981:U:O2'	1:1:982:C:OP1	2.12	0.65
38:m:423:ASP:O	38:m:426:GLU:N	2.30	0.65
1:1:3350:C:O3'	1:1:3352:U:OP1	2.15	0.65
1:1:94:G:O2'	1:1:95:A:O4'	2.15	0.64
5:B:10:ARG:NH1	5:B:11:HIS:O	2.29	0.64
1:1:1408:G:OP2	30:e:31:ASN:ND2	2.30	0.64
1:1:1721:U:OP2	17:R:103:ARG:NH2	2.31	0.64
1:1:3292:A:O2'	1:1:3293:U:O5'	2.12	0.64
1:1:596:C:OP1	8:F:37:ASN:ND2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:675:C:O2'	1:1:679:U:OP1	2.14	0.64
4:A:30:ARG:NH2	4:A:33:ASP:OD2	2.31	0.64
1:1:349:A:O4'	2:2:24:G:O2'	2.12	0.64
1:1:2125:A:OP1	38:m:437:ARG:NH1	2.31	0.64
1:1:23:A:OP1	35:j:44:THR:N	2.31	0.64
1:1:1861:G:O2'	1:1:3066:U:OP1	2.09	0.64
1:1:2899:C:O2	10:H:173:ARG:NH1	2.31	0.63
19:T:154:VAL:O	19:T:156:TYR:N	2.32	0.63
25:Z:76:ASN:OD1	25:Z:77:TYR:N	2.31	0.63
1:1:361:A:O3'	35:j:45:ARG:NH2	2.30	0.63
1:1:2137:U:OP2	1:1:2142:A:N6	2.16	0.63
41:u:137:ARG:NH2	41:u:138:GLU:OE2	2.32	0.63
1:1:3258:U:O2'	1:1:3260:G:OP1	2.17	0.63
1:1:1559:A:O2'	1:1:1582:C:O2	2.17	0.63
1:1:1312:C:O2'	14:O:83:ALA:O	2.15	0.63
2:2:150:G:O2'	9:G:59:GLN:NE2	2.31	0.63
22:W:30:VAL:HG22	22:W:66:ILE:HG21	1.81	0.63
1:1:1579:C:O2'	1:1:1580:A:O4'	2.17	0.62
2:2:13:A:C2	2:2:14:C:C5	2.86	0.62
11:L:42:ARG:NH1	11:L:51:LEU:O	2.32	0.62
28:c:13:LYS:O	28:c:17:VAL:HG23	1.98	0.62
1:1:2555:G:N2	25:Z:135:ARG:O	2.32	0.62
1:1:1315:U:OP2	14:O:44:SER:OG	2.11	0.62
11:L:161:ASP:OD2	26:a:139:ARG:NH2	2.32	0.62
1:1:3049:A:O2'	5:B:55:THR:HG23	2.00	0.62
24:Y:43:TYR:O	24:Y:125:LYS:N	2.33	0.62
38:m:413:GLU:O	38:m:417:GLU:N	2.33	0.62
1:1:837:A:OP1	39:p:5:THR:OG1	2.16	0.62
1:1:2158:A:OP2	4:A:156:LYS:NZ	2.33	0.62
1:1:687:U:OP2	11:L:36:ARG:NH2	2.33	0.62
1:1:1392:G:O2'	1:1:1393:A:OP2	2.16	0.62
1:1:3042:U:OP2	1:1:3092:C:N4	2.32	0.62
21:V:33:ASN:OD1	21:V:64:LYS:N	2.33	0.62
21:V:136:VAL:HG12	21:V:137:VAL:HG23	1.80	0.62
42:y:21:ASN:ND2	42:y:112:ASP:OD2	2.33	0.62
1:1:250:U:OP2	1:1:251:G:O2'	2.11	0.61
1:1:421:G:O6	1:1:2383:C:O2'	2.14	0.61
7:E:76:LEU:N	7:E:138:GLN:OE1	2.33	0.61
1:1:2902:A:OP1	1:1:3032:A:O2'	2.15	0.61
9:G:98:ARG:NH2	9:G:191:ASN:OD1	2.34	0.61
1:1:1243:G:N2	1:1:1270:A:O2'	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:152:ALA:O	19:T:154:VAL:HG23	1.99	0.61
1:1:2612:U:O2'	1:1:2803:A:O2'	2.13	0.61
8:F:156:ILE:HG22	8:F:157:ASN:H	1.66	0.61
15:P:126:ARG:NH2	15:P:140:GLU:OE1	2.34	0.61
1:1:516:A:N6	1:1:517:G:O6	2.34	0.60
1:1:517:G:OP1	8:F:60:ARG:NH1	2.34	0.60
1:1:1928:G:N2	1:1:2320:A:O2'	2.34	0.60
1:1:2920:U:O2'	1:1:2921:U:O4'	2.09	0.60
2:2:126:A:O2'	2:2:129:C:N4	2.34	0.60
41:u:84:GLU:O	41:u:88:THR:HG23	2.01	0.60
1:1:1146:C:OP1	30:e:47:ARG:N	2.34	0.60
1:1:2813:A:OP1	6:C:67:THR:OG1	2.06	0.60
1:1:351:A:N6	37:l:37:TYR:O	2.34	0.60
25:Z:23:VAL:HG12	25:Z:45:GLY:HA3	1.82	0.60
16:Q:116:LYS:NZ	26:a:88:ASP:OD2	2.20	0.60
1:1:1807:G:O2'	1:1:2559:U:O4	2.20	0.60
15:P:30:ARG:HA	15:P:119:VAL:HG11	1.83	0.60
38:m:224:VAL:HG13	38:m:318:VAL:HG23	1.83	0.60
1:1:117:U:O2'	1:1:119:U:OP2	2.04	0.60
1:1:1630:U:OP1	25:Z:67:LYS:NZ	2.27	0.60
42:y:154:LEU:HD11	42:y:179:VAL:HG21	1.83	0.60
1:1:3049:A:N6	1:1:3095:U:O4'	2.35	0.59
1:1:296:A:O2'	1:1:297:G:O4'	2.16	0.59
1:1:647:A:N6	1:1:2371:G:O2'	2.30	0.59
1:1:364:G:OP1	6:C:60:THR:OG1	2.17	0.59
1:1:1314:C:OP1	14:O:17:GLY:N	2.35	0.59
1:1:1145:G:N2	1:1:1331:U:O2'	2.35	0.59
1:1:1721:U:O2'	1:1:1723:A:N7	2.28	0.59
11:L:165:SER:O	11:L:168:ARG:N	2.35	0.59
22:W:74:GLN:O	22:W:78:GLY:N	2.35	0.59
27:b:150:LEU:HA	27:b:153:VAL:HG22	1.84	0.59
27:b:250:VAL:HG21	27:b:278:PHE:CE1	2.38	0.59
27:b:87:GLU:O	27:b:90:HIS:N	2.35	0.59
1:1:1491:A:HO2'	1:1:1843:C:HO2'	1.50	0.59
11:L:42:ARG:O	11:L:46:ILE:N	2.36	0.59
28:c:30:THR:HG22	28:c:91:SER:CB	2.32	0.59
1:1:1262:G:O6	1:1:1264:G:N2	2.33	0.59
20:U:33:TYR:HE1	20:U:80:THR:HG22	1.67	0.59
1:1:1062:A:N3	19:T:130:ARG:NH2	2.51	0.58
1:1:2828:G:N2	27:b:19:ASP:OD1	2.35	0.58
1:1:981:U:HO2'	1:1:982:C:P	2.25	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:283:VAL:HB	27:b:315:VAL:HG12	1.85	0.58
42:y:28:VAL:HG12	42:y:50:HIS:HB3	1.84	0.58
11:L:61:PRO:O	11:L:62:THR:OG1	2.21	0.58
1:1:422:A:N1	1:1:2362:C:O2'	2.25	0.58
1:1:2877:G:O2'	1:1:2878:G:OP2	2.16	0.58
1:1:2947:G:N3	5:B:250:ALA:HB1	2.18	0.58
1:1:2988:C:OP1	14:O:65:ASN:ND2	2.36	0.58
5:B:299:ASP:OD2	5:B:301:THR:OG1	2.21	0.58
22:W:212:GLU:N	22:W:212:GLU:OE1	2.37	0.58
1:1:1488:G:O2'	32:g:10:ARG:O	2.22	0.58
17:R:105:LEU:HD22	17:R:138:LEU:HD22	1.86	0.58
1:1:44:U:OP1	13:N:85:THR:OG1	2.11	0.58
1:1:2605:G:O2'	1:1:2607:G:N7	2.37	0.58
9:G:153:ILE:HG23	9:G:163:VAL:HG21	1.84	0.58
9:G:160:ILE:O	9:G:164:VAL:HG13	2.03	0.58
19:T:152:ALA:O	19:T:154:VAL:N	2.36	0.58
1:1:725:G:O6	1:1:746:A:N6	2.36	0.57
1:1:1864:A:OP1	17:R:83:GLY:N	2.35	0.57
8:F:154:GLY:HA3	8:F:163:LEU:HD21	1.86	0.57
42:y:11:ASN:ND2	42:y:209:ASP:OD2	2.37	0.57
1:1:292:U:OP2	13:N:68:ARG:NH2	2.36	0.57
1:1:406:G:N2	2:2:16:G:O2'	2.36	0.57
42:y:61:ARG:NE	42:y:106:ASN:OD1	2.37	0.57
1:1:415:G:O6	2:2:9:A:N6	2.37	0.57
1:1:2386:A:O2'	2:2:3:A:N1	2.30	0.57
1:1:2613:U:O2'	1:1:2805:G:OP2	2.19	0.57
5:B:375:GLU:OE1	41:u:14:TYR:OH	2.22	0.57
42:y:108:ILE:HG12	42:y:117:VAL:HG12	1.87	0.57
1:1:1395:G:O2'	2:2:18:U:O2	2.23	0.57
1:1:2808:A:O2'	1:1:2969:A:OP1	2.20	0.57
42:y:156:ASN:ND2	42:y:201:ASP:OD2	2.36	0.57
1:1:336:A:O2'	6:C:48:GLN:NE2	2.38	0.57
1:1:3156:U:O2'	1:1:3157:U:OP1	2.22	0.57
2:2:66:A:OP1	33:h:10:ARG:NH2	2.38	0.57
1:1:2989:U:O2'	5:B:232:ARG:NH1	2.38	0.56
27:b:57:PHE:CE1	27:b:140:VAL:HG21	2.40	0.56
27:b:443:ASP:O	41:u:75:ARG:NE	2.37	0.56
5:B:25:ILE:HD12	5:B:26:ARG:N	2.20	0.56
10:H:20:ILE:HG13	12:M:7:VAL:HG22	1.86	0.56
15:P:51:VAL:HG11	15:P:88:VAL:HG21	1.88	0.56
27:b:178:VAL:HG22	27:b:255:ASP:HB2	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1805:C:O2	1:1:1806:A:N7	2.39	0.56
20:U:33:TYR:CE1	20:U:80:THR:HG22	2.39	0.56
37:l:20:ASN:OD1	37:l:41:ARG:NE	2.38	0.56
1:1:2425:G:OP1	13:N:72:LYS:NZ	2.36	0.56
1:1:2588:U:OP1	9:G:241:LYS:NZ	2.30	0.56
16:Q:36:LEU:O	16:Q:40:THR:OG1	2.16	0.56
26:a:130:VAL:HG11	26:a:145:VAL:HG11	1.88	0.56
27:b:398:LEU:O	27:b:400:ARG:N	2.39	0.56
42:y:182:VAL:HG23	42:y:221:ILE:HD13	1.88	0.56
1:1:768:C:OP1	11:L:186:ARG:NH1	2.39	0.56
1:1:1929:G:OP2	1:1:1930:A:O2'	2.22	0.56
8:F:156:ILE:HD12	8:F:161:VAL:HG21	1.87	0.56
1:1:3113:A:P	10:H:73:SER:HG	2.29	0.56
1:1:283:G:O2'	1:1:284:A:OP1	2.21	0.56
1:1:1202:A:O2'	1:1:1203:A:O5'	2.24	0.56
1:1:1940:G:H21	1:1:3362:A:H8	1.53	0.56
15:P:114:VAL:HG13	15:P:114:VAL:O	2.05	0.56
1:1:2222:A:N6	1:1:2782:U:O2'	2.39	0.56
1:1:1468:A:N6	1:1:1881:A:O2'	2.39	0.55
1:1:1914:G:O2'	17:R:82:LYS:O	2.20	0.55
1:1:3267:A:OP1	1:1:3268:A:N6	2.38	0.55
1:1:1270:A:O2'	1:1:1271:A:OP1	2.21	0.55
1:1:1942:U:O2'	1:1:3345:G:N3	2.39	0.55
1:1:3349:C:HO2'	1:1:3350:C:P	2.28	0.55
21:V:53:SER:N	21:V:56:ASP:OD2	2.40	0.55
38:m:432:ALA:CB	38:m:449:VAL:HG21	2.36	0.55
1:1:36:C:O2'	1:1:934:G:N3	2.39	0.55
1:1:1283:C:OP1	22:W:70:ARG:NH1	2.39	0.55
1:1:64:G:O2'	1:1:77:A:O2'	2.24	0.55
1:1:3027:A:H61	27:b:162:SER:H	1.55	0.55
1:1:600:G:N2	1:1:603:A:OP2	2.27	0.55
1:1:2117:A:OP2	1:1:2119:A:N6	2.40	0.55
1:1:3190:C:OP1	14:O:172:ARG:NH1	2.38	0.55
11:L:46:ILE:HG22	11:L:46:ILE:O	2.07	0.55
1:1:67:A:O2'	1:1:315:C:O2	2.25	0.55
1:1:1113:G:HO2'	1:1:1114:U:P	2.28	0.55
1:1:608:A:O3'	6:C:326:ARG:NH1	2.40	0.54
1:1:2888:U:OP1	27:b:27:ARG:NH2	2.38	0.54
1:1:1757:A:O2'	20:U:104:ARG:NH2	2.40	0.54
6:C:257:LYS:O	6:C:261:VAL:HG23	2.07	0.54
1:1:701:G:N2	1:1:788:C:O3'	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:93:VAL:HG22	7:E:93:VAL:O	2.08	0.54
25:Z:58:GLY:O	25:Z:62:VAL:HG23	2.06	0.54
1:1:1112:A:N3	1:1:1370:G:O2'	2.33	0.54
22:W:177:ALA:O	22:W:179:LYS:N	2.40	0.54
1:1:607:A:C2	7:E:26:ARG:NH2	2.76	0.54
4:A:13:GLY:O	4:A:14:SER:OG	2.21	0.54
6:C:283:THR:HG22	6:C:285:ASP:H	1.71	0.54
13:N:99:ARG:NH2	13:N:118:SER:O	2.41	0.54
1:1:424:G:O2'	30:e:23:ASP:OD2	2.25	0.54
1:1:1447:G:OP1	15:P:65:SER:OG	2.26	0.54
5:B:299:ASP:OD2	5:B:303:LYS:NZ	2.40	0.54
11:L:27:ASP:OD2	11:L:31:LYS:NZ	2.31	0.54
4:A:136:ILE:HG13	4:A:148:VAL:HG12	1.88	0.54
5:B:238:LEU:HD23	5:B:242:THR:HG21	1.90	0.54
42:y:14:GLY:HA2	42:y:198:VAL:HG13	1.89	0.54
4:A:19:HIS:ND1	4:A:190:ARG:O	2.37	0.54
10:H:67:ALA:O	10:H:71:VAL:HG23	2.08	0.54
12:M:40:ASP:OD1	12:M:43:LYS:N	2.40	0.54
17:R:105:LEU:HD22	17:R:138:LEU:CD2	2.38	0.54
28:c:60:ALA:O	28:c:64:LYS:N	2.41	0.54
42:y:140:GLN:NE2	42:y:172:GLU:OE1	2.41	0.54
1:1:87:U:H3	1:1:99:A:H62	1.56	0.53
6:C:222:VAL:HG13	6:C:225:VAL:HB	1.90	0.53
27:b:46:TYR:HB3	27:b:116:LEU:HD21	1.90	0.53
29:d:88:PRO:O	29:d:89:LEU:HD12	2.08	0.53
4:A:45:VAL:HG13	4:A:45:VAL:O	2.08	0.53
18:S:139:TYR:CD2	18:S:140:VAL:HG23	2.43	0.53
1:1:103:G:OP1	11:L:70:ARG:NE	2.40	0.53
1:1:1216:C:HO2'	1:1:1217:A:H8	1.55	0.53
1:1:2836:C:O2'	1:1:2837:A:O5'	2.26	0.53
1:1:439:C:HO2'	1:1:494:G:HO2'	1.39	0.53
1:1:631:U:O2	1:1:632:G:N7	2.42	0.53
1:1:1765:U:O2'	1:1:1766:G:O5'	2.20	0.53
8:F:77:VAL:HG12	18:S:59:VAL:O	2.09	0.53
22:W:41:TRP:HE3	22:W:217:VAL:HG21	1.71	0.53
1:1:2872:A:O2'	27:b:43:ARG:NH2	2.42	0.53
42:y:82:GLN:NE2	42:y:86:ASN:OD1	2.41	0.53
42:y:199:VAL:HG11	42:y:222:PHE:CZ	2.44	0.53
1:1:66:A:O5'	13:N:176:LYS:NZ	2.42	0.53
1:1:2563:G:H5''	9:G:27:THR:HG22	1.91	0.53
1:1:2569:A:O2'	1:1:2570:U:OP2	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:98:LYS:O	8:F:102:VAL:HG23	2.09	0.53
10:H:71:VAL:O	10:H:75:VAL:HG23	2.08	0.53
1:1:1543:G:OP1	13:N:35:VAL:HG23	2.09	0.53
1:1:3292:A:HO2'	1:1:3293:U:P	2.32	0.53
4:A:144:ASN:ND2	4:A:144:ASN:O	2.41	0.53
6:C:156:LEU:HD22	6:C:159:ILE:HD12	1.89	0.53
1:1:172:G:O6	1:1:247:C:N4	2.42	0.53
1:1:1861:G:N2	1:1:3065:G:O2'	2.41	0.53
38:m:455:ASN:OD1	38:m:459:ARG:NH1	2.42	0.53
1:1:289:A:O2'	13:N:93:LYS:O	2.26	0.53
1:1:80:G:OP1	13:N:193:ARG:NH1	2.41	0.52
3:3:75:G:O2'	3:3:104:A:N6	2.41	0.52
25:Z:47:GLU:N	25:Z:69:LYS:O	2.41	0.52
1:1:2166:A:H4'	1:1:2167:A:OP1	2.09	0.52
1:1:2432:A:N6	1:1:2598:G:O6	2.42	0.52
1:1:1514:G:N7	1:1:1841:A:O2'	2.29	0.52
1:1:1562:C:O2'	1:1:1563:C:P	2.66	0.52
2:2:95:G:O2'	35:j:81:GLY:O	2.27	0.52
10:H:72:LYS:NZ	10:H:76:ASP:OD2	2.41	0.52
22:W:38:ARG:NH2	22:W:224:ASP:OD2	2.42	0.52
1:1:100:A:O2'	1:1:101:G:O4'	2.22	0.52
1:1:2100:A:C2'	1:1:2101:C:O5'	2.58	0.52
1:1:2511:A:O2'	1:1:2512:C:OP2	2.22	0.52
6:C:334:PHE:CD1	6:C:339:LEU:HD12	2.44	0.52
7:E:55:LEU:HD11	7:E:66:SER:HB2	1.92	0.52
15:P:16:SER:HB3	15:P:149:VAL:HG22	1.92	0.52
42:y:99:GLU:OE1	42:y:125:THR:OG1	2.23	0.52
10:H:61:GLY:O	10:H:65:VAL:HG23	2.09	0.52
15:P:13:LYS:NZ	15:P:154:GLU:OE2	2.43	0.52
1:1:88:A:O2'	26:a:60:TYR:O	2.22	0.52
1:1:98:G:N7	11:L:13:HIS:NE2	2.57	0.52
1:1:2920:U:HO2'	1:1:2921:U:C4'	2.23	0.52
3:3:87:G:OP1	8:F:218:ARG:NE	2.43	0.52
1:1:620:U:O2'	1:1:622:A:N7	2.38	0.52
8:F:116:PHE:O	8:F:199:ASN:ND2	2.41	0.52
9:G:161:GLU:OE1	13:N:26:ARG:NH2	2.42	0.52
1:1:1202:A:O2'	1:1:1203:A:O4'	2.28	0.52
5:B:160:VAL:HG23	5:B:183:LEU:HG	1.92	0.52
17:R:105:LEU:HD23	17:R:105:LEU:C	2.35	0.52
26:a:130:VAL:HG11	26:a:145:VAL:CG1	2.40	0.52
23:X:68:THR:HG21	33:h:36:LEU:HD13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:441:VAL:HG22	41:u:93:MET:HE1	1.91	0.51
1:1:1097:G:H4'	1:1:1098:A:O5'	2.11	0.51
1:1:1750:A:OP2	36:k:28:ASN:ND2	2.41	0.51
1:1:2549:G:O2'	9:G:38:GLN:NE2	2.43	0.51
1:1:164:A:O2'	1:1:165:A:O5'	2.23	0.51
1:1:1467:A:H1'	1:1:1469:C:OP1	2.10	0.51
1:1:1447:G:N7	15:P:25:SER:OG	2.42	0.51
1:1:1491:A:O2'	1:1:1843:C:O2'	2.22	0.51
27:b:250:VAL:HG21	27:b:278:PHE:CD1	2.45	0.51
1:1:929:A:O2'	35:j:49:TRP:O	2.29	0.51
1:1:3123:A:O2'	10:H:40:HIS:ND1	2.43	0.51
5:B:61:ASP:OD2	27:b:413:ASN:ND2	2.42	0.51
12:M:14:LEU:H	12:M:14:LEU:HD23	1.74	0.51
20:U:16:THR:OG1	20:U:102:GLU:OE1	2.20	0.51
1:1:196:G:N1	1:1:199:A:OP2	2.41	0.51
1:1:3100:U:O2'	1:1:3101:G:OP2	2.23	0.51
4:A:117:GLU:OE2	4:A:123:ARG:N	2.44	0.51
16:Q:44:PHE:O	16:Q:48:VAL:HG23	2.11	0.51
42:y:101:LEU:O	42:y:101:LEU:HD12	2.10	0.51
1:1:1389:G:O2'	1:1:1418:A:N1	2.39	0.51
2:2:52:A:OP1	37:l:21:ARG:NH1	2.42	0.51
1:1:761:A:O2'	1:1:762:U:O4'	2.28	0.51
1:1:789:A:O2'	6:C:114:ASN:ND2	2.44	0.51
1:1:989:A:O2'	19:T:104:GLU:OE1	2.26	0.51
1:1:1303:A:O2'	1:1:1304:A:O5'	2.28	0.51
28:c:30:THR:HG22	28:c:91:SER:HB2	1.91	0.51
1:1:1646:G:O2'	1:1:1647:A:OP2	2.24	0.51
1:1:282:G:O2'	1:1:283:G:P	2.69	0.51
13:N:180:PHE:O	13:N:184:LYS:N	2.45	0.50
42:y:70:LEU:N	42:y:93:LYS:O	2.44	0.50
5:B:317:ILE:HG22	5:B:319:ASN:H	1.75	0.50
1:1:47:C:P	1:1:48:A:HO2'	2.28	0.50
1:1:1557:A:N7	1:1:1559:A:N6	2.59	0.50
21:V:118:VAL:HG21	21:V:133:SER:OG	2.11	0.50
1:1:705:A:O4'	1:1:715:A:N6	2.45	0.50
17:R:41:ILE:O	17:R:45:VAL:HG23	2.11	0.50
17:R:97:ARG:O	17:R:101:VAL:HG23	2.10	0.50
10:H:20:ILE:CG1	12:M:7:VAL:HG22	2.41	0.50
1:1:835:G:O2'	1:1:857:G:N2	2.41	0.50
1:1:2970:C:N4	1:1:2972:G:O6	2.45	0.50
1:1:3114:A:OP2	1:1:3115:C:O2'	2.22	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:142:C:OP1	13:N:38:ARG:NH1	2.41	0.50
42:y:85:ARG:NH1	42:y:89:PRO:O	2.45	0.50
1:1:113:C:OP1	13:N:147:ARG:NE	2.44	0.50
1:1:1343:A:OP1	16:Q:13:SER:N	2.40	0.50
1:1:2569:A:O2'	1:1:2570:U:P	2.70	0.50
1:1:2914:G:O2'	1:1:2934:A:N1	2.34	0.50
1:1:3047:U:OP1	5:B:222:LYS:N	2.39	0.50
1:1:436:A:OP2	1:1:621:A:N6	2.44	0.50
1:1:1300:G:O6	1:1:1301:A:N6	2.45	0.50
1:1:2432:A:N6	1:1:2598:G:C6	2.80	0.50
1:1:2955:U:OP2	1:1:2977:G:N1	2.42	0.50
18:S:11:GLY:N	18:S:41:TYR:OH	2.45	0.50
24:Y:58:VAL:HG22	24:Y:104:LEU:HD22	1.92	0.50
1:1:3291:G:HO2'	1:1:3292:A:C5'	2.16	0.49
36:k:28:ASN:O	36:k:40:GLN:N	2.44	0.49
1:1:122:A:N1	1:1:145:G:O2'	2.38	0.49
1:1:1355:A:O2'	1:1:1356:U:OP2	2.16	0.49
9:G:55:TYR:CE1	9:G:56:VAL:HG23	2.47	0.49
9:G:82:LEU:HD22	9:G:82:LEU:H	1.77	0.49
16:Q:123:THR:OG1	16:Q:125:ASP:OD1	2.25	0.49
26:a:112:ILE:HB	26:a:130:VAL:HG12	1.93	0.49
1:1:90:C:OP1	26:a:59:ARG:NH1	2.44	0.49
1:1:708:G:N2	1:1:711:A:OP2	2.39	0.49
1:1:806:A:HO2'	1:1:807:A:P	2.29	0.49
1:1:3277:U:OP2	1:1:3278:C:N4	2.42	0.49
15:P:18:ARG:NH2	15:P:147:GLU:OE1	2.44	0.49
38:m:289:SER:O	38:m:334:THR:OG1	2.21	0.49
1:1:1685:C:H2'	1:1:1686:U:O4'	2.13	0.49
21:V:45:ARG:HD2	21:V:48:ARG:HD2	1.94	0.49
1:1:1152:G:H8	1:1:2370:G:HO2'	1.60	0.49
1:1:2148:U:H2'	1:1:2149:A:C8	2.48	0.49
9:G:134:TYR:O	9:G:197:VAL:HG23	2.11	0.49
1:1:1318:A:N7	14:O:18:ARG:NH1	2.61	0.49
1:1:2593:A:H1'	1:1:2594:C:OP2	2.13	0.49
2:2:75:G:OP2	24:Y:74:TYR:OH	2.22	0.49
5:B:264:VAL:HG23	5:B:266:ARG:HD2	1.95	0.49
13:N:183:THR:O	13:N:183:THR:OG1	2.31	0.49
1:1:2898:G:N3	40:r:7:ILE:HD12	2.27	0.49
41:u:32:CYS:SG	41:u:33:ARG:NH2	2.86	0.49
1:1:3002:C:O2'	5:B:180:GLU:OE2	2.28	0.49
1:1:3098:G:OP1	5:B:279:ASN:ND2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:154:VAL:N	19:T:155:PRO:HD3	2.27	0.49
1:1:796:U:C2	1:1:797:U:C5	3.00	0.49
1:1:1831:U:C2	1:1:1832:C:C5	3.00	0.49
1:1:1920:U:O2'	1:1:1932:A:N7	2.41	0.49
1:1:2593:A:H4'	1:1:2594:C:O5'	2.12	0.49
10:H:13:PRO:HG2	10:H:16:VAL:HG22	1.95	0.49
20:U:76:LEU:O	20:U:80:THR:HG23	2.12	0.49
1:1:626:U:H2'	1:1:627:U:O4'	2.12	0.49
1:1:3008:A:N6	1:1:3139:A:N6	2.61	0.49
6:C:259:ASP:O	6:C:263:GLY:N	2.46	0.49
1:1:3271:G:OP1	15:P:171:ARG:NH1	2.46	0.48
1:1:2132:C:H2'	1:1:2132:C:O2	2.13	0.48
34:i:68:ARG:O	34:i:72:VAL:HG23	2.13	0.48
1:1:2900:A:OP1	40:r:6:TYR:OH	2.28	0.48
5:B:108:GLU:N	5:B:108:GLU:OE1	2.47	0.48
8:F:156:ILE:O	8:F:157:ASN:C	2.55	0.48
20:U:98:THR:OG1	20:U:104:ARG:NE	2.43	0.48
28:c:34:LEU:HD11	28:c:42:ILE:HG21	1.96	0.48
30:e:42:VAL:O	30:e:52:GLN:NE2	2.45	0.48
38:m:390:VAL:O	38:m:393:VAL:HG22	2.13	0.48
1:1:619:A:OP1	15:P:167:ARG:NE	2.46	0.48
2:2:149:A:N3	9:G:55:TYR:OH	2.36	0.48
25:Z:110:ALA:O	25:Z:114:VAL:HG23	2.12	0.48
1:1:1148:G:OP1	31:f:21:ARG:NH1	2.45	0.48
1:1:1561:G:H22	1:1:1578:C:H42	1.60	0.48
1:1:3206:C:OP1	18:S:166:LYS:NZ	2.45	0.48
8:F:88:ARG:HA	8:F:134:VAL:HG12	1.95	0.48
23:X:139:ILE:HD11	23:X:141:TYR:CE1	2.48	0.48
1:1:670:C:OP2	16:Q:147:ARG:NH2	2.46	0.48
1:1:1420:C:OP2	6:C:193:LYS:NZ	2.45	0.48
1:1:1803:C:C2	1:1:1804:A:C8	3.01	0.48
1:1:3284:G:H2'	1:1:3285:C:C6	2.48	0.48
27:b:294:ARG:O	27:b:296:GLU:N	2.46	0.48
31:f:11:GLY:O	31:f:98:VAL:N	2.39	0.48
4:A:118:GLU:OE2	4:A:156:LYS:NZ	2.46	0.48
6:C:263:GLY:HA3	6:C:267:VAL:HG23	1.96	0.48
1:1:289:A:C2	1:1:290:G:N7	2.82	0.48
1:1:1097:G:H1'	1:1:1098:A:OP2	2.14	0.48
1:1:3108:G:N3	10:H:163:GLN:NE2	2.57	0.48
17:R:36:ASN:OD1	17:R:37:SER:N	2.47	0.48
1:1:3228:C:O2'	1:1:3229:G:P	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3369:G:N1	5:B:380:MET:O	2.44	0.48
9:G:78:PHE:O	9:G:79:GLN:HG2	2.14	0.48
29:d:23:VAL:HG21	29:d:31:ARG:HD3	1.95	0.48
38:m:47:GLU:OE2	38:m:49:ARG:NH2	2.46	0.48
1:1:2330:C:C2	1:1:2331:C:C5	3.02	0.48
27:b:104:LEU:O	27:b:108:VAL:HG23	2.14	0.48
38:m:462:ILE:HD12	38:m:463:PRO:HD2	1.96	0.48
1:1:1493:G:O6	37:l:2:ALA:N	2.47	0.47
2:2:12:A:C6	2:2:13:A:N7	2.82	0.47
3:3:97:A:OP1	18:S:40:ARG:NH1	2.47	0.47
13:N:136:ASP:OD1	13:N:138:GLN:NE2	2.47	0.47
19:T:154:VAL:N	19:T:155:PRO:CD	2.77	0.47
1:1:99:A:O2'	1:1:100:A:O5'	2.33	0.47
1:1:813:G:O2'	35:j:45:ARG:NH1	2.45	0.47
1:1:2098:C:N3	1:1:2099:A:N6	2.62	0.47
1:1:2966:G:O6	38:m:31:ARG:NH2	2.47	0.47
1:1:3049:A:C4	5:B:75:ALA:HB2	2.48	0.47
1:1:3060:C:O2	1:1:3332:U:O2'	2.31	0.47
1:1:3084:C:H2'	1:1:3085:G:O4'	2.14	0.47
10:H:20:ILE:HB	12:M:7:VAL:HG22	1.95	0.47
1:1:591:G:O2'	7:E:17:ALA:O	2.27	0.47
2:2:4:C:C2	2:2:5:U:C5	3.01	0.47
1:1:627:U:H2'	1:1:628:A:H8	1.79	0.47
1:1:116:A:OP1	34:i:36:ARG:NH2	2.45	0.47
1:1:1719:G:OP2	17:R:121:HIS:ND1	2.45	0.47
1:1:3347:A:C2	1:1:3348:G:N7	2.82	0.47
5:B:37:ARG:NH2	5:B:156:SER:O	2.47	0.47
25:Z:26:VAL:HG22	25:Z:42:LEU:O	2.14	0.47
25:Z:53:VAL:CG2	25:Z:62:VAL:HG22	2.43	0.47
40:r:5:ASP:C	40:r:5:ASP:OD1	2.57	0.47
1:1:597:G:O3'	8:F:41:ARG:NH2	2.48	0.47
1:1:1786:G:H2'	1:1:1787:A:C8	2.50	0.47
1:1:217:U:O2	24:Y:103:LYS:NZ	2.45	0.47
1:1:629:U:O2	1:1:630:A:C8	2.68	0.47
1:1:1449:A:O2'	1:1:2983:C:N3	2.43	0.47
1:1:1608:C:C2	1:1:1609:C:C5	3.03	0.47
1:1:1747:G:O6	1:1:1748:G:N1	2.48	0.47
1:1:2881:C:OP1	5:B:11:HIS:NE2	2.47	0.47
1:1:3181:C:HO2'	14:O:164:SER:HG	1.60	0.47
2:2:125:U:O2'	2:2:126:A:OP1	2.26	0.47
11:L:62:THR:O	11:L:64:LYS:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:274:ILE:HG22	27:b:274:ILE:O	2.14	0.47
28:c:17:VAL:HG21	28:c:100:ILE:HD13	1.96	0.47
1:1:164:A:O2'	1:1:165:A:O4'	2.32	0.47
9:G:150:LEU:HD23	9:G:151:VAL:N	2.30	0.47
28:c:30:THR:HG22	28:c:91:SER:HB3	1.96	0.47
1:1:1150:A:H61	1:1:2369:G:H1'	1.79	0.47
1:1:2329:C:C2	1:1:2330:C:C5	3.03	0.47
1:1:2888:U:O4'	1:1:2911:A:N6	2.47	0.47
1:1:611:A:O2'	1:1:612:U:OP2	2.26	0.47
1:1:795:G:C2	1:1:796:U:C5	3.03	0.46
1:1:269:G:OP2	13:N:44:ARG:NH2	2.45	0.46
33:h:53:CYS:O	33:h:57:VAL:HG23	2.16	0.46
1:1:65:A:H4'	1:1:66:A:O5'	2.15	0.46
1:1:67:A:N6	1:1:271:C:O2'	2.49	0.46
1:1:1113:G:C2'	1:1:1114:U:O5'	2.62	0.46
1:1:1380:G:OP1	6:C:191:LYS:N	2.43	0.46
2:2:19:C:C2	2:2:20:U:C5	3.02	0.46
41:u:49:LEU:HD23	41:u:51:TRP:NE1	2.31	0.46
1:1:1270:A:OP1	40:r:12:LYS:NZ	2.45	0.46
1:1:3332:U:H2'	1:1:3333:G:O4'	2.15	0.46
2:2:71:A:C5	2:2:85:G:N2	2.84	0.46
6:C:264:SER:OG	6:C:265:GLU:OE1	2.28	0.46
22:W:222:ASP:OD1	22:W:223:ASN:N	2.48	0.46
31:f:16:TYR:OH	31:f:89:LEU:O	2.32	0.46
40:r:11:ILE:O	40:r:15:GLY:N	2.43	0.46
5:B:283:TYR:CG	5:B:354:VAL:HG21	2.51	0.46
13:N:9:GLU:HB3	34:i:44:VAL:HG21	1.97	0.46
1:1:1415:U:H2'	1:1:1416:C:O4'	2.16	0.46
1:1:2828:G:OP2	27:b:129:LYS:NZ	2.39	0.46
2:2:124:G:H3'	2:2:125:U:C5'	2.46	0.46
4:A:7:ASN:OD1	4:A:8:GLN:N	2.49	0.46
10:H:113:GLU:OE1	10:H:115:ARG:NH2	2.48	0.46
9:G:134:TYR:CG	9:G:190:VAL:HG21	2.51	0.46
25:Z:17:ARG:NH1	25:Z:18:TYR:OH	2.49	0.46
28:c:103:THR:HG22	28:c:104:LEU:H	1.81	0.46
38:m:366:ASP:OD1	38:m:366:ASP:N	2.49	0.46
41:u:4:TYR:O	41:u:13:CYS:N	2.46	0.46
1:1:157:A:N7	34:i:26:ILE:HG21	2.30	0.46
1:1:1688:U:C2	1:1:1689:U:C5	3.04	0.46
1:1:3000:A:C6	1:1:3149:G:O6	2.68	0.46
1:1:3350:C:O2	1:1:3353:G:N1	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:52:VAL:HG12	7:E:53:VAL:N	2.31	0.46
1:1:1655:G:N2	1:1:1801:U:O4	2.48	0.46
1:1:2833:A:C6	1:1:2856:G:O6	2.69	0.46
13:N:5:LYS:CG	34:i:40:VAL:HG11	2.46	0.46
13:N:106:VAL:HG11	13:N:132:VAL:HG21	1.98	0.46
13:N:110:ALA:HB1	13:N:113:LEU:HD23	1.97	0.46
16:Q:33:TYR:CZ	16:Q:48:VAL:HG11	2.51	0.46
1:1:1221:A:H3'	1:1:1222:G:H5'	1.97	0.46
1:1:3097:C:OP1	5:B:349:LYS:NZ	2.40	0.46
1:1:3184:A:N3	1:1:3187:A:O2'	2.46	0.46
21:V:58:VAL:O	21:V:76:ALA:N	2.39	0.46
31:f:59:VAL:HG23	31:f:60:ARG:H	1.81	0.46
1:1:812:G:O6	1:1:929:A:N6	2.49	0.45
1:1:1666:G:O2'	1:1:1742:U:O3'	2.34	0.45
1:1:2341:A:OP2	5:B:247:ARG:NH1	2.43	0.45
1:1:3170:A:O5'	31:f:56:SER:OG	2.24	0.45
6:C:338:LYS:O	6:C:340:GLY:N	2.49	0.45
1:1:269:G:OP2	13:N:44:ARG:NH1	2.49	0.45
1:1:406:G:OP1	1:1:1415:U:O2'	2.32	0.45
1:1:1690:C:C2	1:1:1691:U:C5	3.04	0.45
9:G:54:GLU:O	9:G:58:VAL:HG23	2.16	0.45
1:1:99:A:C2'	1:1:100:A:O5'	2.65	0.45
1:1:106:A:N6	1:1:107:A:N1	2.64	0.45
1:1:198:A:N7	1:1:219:A:N6	2.64	0.45
1:1:3163:A:H2'	1:1:3164:C:H5'	1.98	0.45
1:1:3217:C:H6	1:1:3266:G:H21	1.65	0.45
1:1:3217:C:N3	15:P:182:ILE:HG23	2.32	0.45
6:C:77:VAL:HG23	6:C:87:GLN:O	2.16	0.45
9:G:196:ALA:O	9:G:197:VAL:HG13	2.17	0.45
18:S:87:THR:HG23	19:T:156:TYR:CZ	2.50	0.45
27:b:178:VAL:HG22	27:b:255:ASP:CB	2.47	0.45
1:1:498:A:OP1	31:f:86:ARG:NE	2.46	0.45
1:1:1830:G:N2	2:2:115:C:OP2	2.49	0.45
1:1:2801:A:O2'	1:1:2803:A:OP2	2.26	0.45
7:E:2:SER:N	30:e:81:ASP:OD2	2.50	0.45
7:E:40:LEU:N	7:E:52:VAL:O	2.37	0.45
1:1:164:A:HO2'	1:1:165:A:C5'	2.29	0.45
1:1:629:U:O2	1:1:630:A:N7	2.50	0.45
1:1:1113:G:H2'	1:1:1114:U:C5	2.52	0.45
1:1:345:G:O2'	2:2:25:G:N3	2.50	0.45
1:1:925:A:OP2	1:1:2413:A:O2'	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1336:U:O2	1:1:1337:A:C8	2.70	0.45
1:1:1703:U:N3	1:1:1740:U:O2	2.49	0.45
7:E:43:LEU:HD21	7:E:85:ILE:HD12	1.98	0.45
7:E:52:VAL:HG11	7:E:65:ILE:HD13	1.98	0.45
10:H:139:ASN:OD1	10:H:139:ASN:C	2.59	0.45
13:N:27:VAL:HG23	13:N:129:TYR:CE2	2.52	0.45
28:c:75:ASN:OD1	28:c:86:ARG:NH1	2.50	0.45
1:1:189:G:O2'	1:1:190:U:O4'	2.34	0.45
1:1:208:C:H2'	1:1:209:A:O4'	2.17	0.45
1:1:1720:U:OP2	17:R:120:TYR:OH	2.30	0.45
1:1:1791:C:OP1	39:p:34:HIS:NE2	2.50	0.45
1:1:3156:U:HO2'	1:1:3157:U:P	2.39	0.45
1:1:3177:G:N7	7:E:167:ASN:ND2	2.61	0.45
38:m:233:ASP:OD1	38:m:233:ASP:N	2.50	0.45
42:y:107:VAL:HG13	42:y:118:HIS:HB2	1.97	0.45
1:1:707:U:HO2'	1:1:754:G:C2'	2.26	0.45
1:1:1804:A:O2'	32:g:78:GLY:O	2.34	0.45
4:A:179:LEU:O	4:A:184:ARG:NH1	2.43	0.45
9:G:83:ASP:OD1	9:G:83:ASP:N	2.50	0.45
1:1:1307:G:O2'	1:1:1308:A:OP2	2.26	0.45
1:1:1421:G:C2	1:1:1422:G:N7	2.84	0.45
2:2:139:U:O2	2:2:140:G:C8	2.70	0.45
6:C:156:LEU:CD2	6:C:159:ILE:HD12	2.47	0.45
7:E:142:ASP:O	7:E:146:ILE:N	2.41	0.45
8:F:223:PHE:N	8:F:229:PHE:O	2.50	0.45
9:G:112:GLU:O	9:G:116:VAL:HG23	2.17	0.45
35:j:5:THR:N	35:j:6:PRO:HD2	2.32	0.45
1:1:210:U:OP2	6:C:162:THR:N	2.40	0.45
1:1:832:G:O6	1:1:863:C:N4	2.50	0.45
1:1:1724:U:H1'	1:1:1725:C:C5	2.51	0.45
5:B:49:TYR:O	5:B:80:ASP:N	2.43	0.45
6:C:34:ILE:O	6:C:38:VAL:HG23	2.17	0.45
15:P:87:SER:O	15:P:91:VAL:HG23	2.16	0.45
1:1:288:C:C2	1:1:289:A:C8	3.05	0.44
1:1:1493:G:C4	37:l:13:MET:HE2	2.52	0.44
1:1:2433:U:OP2	1:1:2434:U:H2'	2.17	0.44
5:B:261:MET:O	5:B:264:VAL:HG22	2.16	0.44
9:G:163:VAL:HG22	9:G:163:VAL:O	2.16	0.44
17:R:118:HIS:O	17:R:122:VAL:HG23	2.18	0.44
31:f:19:SER:N	31:f:22:VAL:O	2.42	0.44
1:1:170:G:N3	1:1:250:U:O2'	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1240:A:H3'	1:1:1241:U:H5'	1.99	0.44
1:1:1412:G:OP1	30:e:105:ARG:NH2	2.47	0.44
1:1:1636:U:O2'	25:Z:79:HIS:ND1	2.50	0.44
5:B:85:VAL:HG23	5:B:201:LYS:O	2.17	0.44
1:1:1114:U:C2'	1:1:1115:G:O4'	2.66	0.44
1:1:1689:U:C2	1:1:1690:C:C5	3.04	0.44
4:A:104:LEU:HD11	4:A:116:VAL:HG23	1.99	0.44
6:C:68:GLY:O	6:C:70:ALA:N	2.47	0.44
27:b:414:VAL:HG21	42:y:32:GLU:CD	2.43	0.44
1:1:790:U:O2	1:1:791:A:C8	2.70	0.44
1:1:1216:C:O2'	1:1:1217:A:O4'	2.35	0.44
1:1:1329:U:OP1	31:f:17:GLN:NE2	2.50	0.44
1:1:2878:G:C4	1:1:2879:C:C5	3.05	0.44
8:F:165:ASP:OD1	8:F:166:ASN:N	2.51	0.44
10:H:43:VAL:HG21	10:H:71:VAL:HG11	1.99	0.44
23:X:80:ASN:OD1	23:X:132:ALA:N	2.41	0.44
42:y:101:LEU:HD13	42:y:107:VAL:HG11	2.00	0.44
1:1:1355:A:H1'	1:1:1356:U:OP2	2.16	0.44
1:1:1560:G:H2'	1:1:1561:G:O4'	2.18	0.44
1:1:3302:U:H2'	1:1:3303:G:O4'	2.18	0.44
22:W:224:ASP:OD1	22:W:225:SER:N	2.51	0.44
1:1:346:C:O2	1:1:348:A:N6	2.50	0.44
1:1:2778:G:C2	1:1:2779:A:N7	2.85	0.44
13:N:4:TYR:CG	13:N:5:LYS:N	2.86	0.44
22:W:41:TRP:CE3	22:W:217:VAL:HG21	2.52	0.44
1:1:712:G:OP1	11:L:174:ARG:NH2	2.50	0.44
1:1:3304:U:O3'	5:B:334:ARG:NH2	2.51	0.44
11:L:115:ARG:NH2	11:L:145:PHE:O	2.42	0.44
27:b:210:ASP:OD1	27:b:215:ARG:NH1	2.50	0.44
1:1:1544:G:O6	1:1:1550:C:N4	2.50	0.44
1:1:1686:U:H2'	1:1:1688:U:O4'	2.18	0.44
1:1:2221:G:N2	1:1:2224:A:OP2	2.42	0.44
1:1:2508:U:H2'	1:1:2509:U:C6	2.53	0.44
1:1:3181:C:O2	1:1:3181:C:O4'	2.34	0.44
1:1:3349:C:H2'	1:1:3350:C:O4'	2.18	0.44
13:N:153:ASP:HB3	13:N:155:VAL:HG22	1.99	0.44
1:1:340:C:OP2	6:C:195:ARG:NH2	2.51	0.44
1:1:846:A:H4'	1:1:847:A:OP1	2.18	0.44
1:1:1881:A:C6	1:1:2352:A:N6	2.86	0.44
5:B:187:SER:OG	5:B:190:GLU:OE1	2.35	0.44
21:V:130:ALA:O	42:y:106:ASN:ND2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:m:338:LYS:HG3	38:m:340:VAL:HG23	1.99	0.44
1:1:267:G:N2	13:N:50:ARG:O	2.50	0.43
1:1:1650:G:C6	1:1:1806:A:N6	2.86	0.43
1:1:1296:C:N3	1:1:1297:C:C5	2.86	0.43
1:1:3205:G:P	1:1:3206:C:H41	2.41	0.43
41:u:6:CYS:SG	41:u:9:CYS:N	2.89	0.43
1:1:164:A:HO2'	1:1:165:A:C4'	2.31	0.43
1:1:705:A:N6	1:1:715:A:OP2	2.46	0.43
1:1:1806:A:H2'	1:1:1807:G:O5'	2.19	0.43
1:1:3040:A:C2	1:1:3041:U:C5	3.06	0.43
2:2:142:C:C2	2:2:143:U:C5	3.06	0.43
5:B:95:THR:OG1	5:B:98:GLY:O	2.24	0.43
5:B:264:VAL:HG23	5:B:266:ARG:CD	2.48	0.43
27:b:420:TYR:OH	27:b:428:LYS:O	2.26	0.43
38:m:412:LEU:HA	38:m:462:ILE:HD13	1.99	0.43
1:1:525:C:OP2	12:M:77:ARG:NE	2.50	0.43
1:1:633:C:O2'	31:f:21:ARG:O	2.37	0.43
1:1:1517:G:OP1	37:l:41:ARG:NH1	2.49	0.43
1:1:1589:A:N6	1:1:1854:C:O2'	2.52	0.43
1:1:1689:U:N3	1:1:1690:C:C5	2.86	0.43
1:1:2971:A:O2'	40:r:166:VAL:HG11	2.19	0.43
1:1:3181:C:C6	1:1:3182:G:C8	3.06	0.43
9:G:55:TYR:CZ	9:G:56:VAL:HG23	2.54	0.43
15:P:122:ALA:N	15:P:143:PRO:O	2.38	0.43
1:1:12:A:H4'	23:X:34:LEU:HD21	2.01	0.43
1:1:53:G:OP2	35:j:48:ASN:ND2	2.43	0.43
1:1:628:A:H2'	1:1:629:U:O4'	2.19	0.43
1:1:1241:U:O2'	1:1:1243:G:OP2	2.30	0.43
1:1:1927:G:N7	39:p:16:VAL:HG12	2.33	0.43
1:1:2526:C:OP1	4:A:37:ARG:NH1	2.49	0.43
1:1:3273:A:OP2	7:E:77:ARG:NH2	2.46	0.43
10:H:129:ARG:O	10:H:132:VAL:HG12	2.19	0.43
20:U:100:THR:HG23	20:U:100:THR:O	2.19	0.43
25:Z:26:VAL:HG12	25:Z:89:VAL:HG23	1.99	0.43
1:1:209:A:O2'	1:1:211:A:OP2	2.32	0.43
1:1:753:C:C2	1:1:754:G:C8	3.07	0.43
1:1:1178:G:N2	1:1:1328:C:O2	2.50	0.43
1:1:3049:A:C5	1:1:3050:U:C5	3.06	0.43
6:C:326:ARG:O	8:F:41:ARG:NH1	2.51	0.43
1:1:66:A:HO2'	1:1:315:C:HO2'	1.65	0.43
1:1:173:G:N1	1:1:246:U:O2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:752:C:N3	1:1:753:C:C5	2.87	0.43
1:1:968:G:H2'	1:1:969:C:O4'	2.19	0.43
1:1:3369:G:N1	41:u:62:GLU:OE2	2.52	0.43
18:S:79:VAL:HG21	18:S:106:LEU:HD21	2.00	0.43
27:b:46:TYR:CB	27:b:116:LEU:HD21	2.48	0.43
1:1:356:C:O2'	6:C:81:GLY:O	2.29	0.43
1:1:561:C:OP1	12:M:77:ARG:N	2.44	0.43
1:1:1315:U:O2	1:1:1317:A:N6	2.51	0.43
1:1:2217:U:O2	1:1:2218:G:C8	2.71	0.43
1:1:2431:C:N4	1:1:2432:A:H62	2.17	0.43
1:1:3019:U:H3	1:1:3035:A:H61	1.65	0.43
1:1:3157:U:P	1:1:3157:U:O4'	2.77	0.43
2:2:71:A:O3'	24:Y:52:ARG:NH2	2.52	0.43
35:j:5:THR:HG23	35:j:6:PRO:HD3	2.00	0.43
1:1:1437:C:O2	1:1:1437:C:H2'	2.19	0.43
10:H:41:ILE:CG2	10:H:43:VAL:HG22	2.48	0.43
10:H:57:VAL:HG23	10:H:68:LEU:HD23	2.01	0.43
12:M:113:THR:HG22	12:M:114:ASP:N	2.34	0.43
38:m:418:ILE:HD13	38:m:434:LYS:HG3	2.00	0.43
42:y:166:SER:OG	42:y:169:ASP:OD2	2.36	0.43
1:1:1688:U:O2	1:1:1689:U:C5	2.72	0.43
1:1:1948:G:C2	1:1:2099:A:N1	2.87	0.43
4:A:101:VAL:C	4:A:102:LEU:HD12	2.44	0.43
1:1:67:A:N1	1:1:300:G:O2'	2.47	0.42
1:1:82:C:H2'	1:1:83:U:O4'	2.19	0.42
1:1:439:C:H2'	1:1:439:C:O2	2.17	0.42
1:1:831:G:O2'	1:1:1864:A:N3	2.40	0.42
1:1:1281:G:C6	1:1:1282:G:C6	3.07	0.42
1:1:1805:C:O2	1:1:1805:C:H2'	2.18	0.42
1:1:2234:G:O2'	1:1:2603:G:O2'	2.01	0.42
2:2:79:A:H3'	2:2:80:A:H4'	2.00	0.42
1:1:59:G:H2'	2:2:33:A:C8	2.54	0.42
1:1:195:U:H2'	1:1:196:G:O4'	2.19	0.42
1:1:406:G:O2'	1:1:407:A:OP2	2.34	0.42
1:1:411:U:O4	2:2:13:A:N6	2.52	0.42
1:1:591:G:N2	1:1:612:U:OP1	2.37	0.42
1:1:608:A:P	6:C:315:LYS:HZ3	2.42	0.42
1:1:1193:A:H2'	1:1:1194:G:O4'	2.19	0.42
1:1:1497:C:H2'	1:1:1498:A:H8	1.84	0.42
1:1:1805:C:O2	1:1:1806:A:C8	2.72	0.42
1:1:2882:U:O2'	5:B:261:MET:SD	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3269:U:C4'	1:1:3270:U:OP2	2.67	0.42
1:1:3303:G:H2'	1:1:3305:A:N6	2.35	0.42
1:1:3329:U:HO2'	5:B:363:SER:HG	1.54	0.42
3:3:105:C:C2	3:3:106:U:C5	3.06	0.42
13:N:172:ARG:O	13:N:183:THR:OG1	2.35	0.42
16:Q:16:ARG:NH1	16:Q:53:PHE:O	2.47	0.42
1:1:1150:A:C2	1:1:1151:U:C5	3.07	0.42
1:1:2912:G:H2'	1:1:2913:C:O4'	2.18	0.42
2:2:69:U:H2'	2:2:70:G:O4'	2.19	0.42
2:2:133:G:OP1	23:X:94:GLN:NE2	2.50	0.42
13:N:160:GLU:OE1	13:N:160:GLU:N	2.47	0.42
18:S:99:ARG:O	18:S:103:VAL:HG23	2.19	0.42
29:d:29:ALA:HB3	29:d:30:PRO:HD3	2.01	0.42
1:1:13:A:H4'	1:1:14:U:OP1	2.18	0.42
1:1:637:C:C2	1:1:638:C:C5	3.08	0.42
1:1:720:A:OP1	16:Q:69:ARG:NH1	2.53	0.42
1:1:1903:U:N3	1:1:1906:G:OP2	2.45	0.42
1:1:2503:G:C2	1:1:2504:U:C5	3.08	0.42
1:1:2986:U:C2	1:1:2987:A:C8	3.08	0.42
6:C:106:TRP:CE3	11:L:22:VAL:HG11	2.55	0.42
24:Y:59:VAL:HG13	24:Y:60:ARG:HG2	1.99	0.42
25:Z:134:LEU:HD13	25:Z:135:ARG:N	2.34	0.42
42:y:7:PHE:O	42:y:8:GLU:C	2.62	0.42
1:1:750:G:C2	1:1:751:A:C8	3.07	0.42
1:1:822:G:O6	1:1:904:A:C6	2.73	0.42
1:1:1150:A:C8	1:1:1310:G:O4'	2.72	0.42
1:1:1156:C:OP2	8:F:94:LYS:NZ	2.41	0.42
1:1:1227:C:H2'	1:1:1228:C:C1'	2.49	0.42
1:1:1952:G:H3'	1:1:1953:G:C5'	2.49	0.42
4:A:101:VAL:O	4:A:101:VAL:HG13	2.19	0.42
6:C:139:GLY:O	6:C:141:ARG:NH1	2.52	0.42
15:P:122:ALA:HB1	15:P:123:PRO:HD2	2.02	0.42
28:c:74:ASN:OD1	28:c:75:ASN:N	2.52	0.42
42:y:101:LEU:HD13	42:y:107:VAL:HG21	2.01	0.42
1:1:1927:G:O4'	39:p:8:VAL:HG11	2.19	0.42
5:B:77:THR:N	5:B:324:VAL:O	2.47	0.42
8:F:140:SER:N	8:F:237:ASN:OD1	2.47	0.42
12:M:77:ARG:O	12:M:81:VAL:HG23	2.19	0.42
23:X:62:VAL:HG13	23:X:90:ALA:CB	2.50	0.42
23:X:91:ASN:N	23:X:94:GLN:OE1	2.49	0.42
42:y:154:LEU:HD13	42:y:177:LEU:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:855:U:H4'	17:R:95:TRP:NE1	2.35	0.42
1:1:878:G:H1'	1:1:880:G:H21	1.84	0.42
1:1:2100:A:HO2'	1:1:2101:C:P	2.43	0.42
2:2:71:A:H62	2:2:87:G:N2	2.18	0.42
16:Q:64:VAL:HG13	16:Q:93:ILE:HD11	2.01	0.42
1:1:781:G:N3	1:1:781:G:H2'	2.35	0.42
1:1:986:U:OP1	8:F:98:LYS:NZ	2.46	0.42
1:1:2214:A:C4	1:1:2215:A:C8	3.08	0.42
1:1:2901:G:H21	1:1:3031:G:C4'	2.32	0.42
1:1:3051:U:C2	1:1:3052:G:C8	3.07	0.42
1:1:3110:C:OP1	40:r:26:LYS:NZ	2.53	0.42
4:A:110:GLY:N	4:A:136:ILE:O	2.44	0.42
6:C:71:VAL:HG22	6:C:72:ALA:N	2.35	0.42
1:1:501:A:C6	1:1:613:G:C6	3.08	0.42
1:1:1112:A:H1'	1:1:1371:G:H5'	2.02	0.42
2:2:12:A:C2	2:2:13:A:C8	3.07	0.42
40:r:4:ASN:O	40:r:5:ASP:OD1	2.37	0.42
1:1:353:G:O6	35:j:55:ARG:NH2	2.52	0.42
1:1:978:G:O2'	1:1:979:U:O4'	2.36	0.42
1:1:1423:C:C2	1:1:1424:C:C5	3.08	0.42
1:1:1833:G:H2'	1:1:1834:U:O4'	2.20	0.42
2:2:21:C:OP2	6:C:194:TYR:OH	2.26	0.42
4:A:114:SER:O	4:A:165:VAL:HG12	2.19	0.42
27:b:164:ASP:O	27:b:167:THR:OG1	2.33	0.42
1:1:1149:G:OP2	31:f:21:ARG:NH2	2.53	0.41
1:1:1320:C:O2'	18:S:115:ARG:NH2	2.51	0.41
1:1:1661:G:H2'	1:1:1662:G:C8	2.54	0.41
1:1:2176:U:OP1	4:A:54:ARG:NH2	2.48	0.41
1:1:3138:U:OP2	5:B:30:LYS:NZ	2.42	0.41
6:C:216:VAL:HG23	6:C:227:THR:OG1	2.19	0.41
8:F:163:LEU:HD22	8:F:169:ILE:HG12	2.02	0.41
9:G:136:LEU:O	9:G:140:VAL:HG23	2.19	0.41
16:Q:51:ALA:CB	16:Q:84:VAL:HG21	2.50	0.41
23:X:139:ILE:HD11	23:X:141:TYR:CD1	2.55	0.41
1:1:916:G:H4'	1:1:917:A:O5'	2.21	0.41
1:1:1281:G:H2'	1:1:1282:G:C8	2.55	0.41
1:1:1648:A:H2'	1:1:1649:U:O4'	2.20	0.41
1:1:1881:A:N1	1:1:2352:A:N6	2.68	0.41
35:j:19:CYS:O	35:j:23:GLY:N	2.53	0.41
1:1:523:A:N6	1:1:569:A:C2	2.81	0.41
1:1:970:A:H2'	1:1:971:G:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1578:C:C2'	1:1:1579:C:O5'	2.68	0.41
1:1:1619:A:C2'	1:1:1620:U:O5'	2.68	0.41
1:1:2900:A:OP2	40:r:7:ILE:HD11	2.19	0.41
15:P:47:TYR:O	15:P:51:VAL:HG23	2.20	0.41
42:y:107:VAL:HG13	42:y:118:HIS:CB	2.50	0.41
42:y:145:ASN:OD1	42:y:162:HIS:NE2	2.54	0.41
1:1:860:G:N3	1:1:860:G:H3'	2.35	0.41
1:1:1203:A:H3'	1:1:1300:G:H22	1.85	0.41
1:1:1303:A:HO2'	1:1:1304:A:C4'	2.28	0.41
1:1:2166:A:C2	13:N:74:PRO:HB3	2.54	0.41
28:c:25:LEU:HD22	28:c:90:VAL:HG22	2.02	0.41
1:1:360:G:H21	1:1:815:G:H1'	1.85	0.41
1:1:1422:G:C5	1:1:1423:C:C5	3.08	0.41
1:1:1655:G:OP2	1:1:1656:A:O2'	2.32	0.41
1:1:1881:A:C2	1:1:1882:G:N7	2.88	0.41
1:1:2160:G:C2	1:1:2161:G:N7	2.89	0.41
5:B:57:VAL:HG13	5:B:57:VAL:O	2.21	0.41
7:E:98:VAL:HG13	7:E:101:PHE:HD2	1.85	0.41
21:V:87:ARG:HH22	21:V:137:VAL:HG22	1.85	0.41
1:1:1188:U:O2'	1:1:1190:A:N7	2.50	0.41
1:1:1223:A:C2	1:1:1224:C:C6	3.09	0.41
1:1:2552:C:H2'	28:c:50:VAL:HG11	2.01	0.41
1:1:3228:C:H4'	1:1:3229:G:O5'	2.21	0.41
20:U:54:VAL:HG12	20:U:67:SER:CB	2.50	0.41
32:g:20:ILE:HG23	32:g:32:ALA:HB1	2.03	0.41
1:1:72:C:H4'	11:L:63:VAL:HG13	2.03	0.41
1:1:3164:C:O2'	1:1:3165:A:H8	2.04	0.41
1:1:3291:G:C2'	1:1:3292:A:O5'	2.68	0.41
5:B:37:ARG:HA	5:B:185:GLY:O	2.21	0.41
7:E:55:LEU:HD12	7:E:64:LEU:CD1	2.51	0.41
16:Q:80:THR:O	16:Q:138:LEU:N	2.51	0.41
20:U:80:THR:HG21	20:U:95:PHE:CE1	2.55	0.41
27:b:368:ALA:O	27:b:370:ASP:N	2.54	0.41
35:j:17:THR:HG22	35:j:18:LEU:H	1.85	0.41
1:1:297:G:O2'	34:i:31:GLY:O	2.35	0.41
1:1:1491:A:N7	37:l:2:ALA:HB2	2.34	0.41
1:1:1618:G:H2'	1:1:1619:A:C8	2.55	0.41
1:1:3349:C:O2'	1:1:3350:C:P	2.76	0.41
2:2:9:A:C2	2:2:10:A:C5	3.09	0.41
2:2:136:G:OP1	23:X:48:SER:OG	2.26	0.41
27:b:149:TYR:O	27:b:153:VAL:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:j:17:THR:HG22	35:j:18:LEU:N	2.36	0.41
38:m:438:LEU:H	38:m:438:LEU:HD23	1.85	0.41
1:1:829:U:O2'	1:1:866:A:N1	2.44	0.41
1:1:981:U:O2'	1:1:982:C:P	2.75	0.41
1:1:1114:U:H2'	1:1:1115:G:C4	2.56	0.41
1:1:1153:A:O2'	1:1:1154:A:O4'	2.31	0.41
1:1:1297:C:C2	1:1:1298:C:C5	3.09	0.41
1:1:1748:G:OP1	36:k:44:LYS:NZ	2.48	0.41
1:1:2522:G:O2'	23:X:31:THR:OG1	2.39	0.41
1:1:2933:A:N7	1:1:3014:U:O2'	2.54	0.41
1:1:2944:U:O2'	1:1:2947:G:N7	2.48	0.41
1:1:2951:G:H2'	1:1:2951:G:N3	2.36	0.41
1:1:2961:G:C6	1:1:2972:G:C6	3.09	0.41
1:1:3072:C:H4'	1:1:3336:A:H4'	2.02	0.41
1:1:3152:U:O5'	1:1:3158:G:N2	2.54	0.41
1:1:3220:G:C6	1:1:3266:G:N1	2.88	0.41
2:2:3:A:C4	2:2:4:C:C6	3.08	0.41
9:G:47:SER:O	9:G:50:VAL:HG12	2.20	0.41
12:M:118:PHE:O	12:M:122:VAL:HG23	2.20	0.41
25:Z:33:SER:OG	25:Z:35:SER:O	2.37	0.41
38:m:423:ASP:O	38:m:425:THR:N	2.54	0.41
38:m:431:LEU:HD23	38:m:453:ILE:HD11	2.03	0.41
1:1:91:G:N2	1:1:95:A:OP2	2.54	0.41
1:1:114:A:H2'	1:1:115:A:O4'	2.22	0.41
1:1:501:A:N6	1:1:613:G:O6	2.54	0.41
1:1:556:U:C4	1:1:560:G:C6	3.09	0.41
1:1:636:C:O2	1:1:2377:G:O2'	2.35	0.41
1:1:693:A:OP1	6:C:45:ASN:ND2	2.45	0.41
1:1:1119:C:C2	1:1:1120:A:C8	3.08	0.41
1:1:1338:C:C2	1:1:1339:C:C5	3.09	0.41
1:1:1636:U:C4	25:Z:38:PHE:CE1	3.09	0.41
1:1:1688:U:O2	1:1:1688:U:H2'	2.21	0.41
1:1:2215:A:C4	1:1:2216:G:C8	3.09	0.41
1:1:2907:G:C2	1:1:2908:G:N7	2.88	0.41
10:H:55:VAL:HB	10:H:68:LEU:HD21	2.03	0.41
13:N:119:TYR:OH	13:N:131:GLU:OE1	2.25	0.41
32:g:62:TYR:O	32:g:65:VAL:HG22	2.20	0.41
42:y:118:HIS:O	42:y:121:ILE:HG22	2.21	0.41
1:1:29:C:O2'	13:N:162:ARG:O	2.37	0.40
1:1:150:A:C2	1:1:151:A:C8	3.09	0.40
1:1:835:G:N2	1:1:857:G:O2'	2.43	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1437:C:O2	1:1:1438:U:C5	2.74	0.40
1:1:1470:U:C2	1:1:1471:U:C5	3.09	0.40
1:1:2377:G:OP1	1:1:2378:C:N4	2.53	0.40
1:1:3164:C:O2'	1:1:3165:A:P	2.79	0.40
5:B:3:HIS:O	5:B:4:ARG:CG	2.70	0.40
10:H:38:LEU:O	10:H:41:ILE:HG22	2.21	0.40
17:R:101:VAL:HG22	17:R:104:ARG:HH11	1.86	0.40
1:1:439:C:O2	1:1:439:C:C2'	2.69	0.40
1:1:1112:A:C4	1:1:1370:G:O2'	2.74	0.40
1:1:1490:A:OP2	37:I:2:ALA:HB1	2.22	0.40
1:1:2933:A:OP1	1:1:3015:G:O2'	2.29	0.40
1:1:2959:C:C2	1:1:2960:C:C5	3.10	0.40
1:1:3181:C:O2'	14:O:164:SER:OG	2.32	0.40
3:3:105:C:O2	3:3:105:C:H2'	2.19	0.40
28:c:78:GLY:HA2	28:c:81:VAL:HG22	2.04	0.40
38:m:338:LYS:CG	38:m:340:VAL:HG23	2.51	0.40
1:1:855:U:C4	1:1:856:G:C6	3.09	0.40
1:1:903:U:O3'	1:1:1536:G:O2'	2.39	0.40
1:1:979:U:H1'	1:1:980:A:O5'	2.22	0.40
1:1:3107:U:O4	1:1:3128:G:N2	2.54	0.40
6:C:159:ILE:HD13	6:C:165:ALA:HA	2.03	0.40
9:G:135:GLY:O	9:G:139:VAL:HG23	2.21	0.40
10:H:88:TYR:N	10:H:146:LEU:O	2.48	0.40
1:1:344:A:N6	1:1:349:A:N7	2.53	0.40
1:1:1313:G:C2	1:1:1314:C:C5	3.10	0.40
1:1:1710:C:C2	1:1:1711:C:C5	3.09	0.40
1:1:2530:G:N2	1:1:2531:C:C6	2.89	0.40
1:1:2959:C:N3	1:1:2960:C:C5	2.89	0.40
1:1:3346:U:C2	1:1:3347:A:C8	3.09	0.40
2:2:59:A:OP1	2:2:98:U:O2'	2.36	0.40
2:2:71:A:H4'	2:2:72:A:O5'	2.22	0.40
8:F:191:VAL:HG22	8:F:195:PHE:CD1	2.57	0.40
11:L:76:THR:O	11:L:80:VAL:HG23	2.21	0.40
1:1:610:G:C8	6:C:312:VAL:HG21	2.57	0.40
1:1:1471:U:C2	1:1:1472:U:C5	3.09	0.40
1:1:2509:U:O2'	1:1:2510:U:O4'	2.40	0.40
1:1:2886:U:C4	1:1:2911:A:C5	3.10	0.40
1:1:3034:C:C2	1:1:3035:A:C8	3.09	0.40
3:3:107:C:H2'	3:3:108:A:O4'	2.22	0.40
16:Q:41:ASP:OD1	16:Q:41:ASP:C	2.64	0.40
22:W:50:THR:N	22:W:51:PRO:HD2	2.36	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	A	206/254 (81%)	200 (97%)	6 (3%)	0	100	100
5	B	384/387 (99%)	364 (95%)	20 (5%)	0	100	100
6	C	359/362 (99%)	341 (95%)	18 (5%)	0	100	100
7	E	156/176 (89%)	152 (97%)	4 (3%)	0	100	100
8	F	220/244 (90%)	215 (98%)	5 (2%)	0	100	100
9	G	223/256 (87%)	216 (97%)	7 (3%)	0	100	100
10	H	186/191 (97%)	179 (96%)	7 (4%)	0	100	100
11	L	176/199 (88%)	167 (95%)	9 (5%)	0	100	100
12	M	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
13	N	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
14	O	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
15	P	172/184 (94%)	170 (99%)	2 (1%)	0	100	100
16	Q	144/186 (77%)	141 (98%)	3 (2%)	0	100	100
17	R	152/189 (80%)	146 (96%)	6 (4%)	0	100	100
18	S	168/172 (98%)	157 (94%)	11 (6%)	0	100	100
19	T	59/160 (37%)	54 (92%)	5 (8%)	0	100	100
20	U	100/121 (83%)	96 (96%)	4 (4%)	0	100	100
21	V	134/137 (98%)	134 (100%)	0	0	100	100
22	W	223/236 (94%)	215 (96%)	7 (3%)	1 (0%)	30	61
23	X	118/142 (83%)	115 (98%)	3 (2%)	0	100	100
24	Y	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
25	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	92/149 (62%)	89 (97%)	3 (3%)	0	100	100
27	b	489/647 (76%)	466 (95%)	22 (4%)	1 (0%)	43	73
28	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
29	d	102/113 (90%)	101 (99%)	1 (1%)	0	100	100
30	e	124/130 (95%)	120 (97%)	4 (3%)	0	100	100
31	f	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
32	g	99/121 (82%)	96 (97%)	3 (3%)	0	100	100
33	h	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
34	i	94/100 (94%)	93 (99%)	1 (1%)	0	100	100
35	j	83/88 (94%)	82 (99%)	1 (1%)	0	100	100
36	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
37	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
38	m	215/486 (44%)	207 (96%)	8 (4%)	0	100	100
39	p	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
40	r	93/261 (36%)	86 (92%)	7 (8%)	0	100	100
41	u	136/199 (68%)	134 (98%)	2 (2%)	0	100	100
42	y	222/245 (91%)	217 (98%)	5 (2%)	0	100	100
All	All	6238/7492 (83%)	6036 (97%)	200 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	b	399	ALA
22	W	178	GLY

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	A	164/196 (84%)	162 (99%)	2 (1%)	63	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	322/323 (100%)	318 (99%)	4 (1%)	63	78
6	C	288/289 (100%)	285 (99%)	3 (1%)	68	79
7	E	138/153 (90%)	137 (99%)	1 (1%)	76	82
8	F	186/205 (91%)	186 (100%)	0	100	100
9	G	185/208 (89%)	183 (99%)	2 (1%)	65	78
10	H	168/171 (98%)	167 (99%)	1 (1%)	78	83
11	L	140/159 (88%)	139 (99%)	1 (1%)	76	82
12	M	108/109 (99%)	108 (100%)	0	100	100
13	N	175/176 (99%)	174 (99%)	1 (1%)	78	83
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	141/146 (97%)	141 (100%)	0	100	100
16	Q	120/151 (80%)	119 (99%)	1 (1%)	73	81
17	R	127/154 (82%)	126 (99%)	1 (1%)	73	81
18	S	154/156 (99%)	153 (99%)	1 (1%)	78	83
19	T	50/137 (36%)	50 (100%)	0	100	100
20	U	89/107 (83%)	89 (100%)	0	100	100
21	V	104/105 (99%)	103 (99%)	1 (1%)	68	79
22	W	201/213 (94%)	199 (99%)	2 (1%)	68	79
23	X	104/118 (88%)	103 (99%)	1 (1%)	68	79
24	Y	109/110 (99%)	109 (100%)	0	100	100
25	Z	115/116 (99%)	114 (99%)	1 (1%)	70	80
26	a	77/119 (65%)	76 (99%)	1 (1%)	61	77
27	b	443/573 (77%)	440 (99%)	3 (1%)	76	82
28	c	81/88 (92%)	80 (99%)	1 (1%)	63	78
29	d	91/97 (94%)	90 (99%)	1 (1%)	65	78
30	e	108/111 (97%)	107 (99%)	1 (1%)	70	80
31	f	90/91 (99%)	89 (99%)	1 (1%)	65	78
32	g	86/103 (84%)	84 (98%)	2 (2%)	44	70
33	h	104/105 (99%)	102 (98%)	2 (2%)	50	73
34	i	78/82 (95%)	77 (99%)	1 (1%)	61	77
35	j	69/71 (97%)	68 (99%)	1 (1%)	59	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	k	68/69 (99%)	68 (100%)	0	100	100
37	l	45/46 (98%)	45 (100%)	0	100	100
38	m	197/428 (46%)	195 (99%)	2 (1%)	68	79
39	p	66/72 (92%)	65 (98%)	1 (2%)	57	75
40	r	90/229 (39%)	90 (100%)	0	100	100
41	u	123/180 (68%)	123 (100%)	0	100	100
42	y	192/211 (91%)	191 (100%)	1 (0%)	81	85
All	All	5356/6339 (84%)	5315 (99%)	41 (1%)	70	81

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	32	LEU
4	A	70	ARG
5	B	70	ARG
5	B	84	VAL
5	B	85	VAL
5	B	346	THR
6	C	12	THR
6	C	150	LEU
6	C	182	LEU
7	E	128	LYS
9	G	150	LEU
9	G	166	LEU
10	H	41	ILE
11	L	58	VAL
13	N	153	ASP
16	Q	138	LEU
17	R	99	LEU
18	S	61	ILE
21	V	14	SER
22	W	12	LEU
22	W	175	ILE
23	X	141	TYR
25	Z	99	GLU
26	a	133	LEU
27	b	171	LEU
27	b	312	VAL
27	b	398	LEU
28	c	103	THR

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Mol	Chain	Res	Type
29	d	89	LEU
30	e	21	HIS
31	f	98	VAL
32	g	44	CYS
32	g	90	ILE
33	h	28	LEU
33	h	85	THR
34	i	43	LEU
35	j	25	ARG
38	m	370	ILE
38	m	462	ILE
39	p	60	CYS
42	y	101	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	86	GLN
4	A	144	ASN
4	A	205	ASN
5	B	165	GLN
5	B	184	ASN
5	B	243	HIS
5	B	371	GLN
6	C	48	GLN
6	C	59	GLN
6	C	114	ASN
6	C	116	ASN
6	C	140	HIS
6	C	175	HIS
6	C	260	GLN
6	C	291	ASN
6	C	307	GLN
8	F	25	GLN
8	F	80	GLN
8	F	186	HIS
8	F	197	GLN
8	F	209	ASN
9	G	38	GLN
9	G	59	GLN
9	G	138	HIS
10	H	5	GLN

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Mol	Chain	Res	Type
10	H	8	GLN
10	H	157	ASN
11	L	102	GLN
14	O	42	ASN
15	P	34	GLN
15	P	133	HIS
17	R	150	GLN
20	U	87	ASN
20	U	101	ASN
22	W	88	ASN
22	W	205	GLN
24	Y	4	GLN
25	Z	36	HIS
25	Z	122	HIS
26	a	65	GLN
26	a	89	GLN
26	a	120	ASN
27	b	195	GLN
27	b	208	HIS
27	b	234	ASN
27	b	280	ASN
27	b	288	ASN
29	d	57	GLN
30	e	26	HIS
30	e	31	ASN
30	e	71	HIS
33	h	59	ASN
33	h	68	GLN
35	j	12	HIS
37	l	33	ASN
38	m	392	HIS
39	p	33	GLN
40	r	10	HIS
40	r	20	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2762/3396 (81%)	434 (15%)	31 (1%)
2	2	157/158 (99%)	25 (15%)	1 (0%)
3	3	42/121 (34%)	3 (7%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	2961/3675 (80%)	462 (15%)	32 (1%)

All (462) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	14	U
1	1	26	A
1	1	43	A
1	1	49	A
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	92	G
1	1	99	A
1	1	100	A
1	1	110	G
1	1	111	C
1	1	113	C
1	1	116	A
1	1	122	A
1	1	133	U
1	1	136	G
1	1	156	G
1	1	157	A
1	1	166	C
1	1	187	A
1	1	190	U
1	1	191	U
1	1	200	C
1	1	213	A
1	1	218	G
1	1	219	A
1	1	221	A
1	1	231	G
1	1	234	G
1	1	240	U
1	1	243	G
1	1	245	U
1	1	252	U
1	1	253	A

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Mol	Chain	Res	Type
1	1	269	G
1	1	283	G
1	1	284	A
1	1	286	U
1	1	298	U
1	1	305	U
1	1	315	C
1	1	323	A
1	1	325	A
1	1	329	U
1	1	338	A
1	1	339	C
1	1	350	C
1	1	370	U
1	1	374	A
1	1	375	A
1	1	376	G
1	1	398	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	421	G
1	1	422	A
1	1	429	U
1	1	440	A
1	1	495	G
1	1	503	C
1	1	521	A
1	1	523	A
1	1	535	G
1	1	536	U
1	1	543	C
1	1	544	C
1	1	545	U
1	1	547	G
1	1	548	G
1	1	552	G
1	1	555	U
1	1	557	A
1	1	558	U
1	1	559	A

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Mol	Chain	Res	Type
1	1	560	G
1	1	578	A
1	1	579	G
1	1	589	A
1	1	604	G
1	1	611	A
1	1	620	U
1	1	621	A
1	1	636	C
1	1	637	C
1	1	638	C
1	1	677	A
1	1	681	U
1	1	691	A
1	1	705	A
1	1	715	A
1	1	716	A
1	1	719	U
1	1	737	G
1	1	761	A
1	1	764	U
1	1	767	U
1	1	768	C
1	1	769	G
1	1	776	U
1	1	777	U
1	1	780	A
1	1	781	G
1	1	785	G
1	1	787	G
1	1	806	A
1	1	807	A
1	1	817	A
1	1	830	A
1	1	836	A
1	1	847	A
1	1	857	G
1	1	861	C
1	1	874	U
1	1	879	U
1	1	880	G
1	1	896	A

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Mol	Chain	Res	Type
1	1	907	G
1	1	908	G
1	1	914	A
1	1	916	G
1	1	917	A
1	1	924	G
1	1	937	G
1	1	944	C
1	1	954	U
1	1	955	U
1	1	959	C
1	1	960	U
1	1	974	G
1	1	979	U
1	1	980	A
1	1	981	U
1	1	982	C
1	1	1063	G
1	1	1064	A
1	1	1065	A
1	1	1072	G
1	1	1081	U
1	1	1082	U
1	1	1093	A
1	1	1094	U
1	1	1095	U
1	1	1096	U
1	1	1097	G
1	1	1098	A
1	1	1103	A
1	1	1104	G
1	1	1114	U
1	1	1116	G
1	1	1117	G
1	1	1153	A
1	1	1159	A
1	1	1180	A
1	1	1181	U
1	1	1182	A
1	1	1189	C
1	1	1190	A
1	1	1191	U

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Mol	Chain	Res	Type
1	1	1192	C
1	1	1193	A
1	1	1201	C
1	1	1202	A
1	1	1209	G
1	1	1217	A
1	1	1222	G
1	1	1233	G
1	1	1236	G
1	1	1239	C
1	1	1240	A
1	1	1241	U
1	1	1245	A
1	1	1246	G
1	1	1247	U
1	1	1253	U
1	1	1254	C
1	1	1259	A
1	1	1263	A
1	1	1265	U
1	1	1269	U
1	1	1271	A
1	1	1272	C
1	1	1282	G
1	1	1283	C
1	1	1284	C
1	1	1287	A
1	1	1295	G
1	1	1302	A
1	1	1304	A
1	1	1307	G
1	1	1308	A
1	1	1309	U
1	1	1330	A
1	1	1348	U
1	1	1349	G
1	1	1356	U
1	1	1357	G
1	1	1386	A
1	1	1392	G
1	1	1399	A
1	1	1400	G

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Mol	Chain	Res	Type
1	1	1417	G
1	1	1419	A
1	1	1434	G
1	1	1436	U
1	1	1437	C
1	1	1481	A
1	1	1483	G
1	1	1487	G
1	1	1496	C
1	1	1508	C
1	1	1536	G
1	1	1557	A
1	1	1561	G
1	1	1562	C
1	1	1563	C
1	1	1566	A
1	1	1579	C
1	1	1583	A
1	1	1589	A
1	1	1593	A
1	1	1607	U
1	1	1618	G
1	1	1620	U
1	1	1629	U
1	1	1639	C
1	1	1643	A
1	1	1657	C
1	1	1683	A
1	1	1694	U
1	1	1713	G
1	1	1724	U
1	1	1741	A
1	1	1750	A
1	1	1751	G
1	1	1763	U
1	1	1764	U
1	1	1765	U
1	1	1770	G
1	1	1775	G
1	1	1780	G
1	1	1797	A
1	1	1807	G

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Mol	Chain	Res	Type
1	1	1808	G
1	1	1812	G
1	1	1813	A
1	1	1815	U
1	1	1816	A
1	1	1820	U
1	1	1821	U
1	1	1839	A
1	1	1841	A
1	1	1842	A
1	1	1849	C
1	1	1866	C
1	1	1878	G
1	1	1881	A
1	1	1906	G
1	1	1926	C
1	1	2099	A
1	1	2101	C
1	1	2111	G
1	1	2120	A
1	1	2121	G
1	1	2122	G
1	1	2126	A
1	1	2131	A
1	1	2158	A
1	1	2167	A
1	1	2168	A
1	1	2169	G
1	1	2188	A
1	1	2194	G
1	1	2202	C
1	1	2228	A
1	1	2244	A
1	1	2335	G
1	1	2336	U
1	1	2356	A
1	1	2372	A
1	1	2373	A
1	1	2374	C
1	1	2388	U
1	1	2393	G
1	1	2394	G

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Mol	Chain	Res	Type
1	1	2397	A
1	1	2399	A
1	1	2418	G
1	1	2432	A
1	1	2433	U
1	1	2435	G
1	1	2440	G
1	1	2442	G
1	1	2507	C
1	1	2510	U
1	1	2511	A
1	1	2512	C
1	1	2514	U
1	1	2515	A
1	1	2522	G
1	1	2523	A
1	1	2524	A
1	1	2525	G
1	1	2532	U
1	1	2536	A
1	1	2547	A
1	1	2549	G
1	1	2552	C
1	1	2562	A
1	1	2570	U
1	1	2572	C
1	1	2573	G
1	1	2585	G
1	1	2586	G
1	1	2593	A
1	1	2594	C
1	1	2600	C
1	1	2606	G
1	1	2607	G
1	1	2771	U
1	1	2772	C
1	1	2773	C
1	1	2777	G
1	1	2778	G
1	1	2801	A
1	1	2810	C
1	1	2820	A

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Mol	Chain	Res	Type
1	1	2825	C
1	1	2837	A
1	1	2853	A
1	1	2857	C
1	1	2858	U
1	1	2873	U
1	1	2875	U
1	1	2876	C
1	1	2877	G
1	1	2878	G
1	1	2879	C
1	1	2887	A
1	1	2898	G
1	1	2899	C
1	1	2900	A
1	1	2901	G
1	1	2910	A
1	1	2921	U
1	1	2922	G
1	1	2923	U
1	1	2935	U
1	1	2936	A
1	1	2942	C
1	1	2970	C
1	1	2971	A
1	1	2972	G
1	1	2983	C
1	1	2997	G
1	1	3012	A
1	1	3022	G
1	1	3027	A
1	1	3028	G
1	1	3030	G
1	1	3033	A
1	1	3049	A
1	1	3059	G
1	1	3078	U
1	1	3079	U
1	1	3086	A
1	1	3092	C
1	1	3093	C
1	1	3099	C

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Mol	Chain	Res	Type
1	1	3101	G
1	1	3109	G
1	1	3117	C
1	1	3121	U
1	1	3127	A
1	1	3128	G
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3153	U
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3158	G
1	1	3163	A
1	1	3165	A
1	1	3170	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3181	C
1	1	3187	A
1	1	3196	U
1	1	3198	U
1	1	3207	U
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3229	G
1	1	3239	G
1	1	3245	A
1	1	3247	G
1	1	3253	G
1	1	3259	U
1	1	3260	G
1	1	3270	U
1	1	3273	A
1	1	3276	G
1	1	3279	A
1	1	3281	U

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Mol	Chain	Res	Type
1	1	3292	A
1	1	3293	U
1	1	3294	A
1	1	3304	U
1	1	3316	A
1	1	3319	U
1	1	3320	A
1	1	3334	U
1	1	3335	A
1	1	3341	U
1	1	3342	A
1	1	3350	C
1	1	3352	U
1	1	3353	G
1	1	3355	U
1	1	3368	U
1	1	3369	G
1	1	3375	A
1	1	3378	C
2	2	16	G
2	2	21	C
2	2	23	U
2	2	34	U
2	2	35	C
2	2	39	G
2	2	59	A
2	2	62	C
2	2	63	G
2	2	80	A
2	2	81	U
2	2	82	U
2	2	86	U
2	2	90	U
2	2	95	G
2	2	104	A
2	2	106	C
2	2	111	A
2	2	125	U
2	2	126	A
2	2	127	U
2	2	138	A
2	2	151	C

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Mol	Chain	Res	Type
2	2	152	G
2	2	157	U
3	3	76	A
3	3	102	A
3	3	106	U

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	65	A
1	1	239	G
1	1	282	G
1	1	547	G
1	1	637	C
1	1	806	A
1	1	846	A
1	1	916	G
1	1	979	U
1	1	981	U
1	1	1064	A
1	1	1097	G
1	1	1103	A
1	1	1268	G
1	1	1270	A
1	1	1303	A
1	1	1307	G
1	1	1355	A
1	1	1562	C
1	1	2166	A
1	1	2593	A
1	1	2857	C
1	1	3078	U
1	1	3218	A
1	1	3228	C
1	1	3269	U
1	1	3291	G
1	1	3292	A
1	1	3349	C
1	1	3352	U
2	2	125	U

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](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

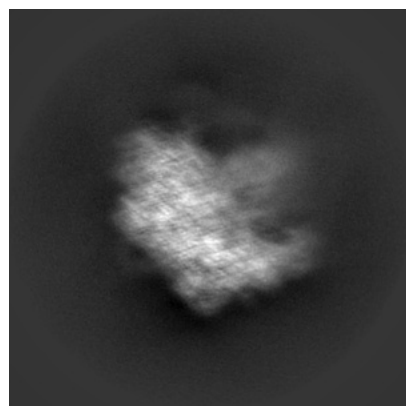
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12866. These allow visual inspection of the internal detail of the map and identification of artifacts.

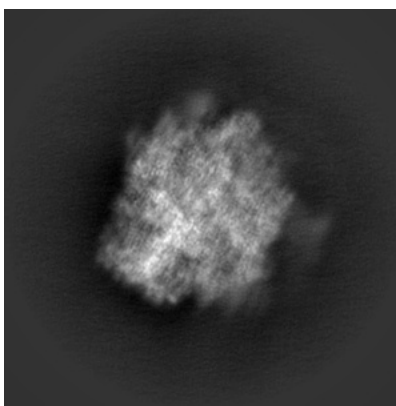
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

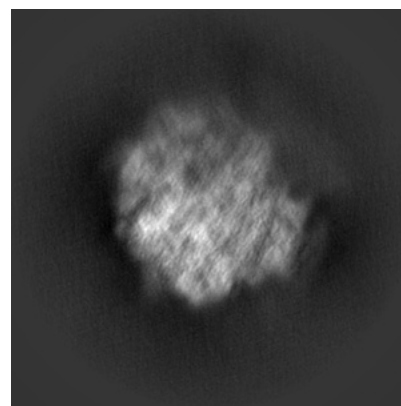
6.1.1 Primary map



X

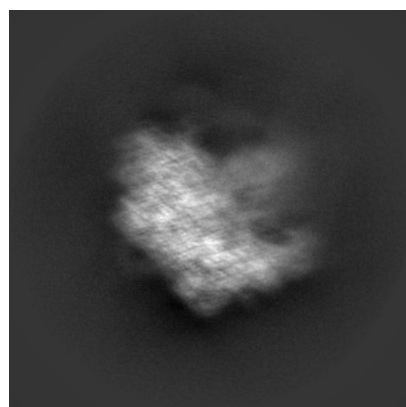


Y

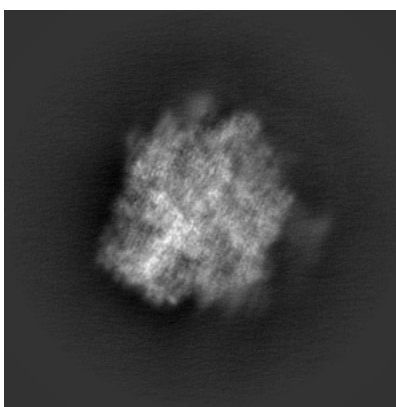


Z

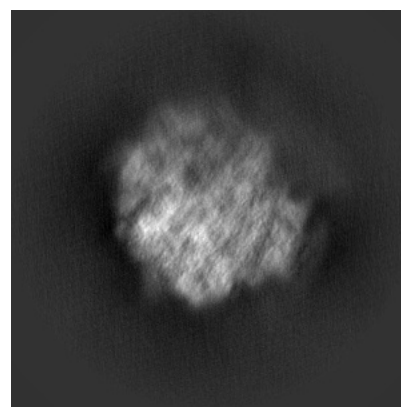
6.1.2 Raw map



X



Y

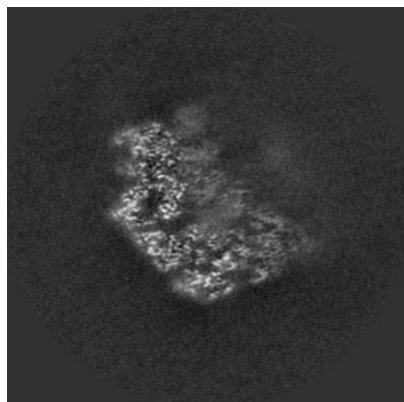


Z

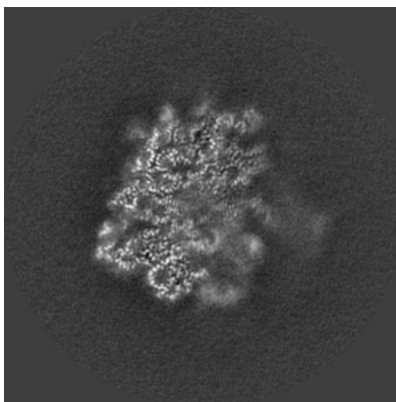
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

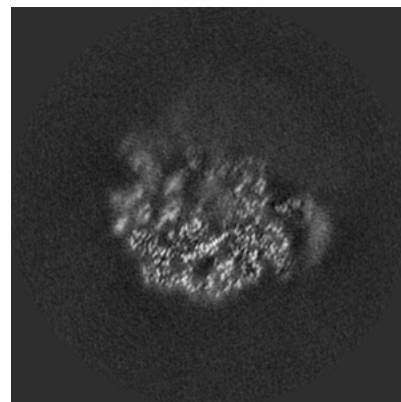
6.2.1 Primary map



X Index: 200

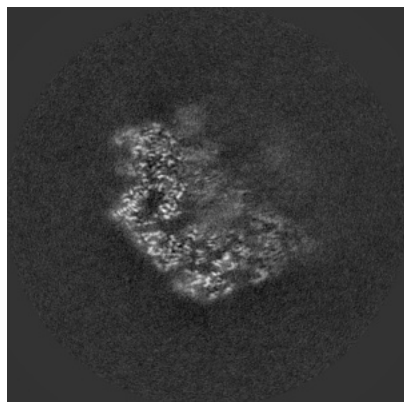


Y Index: 200

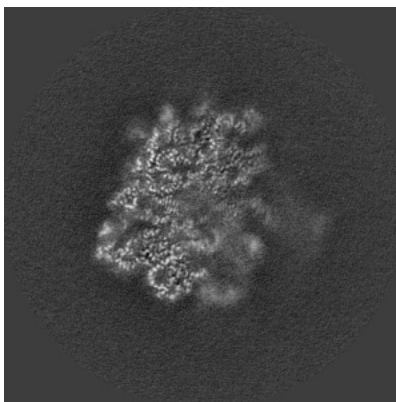


Z Index: 200

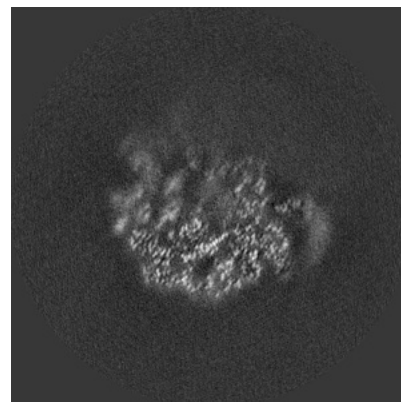
6.2.2 Raw map



X Index: 200



Y Index: 200

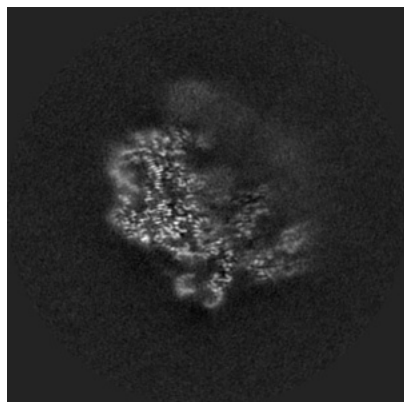


Z Index: 200

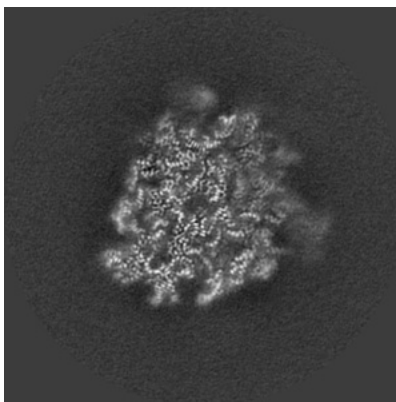
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

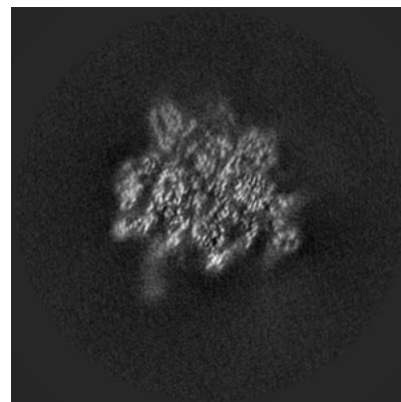
6.3.1 Primary map



X Index: 184

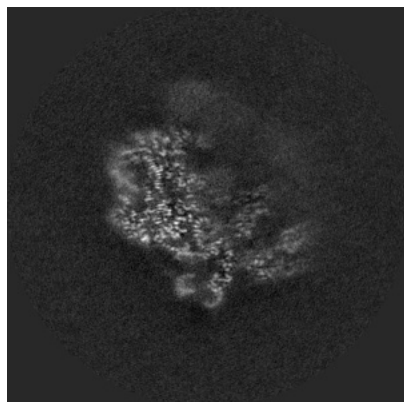


Y Index: 179

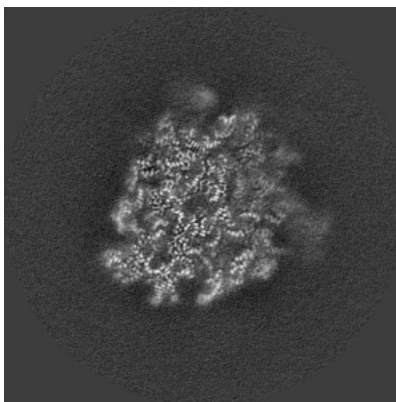


Z Index: 154

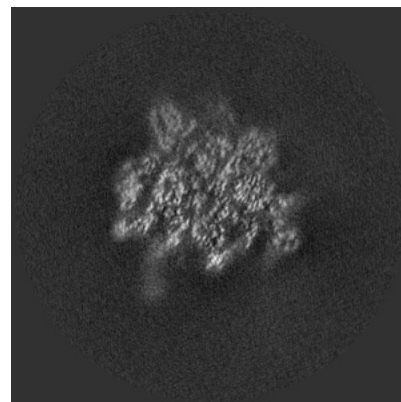
6.3.2 Raw map



X Index: 184



Y Index: 179

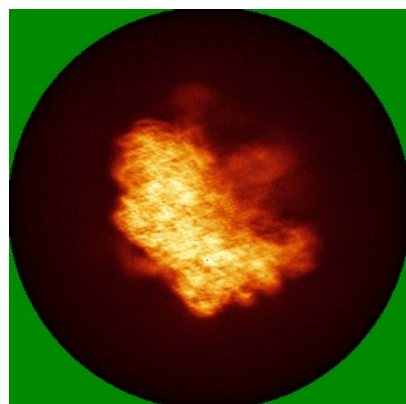


Z Index: 154

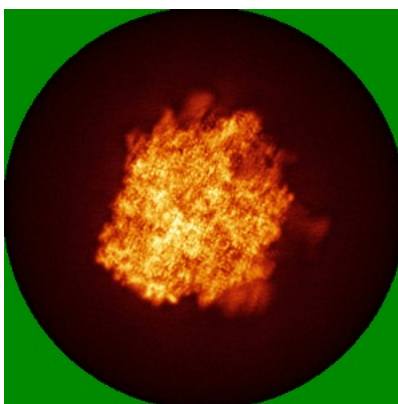
The images above show the largest variance slices of the map in three orthogonal directions.

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

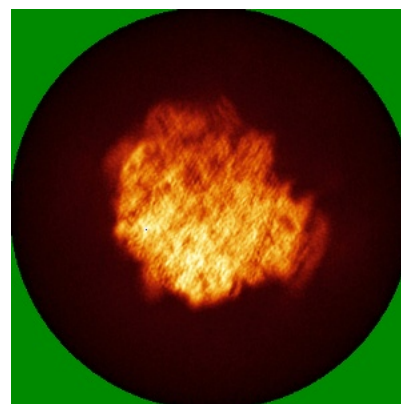
6.4.1 Primary map



X

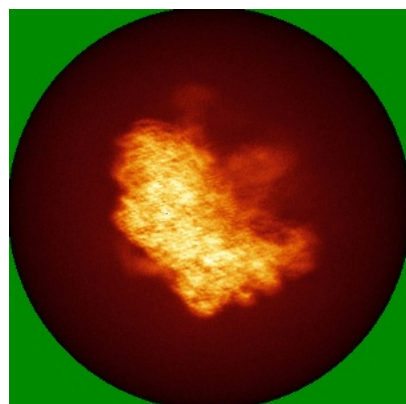


Y

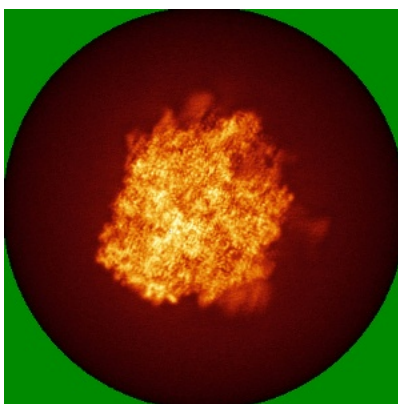


Z

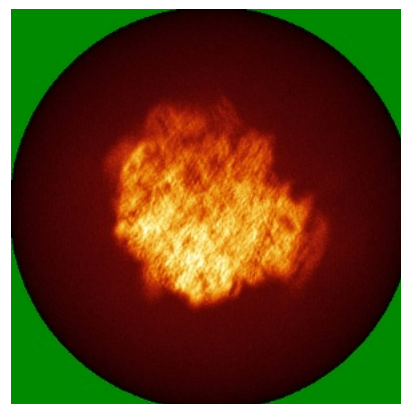
6.4.2 Raw map



X



Y

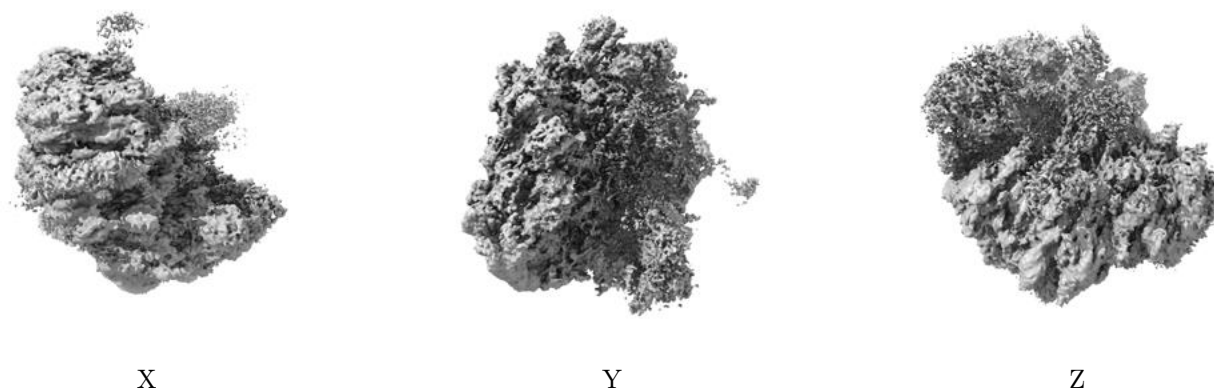


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

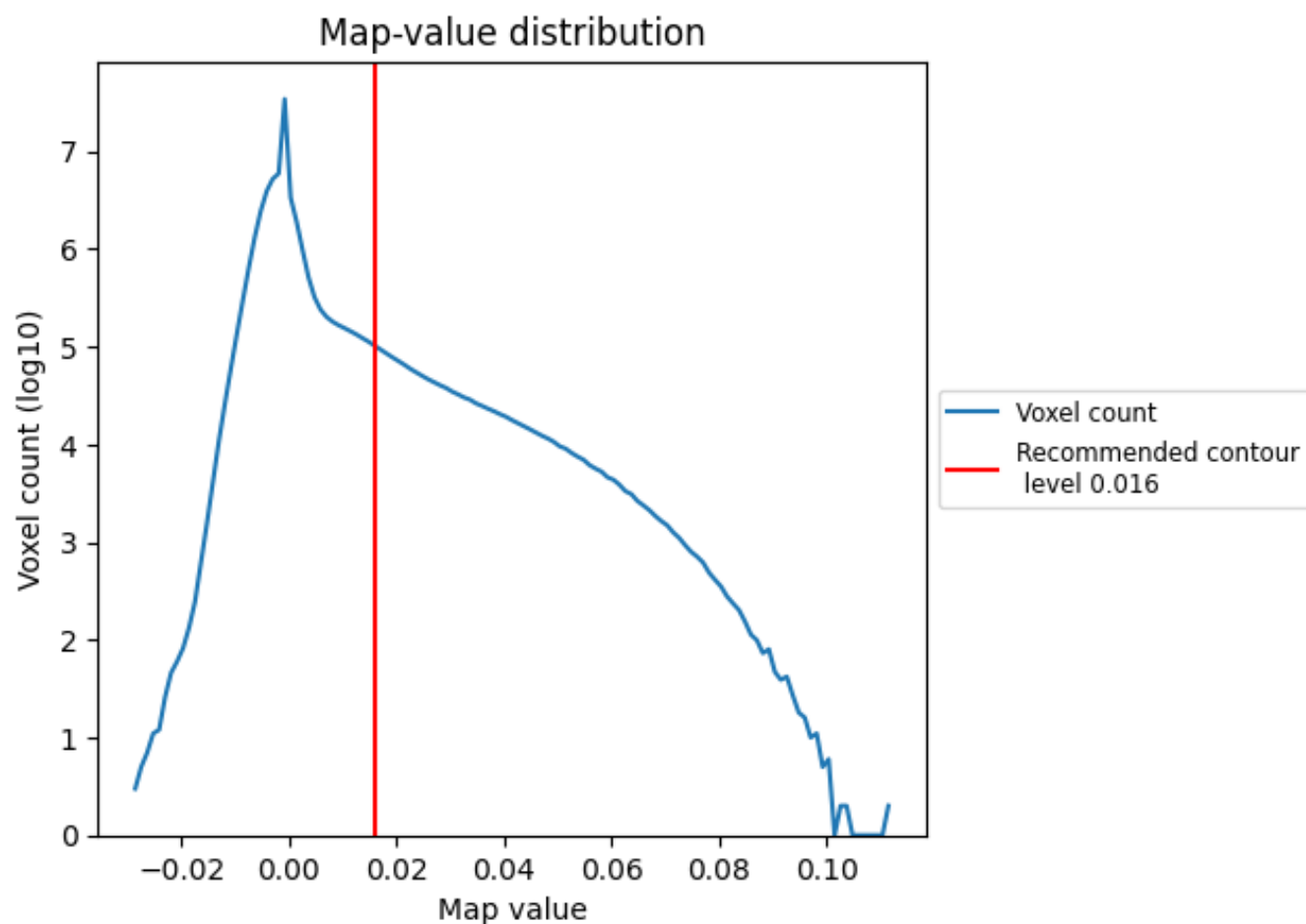
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

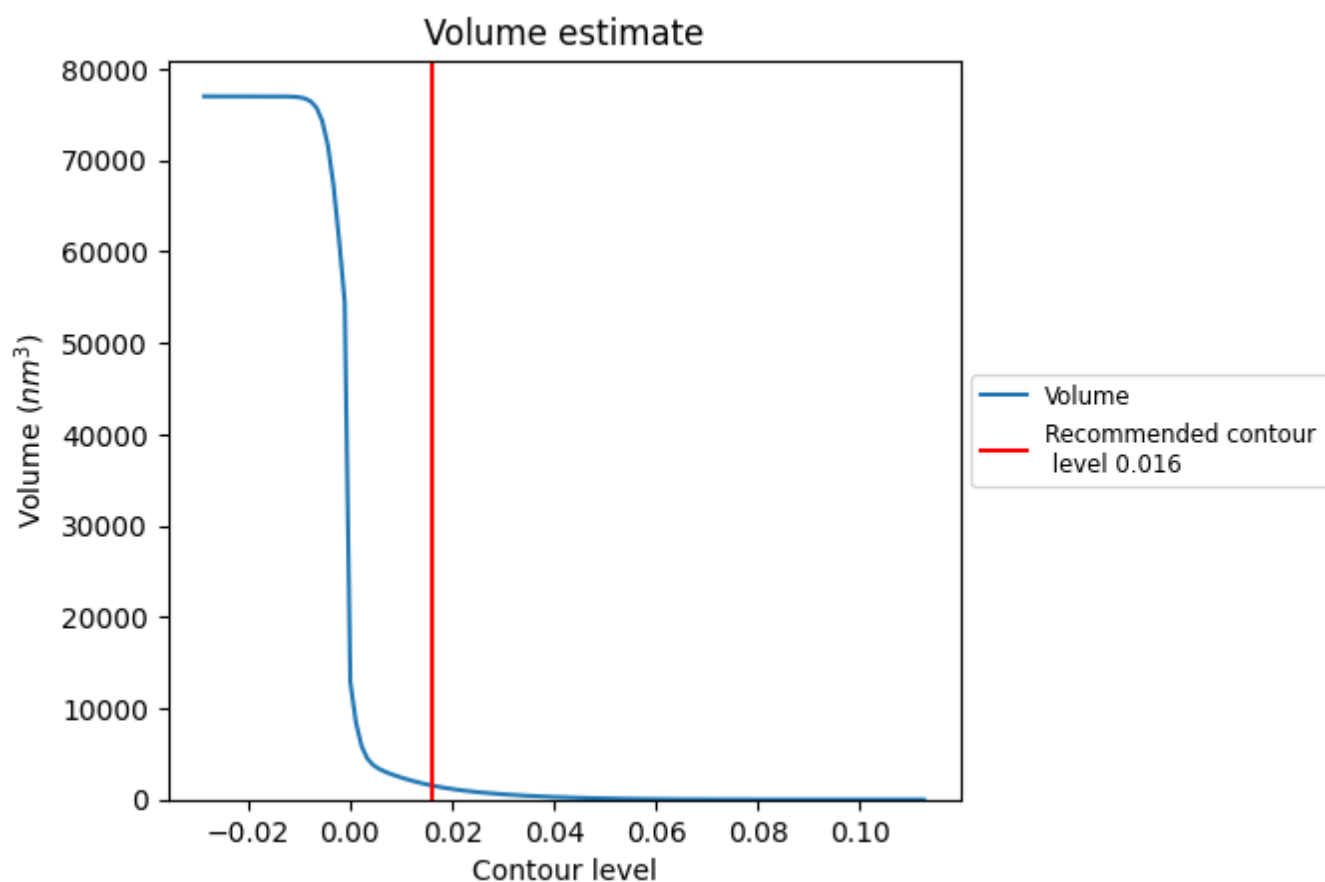
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

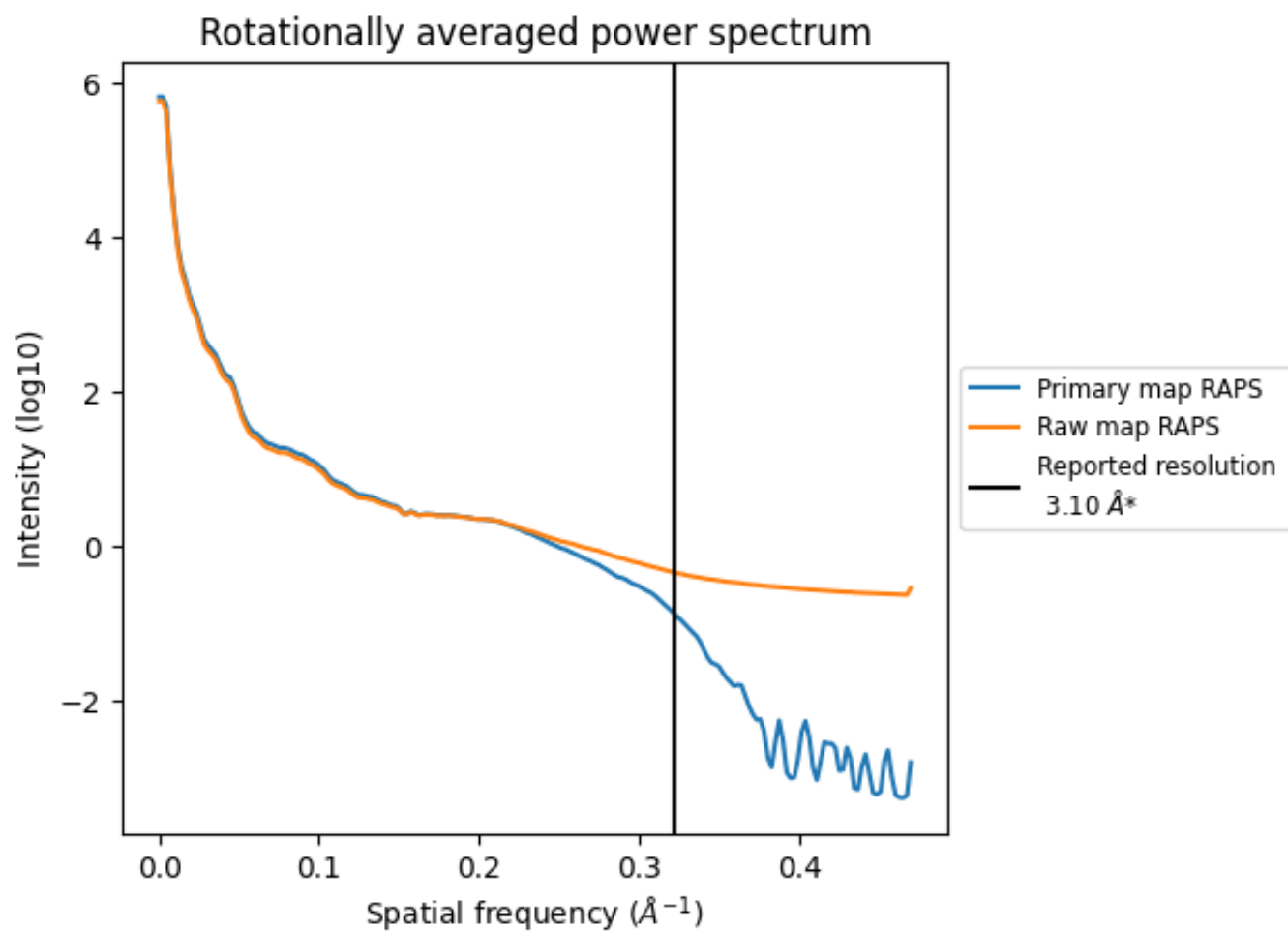
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1549 nm³; this corresponds to an approximate mass of 1400 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](#)

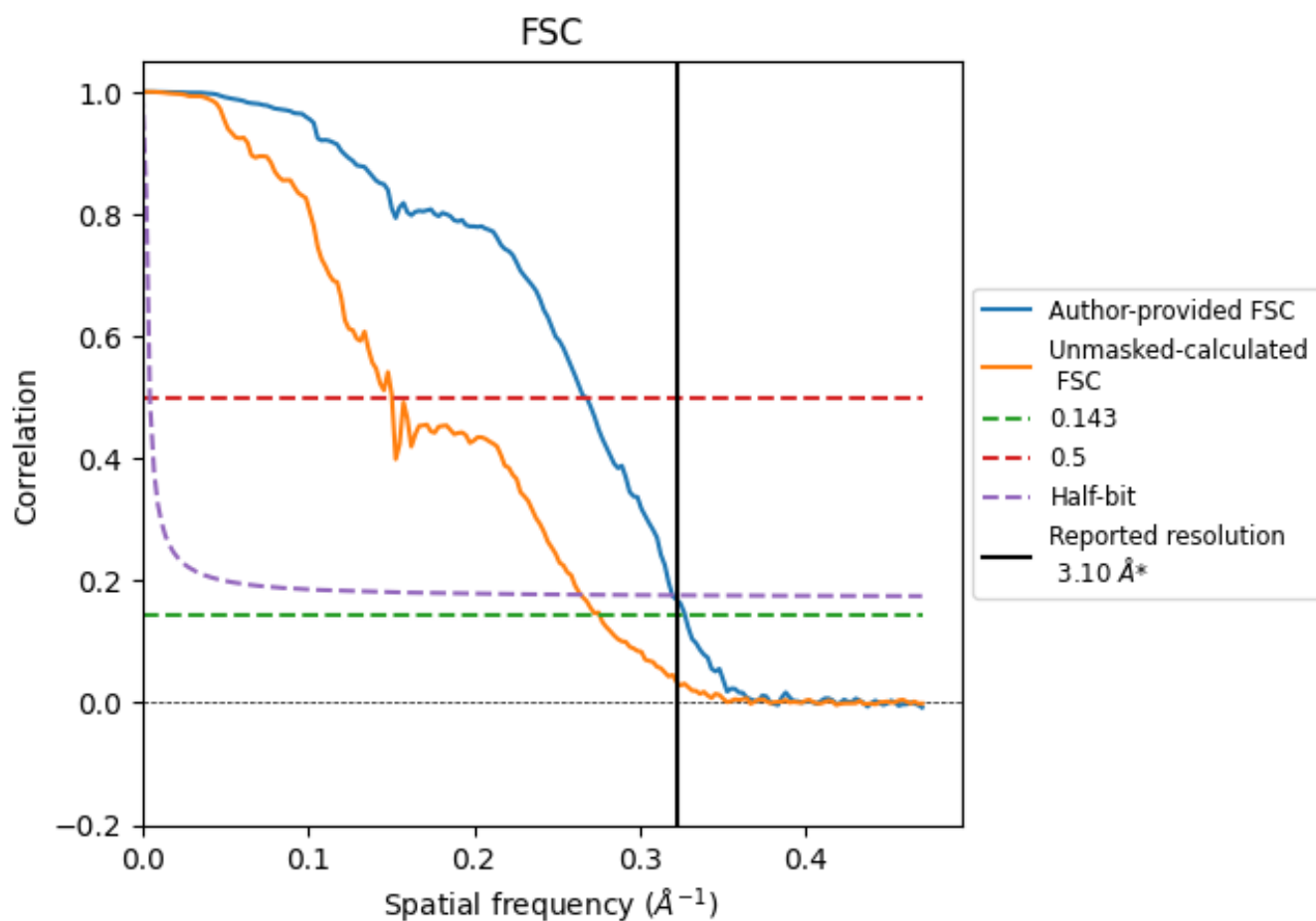


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.323 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.06	3.74	3.13
Unmasked-calculated*	3.63	6.64	3.78

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.63 differs from the reported value 3.1 by more than 10 %

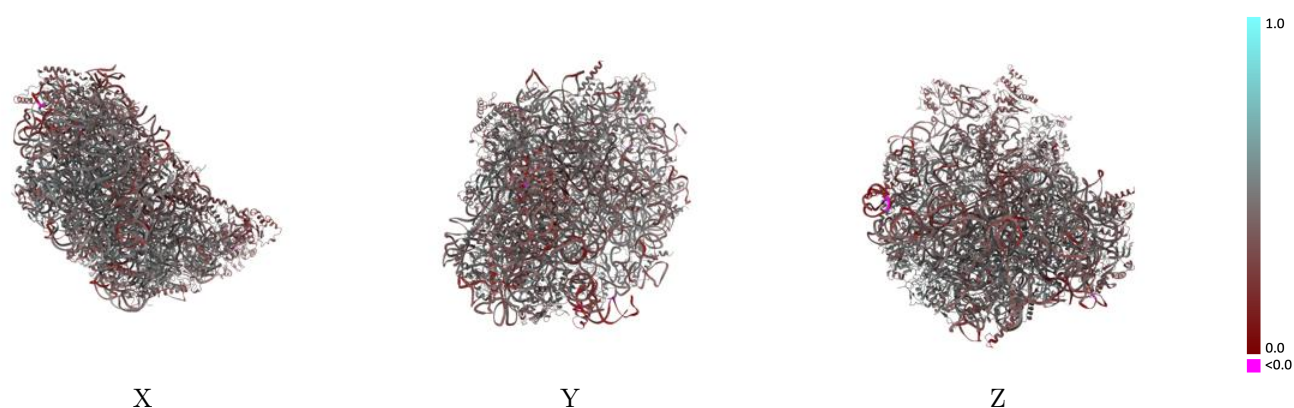
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12866 and PDB model 7OF1. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

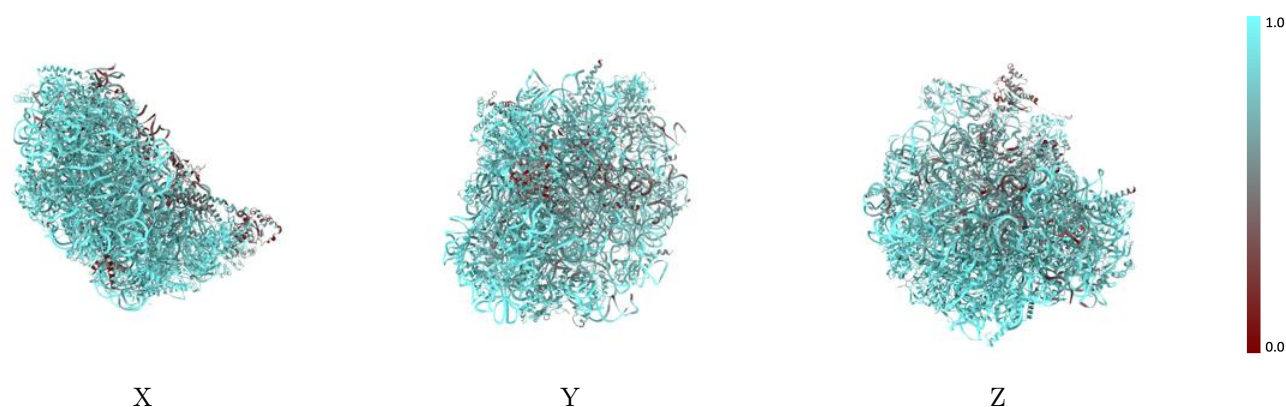
This section was not generated.

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



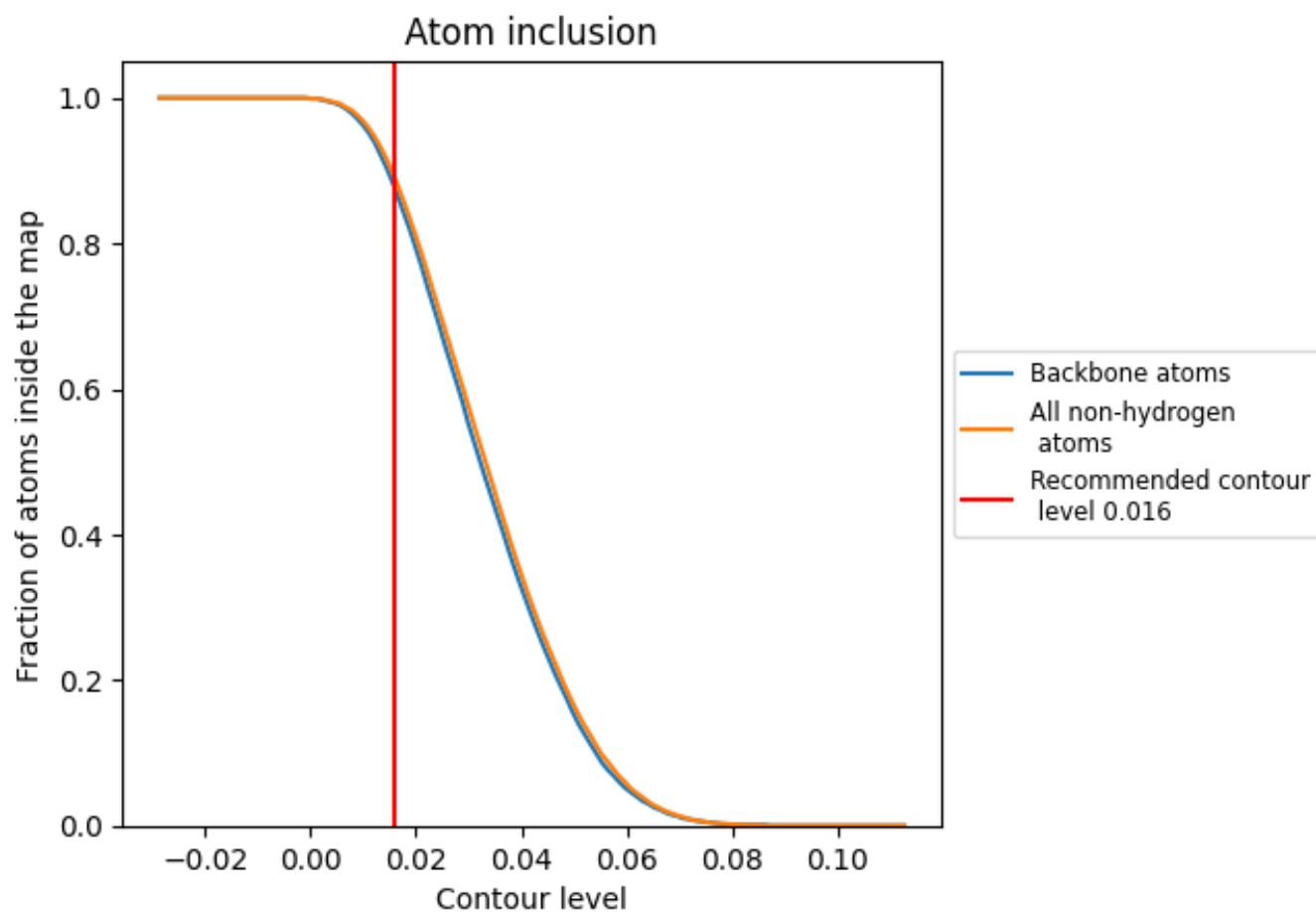
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 89% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8900	 0.4110
1	 0.9300	 0.4010
2	 0.9850	 0.4390
3	 0.7890	 0.3380
A	 0.7200	 0.4180
B	 0.8970	 0.4460
C	 0.9280	 0.4700
E	 0.9260	 0.4410
F	 0.9090	 0.4350
G	 0.8460	 0.3860
H	 0.8520	 0.4350
L	 0.9190	 0.4510
M	 0.9180	 0.4410
N	 0.8570	 0.4500
O	 0.9080	 0.4660
P	 0.9180	 0.4680
Q	 0.8880	 0.4520
R	 0.8180	 0.4380
S	 0.8810	 0.4310
T	 0.7150	 0.2920
U	 0.8300	 0.3900
V	 0.8850	 0.4450
W	 0.7250	 0.3180
X	 0.8970	 0.4650
Y	 0.9660	 0.4760
Z	 0.8500	 0.4010
a	 0.8780	 0.4380
b	 0.5550	 0.3360
c	 0.8660	 0.3970
d	 0.8500	 0.4590
e	 0.9160	 0.4870
f	 0.9370	 0.5000
g	 0.8680	 0.4510
h	 0.9500	 0.4470
i	 0.8400	 0.4170



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Chain	Atom inclusion	Q-score
j	 0.9270	 0.4840
k	 0.7100	 0.4140
l	 0.8890	 0.4770
m	 0.4730	 0.3410
p	 0.6710	 0.4230
r	 0.7490	 0.3820
u	 0.8290	 0.4120
y	 0.9420	 0.4170