



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 09:52 AM UTC

PDB ID : 5ZWN / pdb_00005zwn
EMDB ID : EMD-6973
Title : Cryo-EM structure of the yeast pre-B complex at an average resolution of 3.3 angstrom (Part II: U1 snRNP region)
Authors : Bai, R.; Wan, R.; Yan, C.; Lei, J.; Shi, Y.
Deposited on : 2018-05-16
Resolution : 3.40 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:

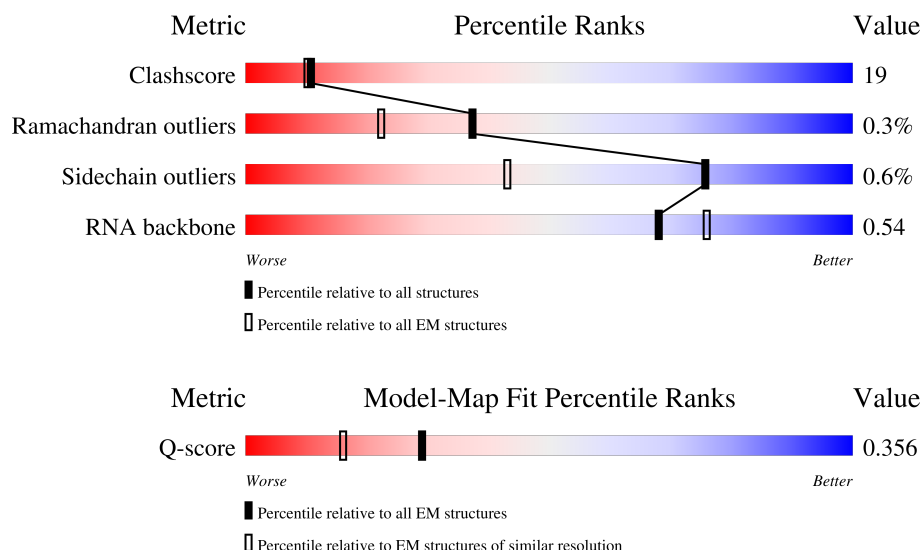
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 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.



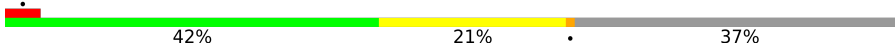
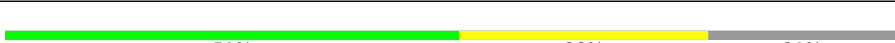
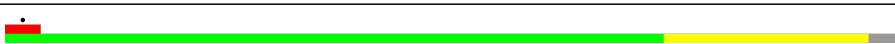
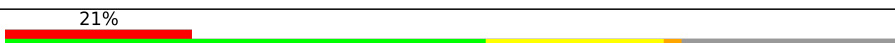
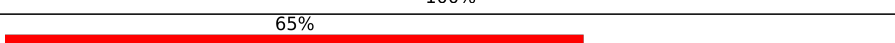
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	G	22	59% 41% 41% 18%
2	P	568	32% 24% 39% 20% 15%
3	Q	300	29% 52% 9% 38%

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Mol	Chain	Length	Quality of chain
4	R	231	
5	S	298	
6	T	544	
7	U	629	
8	V	523	
9	W	492	
10	a	196	
11	b	146	
12	c	110	
13	d	101	
14	e	94	
15	f	86	
16	g	77	
17	X	619	
18	Y	261	
19	x	49	
20	y	588	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 33559 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	22	Total	C	N	O	P	0	0
			477	215	95	145	22		

- Molecule 2 is a RNA chain called U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	480	Total	C	N	O	P	0	0
			10138	4535	1715	3408	480		

- Molecule 3 is a protein called U1 small nuclear ribonucleoprotein 70 kDa homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	186	Total	C	N	O	S	0	0
			1219	752	232	233	2		

- Molecule 4 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	184	Total	C	N	O	S	0	0
			1492	930	289	268	5		

- Molecule 5 is a protein called U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	131	Total	C	N	O	S	0	0
			1045	665	191	186	3		

- Molecule 6 is a protein called U1 small nuclear ribonucleoprotein component PRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	T	539	Total	C	N	O	S	0	0
			4540	2976	716	829	19		

- Molecule 7 is a protein called Pre-mRNA-processing factor 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	U	583	Total	C	N	O	S	0	0
			3940	2498	684	751	7		

- Molecule 8 is a protein called Protein NAM8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	187	Total	C	N	O	S	0	0
			1414	889	244	271	10		

- Molecule 9 is a protein called 56 kDa U1 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	229	Total	C	N	O	S	0	0
			1841	1202	300	328	11		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	a	124	Total	C	N	O	S	0	0
			1009	637	191	178	3		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	b	119	Total	C	N	O	S	0	0
			917	575	163	176	3		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	101	Total	C	N	O	S	0	0
			785	504	149	128	4		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	d	92	Total	C	N	O	S	0	0
			704	448	126	127	3		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	e	74	Total	C	N	O	S	0	0
			526	346	87	90	3		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	f	68	Total	C	N	O	S	0	0
			518	337	96	84	1		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	g	75	Total	C	N	O	S	0	0
			552	350	98	103	1		

- Molecule 17 is a protein called U1 small nuclear ribonucleoprotein component SNU71.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	X	49	Total	C	N	O	0	0
			395	252	68	75		

- Molecule 18 is a protein called Protein LUC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	196	Total	C	N	O	S	0	0
			1400	874	258	257	11		

- Molecule 19 is a protein called U1 snRNP.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	x	49	Total	C	N	O	0	0
			245	147	49	49		

- Molecule 20 is a protein called Pre-mRNA-splicing ATP-dependent RNA helicase PRP28.

Mol	Chain	Residues	Atoms	AltConf	Trace
20	y	399	Total C 399 399	0	399

- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
21	R	1	Total 1	Zn 1	0
21	Y	2	Total 2	Zn 2	0

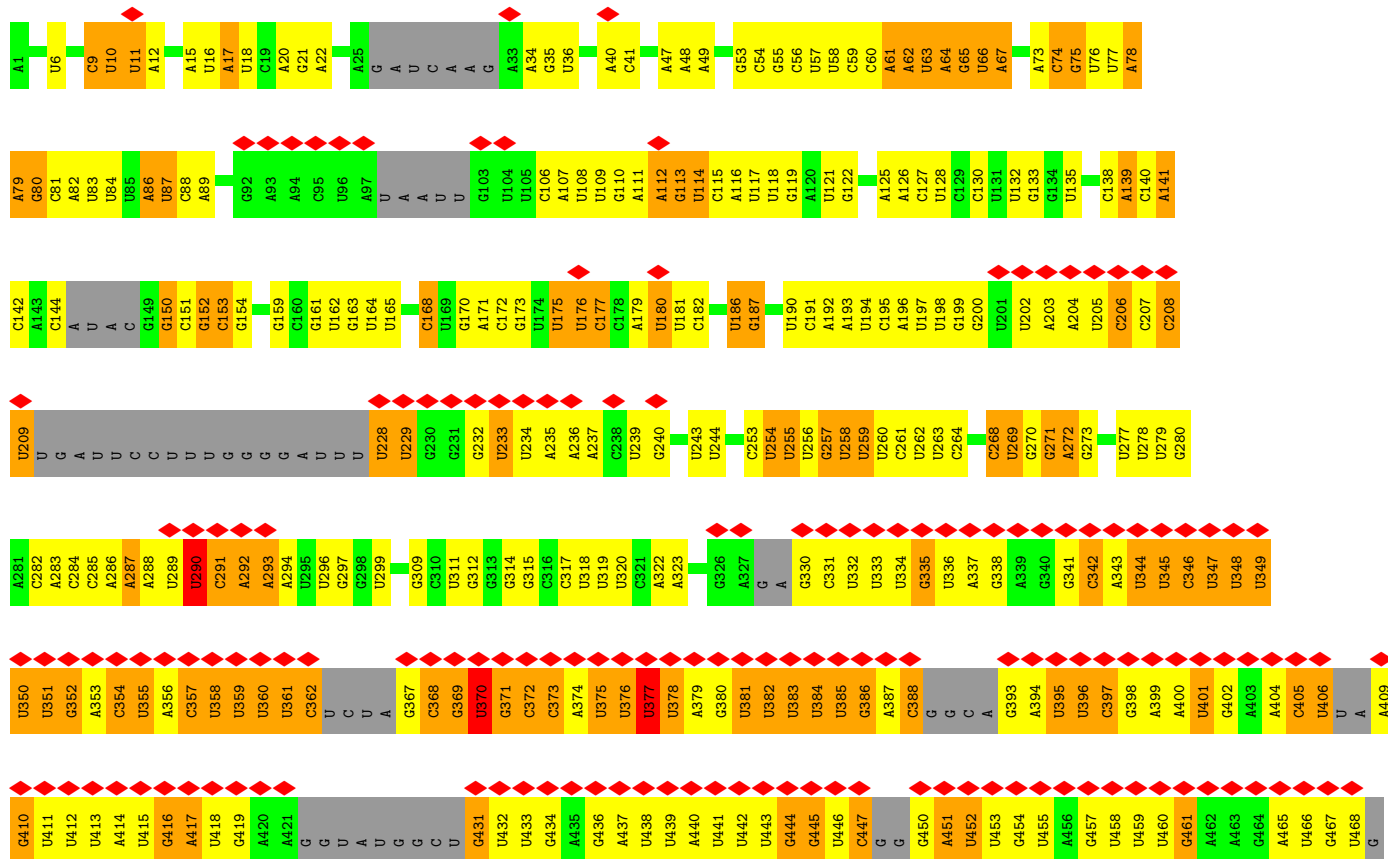
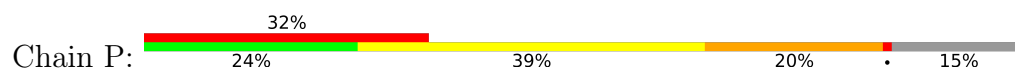
3 Residue-property plots

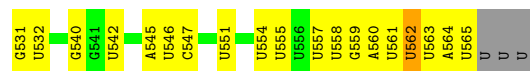
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

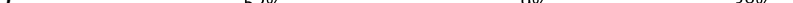
• Molecule 1: pre-mRNA

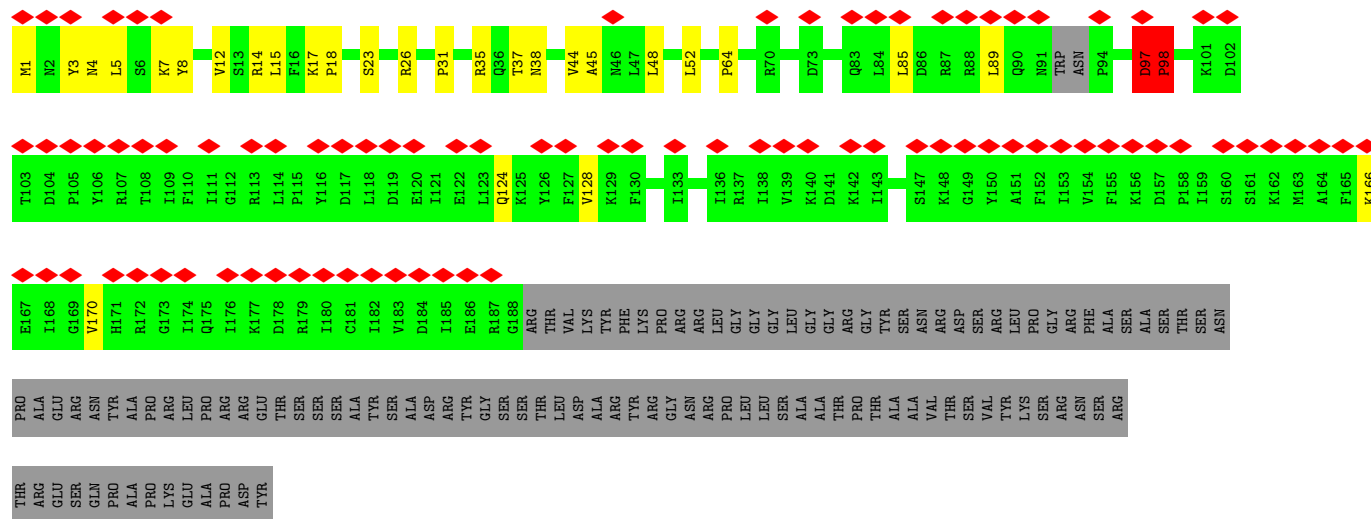


• Molecule 2: U1 snRNA

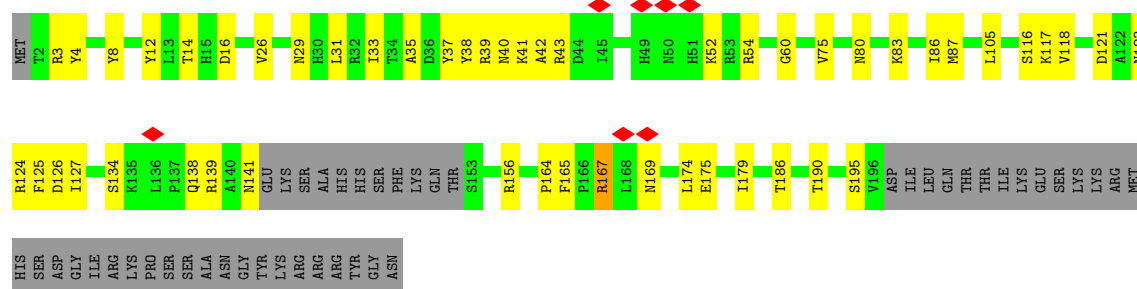


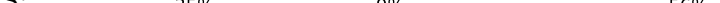


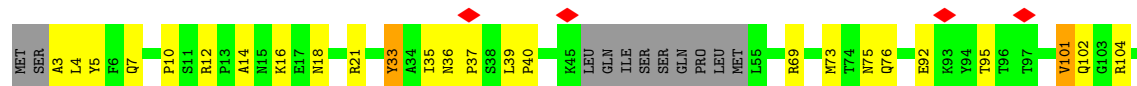
- Chain Q: 

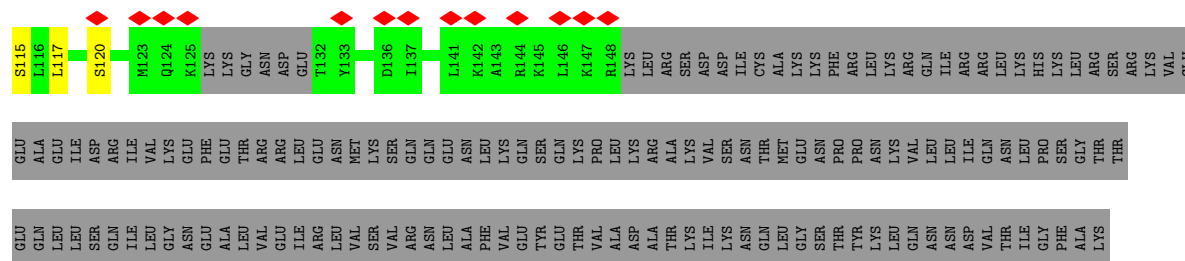


- Chain R:



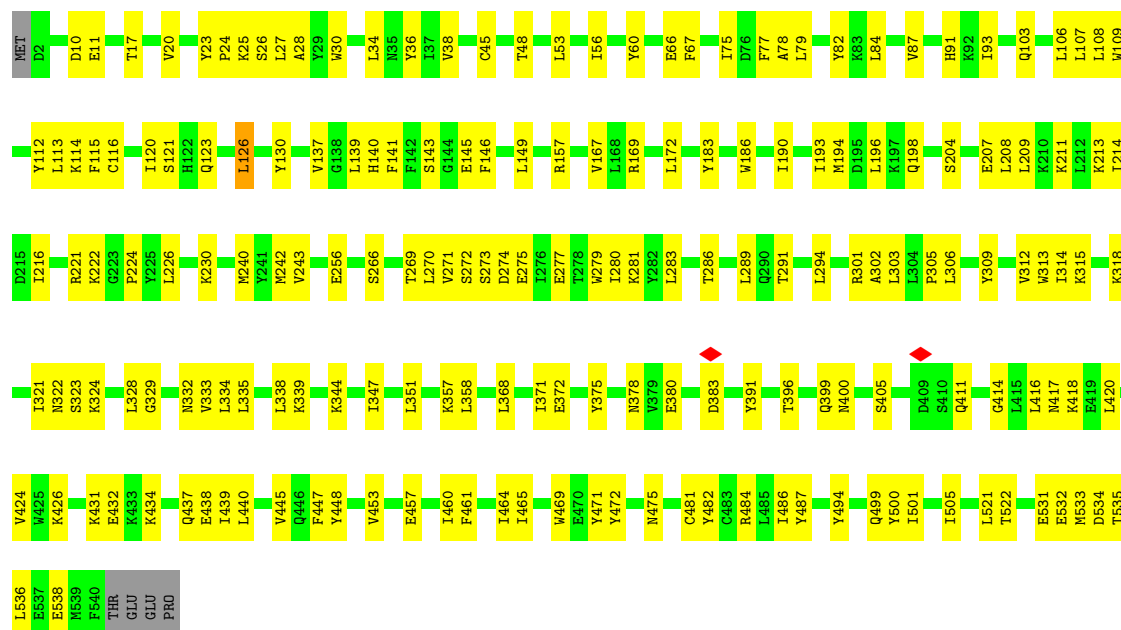
- Chain S: 





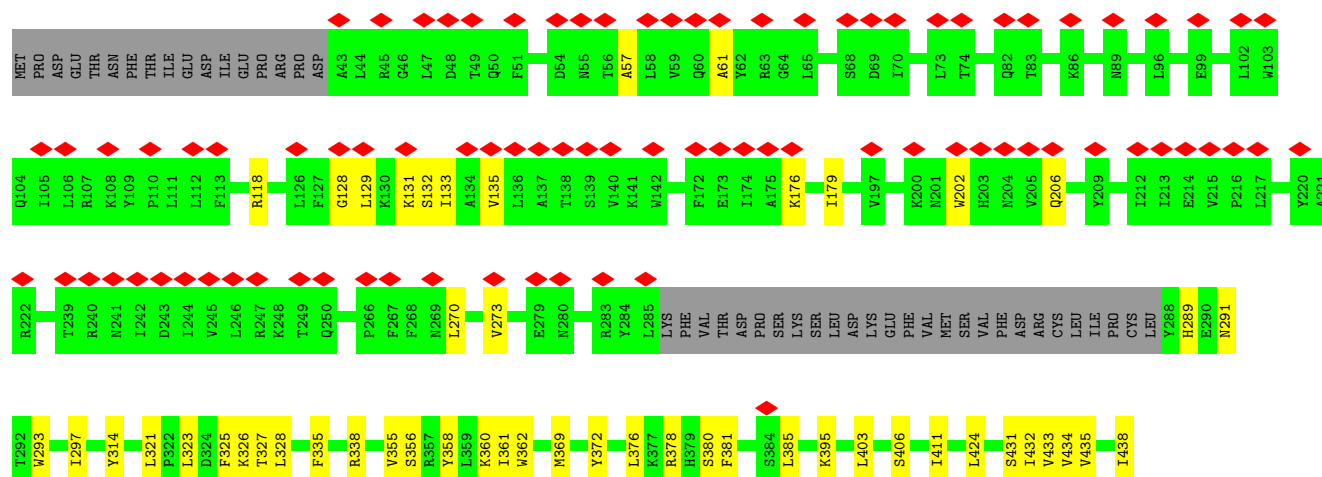
• Molecule 6: U1 small nuclear ribonucleoprotein component PRP42

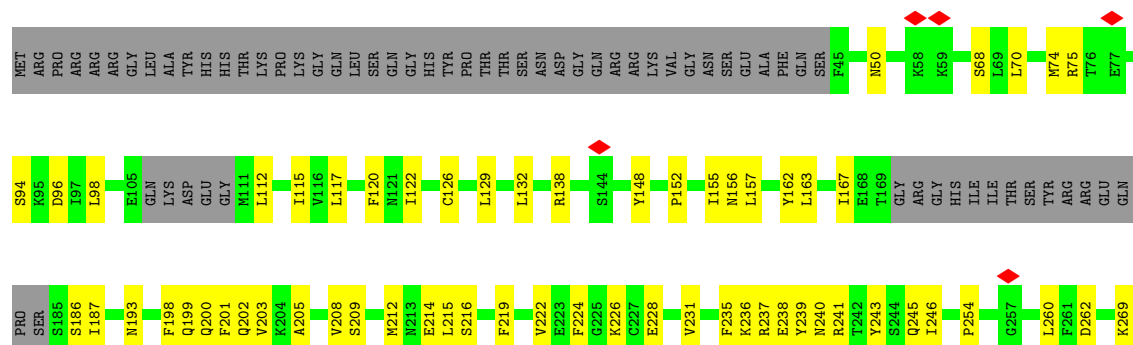
Chain T: 65% 34%

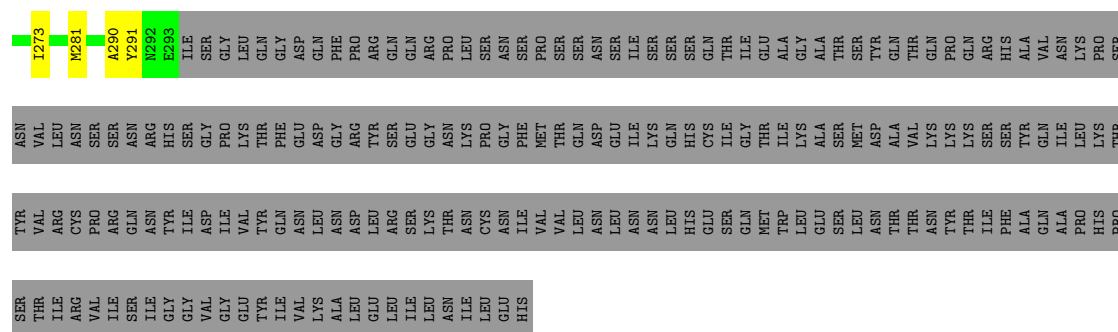


• Molecule 7: Pre-mRNA-processing factor 39

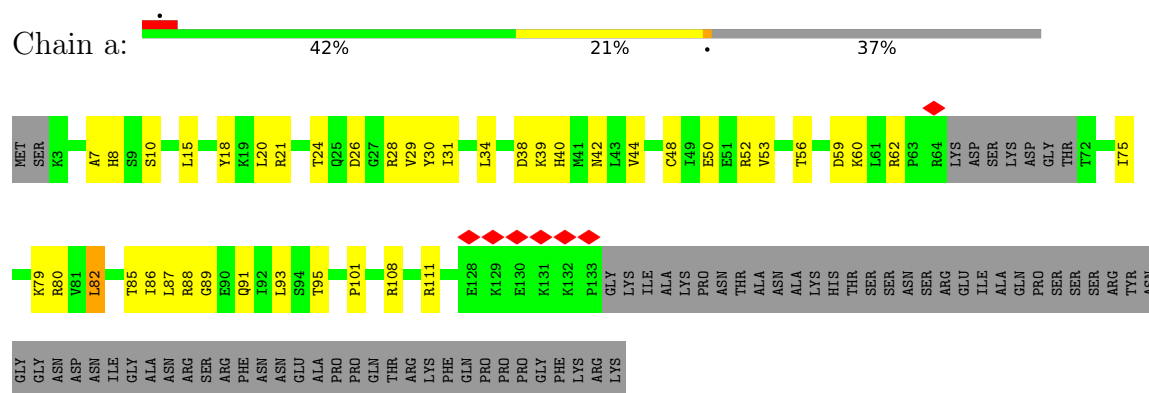
Chain U: 15% 74% 18% 7%



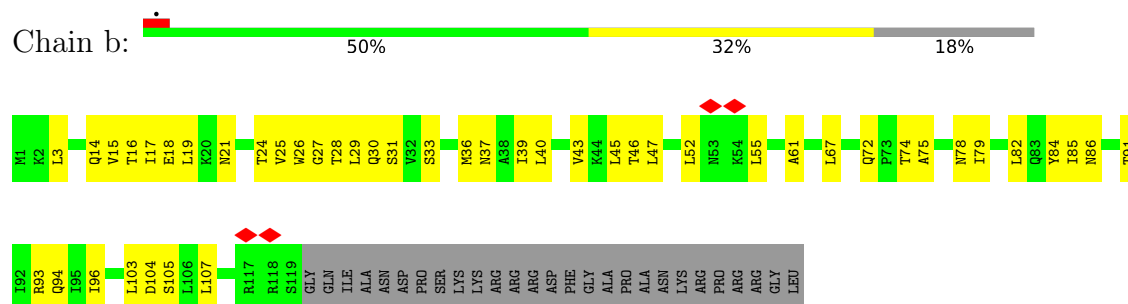




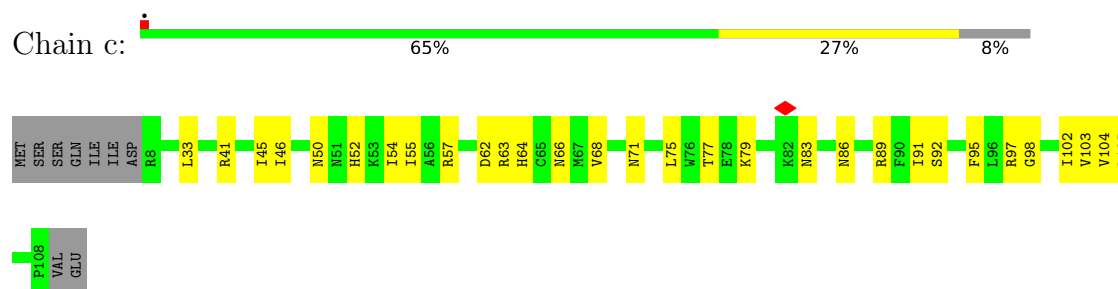
• Molecule 10: Small nuclear ribonucleoprotein-associated protein B



• Molecule 11: Small nuclear ribonucleoprotein Sm D1

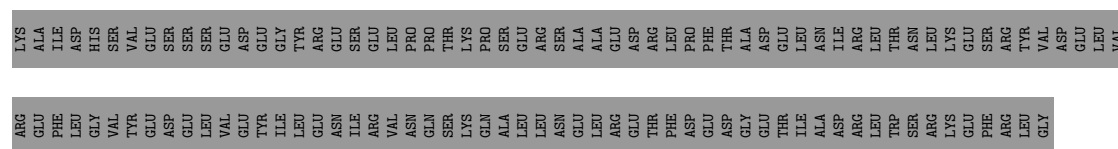


• Molecule 12: Small nuclear ribonucleoprotein Sm D2

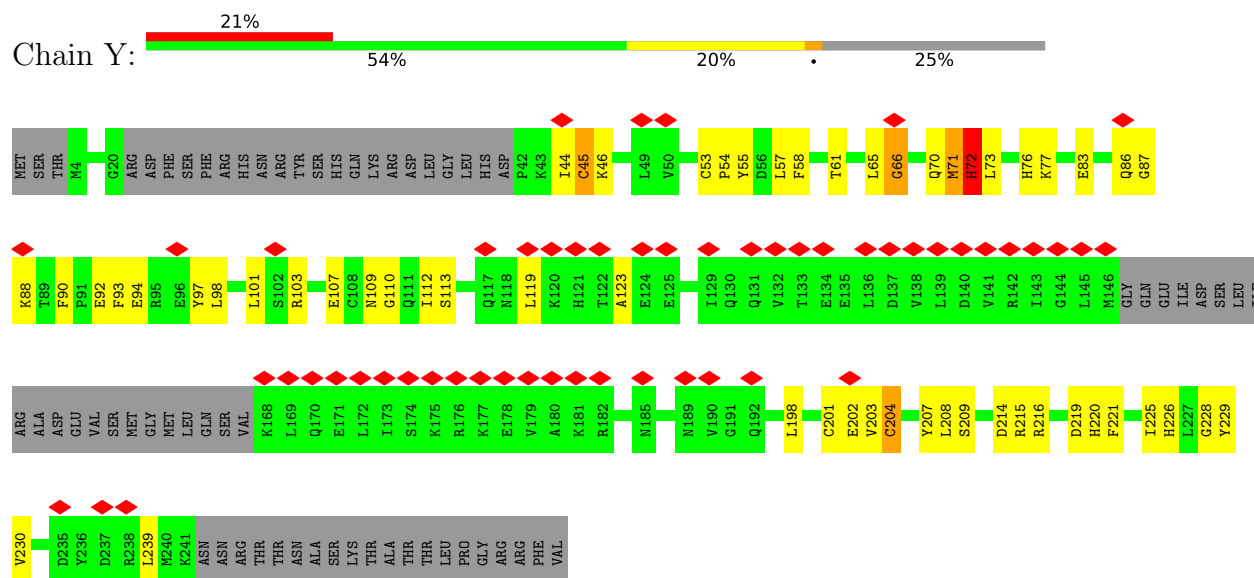


• Molecule 13: Small nuclear ribonucleoprotein Sm D3

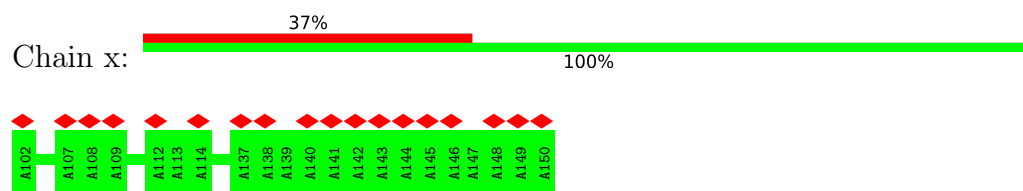




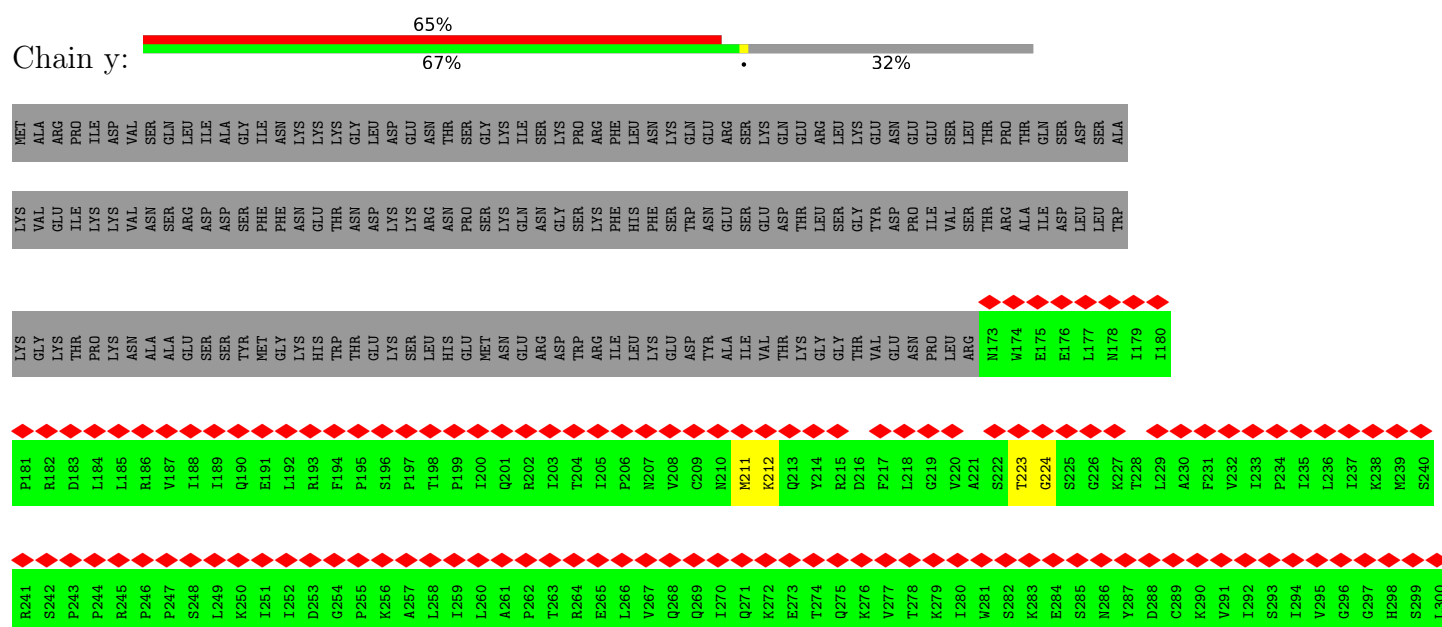
• Molecule 18: Protein LUC7



• Molecule 19: U1 snRNP



• Molecule 20: Pre-mRNA-splicing ATP-dependent RNA helicase PRP28



E301	E302	I303	S304	F305	S306	L307	S308	E309	G310	C311	D312	I313	L314	V315	A316	T317	P318	G319	R320	L321	I322	D323	S324	L325	E326	N327	H328	L329	L330	V331	M332	K333	Q334	V335	E336	T337	L338	V339	L340	D341	E342	A343	D344	K345	M346	I347	D348	L349	G350	F351	E352	D353	Q354	V355	T356	N357	I358	L359	T360
K361	V362	D363	I364	N365	A366	D367	S368	A369	V370	N371	R372	Q373	T374	L375	M376	F377	T378	A379	T380	M381	T382	P383	V384	I385	E386	K387	I388	A389	A390	G391	Y392	M393	Q394	K395	P396	V397	Y398	A399	T400	I401	G402	A403	D404	K405	M406	I407	D408	P409	L410	I411	Q412	Q413	V414	V415	E416	Y417	A418	D419	N420
D421	E422	D423	K424	F425	K426	K427	L428	K429	P430	I431	V432	A433	K434	Y435	D436	P437	P438	I439	I440	I441	F442	I443	N444	Y445	K446	Q447	T448	A449	D450	W451	L452	A453	E454	K455	F456	Q457	K458	E459	T460	N461	M462	K463	V464	T465	I466	L467	H468	G469	S470	K471	S472	Q473	E474	Q475	R476	E477	H478	S479	L480
Q481	L482	F483	R484	T485	N486	K487	V488	Q489	I490	M491	I492	A493	T494	N495	V496	A497	A498	R499	G500	L501	D502	I503	P504	N505	V506	S507	L508	V509	V510	N511	F512	M513	K516	K517	M518	D519	D520	Y521	I522	H523	R524	I525	G526	R527	T528	G529	R530	A531	A532	N533	E534	G535	T536	A537	V538	S539	F540	V541	
S542	A543	A544	E545	D546	E547	S548	L549	I550	R551	E552	L553	Y554	K555	Y556	V557	R558	K559	H560	D561	P562	L563	N564	S565	N566	I567	F568	S569	E570	A571	V572	K573	N574	K575	Y576	N577	V578	G579	L580	G581	L582	S583	A584	I585	T586	N587	L588	S589	F590	L591	N592	D593	L594	N595	L596	N597	L598	N599	L600	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	500657	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.347	Depositor
Minimum map value	-0.196	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.338, 1.338, 1.338	Depositor

5 Model quality

5.1 Standard geometry

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

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	G	0.13	0/537	0.35	0/835
2	P	0.57	46/11309 (0.4%)	0.72	5/17577 (0.0%)
3	Q	0.24	0/1237	0.93	5/1691 (0.3%)
4	R	0.20	0/1522	0.50	0/2047
5	S	0.20	0/1059	0.59	1/1422 (0.1%)
6	T	0.20	0/4654	0.49	0/6289
7	U	0.23	2/4002 (0.0%)	0.57	2/5497 (0.0%)
8	V	0.20	0/1441	0.56	1/1957 (0.1%)
9	W	0.18	0/1882	0.47	0/2537
10	a	0.20	0/1016	0.56	0/1355
11	b	0.17	0/926	0.55	0/1257
12	c	0.18	0/799	0.51	0/1078
13	d	0.22	0/716	0.56	0/970
14	e	0.17	0/535	0.45	0/730
15	f	0.17	0/529	0.51	0/715
16	g	0.19	0/557	0.57	0/756
17	X	0.23	0/403	0.47	0/543
18	Y	0.27	0/1417	0.73	5/1907 (0.3%)
19	x	0.14	0/244	0.28	0/340
All	All	0.37	48/34785 (0.1%)	0.62	19/49503 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	Q	0	2
4	R	0	1
8	V	0	2
18	Y	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	7

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	346	C	C1'-N1	7.35	1.59	1.48
2	P	496	C	C1'-N1	7.30	1.59	1.48
2	P	361	U	C1'-N1	7.09	1.59	1.48
2	P	209	U	C1'-N1	7.07	1.59	1.48
2	P	381	U	C1'-N1	6.90	1.58	1.48
2	P	491	U	C1'-N1	6.90	1.58	1.48
2	P	395	U	C1'-N1	6.89	1.58	1.48
2	P	406	U	C1'-N1	6.89	1.58	1.48
2	P	375	U	C1'-N1	6.86	1.58	1.48
2	P	228	U	C1'-N1	6.85	1.58	1.48
2	P	490	U	C1'-N1	6.83	1.58	1.48
2	P	483	U	C1'-N1	6.83	1.58	1.48
2	P	359	U	C1'-N1	6.81	1.58	1.48
2	P	396	U	C1'-N1	6.77	1.58	1.48
2	P	358	U	C1'-N1	6.76	1.58	1.48
2	P	382	U	C1'-N1	6.76	1.58	1.48
2	P	492	U	C1'-N1	6.76	1.58	1.48
2	P	355	U	C1'-N1	6.76	1.58	1.48
2	P	495	U	C1'-N1	6.76	1.58	1.48
2	P	485	U	C1'-N1	6.75	1.58	1.48
2	P	348	U	C1'-N1	6.72	1.58	1.48
2	P	229	U	C1'-N1	6.71	1.58	1.48
2	P	349	U	C1'-N1	6.71	1.58	1.48
2	P	233	U	C1'-N1	6.70	1.58	1.48
2	P	401	U	C1'-N1	6.68	1.58	1.48
2	P	347	U	C1'-N1	6.65	1.58	1.48
2	P	362	C	C1'-N1	6.54	1.58	1.48
2	P	360	U	C1'-N1	6.53	1.58	1.48
2	P	290	U	C1'-N1	6.42	1.58	1.48
2	P	357	C	C1'-N1	6.33	1.57	1.48
2	P	494	C	C1'-N1	6.32	1.57	1.48
2	P	486	C	C1'-N1	6.30	1.57	1.48
2	P	397	C	C1'-N1	6.29	1.57	1.48
2	P	368	C	C1'-N1	6.27	1.57	1.48
2	P	484	C	C1'-N1	6.23	1.57	1.48
2	P	489	C	C1'-N1	6.19	1.57	1.48
2	P	405	C	C1'-N1	6.15	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	354	C	C1'-N1	6.15	1.57	1.48
2	P	388	C	C1'-N1	6.09	1.57	1.48
2	P	370	U	C1'-N1	6.02	1.56	1.47
7	U	580	ARG	C-N	5.70	1.41	1.33
2	P	345	U	C1'-N1	5.61	1.56	1.48
2	P	377	U	C1'-N1	5.36	1.56	1.48
7	U	581	PRO	N-CD	5.20	1.55	1.47
2	P	410	G	C1'-N9	-5.04	1.40	1.48
2	P	335	G	C1'-N9	-5.04	1.40	1.48
2	P	461	G	C1'-N9	-5.03	1.40	1.48
2	P	431	G	C1'-N9	-5.01	1.40	1.48

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	97	ASP	CA-C-N	19.70	144.46	119.84
3	Q	97	ASP	C-N-CA	19.70	144.46	119.84
2	P	360	U	O3'-P-O5'	-8.64	91.03	104.00
2	P	361	U	O3'-P-O5'	-8.59	91.12	104.00
18	Y	66	GLY	N-CA-C	8.54	133.42	113.18
2	P	208	C	O3'-P-O5'	-8.29	91.57	104.00
18	Y	71	MET	N-CA-C	7.69	122.29	107.44
18	Y	72	HIS	CA-C-N	7.34	132.54	122.19
18	Y	72	HIS	C-N-CA	7.34	132.54	122.19
3	Q	98	PRO	CA-C-N	-7.05	110.08	120.38
3	Q	98	PRO	C-N-CA	-7.05	110.08	120.38
7	U	580	ARG	CA-C-N	-6.51	113.27	119.85
7	U	580	ARG	C-N-CA	-6.51	113.27	119.85
18	Y	70	GLN	CB-CA-C	-5.36	109.42	115.79
8	V	412	GLN	N-CA-C	5.21	121.32	109.81
2	P	370	U	C2'-C3'-O3'	5.19	117.29	109.50
5	S	33	TYR	CA-CB-CG	5.12	123.11	113.90
2	P	206	C	N1-C1'-C2'	5.07	119.60	112.00
3	Q	97	ASP	N-CA-C	5.05	120.96	109.81

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	Q	97	ASP	Peptide
3	Q	98	PRO	Peptide
4	R	167	ARG	Peptide

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Mol	Chain	Res	Type	Group
8	V	412	GLN	Peptide
8	V	413	PRO	Peptide
18	Y	123	ALA	Peptide
18	Y	65	LEU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	477	0	238	7	0
2	P	10138	0	5108	542	0
3	Q	1219	0	943	27	0
4	R	1492	0	1493	54	0
5	S	1045	0	1093	25	0
6	T	4540	0	4531	151	0
7	U	3940	0	3175	106	0
8	V	1414	0	1363	55	0
9	W	1841	0	1813	55	0
10	a	1009	0	1100	35	0
11	b	917	0	961	36	0
12	c	785	0	802	28	0
13	d	704	0	735	22	0
14	e	526	0	515	10	0
15	f	518	0	502	17	0
16	g	552	0	553	13	0
17	X	395	0	391	12	0
18	Y	1400	0	1254	55	0
19	x	245	0	244	0	0
20	y	399	0	0	3	0
21	R	1	0	0	0	0
21	Y	2	0	0	0	0
All	All	33559	0	26814	1117	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 19.

All (1117) 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:P:445:G:O2'	2:P:446:U:H5'	1.48	1.11
2:P:234:U:H2'	2:P:235:A:C8	1.84	1.11
2:P:382:U:C2'	2:P:383:U:H5'	1.83	1.08
2:P:445:G:O2'	2:P:446:U:C5'	2.01	1.08
2:P:415:U:H5''	2:P:416:G:OP1	1.53	1.07
7:U:529:ILE:HG23	7:U:535:PHE:O	1.54	1.07
2:P:450:G:H2'	2:P:451:A:C8	1.90	1.06
2:P:445:G:H2'	2:P:446:U:C6	1.91	1.05
2:P:383:U:H2'	2:P:384:U:H5'	1.40	1.04
7:U:450:GLN:HA	7:U:450:GLN:HE21	1.24	1.03
7:U:502:THR:HG21	8:V:368:MET:HE3	1.38	1.02
2:P:382:U:H2'	2:P:383:U:H5'	1.42	1.00
2:P:78:A:H4'	2:P:79:A:H5'	1.44	0.98
6:T:126:LEU:HD12	6:T:157:ARG:HH22	1.28	0.97
2:P:368:C:C2'	2:P:369:G:H5'	1.94	0.97
7:U:502:THR:CG2	8:V:368:MET:CE	2.43	0.97
7:U:502:THR:CG2	8:V:368:MET:HE3	1.94	0.96
7:U:502:THR:HG23	8:V:368:MET:CE	1.95	0.95
2:P:486:C:H3'	2:P:487:A:C2	2.01	0.95
7:U:580:ARG:HH11	7:U:580:ARG:HG2	1.32	0.94
2:P:361:U:H3	2:P:450:G:H22	1.05	0.94
2:P:450:G:H2'	2:P:451:A:H8	1.32	0.90
2:P:371:G:H2'	2:P:372:C:H6	1.38	0.89
2:P:234:U:C2'	2:P:235:A:C8	2.57	0.88
2:P:202:U:H2'	2:P:203:A:H8	1.39	0.88
2:P:368:C:H2'	2:P:369:G:H5'	1.55	0.88
6:T:126:LEU:HD12	6:T:157:ARG:NH2	1.88	0.88
2:P:415:U:H3'	2:P:417:A:C8	2.09	0.88
7:U:128:GLY:O	7:U:131:LYS:O	1.91	0.87
2:P:487:A:N3	2:P:487:A:O5'	2.07	0.87
2:P:486:C:H3'	2:P:487:A:H2	1.39	0.87
2:P:383:U:C2'	2:P:384:U:H5'	2.04	0.87
2:P:383:U:O2'	2:P:384:U:OP1	1.92	0.87
2:P:376:U:H2'	2:P:378:U:H6	1.39	0.86
18:Y:46:LYS:HD3	18:Y:72:HIS:HB3	1.58	0.85
2:P:320:U:H3	2:P:521:G:H1	1.25	0.83
2:P:416:G:H4'	2:P:417:A:OP2	1.76	0.82
2:P:376:U:H2'	2:P:378:U:C6	2.14	0.82
18:Y:221:PHE:HA	18:Y:226:HIS:ND1	1.94	0.82
2:P:382:U:C2	2:P:383:U:C5	2.67	0.82
2:P:445:G:H2'	2:P:446:U:C5	2.13	0.82
9:W:98:LEU:HD12	9:W:117:LEU:HD12	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:443:U:H2'	2:P:444:G:H5''	1.61	0.81
2:P:361:U:H3	2:P:450:G:N2	1.79	0.80
9:W:186:SER:HB3	9:W:214:GLU:HG2	1.64	0.80
11:b:72:GLN:HE22	11:b:79:ILE:HD11	1.46	0.80
13:d:31:GLY:HA3	13:d:47:VAL:HG12	1.63	0.80
2:P:385:U:OP1	2:P:385:U:H3'	1.81	0.79
2:P:202:U:H2'	2:P:203:A:C8	2.17	0.79
6:T:400:ASN:HD21	6:T:414:GLY:HA2	1.46	0.79
2:P:446:U:H2'	2:P:447:C:H6	1.48	0.78
9:W:187:ILE:HG12	9:W:203:VAL:HG12	1.62	0.78
2:P:351:U:O2'	2:P:352:G:OP1	2.02	0.77
2:P:378:U:H2'	2:P:379:A:H8	1.50	0.77
2:P:198:U:H3	2:P:240:G:H1	1.33	0.77
9:W:152:PRO:HG2	9:W:155:ILE:HD12	1.67	0.77
2:P:377:U:H4'	2:P:378:U:OP2	1.85	0.76
7:U:457:LEU:O	7:U:457:LEU:HD23	1.85	0.76
8:V:396:MET:SD	8:V:402:GLN:NE2	2.58	0.76
9:W:241:ARG:HH11	9:W:241:ARG:HB2	1.50	0.76
7:U:488:ASN:ND2	7:U:512:TYR:OH	2.19	0.76
2:P:350:U:H2'	2:P:352:G:H8	1.50	0.76
7:U:562:TRP:O	7:U:563:HIS:ND1	2.19	0.76
6:T:38:VAL:HG22	6:T:56:ILE:HD11	1.66	0.76
7:U:326:LYS:CB	7:U:362:TRP:CH2	2.69	0.76
2:P:487:A:H2	2:P:487:A:OP2	1.67	0.75
2:P:170:G:H2'	2:P:171:A:H8	1.51	0.75
6:T:322:ASN:OD1	6:T:323:SER:N	2.19	0.75
7:U:450:GLN:HA	7:U:450:GLN:NE2	2.02	0.75
2:P:371:G:H2'	2:P:372:C:C6	2.21	0.75
7:U:128:GLY:O	7:U:131:LYS:C	2.29	0.75
7:U:555:ASN:ND2	7:U:557:THR:OG1	2.18	0.75
2:P:16:U:O2'	2:P:168:C:OP2	2.05	0.74
6:T:328:LEU:HD23	6:T:358:LEU:HD11	1.69	0.74
18:Y:221:PHE:CD1	18:Y:226:HIS:CE1	2.76	0.74
13:d:35:GLU:HB2	13:d:43:GLN:HG2	1.68	0.74
2:P:445:G:C2	2:P:446:U:N3	2.56	0.74
2:P:344:U:H2'	2:P:345:U:H6	1.51	0.73
2:P:111:A:H2'	2:P:112:A:C8	2.23	0.73
2:P:256:U:H3	6:T:194:MET:HB3	1.53	0.73
3:Q:1:MET:HB3	3:Q:4:ASN:HD21	1.54	0.72
2:P:383:U:HO2'	2:P:384:U:P	2.13	0.72
15:f:34:ASN:HB3	15:f:36:THR:HG23	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:286:A:H2'	2:P:287:A:C8	2.26	0.71
2:P:234:U:C3'	2:P:235:A:C8	2.73	0.71
2:P:487:A:C2	2:P:487:A:OP2	2.43	0.71
2:P:415:U:C3'	2:P:417:A:C8	2.73	0.71
18:Y:46:LYS:CD	18:Y:72:HIS:HB3	2.20	0.71
7:U:580:ARG:HG2	7:U:580:ARG:NH1	2.06	0.71
3:Q:124:GLN:O	3:Q:128:VAL:CB	2.39	0.71
15:f:68:LEU:HD23	15:f:71:ILE:HD11	1.73	0.71
2:P:445:G:H2'	2:P:446:U:H6	1.56	0.70
2:P:384:U:H6	2:P:384:U:H3'	1.55	0.70
3:Q:23:SER:O	10:a:80:ARG:NH1	2.23	0.70
2:P:6:U:O2	18:Y:216:ARG:NH2	2.25	0.70
9:W:167:ILE:HA	9:W:224:PHE:HB3	1.73	0.70
7:U:202:TRP:O	7:U:206:GLN:CB	2.40	0.70
2:P:341:G:C2'	2:P:342:C:H5'	2.22	0.70
11:b:39:ILE:HD11	11:b:84:TYR:HE1	1.56	0.70
3:Q:5:LEU:O	13:d:32:LYS:NZ	2.21	0.69
2:P:384:U:H3	2:P:434:G:H1	1.40	0.69
2:P:114:U:H1'	13:d:56:VAL:HG12	1.75	0.69
6:T:24:PRO:O	6:T:30:TRP:NE1	2.23	0.69
2:P:382:U:H2'	2:P:383:U:H6	1.57	0.69
2:P:445:G:O2'	2:P:446:U:O5'	2.11	0.69
9:W:50:ASN:HD21	9:W:209:SER:HA	1.57	0.69
10:a:50:GLU:OE2	10:a:80:ARG:NE	2.23	0.69
13:d:20:SER:HB2	13:d:73:VAL:HB	1.75	0.69
14:e:29:ILE:HG22	14:e:90:ILE:HA	1.75	0.68
10:a:82:LEU:HD13	10:a:85:THR:HG21	1.75	0.68
2:P:199:G:H1	2:P:239:U:H3	1.38	0.68
6:T:531:GLU:HG3	6:T:532:GLU:HG3	1.75	0.68
9:W:122:ILE:HD11	9:W:216:SER:HA	1.76	0.68
2:P:382:U:H3	2:P:436:G:H1	1.41	0.68
1:G:-1:A:H1'	1:G:0:A:H5'	1.75	0.68
5:S:35:ILE:HG13	5:S:37:PRO:HD2	1.75	0.68
7:U:450:GLN:HG3	7:U:454:TYR:CE2	2.29	0.68
9:W:138:ARG:HH12	9:W:148:TYR:HA	1.58	0.68
7:U:439:LYS:HG3	7:U:443:LEU:HD12	1.75	0.68
2:P:402:G:H1	2:P:413:U:H3	1.42	0.68
2:P:486:C:H2'	2:P:487:A:N3	2.09	0.68
4:R:3:ARG:HD3	4:R:12:TYR:CD2	2.29	0.68
18:Y:72:HIS:ND1	18:Y:72:HIS:N	2.42	0.68
2:P:380:G:H1	2:P:438:U:H3	1.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:344:U:H2'	2:P:345:U:C6	2.29	0.67
2:P:376:U:C2'	2:P:378:U:H6	2.07	0.67
2:P:445:G:C2'	2:P:446:U:C6	2.76	0.67
9:W:241:ARG:HB2	9:W:241:ARG:NH1	2.08	0.67
2:P:349:U:H3	2:P:461:G:H1	1.41	0.67
2:P:446:U:H6	2:P:446:U:O5'	1.78	0.67
2:P:186:U:O2'	2:P:187:G:OP2	2.13	0.67
18:Y:46:LYS:CG	18:Y:72:HIS:HB3	2.24	0.67
2:P:341:G:H1	2:P:483:U:H3	1.42	0.67
2:P:352:G:H1	2:P:459:U:H3	1.43	0.67
2:P:386:G:H1	2:P:433:U:H3	1.43	0.67
13:d:34:VAL:HG12	13:d:35:GLU:HG2	1.77	0.66
2:P:349:U:C2'	2:P:350:U:H5'	2.26	0.66
7:U:323:LEU:HD22	7:U:361:ILE:HD11	1.77	0.66
10:a:44:VAL:HG22	10:a:86:ILE:HG22	1.77	0.66
1:G:-5:A:O2'	1:G:-4:A:N7	2.28	0.66
2:P:558:U:H3	12:c:66:ASN:HD22	1.44	0.66
8:V:316:PHE:HA	8:V:352:PHE:HB3	1.77	0.66
18:Y:46:LYS:HG3	18:Y:77:LYS:HE2	1.78	0.66
2:P:514:A:H2'	2:P:515:A:H8	1.61	0.65
10:a:60:LYS:HD2	10:a:75:ILE:HD13	1.78	0.65
2:P:443:U:H6	2:P:443:U:O5'	1.78	0.65
9:W:74:MET:HE3	9:W:115:ILE:HG13	1.77	0.65
12:c:41:ARG:O	12:c:57:ARG:NH1	2.29	0.65
12:c:45:ILE:HD12	12:c:55:ILE:HG12	1.78	0.65
9:W:198:PHE:HE2	9:W:235:PHE:HB2	1.60	0.65
10:a:93:LEU:HD11	11:b:21:ASN:HD21	1.60	0.65
2:P:73:A:H2'	2:P:75:G:H8	1.62	0.65
2:P:450:G:O5'	2:P:450:G:H8	1.80	0.65
6:T:204:SER:OG	6:T:207:GLU:OE1	2.15	0.65
6:T:243:VAL:HG22	7:U:581:PRO:HB2	1.79	0.65
2:P:398:G:H1	2:P:418:U:H3	1.42	0.65
2:P:386:G:OP2	2:P:386:G:H3'	1.97	0.64
10:a:29:VAL:HG21	11:b:67:LEU:HB3	1.79	0.64
2:P:384:U:H3'	2:P:384:U:C6	2.32	0.64
2:P:446:U:H2'	2:P:447:C:C6	2.30	0.64
10:a:88:ARG:NH1	13:d:40:MET:SD	2.71	0.64
2:P:314:G:H2'	2:P:315:G:H8	1.62	0.64
2:P:191:C:H2'	2:P:192:A:H8	1.62	0.64
2:P:370:U:H4'	2:P:371:G:OP1	1.98	0.64
6:T:78:ALA:HB2	6:T:93:ILE:HD11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:457:LEU:HD22	7:U:458:TYR:CE1	2.33	0.64
7:U:570:GLU:HB3	7:U:573:HIS:O	1.98	0.64
18:Y:46:LYS:HD3	18:Y:72:HIS:CB	2.28	0.64
3:Q:1:MET:HB3	3:Q:4:ASN:ND2	2.12	0.64
4:R:116:SER:O	4:R:123:ASN:ND2	2.26	0.64
7:U:176:LYS:O	7:U:179:ILE:N	2.30	0.64
2:P:445:G:C2	2:P:446:U:C4	2.86	0.64
2:P:376:U:O2'	2:P:378:U:O4'	2.14	0.63
14:e:58:VAL:HG12	14:e:76:PRO:HA	1.79	0.63
6:T:332:ASN:OD1	9:W:200:GLN:NE2	2.32	0.63
3:Q:166:LYS:O	3:Q:170:VAL:CB	2.46	0.63
16:g:27:GLY:HA3	16:g:40:LEU:HD13	1.80	0.63
7:U:457:LEU:HD23	7:U:457:LEU:C	2.24	0.63
2:P:415:U:H2'	2:P:417:A:C8	2.34	0.62
3:Q:44:VAL:HG23	15:f:68:LEU:HD21	1.80	0.62
5:S:39:LEU:HD12	5:S:40:PRO:HD2	1.80	0.62
2:P:368:C:O2'	2:P:369:G:H5'	2.00	0.62
11:b:3:LEU:HD21	12:c:68:VAL:HG23	1.81	0.62
12:c:50:ASN:ND2	12:c:52:HIS:HE1	1.96	0.62
2:P:208:C:H2'	2:P:209:U:H6	1.65	0.62
2:P:444:G:H3'	2:P:445:G:H5'	1.81	0.62
7:U:326:LYS:CB	7:U:362:TRP:CZ2	2.82	0.62
10:a:42:ASN:HB3	10:a:89:GLY:H	1.65	0.62
7:U:576:ILE:HG12	7:U:616:ILE:HG12	1.82	0.62
4:R:117:LYS:HE3	4:R:156:ARG:HE	1.65	0.61
7:U:376:LEU:O	7:U:380:SER:OG	2.17	0.61
18:Y:204:CYS:SG	18:Y:226:HIS:CD2	2.92	0.61
6:T:23:TYR:CG	9:W:262:ASP:HB2	2.34	0.61
7:U:502:THR:HG23	8:V:368:MET:HE1	1.78	0.61
8:V:410:LEU:HD22	8:V:412:GLN:NE2	2.15	0.61
18:Y:198:LEU:HD13	18:Y:207:TYR:HB3	1.82	0.61
6:T:405:SER:OG	6:T:411:GLN:O	2.19	0.61
2:P:236:A:H2'	2:P:237:A:H8	1.65	0.61
4:R:75:VAL:HB	6:T:224:PRO:HB3	1.83	0.61
7:U:355:VAL:HG11	7:U:372:TYR:HB2	1.83	0.61
17:X:13:LEU:HB3	17:X:50:ARG:HH12	1.65	0.61
2:P:296:U:H2'	2:P:297:G:H8	1.66	0.61
2:P:452:U:O5'	2:P:452:U:H6	1.83	0.61
1:G:7:U:OP1	4:R:141:ASN:ND2	2.34	0.60
18:Y:55:TYR:OH	18:Y:66:GLY:O	2.13	0.60
18:Y:208:LEU:HD11	18:Y:220:HIS:NE2	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:382:U:O2'	2:P:383:U:H5'	2.00	0.60
4:R:83:LYS:HA	4:R:86:ILE:HG22	1.82	0.60
3:Q:37:THR:HG22	3:Q:38:ASN:H	1.67	0.60
4:R:124:ARG:HH21	6:T:79:LEU:HD21	1.65	0.60
2:P:486:C:C3'	2:P:487:A:C2	2.81	0.60
2:P:234:U:C3'	2:P:235:A:H8	2.13	0.60
2:P:352:G:H2'	2:P:353:A:H8	1.67	0.60
7:U:369:MET:HG3	7:U:432:ILE:HD11	1.84	0.60
10:a:28:ARG:HD3	10:a:52:ARG:HE	1.65	0.60
2:P:170:G:H2'	2:P:171:A:C8	2.37	0.60
2:P:203:A:H2'	2:P:204:A:H8	1.67	0.59
12:c:46:ILE:HD12	12:c:54:ILE:HD11	1.84	0.59
2:P:444:G:C3'	2:P:445:G:H5'	2.32	0.59
6:T:286:THR:HG23	6:T:294:LEU:HD23	1.85	0.59
12:c:62:ASP:OD1	12:c:63:ARG:N	2.33	0.59
18:Y:208:LEU:HD11	18:Y:220:HIS:CD2	2.37	0.59
4:R:105:LEU:HB2	6:T:145:GLU:OE2	2.02	0.59
2:P:384:U:H2'	2:P:386:G:O5'	2.03	0.59
2:P:445:G:N2	2:P:446:U:N3	2.50	0.59
7:U:411:ILE:CD1	7:U:461:ASN:OD1	2.51	0.59
2:P:373:C:N4	2:P:445:G:C2	2.70	0.59
2:P:384:U:O2'	2:P:386:G:H5'	2.03	0.59
3:Q:18:PRO:HG3	13:d:18:ILE:HB	1.83	0.59
2:P:376:U:O2'	2:P:378:U:H5'	2.02	0.59
7:U:457:LEU:HD22	7:U:458:TYR:CD1	2.37	0.59
7:U:529:ILE:CG2	7:U:535:PHE:O	2.40	0.59
2:P:360:U:H2'	2:P:361:U:H6	1.68	0.59
8:V:421:SER:OG	8:V:442:GLN:NE2	2.36	0.59
6:T:10:ASP:OD2	6:T:36:TYR:OH	2.21	0.58
2:P:378:U:H2'	2:P:379:A:C8	2.36	0.58
7:U:131:LYS:C	7:U:133:ILE:H	2.11	0.58
7:U:381:PHE:HD1	7:U:395:LYS:HE3	1.67	0.58
2:P:114:U:H2'	2:P:115:C:C6	2.39	0.58
2:P:417:A:OP2	2:P:417:A:H3'	2.03	0.58
9:W:112:LEU:HD11	9:W:239:TYR:HE2	1.67	0.58
6:T:481:CYS:SG	6:T:484:ARG:NH2	2.77	0.58
9:W:162:TYR:CE1	9:W:200:GLN:HB3	2.39	0.58
11:b:16:THR:OG1	11:b:96:ILE:HB	2.03	0.58
2:P:121:U:H5''	3:Q:26:ARG:HH12	1.67	0.58
3:Q:45:ALA:HB3	3:Q:48:LEU:H	1.68	0.58
6:T:438:GLU:OE2	6:T:475:ASN:ND2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:23:SER:HA	6:T:121:SER:HB2	1.85	0.57
6:T:140:HIS:HB3	6:T:143:SER:HB2	1.86	0.57
9:W:68:SER:HA	9:W:224:PHE:CE2	2.39	0.57
17:X:8:SER:HB2	17:X:28:PHE:CD1	2.39	0.57
4:R:179:ILE:HG22	8:V:295:ILE:O	2.05	0.57
7:U:131:LYS:O	7:U:133:ILE:N	2.37	0.57
2:P:286:A:H4'	4:R:39:ARG:NH1	2.19	0.57
4:R:167:ARG:NH2	8:V:412:GLN:O	2.37	0.57
12:c:46:ILE:HG12	12:c:104:VAL:HG22	1.87	0.57
2:P:21:G:H2'	2:P:22:A:H8	1.69	0.57
16:g:47:ASN:OD1	16:g:48:GLY:N	2.31	0.57
18:Y:58:PHE:O	18:Y:61:THR:OG1	2.20	0.57
18:Y:97:TYR:CZ	18:Y:101:LEU:HD11	2.39	0.57
2:P:487:A:C2	2:P:487:A:P	2.98	0.57
15:f:58:GLU:O	15:f:65:HIS:N	2.38	0.57
2:P:376:U:C2	2:P:378:U:C5	2.93	0.57
2:P:444:G:C5	2:P:445:G:N7	2.72	0.56
2:P:524:G:H2'	2:P:525:G:H8	1.70	0.56
6:T:17:THR:HG21	17:X:31:ILE:HA	1.86	0.56
2:P:384:U:C6	2:P:384:U:C3'	2.88	0.56
2:P:417:A:C2	2:P:418:U:O4	2.57	0.56
18:Y:73:LEU:HB2	18:Y:76:HIS:HD2	1.69	0.56
2:P:361:U:H2'	2:P:362:C:H6	1.71	0.56
2:P:445:G:C2'	2:P:446:U:O5'	2.53	0.56
10:a:91:GLN:HG3	13:d:70:LYS:HG3	1.87	0.56
7:U:455:PHE:O	7:U:459:GLN:HB2	2.06	0.56
9:W:156:ASN:HD22	9:W:205:ALA:HB1	1.71	0.56
2:P:125:A:H2'	2:P:126:A:C8	2.41	0.56
10:a:29:VAL:O	10:a:50:GLU:HA	2.05	0.56
2:P:382:U:C2	2:P:383:U:C6	2.93	0.56
3:Q:12:VAL:HG21	4:R:35:ALA:HB1	1.88	0.56
2:P:361:U:C2	2:P:362:C:C5	2.94	0.56
4:R:40:ASN:HD22	4:R:43:ARG:HE	1.53	0.56
6:T:378:ASN:OD1	6:T:426:LYS:NZ	2.36	0.56
2:P:376:U:HO2'	2:P:378:U:H6	1.52	0.56
6:T:20:VAL:HG12	17:X:29:ILE:HD13	1.87	0.56
7:U:493:GLU:CD	7:U:497:GLU:OE2	2.49	0.56
2:P:112:A:O2'	2:P:113:G:OP1	2.19	0.56
2:P:445:G:N2	2:P:446:U:C2	2.74	0.56
4:R:139:ARG:NH1	18:Y:219:ASP:OD2	2.39	0.56
6:T:335:LEU:HD12	6:T:351:LEU:HD11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:382:U:C3'	2:P:383:U:H5'	2.36	0.56
3:Q:3:TYR:HB3	4:R:127:ILE:HD11	1.88	0.56
2:P:141:A:H2	5:S:7:GLN:HE22	1.54	0.55
2:P:415:U:H3'	2:P:417:A:N7	2.21	0.55
11:b:36:MET:SD	12:c:97:ARG:NH2	2.79	0.55
11:b:39:ILE:HD11	11:b:84:TYR:CE1	2.40	0.55
12:c:102:ILE:HG13	12:c:103:VAL:H	1.70	0.55
2:P:369:G:O3'	2:P:370:U:O3'	2.24	0.55
2:P:394:A:C4	2:P:395:U:C5	2.95	0.55
7:U:325:PHE:CE2	7:U:327:THR:HG22	2.41	0.55
2:P:254:U:H1'	4:R:54:ARG:HH11	1.71	0.55
7:U:502:THR:OG1	8:V:332:TYR:O	2.20	0.55
11:b:25:VAL:HG22	11:b:45:LEU:HB2	1.87	0.55
2:P:490:U:C2	2:P:491:U:C5	2.95	0.55
18:Y:221:PHE:HD1	18:Y:226:HIS:CE1	2.24	0.55
2:P:381:U:C2	2:P:382:U:C5	2.95	0.55
4:R:167:ARG:O	8:V:415:TYR:OH	2.23	0.55
13:d:63:PHE:O	16:g:71:LEU:N	2.28	0.55
2:P:73:A:H2'	2:P:75:G:C8	2.42	0.55
16:g:7:LEU:HD23	16:g:29:LEU:HD11	1.87	0.55
4:R:4:TYR:HB2	4:R:16:ASP:HB2	1.89	0.55
2:P:376:U:C3'	2:P:378:U:H5'	2.37	0.55
2:P:489:C:H2'	2:P:490:U:H6	1.72	0.55
2:P:490:U:H2'	2:P:491:U:H6	1.72	0.55
4:R:37:TYR:CE2	13:d:82:PRO:HD3	2.42	0.55
8:V:392:LEU:HD21	8:V:404:GLN:NE2	2.21	0.55
4:R:3:ARG:CD	4:R:12:TYR:CE2	2.90	0.54
6:T:424:VAL:HG13	6:T:440:LEU:HD21	1.88	0.54
7:U:297:ILE:HG13	7:U:314:TYR:OH	2.06	0.54
2:P:34:A:H2'	2:P:35:G:C8	2.43	0.54
2:P:233:U:H2'	2:P:234:U:H6	1.71	0.54
2:P:255:U:O2	2:P:259:U:H5''	2.07	0.54
2:P:282:C:H2'	2:P:283:A:H8	1.73	0.54
2:P:405:C:C2	2:P:406:U:C5	2.95	0.54
2:P:415:U:H5''	2:P:416:G:P	2.46	0.54
6:T:91:HIS:CD2	6:T:115:PHE:HE2	2.26	0.54
8:V:314:THR:HA	8:V:354:GLN:HA	1.89	0.54
2:P:360:U:C2	2:P:361:U:C5	2.95	0.54
6:T:116:CYS:SG	6:T:120:ILE:HD12	2.48	0.54
6:T:143:SER:O	6:T:146:PHE:HB3	2.07	0.54
6:T:270:LEU:HB3	8:V:415:TYR:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:461:PHE:O	6:T:465:ILE:HG12	2.07	0.54
7:U:574:ILE:HG23	8:V:382:TRP:HE1	1.73	0.54
14:e:44:VAL:HB	14:e:53:VAL:HG23	1.89	0.54
2:P:495:U:C2	2:P:496:C:C5	2.95	0.54
6:T:196:LEU:HD12	6:T:226:LEU:HD12	1.88	0.54
16:g:35:PHE:HB2	16:g:37:ASN:ND2	2.23	0.54
2:P:356:A:C4	2:P:357:C:C5	2.96	0.54
2:P:357:C:C2	2:P:358:U:C5	2.96	0.54
2:P:444:G:C6	2:P:445:G:N7	2.76	0.54
5:S:18:ASN:OD1	5:S:21:ARG:NH1	2.38	0.54
2:P:491:U:C2	2:P:492:U:C5	2.96	0.54
2:P:485:U:C2	2:P:486:C:C5	2.95	0.54
6:T:464:ILE:HD11	6:T:472:TYR:CD2	2.42	0.54
8:V:342:VAL:HG23	8:V:343:LYS:H	1.72	0.54
16:g:63:ILE:HG21	16:g:68:ILE:HD11	1.90	0.54
2:P:344:U:C2	2:P:345:U:C5	2.96	0.54
2:P:516:U:H2'	2:P:517:U:C6	2.43	0.54
9:W:236:LYS:O	9:W:240:ASN:ND2	2.34	0.54
10:a:24:THR:OG1	10:a:26:ASP:OD1	2.25	0.54
18:Y:94:GLU:HA	18:Y:97:TYR:HB3	1.89	0.54
2:P:346:C:C2	2:P:347:U:C5	2.96	0.54
2:P:348:U:C2	2:P:349:U:C5	2.96	0.54
2:P:395:U:C2	2:P:396:U:C5	2.97	0.54
2:P:484:C:C2	2:P:485:U:C5	2.96	0.54
7:U:513:LYS:NZ	7:U:538:ILE:O	2.40	0.54
2:P:64:A:OP2	4:R:60:GLY:HA2	2.09	0.53
2:P:233:U:C2	2:P:234:U:C5	2.96	0.53
2:P:382:U:N3	2:P:383:U:C5	2.75	0.53
2:P:394:A:H2'	2:P:395:U:H6	1.71	0.53
2:P:494:C:C2	2:P:495:U:C5	2.96	0.53
2:P:523:A:H2'	2:P:524:G:H8	1.72	0.53
7:U:574:ILE:HG21	8:V:362:GLU:HG2	1.89	0.53
2:P:354:C:C2	2:P:355:U:C5	2.96	0.53
2:P:358:U:C2	2:P:359:U:C5	2.97	0.53
2:P:367:G:C4	2:P:368:C:C5	2.97	0.53
2:P:396:U:C2	2:P:397:C:C5	2.96	0.53
2:P:447:C:H2'	2:P:447:C:O2	2.08	0.53
6:T:277:GLU:HG2	6:T:281:LYS:HE2	1.89	0.53
2:P:345:U:C2	2:P:346:C:C5	2.97	0.53
2:P:372:C:H2'	2:P:372:C:O2	2.09	0.53
2:P:416:G:C4'	2:P:417:A:OP2	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:582:GLN:HE21	7:U:606:ARG:HH11	1.56	0.53
18:Y:214:ASP:OD1	18:Y:215:ARG:N	2.41	0.53
2:P:376:U:C2'	2:P:378:U:C6	2.86	0.53
6:T:482:TYR:CE2	6:T:505:ILE:HG12	2.44	0.53
1:G:0:A:H5''	1:G:1:G:OP2	2.09	0.53
2:P:311:U:H2'	2:P:312:G:H8	1.72	0.53
6:T:501:ILE:HA	6:T:505:ILE:HD12	1.89	0.53
15:f:29:VAL:HG12	15:f:81:ILE:HG12	1.91	0.53
2:P:380:G:C4	2:P:381:U:C5	2.97	0.53
2:P:400:A:C4	2:P:401:U:C5	2.96	0.53
2:P:493:G:C4	2:P:494:C:C5	2.96	0.53
6:T:139:LEU:HB3	6:T:294:LEU:HD12	1.90	0.53
6:T:270:LEU:CB	8:V:415:TYR:HB3	2.39	0.53
6:T:338:LEU:O	6:T:344:LYS:HE3	2.09	0.53
7:U:620:TYR:OH	8:V:389:THR:OG1	2.25	0.53
2:P:359:U:C2	2:P:360:U:C5	2.96	0.53
2:P:369:G:H4'	2:P:370:U:OP1	2.09	0.53
2:P:431:G:C4	2:P:432:U:C5	2.97	0.53
2:P:494:C:H2'	2:P:495:U:H6	1.74	0.53
2:P:208:C:H2'	2:P:209:U:C6	2.44	0.53
2:P:347:U:C2	2:P:348:U:C5	2.96	0.53
2:P:405:C:H2'	2:P:406:U:H6	1.74	0.53
2:P:444:G:C3'	2:P:445:G:C5'	2.87	0.53
2:P:444:G:C6	2:P:445:G:C5	2.97	0.53
4:R:8:TYR:OH	4:R:38:TYR:OH	2.19	0.53
18:Y:98:LEU:HB2	18:Y:239:LEU:HD23	1.91	0.53
2:P:77:U:OP1	7:U:597:GLN:NE2	2.42	0.53
2:P:235:A:H8	2:P:235:A:P	2.32	0.53
2:P:254:U:H5	6:T:222:LYS:HB2	1.74	0.53
2:P:415:U:C2'	2:P:417:A:C8	2.91	0.53
2:P:483:U:C2	2:P:484:C:C5	2.96	0.53
2:P:232:G:C4	2:P:233:U:C5	2.96	0.53
2:P:341:G:C4	2:P:342:C:C5	2.97	0.53
2:P:400:A:H2'	2:P:401:U:H6	1.74	0.53
10:a:108:ARG:HA	10:a:111:ARG:HG2	1.90	0.53
2:P:172:C:H2'	2:P:173:G:H8	1.74	0.52
2:P:192:A:H2'	2:P:193:A:H8	1.75	0.52
2:P:228:U:C2	2:P:229:U:C5	2.97	0.52
2:P:331:C:C2	2:P:332:U:C5	2.97	0.52
2:P:387:A:C4	2:P:388:C:C5	2.97	0.52
6:T:103:GLN:O	6:T:109:TRP:NE1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:277:GLU:HG3	8:V:359:LEU:HD12	1.91	0.52
2:P:374:A:C4	2:P:375:U:C5	2.97	0.52
2:P:404:A:C4	2:P:405:C:C5	2.97	0.52
2:P:523:A:H2'	2:P:524:G:C8	2.45	0.52
5:S:5:TYR:OH	5:S:7:GLN:NE2	2.42	0.52
6:T:273:SER:OG	8:V:412:GLN:NE2	2.39	0.52
8:V:385:SER:O	8:V:389:THR:OG1	2.27	0.52
2:P:353:A:C4	2:P:354:C:C5	2.97	0.52
2:P:489:C:C2	2:P:490:U:C5	2.96	0.52
2:P:207:C:C2	2:P:208:C:C5	2.97	0.52
2:P:412:U:H2'	2:P:413:U:H6	1.75	0.52
10:a:42:ASN:HB3	10:a:89:GLY:N	2.23	0.52
17:X:41:ASP:O	17:X:44:LYS:HG2	2.09	0.52
2:P:208:C:C2	2:P:209:U:C5	2.97	0.52
2:P:367:G:H2'	2:P:368:C:H6	1.75	0.52
2:P:458:U:C2	2:P:459:U:C5	2.97	0.52
5:S:14:ALA:O	5:S:69:ARG:NH1	2.37	0.52
6:T:126:LEU:O	6:T:126:LEU:HD22	2.10	0.52
6:T:226:LEU:HD21	6:T:230:LYS:HE3	1.92	0.52
2:P:373:C:H2'	2:P:373:C:O2	2.09	0.52
2:P:385:U:H3'	2:P:385:U:P	2.48	0.52
2:P:432:U:C2	2:P:433:U:C5	2.98	0.52
2:P:493:G:H2'	2:P:494:C:H6	1.75	0.52
2:P:495:U:H2'	2:P:496:C:H6	1.75	0.52
6:T:383:ASP:OD1	6:T:434:LYS:NZ	2.42	0.52
12:c:71:ASN:N	12:c:92:SER:O	2.41	0.52
15:f:32:LYS:HA	15:f:79:LEU:HD12	1.92	0.52
2:P:482:G:C4	2:P:483:U:C5	2.97	0.52
4:R:164:PRO:HB3	9:W:269:LYS:HD2	1.91	0.52
12:c:45:ILE:HB	12:c:105:LEU:HG	1.90	0.52
2:P:62:A:H4'	5:S:104:ARG:HG3	1.92	0.52
2:P:410:G:C4	2:P:411:U:C5	2.98	0.52
2:P:487:A:H2	2:P:487:A:P	2.31	0.52
2:P:488:A:C4	2:P:489:C:C5	2.97	0.52
10:a:18:TYR:CE1	10:a:101:PRO:HD3	2.44	0.52
15:f:23:VAL:HA	15:f:42:LEU:HD22	1.92	0.52
2:P:206:C:C2	2:P:207:C:C5	2.98	0.52
2:P:441:U:C2	2:P:442:U:C5	2.98	0.52
2:P:459:U:C2	2:P:460:U:C5	2.98	0.52
2:P:467:G:C4	2:P:468:U:C5	2.98	0.52
5:S:35:ILE:HG22	11:b:74:THR:HG21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:268:C:H4'	2:P:269:U:O5'	2.08	0.52
7:U:570:GLU:HG2	7:U:576:ILE:O	2.10	0.52
9:W:198:PHE:CE2	9:W:235:PHE:HB2	2.43	0.52
2:P:332:U:C2	2:P:333:U:C5	2.98	0.51
2:P:377:U:H5'	2:P:377:U:C6	2.44	0.51
2:P:438:U:C2	2:P:439:U:C5	2.98	0.51
2:P:454:G:C4	2:P:455:U:C5	2.98	0.51
9:W:243:TYR:HA	9:W:246:ILE:HG12	1.92	0.51
2:P:203:A:C6	2:P:236:A:C2	2.97	0.51
2:P:207:C:H2'	2:P:208:C:H6	1.74	0.51
2:P:376:U:C2'	2:P:378:U:H5'	2.41	0.51
2:P:457:G:C4	2:P:458:U:C5	2.98	0.51
10:a:53:VAL:HG23	11:b:67:LEU:HD11	1.92	0.51
11:b:30:GLN:HB2	11:b:39:ILE:HG23	1.92	0.51
17:X:8:SER:HB2	17:X:28:PHE:CE1	2.45	0.51
2:P:159:G:H5''	10:a:8:HIS:HB2	1.92	0.51
2:P:331:C:H2'	2:P:332:U:H6	1.75	0.51
2:P:382:U:O2	2:P:383:U:C6	2.63	0.51
2:P:387:A:H2'	2:P:388:C:H6	1.74	0.51
2:P:437:A:C4	2:P:438:U:C5	2.99	0.51
2:P:440:A:C4	2:P:441:U:C5	2.98	0.51
6:T:289:LEU:HA	7:U:568:TRP:HZ3	1.76	0.51
18:Y:83:GLU:HA	18:Y:86:GLN:HB2	1.91	0.51
2:P:141:A:H61	5:S:75:ASN:HB2	1.75	0.51
2:P:341:G:H2'	2:P:342:C:H5'	1.92	0.51
7:U:434:VAL:O	7:U:438:ILE:HG12	2.10	0.51
2:P:48:A:H2'	2:P:49:A:C8	2.44	0.51
2:P:349:U:H2'	2:P:350:U:H5'	1.93	0.51
2:P:371:G:C4	2:P:372:C:C5	2.98	0.51
2:P:414:A:C4	2:P:415:U:C5	2.99	0.51
2:P:48:A:H2'	2:P:49:A:H8	1.75	0.51
2:P:57:U:H2'	2:P:58:U:H6	1.75	0.51
2:P:341:G:H2'	2:P:342:C:H6	1.75	0.51
2:P:412:U:C2	2:P:413:U:C5	2.98	0.51
6:T:375:TYR:CE1	9:W:254:PRO:HB3	2.45	0.51
20:y:437:PRO:CA	20:y:438:PRO:CA	2.88	0.51
2:P:317:C:H2'	2:P:318:U:C6	2.46	0.51
2:P:330:G:C4	2:P:331:C:C5	2.98	0.51
2:P:333:U:C2	2:P:334:U:C5	2.99	0.51
2:P:411:U:H2'	2:P:412:U:H6	1.76	0.51
11:b:17:ILE:HD12	11:b:40:LEU:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:228:U:H2'	2:P:229:U:H6	1.75	0.51
2:P:376:U:H6	2:P:376:U:O5'	1.93	0.51
2:P:411:U:C2	2:P:412:U:C5	2.98	0.51
2:P:415:U:C3'	2:P:417:A:H8	2.21	0.51
2:P:440:A:H2'	2:P:441:U:H6	1.76	0.51
2:P:520:G:H2'	2:P:521:G:H8	1.75	0.51
2:P:562:U:O4	12:c:50:ASN:ND2	2.44	0.51
10:a:85:THR:HG22	13:d:73:VAL:HG22	1.93	0.51
11:b:16:THR:HA	11:b:25:VAL:O	2.11	0.51
2:P:483:U:H2'	2:P:484:C:H6	1.76	0.51
18:Y:88:LYS:HE2	18:Y:90:PHE:CE1	2.46	0.51
2:P:284:C:H2'	2:P:285:C:H6	1.75	0.51
2:P:348:U:H2'	2:P:349:U:H6	1.76	0.51
2:P:382:U:O2'	2:P:383:U:C5'	2.59	0.51
2:P:454:G:H2'	2:P:455:U:H6	1.76	0.51
2:P:465:A:C4	2:P:466:U:C5	2.99	0.51
2:P:485:U:H2'	2:P:486:C:H6	1.75	0.51
6:T:172:LEU:HG	6:T:183:TYR:CE1	2.46	0.51
6:T:487:TYR:HE2	7:U:443:LEU:HD13	1.76	0.51
2:P:205:U:H2'	2:P:206:C:H6	1.76	0.50
2:P:396:U:H2'	2:P:397:C:H6	1.76	0.50
2:P:459:U:H2'	2:P:460:U:H6	1.76	0.50
6:T:457:GLU:OE2	6:T:500:TYR:OH	2.25	0.50
8:V:417:TYR:HB2	9:W:281:MET:HE1	1.93	0.50
2:P:254:U:C5	6:T:222:LYS:HB2	2.46	0.50
2:P:514:A:H2'	2:P:515:A:C8	2.44	0.50
20:y:223:THR:CA	20:y:224:GLY:CA	2.89	0.50
2:P:20:A:H2'	2:P:21:G:H8	1.76	0.50
2:P:89:A:C6	2:P:110:G:C6	3.00	0.50
2:P:204:A:C4	2:P:205:U:C5	2.99	0.50
2:P:290:U:C4	2:P:291:C:O2	2.64	0.50
2:P:296:U:H2'	2:P:297:G:C8	2.46	0.50
2:P:432:U:H2'	2:P:433:U:H6	1.76	0.50
2:P:458:U:H2'	2:P:459:U:H6	1.77	0.50
11:b:19:LEU:HD22	11:b:91:THR:HG22	1.93	0.50
2:P:314:G:H2'	2:P:315:G:C8	2.45	0.50
2:P:335:G:C4	2:P:336:U:C5	2.99	0.50
2:P:395:U:H2'	2:P:396:U:H6	1.77	0.50
2:P:431:G:H2'	2:P:432:U:H6	1.75	0.50
2:P:482:G:H2'	2:P:483:U:H6	1.77	0.50
3:Q:44:VAL:HG21	12:c:105:LEU:HD23	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:303:LEU:HD11	6:T:313:TRP:CE2	2.46	0.50
2:P:195:C:H2'	2:P:196:A:C8	2.46	0.50
2:P:332:U:H2'	2:P:333:U:H6	1.76	0.50
2:P:353:A:H2'	2:P:354:C:H6	1.77	0.50
2:P:354:C:H2'	2:P:355:U:H6	1.77	0.50
2:P:356:A:H2'	2:P:357:C:H6	1.76	0.50
2:P:484:C:H2'	2:P:485:U:H6	1.77	0.50
2:P:57:U:H2'	2:P:58:U:C6	2.46	0.50
2:P:318:U:H2'	2:P:319:U:H6	1.76	0.50
6:T:318:LYS:HA	6:T:321:ILE:HG22	1.93	0.50
7:U:579:GLU:HB3	7:U:607:ASN:HD21	1.77	0.50
2:P:360:U:H2'	2:P:361:U:C6	2.47	0.50
4:R:186:THR:HG23	6:T:242:MET:HG2	1.93	0.50
6:T:108:LEU:O	6:T:112:TYR:HB2	2.12	0.50
2:P:204:A:H2'	2:P:205:U:H6	1.77	0.50
2:P:205:U:C2	2:P:206:C:C5	2.99	0.50
2:P:380:G:H2'	2:P:381:U:H6	1.77	0.50
6:T:256:GLU:OE1	6:T:301:ARG:NH1	2.45	0.50
8:V:329:LEU:HD21	8:V:353:VAL:HG22	1.94	0.50
8:V:356:VAL:HG11	8:V:446:TYR:CE2	2.47	0.50
18:Y:109:ASN:HA	18:Y:112:ILE:HD12	1.93	0.50
2:P:20:A:H2'	2:P:21:G:C8	2.47	0.50
2:P:330:G:H2'	2:P:331:C:H6	1.76	0.50
2:P:381:U:H2'	2:P:382:U:H6	1.76	0.50
2:P:488:A:H2'	2:P:489:C:H6	1.77	0.50
6:T:108:LEU:O	6:T:112:TYR:CB	2.60	0.50
7:U:540:TYR:CZ	7:U:544:LYS:HD2	2.47	0.50
12:c:63:ARG:HH11	12:c:64:HIS:HE1	1.59	0.50
18:Y:103:ARG:O	18:Y:107:GLU:HG2	2.12	0.50
2:P:21:G:H2'	2:P:22:A:C8	2.47	0.49
2:P:335:G:H2'	2:P:336:U:H6	1.77	0.49
2:P:150:G:H1'	5:S:69:ARG:HB2	1.92	0.49
2:P:203:A:C6	2:P:236:A:N1	2.80	0.49
6:T:431:LYS:HD3	6:T:469:TRP:CG	2.47	0.49
17:X:25:LYS:HE3	17:X:28:PHE:CE2	2.48	0.49
2:P:193:A:H2'	2:P:194:U:C6	2.47	0.49
2:P:437:A:H2'	2:P:438:U:H6	1.76	0.49
6:T:277:GLU:HG3	8:V:359:LEU:HB2	1.94	0.49
6:T:328:LEU:HD12	9:W:202:GLN:HB2	1.95	0.49
7:U:411:ILE:HD12	7:U:461:ASN:OD1	2.12	0.49
16:g:10:TYR:HB3	16:g:15:ILE:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:191:C:H2'	2:P:192:A:C8	2.44	0.49
2:P:234:U:H3'	2:P:235:A:C8	2.47	0.49
14:e:46:PHE:HB3	14:e:52:VAL:HG12	1.94	0.49
2:P:399:A:H61	2:P:417:A:H2	1.61	0.49
2:P:404:A:H2'	2:P:405:C:H6	1.77	0.49
2:P:444:G:H3'	2:P:445:G:C5'	2.43	0.49
6:T:357:LYS:HD3	7:U:539:LEU:HD13	1.93	0.49
9:W:117:LEU:HD23	9:W:120:PHE:CD2	2.48	0.49
2:P:359:U:H2'	2:P:360:U:H6	1.76	0.49
2:P:526:U:H2'	2:P:527:C:C6	2.47	0.49
4:R:195:SER:H	8:V:301:GLN:HE22	1.60	0.49
9:W:68:SER:HA	9:W:224:PHE:HE2	1.76	0.49
9:W:163:LEU:HD12	9:W:201:PHE:CE2	2.48	0.49
11:b:14:GLN:HB3	11:b:26:TRP:CH2	2.48	0.49
2:P:66:U:H4'	2:P:67:A:O5'	2.11	0.49
2:P:465:A:H2'	2:P:466:U:H6	1.78	0.49
3:Q:8:TYR:HB3	3:Q:12:VAL:HB	1.95	0.49
4:R:41:LYS:HB3	13:d:80:ASN:ND2	2.28	0.49
7:U:403:LEU:HD11	7:U:433:VAL:HG13	1.95	0.49
11:b:52:LEU:HD23	11:b:55:LEU:HD22	1.95	0.49
12:c:52:HIS:HB2	12:c:75:LEU:O	2.11	0.49
12:c:68:VAL:HG22	12:c:95:PHE:HD1	1.78	0.49
2:P:81:C:H2'	2:P:82:A:H8	1.78	0.49
2:P:333:U:H2'	2:P:334:U:H6	1.76	0.49
2:P:441:U:H2'	2:P:442:U:H6	1.77	0.49
6:T:534:ASP:OD1	7:U:378:ARG:NH2	2.30	0.49
7:U:358:TYR:HA	7:U:361:ILE:HG22	1.93	0.49
2:P:357:C:H2'	2:P:358:U:H6	1.78	0.49
6:T:126:LEU:HD12	6:T:157:ARG:CZ	2.41	0.49
6:T:372:GLU:OE1	6:T:391:TYR:OH	2.30	0.49
8:V:445:ASN:OD1	8:V:446:TYR:N	2.41	0.49
8:V:506:THR:HG23	8:V:509:MET:HE2	1.95	0.49
18:Y:204:CYS:SG	18:Y:220:HIS:NE2	2.86	0.49
2:P:232:G:H2'	2:P:233:U:H6	1.78	0.49
2:P:350:U:H2'	2:P:352:G:C8	2.39	0.49
4:R:3:ARG:HD2	4:R:12:TYR:CE2	2.48	0.49
11:b:46:THR:OG1	11:b:78:ASN:O	2.29	0.49
2:P:491:U:H2'	2:P:492:U:H6	1.76	0.48
6:T:486:ILE:HG21	6:T:500:TYR:CD2	2.48	0.48
13:d:24:THR:HA	13:d:70:LYS:HE3	1.94	0.48
2:P:554:U:O2'	13:d:65:ARG:NH2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:445:VAL:HG21	6:T:481:CYS:HB3	1.95	0.48
7:U:457:LEU:C	7:U:457:LEU:CD2	2.86	0.48
2:P:110:G:C2	2:P:111:A:C5	3.00	0.48
2:P:272:A:H2'	2:P:273:G:H8	1.78	0.48
2:P:347:U:H2'	2:P:348:U:H6	1.77	0.48
2:P:438:U:H2'	2:P:439:U:H6	1.77	0.48
2:P:467:G:H2'	2:P:468:U:H6	1.77	0.48
6:T:169:ARG:NH2	7:U:602:LEU:HA	2.29	0.48
7:U:458:TYR:HB3	7:U:464:ILE:HD11	1.96	0.48
7:U:533:ASN:OD1	7:U:534:THR:N	2.46	0.48
2:P:206:C:H2'	2:P:207:C:H6	1.78	0.48
2:P:377:U:H5'	2:P:377:U:H6	1.77	0.48
2:P:410:G:H2'	2:P:411:U:H6	1.77	0.48
2:P:414:A:H2'	2:P:415:U:H6	1.78	0.48
2:P:457:G:H2'	2:P:458:U:H6	1.78	0.48
5:S:92:GLU:O	5:S:95:THR:OG1	2.30	0.48
6:T:82:TYR:CD1	6:T:115:PHE:HE1	2.30	0.48
10:a:15:LEU:HD12	10:a:15:LEU:O	2.13	0.48
12:c:89:ARG:NH2	12:c:91:ILE:HD11	2.29	0.48
2:P:285:C:C2	2:P:286:A:C8	3.02	0.48
2:P:358:U:H2'	2:P:359:U:H6	1.78	0.48
2:P:112:A:HO2'	2:P:113:G:P	2.36	0.48
8:V:387:LYS:NZ	9:W:290:ALA:O	2.42	0.48
2:P:62:A:O3'	5:S:104:ARG:HD3	2.13	0.48
2:P:292:A:O2'	2:P:293:A:OP1	2.30	0.48
2:P:452:U:H2'	2:P:453:U:H6	1.78	0.48
6:T:126:LEU:CD1	6:T:157:ARG:NH2	2.72	0.48
7:U:270:LEU:O	7:U:273:VAL:N	2.46	0.48
8:V:500:GLU:HG2	8:V:504:ASN:ND2	2.29	0.48
18:Y:73:LEU:HB2	18:Y:76:HIS:CD2	2.48	0.48
4:R:80:ASN:HA	4:R:83:LYS:HG2	1.95	0.48
7:U:580:ARG:NH1	7:U:580:ARG:CG	2.73	0.48
18:Y:88:LYS:HE2	18:Y:90:PHE:HE1	1.79	0.48
2:P:199:G:H2'	2:P:200:G:C8	2.49	0.48
2:P:317:C:H2'	2:P:318:U:H6	1.79	0.48
2:P:374:A:H2'	2:P:375:U:H6	1.78	0.48
6:T:464:ILE:HD11	6:T:472:TYR:CG	2.49	0.48
18:Y:221:PHE:HD1	18:Y:226:HIS:ND1	2.12	0.48
2:P:198:U:H2'	2:P:199:G:H8	1.79	0.47
2:P:341:G:O2'	2:P:342:C:H5'	2.13	0.47
2:P:385:U:H2'	2:P:386:G:OP1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:494:TYR:OH	6:T:531:GLU:OE2	2.28	0.47
10:a:7:ALA:HB3	10:a:10:SER:HB2	1.96	0.47
7:U:620:TYR:O	7:U:624:PHE:HB3	2.15	0.47
18:Y:203:VAL:HG11	18:Y:230:VAL:HG23	1.94	0.47
4:R:29:ASN:O	4:R:33:ILE:HG12	2.15	0.47
9:W:75:ARG:NH1	9:W:112:LEU:HB2	2.29	0.47
9:W:219:PHE:HA	9:W:222:VAL:HG22	1.95	0.47
2:P:345:U:H2'	2:P:346:C:H6	1.80	0.47
2:P:346:C:H2'	2:P:347:U:H6	1.79	0.47
4:R:190:THR:HG22	8:V:300:GLN:HB2	1.96	0.47
5:S:21:ARG:HE	5:S:36:ASN:CG	2.22	0.47
6:T:240:MET:SD	7:U:603:PRO:HG3	2.54	0.47
2:P:163:G:H2'	2:P:164:U:H6	1.79	0.47
2:P:272:A:H2'	2:P:273:G:C8	2.49	0.47
2:P:35:G:H2'	2:P:36:U:C6	2.49	0.47
2:P:161:G:H2'	2:P:162:U:C6	2.49	0.47
2:P:163:G:H2'	2:P:164:U:C6	2.50	0.47
2:P:190:U:H2'	2:P:191:C:C6	2.50	0.47
2:P:383:U:C2'	2:P:384:U:C5'	2.85	0.47
4:R:3:ARG:HD3	4:R:12:TYR:CE2	2.50	0.47
6:T:306:LEU:HD13	6:T:309:TYR:HD2	1.79	0.47
8:V:328:GLU:HG2	8:V:332:TYR:HE2	1.79	0.47
8:V:417:TYR:HB2	9:W:281:MET:CE	2.45	0.47
2:P:141:A:N6	5:S:75:ASN:HB2	2.29	0.47
2:P:282:C:H2'	2:P:283:A:C8	2.49	0.47
2:P:417:A:N3	2:P:418:U:C5	2.82	0.47
2:P:517:U:H2'	2:P:518:U:C6	2.49	0.47
5:S:10:PRO:HA	5:S:104:ARG:HH21	1.80	0.47
5:S:21:ARG:NH2	5:S:33:TYR:OH	2.48	0.47
6:T:279:TRP:O	6:T:283:LEU:HD13	2.15	0.47
7:U:530:ILE:O	7:U:531:ASP:HB3	2.15	0.47
8:V:392:LEU:HD11	8:V:404:GLN:HE22	1.80	0.47
8:V:410:LEU:HD22	8:V:412:GLN:HE21	1.79	0.47
9:W:74:MET:HE1	9:W:132:LEU:HB3	1.97	0.47
9:W:126:CYS:HB3	9:W:212:MET:SD	2.55	0.47
11:b:47:LEU:HD21	11:b:61:ALA:HB3	1.97	0.47
2:P:361:U:H2'	2:P:362:C:C6	2.50	0.47
5:S:73:MET:HA	5:S:76:GLN:NE2	2.30	0.47
6:T:87:VAL:HG21	13:d:56:VAL:HG13	1.97	0.47
8:V:401:LEU:HB3	8:V:403:VAL:HG23	1.97	0.47
10:a:15:LEU:HB2	10:a:18:TYR:CD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:a:31:ILE:O	10:a:48:CYS:HA	2.15	0.47
11:b:82:LEU:HD11	11:b:85:ILE:HB	1.96	0.47
2:P:75:G:H2'	2:P:76:U:C6	2.49	0.47
2:P:110:G:H2'	2:P:111:A:H8	1.80	0.47
6:T:141:PHE:HB3	6:T:301:ARG:HH22	1.80	0.47
2:P:516:U:H2'	2:P:517:U:H6	1.78	0.47
8:V:314:THR:HG23	8:V:383:GLY:O	2.15	0.47
6:T:53:LEU:HD13	6:T:84:LEU:HD11	1.95	0.46
7:U:403:LEU:O	7:U:406:SER:OG	2.19	0.46
4:R:118:VAL:O	4:R:124:ARG:HD2	2.14	0.46
6:T:329:GLY:O	6:T:333:VAL:HG23	2.14	0.46
8:V:395:ALA:O	8:V:399:ASN:N	2.48	0.46
9:W:163:LEU:HD12	9:W:201:PHE:HE2	1.80	0.46
16:g:15:ILE:HG23	16:g:72:GLU:O	2.16	0.46
2:P:175:U:H4'	2:P:176:U:OP1	2.15	0.46
2:P:415:U:C5'	2:P:416:G:OP1	2.44	0.46
2:P:530:G:H2'	2:P:531:G:H8	1.80	0.46
11:b:33:SER:HB2	11:b:37:ASN:HB2	1.97	0.46
15:f:29:VAL:O	15:f:37:GLU:HA	2.14	0.46
17:X:13:LEU:HB3	17:X:50:ARG:NH1	2.30	0.46
2:P:444:G:C5	2:P:445:G:C8	3.03	0.46
3:Q:7:LYS:HD3	4:R:26:VAL:HA	1.97	0.46
6:T:208:LEU:HD12	6:T:216:ILE:HD11	1.97	0.46
6:T:306:LEU:HD11	6:T:312:VAL:HG23	1.97	0.46
7:U:502:THR:CG2	8:V:368:MET:HE2	2.43	0.46
16:g:74:LEU:HD12	16:g:74:LEU:O	2.15	0.46
2:P:81:C:C2	2:P:82:A:C8	3.04	0.46
2:P:377:U:O2'	2:P:378:U:OP1	2.28	0.46
9:W:70:LEU:HD21	9:W:129:LEU:HD11	1.98	0.46
14:e:81:LEU:HD22	15:f:19:LEU:HD11	1.97	0.46
3:Q:52:LEU:HD13	12:c:45:ILE:HD11	1.97	0.46
6:T:123:GLN:NE2	6:T:157:ARG:HB3	2.30	0.46
6:T:399:GLN:OE1	6:T:420:LEU:HD13	2.16	0.46
6:T:521:LEU:HD23	6:T:536:LEU:HD11	1.98	0.46
6:T:535:THR:HA	6:T:538:GLU:HG2	1.98	0.46
7:U:450:GLN:HE21	7:U:450:GLN:CA	2.02	0.46
2:P:17:A:H2'	2:P:18:U:C6	2.51	0.46
2:P:83:U:H2'	2:P:84:U:C6	2.51	0.46
2:P:258:U:H1'	2:P:259:U:OP2	2.16	0.46
5:S:16:LYS:HG3	5:S:69:ARG:HH12	1.80	0.46
8:V:407:GLN:HG2	9:W:291:TYR:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:c:102:ILE:HG13	12:c:103:VAL:N	2.30	0.46
2:P:114:U:C1'	13:d:56:VAL:HG12	2.45	0.46
2:P:175:U:O2'	2:P:176:U:O5'	2.28	0.46
2:P:382:U:C2'	2:P:383:U:C5'	2.75	0.46
6:T:126:LEU:HD22	6:T:126:LEU:C	2.41	0.46
6:T:334:LEU:HB3	6:T:351:LEU:HD12	1.98	0.46
6:T:347:ILE:O	6:T:351:LEU:HB2	2.15	0.46
16:g:37:ASN:OD1	16:g:64:ARG:HA	2.16	0.46
2:P:80:G:C4	2:P:81:C:C5	3.04	0.46
2:P:394:A:H2'	2:P:395:U:C6	2.50	0.46
3:Q:64:PRO:HA	12:c:41:ARG:HH11	1.80	0.46
6:T:522:THR:HG23	6:T:533:MET:HE1	1.98	0.46
7:U:442:TRP:HB2	7:U:451:THR:HG21	1.98	0.46
7:U:490:PHE:HE2	7:U:508:ILE:HG21	1.80	0.46
12:c:66:ASN:HB3	12:c:98:GLY:H	1.81	0.46
18:Y:90:PHE:O	18:Y:92:GLU:N	2.43	0.46
2:P:322:A:H2'	2:P:323:A:H8	1.81	0.45
2:P:349:U:O2'	2:P:350:U:H5'	2.16	0.45
2:P:490:U:H2'	2:P:491:U:C6	2.51	0.45
5:S:10:PRO:HA	5:S:104:ARG:NH2	2.31	0.45
2:P:195:C:H2'	2:P:196:A:H8	1.80	0.45
2:P:239:U:H2'	2:P:240:G:C8	2.51	0.45
6:T:499:GLN:HA	7:U:385:LEU:HD21	1.99	0.45
7:U:289:HIS:CE1	7:U:291:ASN:HB3	2.51	0.45
2:P:35:G:H2'	2:P:36:U:H6	1.80	0.45
3:Q:14:ARG:O	3:Q:17:LYS:HG3	2.16	0.45
4:R:126:ASP:OD1	4:R:127:ILE:N	2.47	0.45
9:W:157:LEU:HD11	9:W:208:VAL:HG22	1.98	0.45
10:a:95:THR:OG1	11:b:86:ASN:HB3	2.15	0.45
18:Y:71:MET:HB3	18:Y:73:LEU:HG	1.99	0.45
9:W:129:LEU:HD12	9:W:215:LEU:HD11	1.98	0.45
2:P:487:A:C2	2:P:487:A:O5'	2.69	0.45
7:U:584:SER:N	7:U:604:ASN:O	2.42	0.45
2:P:196:A:H2'	2:P:197:U:H6	1.81	0.45
2:P:341:G:H2'	2:P:342:C:C6	2.52	0.45
11:b:27:GLY:HA3	11:b:43:VAL:HG12	1.97	0.45
2:P:61:A:C5	2:P:135:U:H1'	2.52	0.45
2:P:193:A:H2'	2:P:194:U:H6	1.81	0.45
2:P:524:G:H2'	2:P:525:G:C8	2.50	0.45
2:P:557:U:H5	10:a:40:HIS:HA	1.82	0.45
10:a:93:LEU:HD11	11:b:21:ASN:ND2	2.28	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:121:U:C5'	3:Q:26:ARG:HH12	2.29	0.45
2:P:285:C:H2'	2:P:286:A:H8	1.82	0.45
2:P:309:G:O6	2:P:532:U:O2	2.35	0.45
3:Q:15:LEU:HD11	4:R:42:ALA:HB1	1.98	0.45
4:R:124:ARG:NH2	4:R:126:ASP:OD2	2.50	0.45
4:R:125:PHE:HB2	6:T:79:LEU:HB3	1.99	0.45
2:P:207:C:H2'	2:P:208:C:C6	2.51	0.45
2:P:235:A:C8	2:P:235:A:P	3.10	0.45
4:R:40:ASN:HA	4:R:43:ARG:HG2	1.98	0.45
4:R:121:ASP:HA	4:R:124:ARG:CD	2.47	0.45
4:R:124:ARG:HE	6:T:79:LEU:HD21	1.82	0.45
6:T:302:ALA:C	6:T:305:PRO:HD2	2.42	0.45
11:b:14:GLN:NE2	11:b:28:THR:OG1	2.50	0.45
2:P:202:U:C2	2:P:203:A:N7	2.85	0.45
2:P:322:A:H2'	2:P:323:A:C8	2.52	0.45
4:R:52:LYS:HG3	4:R:54:ARG:HH22	1.82	0.45
4:R:186:THR:CG2	6:T:242:MET:HG2	2.48	0.45
10:a:38:ASP:OD1	10:a:39:LYS:N	2.39	0.45
11:b:18:GLU:HG3	11:b:24:THR:HG22	1.98	0.45
17:X:7:VAL:HG13	17:X:19:TRP:HE3	1.82	0.45
2:P:351:U:OP1	2:P:351:U:H3'	2.17	0.44
3:Q:7:LYS:HB3	4:R:31:LEU:HD13	1.98	0.44
6:T:186:TRP:O	6:T:190:ILE:HG12	2.16	0.44
7:U:335:PHE:HD1	7:U:338:ARG:HH11	1.65	0.44
10:a:50:GLU:O	10:a:79:LYS:HA	2.17	0.44
14:e:51:ASN:HB3	14:e:84:GLY:H	1.81	0.44
18:Y:119:LEU:HD21	18:Y:207:TYR:CE1	2.52	0.44
2:P:525:G:H2'	2:P:526:U:C6	2.52	0.44
18:Y:198:LEU:HD22	18:Y:207:TYR:HB3	1.99	0.44
2:P:47:A:H2'	2:P:48:A:H8	1.83	0.44
2:P:271:G:H3'	2:P:272:A:H5'	2.00	0.44
2:P:377:U:C6	2:P:377:U:C3'	3.01	0.44
4:R:165:PHE:CZ	9:W:273:ILE:HG21	2.52	0.44
11:b:72:GLN:NE2	11:b:75:ALA:HB2	2.32	0.44
6:T:25:LYS:CG	9:W:260:LEU:HD13	2.47	0.44
1:G:-1:A:O2'	1:G:0:A:O4'	2.35	0.44
2:P:450:G:C8	2:P:450:G:OP2	2.70	0.44
7:U:494:LEU:HD22	7:U:505:MET:HG3	2.00	0.44
7:U:534:THR:OG1	7:U:552:PRO:HB2	2.18	0.44
15:f:16:LYS:HB3	15:f:17:PRO:HD3	2.00	0.44
15:f:80:TYR:HE1	15:f:82:ARG:HD2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:X:7:VAL:HG13	17:X:19:TRP:CE3	2.52	0.44
2:P:73:A:O2'	2:P:75:G:OP1	2.32	0.44
2:P:77:U:H2'	2:P:78:A:C8	2.53	0.44
2:P:444:G:O6	2:P:445:G:C5	2.70	0.44
6:T:45:CYS:O	6:T:48:THR:HG22	2.18	0.44
2:P:318:U:H2'	2:P:319:U:C6	2.53	0.44
2:P:451:A:C6	2:P:452:U:O4	2.70	0.44
6:T:318:LYS:O	6:T:321:ILE:HG22	2.18	0.44
6:T:339:LYS:HD3	9:W:245:GLN:HB3	2.00	0.44
12:c:33:LEU:HD23	15:f:72:PHE:HB2	1.98	0.44
14:e:31:LEU:HD21	14:e:82:LEU:HD21	2.00	0.44
18:Y:112:ILE:HD11	18:Y:202:GLU:O	2.18	0.44
18:Y:204:CYS:HA	18:Y:229:TYR:CD2	2.53	0.44
2:P:47:A:H2'	2:P:48:A:C8	2.53	0.44
2:P:203:A:H2'	2:P:204:A:C8	2.52	0.44
8:V:410:LEU:O	8:V:410:LEU:HD23	2.17	0.44
9:W:193:ASN:ND2	9:W:198:PHE:O	2.51	0.44
12:c:62:ASP:HB3	12:c:66:ASN:OD1	2.17	0.44
2:P:116:A:N3	2:P:119:G:O2'	2.43	0.44
2:P:330:G:H2'	2:P:331:C:C6	2.53	0.44
2:P:412:U:H2'	2:P:413:U:C6	2.52	0.44
2:P:445:G:N3	2:P:446:U:C4	2.85	0.44
3:Q:37:THR:HG22	3:Q:38:ASN:N	2.31	0.44
7:U:129:LEU:C	7:U:131:LYS:O	2.61	0.44
9:W:193:ASN:HD22	9:W:199:GLN:HA	1.82	0.44
2:P:65:G:O6	4:R:60:GLY:HA3	2.17	0.43
2:P:199:G:H2'	2:P:200:G:H8	1.83	0.43
2:P:361:U:H3	2:P:450:G:H1	1.66	0.43
2:P:376:U:H4'	2:P:377:U:OP2	2.18	0.43
2:P:485:U:H2'	2:P:486:C:C6	2.53	0.43
2:P:489:C:H2'	2:P:490:U:C6	2.51	0.43
2:P:493:G:H2'	2:P:494:C:C6	2.53	0.43
6:T:193:ILE:HG23	6:T:198:GLN:HB2	2.00	0.43
6:T:437:GLN:NE2	6:T:472:TYR:OH	2.49	0.43
7:U:544:LYS:HG2	7:U:544:LYS:O	2.17	0.43
14:e:91:THR:HG21	16:g:57:LEU:HB3	1.99	0.43
18:Y:221:PHE:CD1	18:Y:226:HIS:HE1	2.30	0.43
2:P:254:U:O2	2:P:256:U:N3	2.51	0.43
2:P:387:A:H2'	2:P:388:C:C6	2.52	0.43
4:R:138:GLN:O	18:Y:215:ARG:HG2	2.18	0.43
6:T:306:LEU:HD12	6:T:306:LEU:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Y:83:GLU:O	18:Y:87:GLY:N	2.46	0.43
2:P:138:C:H2'	2:P:139:A:O4'	2.18	0.43
2:P:331:C:H2'	2:P:332:U:C6	2.53	0.43
2:P:368:C:C3'	2:P:369:G:H5'	2.46	0.43
6:T:10:ASP:OD1	6:T:11:GLU:N	2.51	0.43
6:T:437:GLN:HE21	6:T:471:TYR:HE2	1.65	0.43
7:U:431:SER:O	7:U:435:VAL:HG23	2.18	0.43
18:Y:93:PHE:O	18:Y:97:TYR:HB2	2.18	0.43
1:G:5:U:O2	18:Y:216:ARG:NH2	2.40	0.43
2:P:59:C:H2'	2:P:60:C:H6	1.83	0.43
2:P:205:U:H2'	2:P:206:C:C6	2.53	0.43
2:P:243:U:H2'	2:P:244:U:H6	1.83	0.43
2:P:546:U:H2'	2:P:547:C:H6	1.83	0.43
6:T:77:PHE:HD2	6:T:93:ILE:HD13	1.83	0.43
6:T:126:LEU:C	6:T:126:LEU:CD2	2.92	0.43
6:T:368:LEU:HA	6:T:371:ILE:HG22	2.00	0.43
2:P:74:C:O2'	6:T:123:GLN:OE1	2.32	0.43
2:P:356:A:H2'	2:P:357:C:C6	2.54	0.43
2:P:371:G:N3	2:P:372:C:C6	2.87	0.43
2:P:386:G:O5'	2:P:386:G:C8	2.71	0.43
6:T:303:LEU:HD21	6:T:313:TRP:CH2	2.53	0.43
6:T:416:LEU:HG	6:T:447:PHE:CZ	2.53	0.43
6:T:486:ILE:HG21	6:T:500:TYR:HD2	1.83	0.43
6:T:487:TYR:CE2	7:U:443:LEU:HD13	2.53	0.43
9:W:75:ARG:HH11	9:W:112:LEU:HD12	1.83	0.43
9:W:238:GLU:OE2	9:W:241:ARG:NH2	2.51	0.43
11:b:52:LEU:HD11	12:c:83:ASN:O	2.19	0.43
11:b:103:LEU:HD23	11:b:107:LEU:HD11	2.01	0.43
2:P:172:C:H2'	2:P:173:G:C8	2.51	0.43
2:P:234:U:O3'	2:P:235:A:H8	2.02	0.43
6:T:113:LEU:HD13	6:T:130:TYR:CD1	2.54	0.43
6:T:209:LEU:O	6:T:213:LYS:HA	2.19	0.43
11:b:15:VAL:HG11	11:b:29:LEU:HD12	2.00	0.43
12:c:79:LYS:HA	12:c:83:ASN:O	2.19	0.43
14:e:28:THR:N	14:e:91:THR:O	2.49	0.43
3:Q:31:PRO:O	3:Q:35:ARG:HG3	2.18	0.43
6:T:211:LYS:HD3	7:U:602:LEU:HD22	2.01	0.43
6:T:453:VAL:O	6:T:457:GLU:HB2	2.19	0.43
8:V:324:VAL:HG23	8:V:328:GLU:OE1	2.19	0.43
13:d:41:ASN:HB3	13:d:66:GLY:H	1.84	0.43
18:Y:46:LYS:HG2	18:Y:72:HIS:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:203:A:N1	2:P:236:A:C2	2.87	0.43
2:P:370:U:O2'	2:P:371:G:H5''	2.17	0.43
2:P:400:A:H2'	2:P:401:U:C6	2.53	0.43
7:U:619:LEU:HD11	8:V:379:ARG:HH22	1.84	0.43
2:P:64:A:H4'	2:P:65:G:OP2	2.18	0.43
2:P:333:U:H2'	2:P:334:U:C6	2.54	0.43
11:b:31:SER:O	11:b:39:ILE:HG22	2.18	0.43
15:f:67:THR:C	15:f:68:LEU:HD12	2.44	0.43
18:Y:207:TYR:C	18:Y:208:LEU:HD12	2.44	0.43
2:P:444:G:H2'	2:P:445:G:H5'	2.00	0.43
2:P:495:U:H2'	2:P:496:C:C6	2.53	0.43
6:T:106:LEU:HA	6:T:137:VAL:HG21	2.01	0.43
18:Y:57:LEU:HD23	18:Y:228:GLY:CA	2.49	0.43
2:P:118:U:OP2	9:W:226:LYS:HB2	2.19	0.42
2:P:253:C:C5	6:T:221:ARG:HD2	2.53	0.42
3:Q:85:LEU:HD23	3:Q:89:LEU:HD23	2.01	0.42
5:S:4:LEU:HD23	5:S:5:TYR:N	2.34	0.42
6:T:272:SER:HA	8:V:414:ASN:O	2.19	0.42
7:U:131:LYS:C	7:U:133:ILE:N	2.73	0.42
2:P:11:U:H6	2:P:11:U:O5'	2.02	0.42
2:P:17:A:H2'	2:P:18:U:H6	1.84	0.42
2:P:59:C:H2'	2:P:60:C:C6	2.54	0.42
2:P:386:G:H2'	2:P:387:A:H8	1.83	0.42
7:U:356:SER:HA	7:U:424:LEU:HD21	2.01	0.42
2:P:206:C:H2'	2:P:207:C:C6	2.54	0.42
2:P:284:C:H2'	2:P:285:C:C6	2.55	0.42
2:P:411:U:H2'	2:P:412:U:C6	2.54	0.42
2:P:554:U:O4'	16:g:64:ARG:NH1	2.52	0.42
4:R:121:ASP:HA	4:R:124:ARG:HD3	2.02	0.42
6:T:169:ARG:HH22	7:U:602:LEU:HA	1.85	0.42
10:a:21:ARG:HD3	11:b:67:LEU:O	2.19	0.42
15:f:34:ASN:O	15:f:35:SER:OG	2.29	0.42
2:P:9:C:O2'	2:P:10:U:OP1	2.31	0.42
2:P:367:G:H2'	2:P:368:C:C6	2.53	0.42
2:P:377:U:C6	2:P:377:U:H3'	2.55	0.42
2:P:417:A:C2	2:P:418:U:C4	3.08	0.42
2:P:431:G:H2'	2:P:432:U:C6	2.54	0.42
6:T:417:ASN:OD1	6:T:418:LYS:N	2.53	0.42
8:V:317:ILE:HG22	8:V:352:PHE:HA	2.00	0.42
2:P:86:A:O2'	2:P:87:U:OP2	2.29	0.42
2:P:121:U:H2'	2:P:122:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:332:U:H2'	2:P:333:U:C6	2.53	0.42
2:P:405:C:H2'	2:P:406:U:C6	2.53	0.42
2:P:454:G:H2'	2:P:455:U:C6	2.54	0.42
2:P:488:A:H2'	2:P:489:C:C6	2.55	0.42
6:T:432:GLU:OE2	6:T:471:TYR:HB2	2.20	0.42
18:Y:110:GLY:O	18:Y:113:SER:OG	2.24	0.42
2:P:110:G:H2'	2:P:111:A:C8	2.55	0.42
2:P:335:G:H2'	2:P:336:U:C6	2.54	0.42
2:P:348:U:H2'	2:P:349:U:C6	2.55	0.42
2:P:432:U:H2'	2:P:433:U:C6	2.54	0.42
2:P:459:U:H2'	2:P:460:U:C6	2.54	0.42
2:P:467:G:H2'	2:P:468:U:C6	2.55	0.42
6:T:27:LEU:HD12	6:T:67:PHE:CG	2.54	0.42
6:T:291:THR:HG23	7:U:589:GLU:OE2	2.20	0.42
7:U:289:HIS:HE1	7:U:291:ASN:HB3	1.83	0.42
7:U:504:VAL:O	7:U:508:ILE:HD12	2.19	0.42
7:U:576:ILE:HD11	8:V:307:PHE:O	2.19	0.42
9:W:239:TYR:CZ	9:W:243:TYR:HE2	2.37	0.42
13:d:49:ALA:HB2	13:d:59:MET:HE3	2.01	0.42
2:P:386:G:H3'	2:P:386:G:P	2.60	0.42
2:P:393:G:H2'	2:P:394:A:H8	1.85	0.42
2:P:441:U:H2'	2:P:442:U:C6	2.55	0.42
18:Y:119:LEU:HD11	18:Y:207:TYR:CE1	2.55	0.42
20:y:211:MET:CA	20:y:212:LYS:CA	2.98	0.42
2:P:108:U:H2'	2:P:109:U:H6	1.84	0.42
2:P:204:A:H2'	2:P:205:U:C6	2.54	0.42
2:P:383:U:O2'	2:P:384:U:H5'	2.18	0.42
7:U:573:HIS:HD2	7:U:576:ILE:HB	1.84	0.42
8:V:345:PRO:HD2	8:V:351:GLY:HA2	2.00	0.42
9:W:50:ASN:ND2	9:W:212:MET:HG3	2.34	0.42
18:Y:61:THR:HG21	18:Y:225:ILE:HG13	2.02	0.42
2:P:263:U:H2'	2:P:264:C:C6	2.55	0.42
2:P:381:U:H2'	2:P:382:U:C6	2.55	0.42
2:P:440:A:H2'	2:P:441:U:C6	2.54	0.42
6:T:114:LYS:HG3	6:T:149:LEU:HD21	2.00	0.42
6:T:208:LEU:HB3	6:T:214:ILE:HD11	2.02	0.42
7:U:129:LEU:O	7:U:133:ILE:CB	2.67	0.42
2:P:15:A:O2'	2:P:16:U:H5'	2.20	0.42
2:P:453:U:H2'	2:P:454:G:H8	1.85	0.42
2:P:458:U:H2'	2:P:459:U:C6	2.55	0.42
2:P:465:A:H2'	2:P:466:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:482:G:H2'	2:P:483:U:C6	2.55	0.42
2:P:526:U:H2'	2:P:527:C:H6	1.83	0.42
6:T:266:SER:O	6:T:269:THR:HG22	2.20	0.42
6:T:448:TYR:CD2	7:U:480:SER:HA	2.54	0.42
7:U:57:ALA:O	7:U:61:ALA:CB	2.68	0.42
12:c:77:THR:HB	12:c:86:ASN:HD22	1.84	0.42
17:X:13:LEU:HD21	17:X:43:LEU:HD23	2.02	0.42
18:Y:198:LEU:HA	18:Y:209:SER:HA	2.02	0.42
2:P:198:U:H2'	2:P:199:G:C8	2.55	0.41
6:T:53:LEU:HA	6:T:56:ILE:HG22	2.01	0.41
2:P:121:U:H2'	2:P:122:G:H8	1.85	0.41
2:P:354:C:H2'	2:P:355:U:C6	2.56	0.41
2:P:369:G:H2'	2:P:371:G:H8	1.84	0.41
3:Q:5:LEU:HG	4:R:134:SER:HA	2.02	0.41
6:T:77:PHE:HE2	6:T:93:ILE:HG21	1.83	0.41
6:T:271:VAL:HG22	6:T:309:TYR:OH	2.21	0.41
6:T:460:ILE:HG23	6:T:461:PHE:H	1.84	0.41
7:U:293:TRP:CD1	7:U:321:LEU:HD21	2.56	0.41
16:g:33:ASP:OD1	16:g:37:ASN:N	2.51	0.41
2:P:63:U:O2'	2:P:64:A:O5'	2.37	0.41
2:P:81:C:H2'	2:P:82:A:C8	2.55	0.41
2:P:395:U:H2'	2:P:396:U:C6	2.55	0.41
2:P:404:A:H2'	2:P:405:C:C6	2.55	0.41
6:T:405:SER:HG	6:T:411:GLN:C	2.25	0.41
7:U:451:THR:HG22	7:U:455:PHE:CE2	2.56	0.41
10:a:18:TYR:HE1	10:a:101:PRO:HD3	1.84	0.41
2:P:88:C:H2'	2:P:89:A:H8	1.85	0.41
2:P:286:A:H4'	4:R:39:ARG:HH11	1.85	0.41
2:P:353:A:H2'	2:P:354:C:C6	2.55	0.41
2:P:377:U:O2'	2:P:378:U:P	2.79	0.41
2:P:396:U:H2'	2:P:397:C:C6	2.54	0.41
2:P:410:G:H2'	2:P:411:U:C6	2.54	0.41
6:T:30:TRP:CZ2	6:T:66:GLU:HG3	2.55	0.41
6:T:280:ILE:HG23	6:T:315:LYS:NZ	2.35	0.41
7:U:356:SER:O	7:U:360:LYS:HG2	2.20	0.41
9:W:50:ASN:ND2	9:W:209:SER:HA	2.32	0.41
2:P:386:G:O5'	2:P:386:G:H8	2.04	0.41
4:R:124:ARG:HE	6:T:79:LEU:CD2	2.33	0.41
7:U:489:LYS:HA	7:U:492:ARG:HG2	2.01	0.41
9:W:94:SER:O	9:W:96:ASP:N	2.53	0.41
9:W:228:GLU:HB3	9:W:231:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:e:35:ILE:HG22	14:e:37:ILE:HG12	2.02	0.41
15:f:30:LYS:HD2	15:f:80:TYR:CE2	2.55	0.41
2:P:78:A:H4'	2:P:79:A:C5'	2.32	0.41
2:P:196:A:H2'	2:P:197:U:C6	2.55	0.41
2:P:286:A:C6	2:P:297:G:C6	3.09	0.41
2:P:337:A:H2'	2:P:338:G:H8	1.86	0.41
2:P:380:G:H2'	2:P:381:U:C6	2.55	0.41
2:P:451:A:H8	2:P:451:A:O5'	2.04	0.41
2:P:452:U:H2'	2:P:453:U:C6	2.56	0.41
2:P:460:U:H2'	2:P:461:G:H8	1.86	0.41
6:T:314:ILE:O	6:T:318:LYS:HG2	2.20	0.41
7:U:452:ARG:HA	7:U:455:PHE:HD2	1.84	0.41
9:W:162:TYR:CD1	9:W:200:GLN:HB3	2.55	0.41
17:X:19:TRP:CZ2	17:X:20:LYS:HD3	2.55	0.41
2:P:152:G:O2'	2:P:153:C:OP1	2.34	0.41
2:P:233:U:O2'	2:P:234:U:H5'	2.20	0.41
2:P:257:G:C4	4:R:87:MET:HG3	2.56	0.41
2:P:334:U:H2'	2:P:335:G:H8	1.86	0.41
2:P:370:U:O2'	2:P:371:G:P	2.79	0.41
2:P:414:A:H2'	2:P:415:U:C6	2.55	0.41
2:P:494:C:H2'	2:P:495:U:C6	2.53	0.41
5:S:16:LYS:HG3	5:S:69:ARG:NH1	2.36	0.41
11:b:93:ARG:NH1	12:c:50:ASN:HB2	2.35	0.41
2:P:106:C:H2'	2:P:107:A:C8	2.56	0.41
2:P:122:G:H5'	10:a:56:THR:HG21	2.03	0.41
2:P:127:C:H2'	2:P:128:U:C6	2.55	0.41
2:P:176:U:H3'	2:P:177:C:H5''	2.02	0.41
2:P:371:G:C4	2:P:372:C:C6	3.08	0.41
2:P:438:U:H2'	2:P:439:U:C6	2.55	0.41
2:P:450:G:C6	2:P:451:A:N6	2.89	0.41
4:R:174:LEU:HD23	4:R:175:GLU:O	2.20	0.41
6:T:396:THR:HG23	6:T:414:GLY:O	2.20	0.41
8:V:314:THR:HA	8:V:353:VAL:O	2.21	0.41
8:V:328:GLU:HG2	8:V:332:TYR:CE2	2.56	0.41
9:W:198:PHE:CD2	9:W:235:PHE:HD1	2.39	0.41
13:d:33:LEU:HA	13:d:44:LEU:HD23	2.03	0.41
15:f:45:THR:HA	15:f:50:ASN:O	2.20	0.41
18:Y:204:CYS:SG	18:Y:226:HIS:CG	3.14	0.41
2:P:179:A:H3'	2:P:180:U:C6	2.56	0.41
2:P:299:U:O2	4:R:43:ARG:NH2	2.54	0.41
2:P:413:U:H2'	2:P:414:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:437:A:H2'	2:P:438:U:C6	2.54	0.41
7:U:530:ILE:HG13	7:U:532:SER:H	1.85	0.41
8:V:329:LEU:HD21	8:V:353:VAL:CG2	2.51	0.41
11:b:104:ASP:OD1	11:b:105:SER:N	2.53	0.41
2:P:132:U:O2'	2:P:133:G:H5'	2.20	0.40
2:P:232:G:H2'	2:P:233:U:C6	2.56	0.40
2:P:379:A:H2'	2:P:380:G:H8	1.86	0.40
2:P:530:G:H2'	2:P:531:G:C8	2.57	0.40
4:R:14:THR:HG21	13:d:96:ARG:HD3	2.02	0.40
5:S:3:ALA:HB2	5:S:115:SER:HB3	2.03	0.40
6:T:274:ASP:OD1	6:T:275:GLU:N	2.53	0.40
7:U:327:THR:HG23	7:U:328:LEU:N	2.36	0.40
8:V:340:VAL:O	8:V:354:GLN:HB3	2.21	0.40
18:Y:53:CYS:SG	18:Y:54:PRO:HD2	2.62	0.40
2:P:444:G:C2'	2:P:445:G:H5'	2.51	0.40
2:P:484:C:H2'	2:P:485:U:C6	2.55	0.40
6:T:25:LYS:HG3	9:W:260:LEU:HD13	2.03	0.40
6:T:26:SER:C	6:T:28:ALA:H	2.29	0.40
2:P:228:U:H2'	2:P:229:U:C6	2.55	0.40
2:P:491:U:H2'	2:P:492:U:C6	2.55	0.40
5:S:101:VAL:O	5:S:102:GLN:C	2.64	0.40
6:T:34:LEU:HD11	6:T:60:TYR:CZ	2.56	0.40
6:T:75:ILE:HD11	6:T:107:LEU:HG	2.02	0.40
6:T:380:GLU:H	6:T:380:GLU:CD	2.30	0.40
6:T:439:ILE:HD11	8:V:507:ASN:HA	2.03	0.40
13:d:21:LEU:CD2	13:d:72:ILE:HG12	2.51	0.40
18:Y:204:CYS:HB3	18:Y:226:HIS:HA	2.03	0.40
1:G:5:U:H2'	1:G:6:G:C8	2.56	0.40
2:P:61:A:OP1	5:S:12:ARG:NE	2.54	0.40
2:P:418:U:H2'	2:P:419:G:H8	1.85	0.40
6:T:141:PHE:CB	6:T:301:ARG:HH22	2.34	0.40
6:T:167:VAL:HG22	7:U:592:SER:OG	2.22	0.40
6:T:324:LYS:HB3	6:T:324:LYS:HE3	1.87	0.40
10:a:20:LEU:HD12	10:a:34:LEU:HB2	2.03	0.40
10:a:29:VAL:CG2	11:b:67:LEU:HB3	2.49	0.40
10:a:30:TYR:HD2	10:a:87:LEU:HD21	1.86	0.40
10:a:59:ASP:HA	10:a:62:ARG:HH21	1.86	0.40
15:f:79:LEU:HD22	15:f:80:TYR:HD2	1.86	0.40
18:Y:97:TYR:CE2	18:Y:101:LEU:HD11	2.57	0.40
18:Y:226:HIS:O	18:Y:230:VAL:HG23	2.22	0.40
2:P:6:U:H1'	18:Y:216:ARG:HH22	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:164:U:H2'	2:P:165:U:C6	2.56	0.40
2:P:290:U:O4	2:P:291:C:O2	2.40	0.40
2:P:409:A:H2'	2:P:410:G:H8	1.87	0.40
2:P:436:G:H2'	2:P:437:A:H8	1.86	0.40
2:P:457:G:H2'	2:P:458:U:C6	2.55	0.40
5:S:117:LEU:O	5:S:120:SER:OG	2.35	0.40
7:U:467:SER:HB3	7:U:470:PHE:HB3	2.03	0.40
7:U:582:GLN:HE21	7:U:606:ARG:HD2	1.87	0.40
11:b:93:ARG:HG2	11:b:94:GLN:HG3	2.03	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	
3	Q	182/300 (61%)	168 (92%)	12 (7%)	2 (1%)	11	38
4	R	180/231 (78%)	169 (94%)	10 (6%)	1 (1%)	21	50
5	S	125/298 (42%)	118 (94%)	6 (5%)	1 (1%)	16	44
6	T	537/544 (99%)	515 (96%)	22 (4%)	0	100	100
7	U	579/629 (92%)	544 (94%)	32 (6%)	3 (0%)	24	54
8	V	181/523 (35%)	165 (91%)	16 (9%)	0	100	100
9	W	223/492 (45%)	213 (96%)	10 (4%)	0	100	100
10	a	120/196 (61%)	113 (94%)	7 (6%)	0	100	100
11	b	117/146 (80%)	108 (92%)	9 (8%)	0	100	100
12	c	99/110 (90%)	94 (95%)	5 (5%)	0	100	100
13	d	90/101 (89%)	85 (94%)	5 (6%)	0	100	100
14	e	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
15	f	64/86 (74%)	61 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	g	73/77 (95%)	66 (90%)	7 (10%)	0	100	100
17	X	47/619 (8%)	47 (100%)	0	0	100	100
18	Y	190/261 (73%)	170 (90%)	18 (10%)	2 (1%)	11	38
19	x	47/49 (96%)	47 (100%)	0	0	100	100
All	All	2924/4756 (62%)	2750 (94%)	165 (6%)	9 (0%)	37	65

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	Q	98	PRO
4	R	169	ASN
3	Q	97	ASP
7	U	132	SER
18	Y	44	ILE
7	U	118	ARG
18	Y	45	CYS
5	S	101	VAL
7	U	135	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Q	84/265 (32%)	84 (100%)	0	100	100
4	R	165/214 (77%)	165 (100%)	0	100	100
5	S	114/273 (42%)	114 (100%)	0	100	100
6	T	509/519 (98%)	508 (100%)	1 (0%)	87	85
7	U	301/603 (50%)	295 (98%)	6 (2%)	48	65
8	V	154/451 (34%)	153 (99%)	1 (1%)	78	80
9	W	199/448 (44%)	198 (100%)	1 (0%)	81	81
10	a	113/176 (64%)	112 (99%)	1 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	b	106/129 (82%)	106 (100%)	0	100	100
12	c	82/103 (80%)	82 (100%)	0	100	100
13	d	79/89 (89%)	79 (100%)	0	100	100
14	e	52/83 (63%)	52 (100%)	0	100	100
15	f	51/77 (66%)	51 (100%)	0	100	100
16	g	56/66 (85%)	56 (100%)	0	100	100
17	X	45/567 (8%)	45 (100%)	0	100	100
18	Y	121/234 (52%)	117 (97%)	4 (3%)	33	57
All	All	2231/4297 (52%)	2217 (99%)	14 (1%)	76	80

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	T	126	LEU
7	U	450	GLN
7	U	461	ASN
7	U	508	ILE
7	U	529	ILE
7	U	570	GLU
7	U	580	ARG
8	V	307	PHE
9	W	237	ARG
10	a	82	LEU
18	Y	45	CYS
18	Y	72	HIS
18	Y	201	CYS
18	Y	204	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
3	Q	4	ASN
4	R	10	HIS
4	R	40	ASN
5	S	7	GLN
5	S	75	ASN
6	T	9	HIS
6	T	72	ASN

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Mol	Chain	Res	Type
6	T	123	GLN
6	T	125	GLN
6	T	217	ASN
6	T	245	GLN
6	T	300	GLN
6	T	332	ASN
6	T	400	ASN
6	T	437	GLN
6	T	459	ASN
7	U	289	HIS
7	U	344	ASN
7	U	383	ASN
7	U	450	GLN
7	U	488	ASN
7	U	519	HIS
7	U	555	ASN
7	U	573	HIS
7	U	582	GLN
8	V	301	GLN
8	V	404	GLN
8	V	442	GLN
9	W	50	ASN
9	W	80	GLN
9	W	81	GLN
9	W	154	ASN
9	W	166	ASN
9	W	200	GLN
10	a	8	HIS
11	b	12	ASN
11	b	14	GLN
11	b	21	ASN
12	c	52	HIS
12	c	66	ASN
12	c	86	ASN
13	d	68	GLN
14	e	24	GLN
14	e	86	ASN
16	g	20	ASN
18	Y	76	HIS
18	Y	226	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	G	21/22 (95%)	8 (38%)	1 (4%)
2	P	467/568 (82%)	104 (22%)	22 (4%)
All	All	488/590 (82%)	112 (22%)	23 (4%)

All (112) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	G	-6	A
1	G	-5	A
1	G	-4	A
1	G	-2	A
1	G	-1	A
1	G	0	A
1	G	11	A
1	G	12	A
2	P	9	C
2	P	10	U
2	P	12	A
2	P	17	A
2	P	40	A
2	P	41	C
2	P	53	G
2	P	54	C
2	P	55	G
2	P	56	C
2	P	61	A
2	P	62	A
2	P	63	U
2	P	64	A
2	P	65	G
2	P	67	A
2	P	74	C
2	P	75	G
2	P	78	A
2	P	79	A
2	P	80	G
2	P	86	A
2	P	87	U
2	P	113	G
2	P	114	U
2	P	117	U
2	P	130	C
2	P	139	A

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Mol	Chain	Res	Type
2	P	140	C
2	P	141	A
2	P	142	C
2	P	144	C
2	P	150	G
2	P	151	C
2	P	152	G
2	P	153	C
2	P	154	G
2	P	168	C
2	P	176	U
2	P	177	C
2	P	180	U
2	P	181	U
2	P	182	C
2	P	186	U
2	P	187	G
2	P	254	U
2	P	255	U
2	P	257	G
2	P	258	U
2	P	259	U
2	P	260	U
2	P	262	U
2	P	269	U
2	P	270	G
2	P	271	G
2	P	272	A
2	P	278	U
2	P	279	U
2	P	280	G
2	P	287	A
2	P	288	A
2	P	289	U
2	P	290	U
2	P	291	C
2	P	292	A
2	P	293	A
2	P	294	A
2	P	342	C
2	P	343	A
2	P	344	U

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Mol	Chain	Res	Type
2	P	350	U
2	P	351	U
2	P	352	G
2	P	369	G
2	P	370	U
2	P	371	G
2	P	372	C
2	P	373	C
2	P	376	U
2	P	377	U
2	P	378	U
2	P	383	U
2	P	384	U
2	P	385	U
2	P	386	G
2	P	416	G
2	P	417	A
2	P	444	G
2	P	445	G
2	P	447	C
2	P	451	A
2	P	452	U
2	P	540	G
2	P	542	U
2	P	545	A
2	P	551	U
2	P	555	U
2	P	559	G
2	P	560	A
2	P	561	U
2	P	562	U
2	P	563	U
2	P	564	A
2	P	565	U

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	G	-3	A
2	P	9	C
2	P	11	U
2	P	63	U

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Mol	Chain	Res	Type
2	P	64	A
2	P	66	U
2	P	86	A
2	P	112	A
2	P	113	G
2	P	152	G
2	P	175	U
2	P	186	U
2	P	258	U
2	P	261	C
2	P	268	C
2	P	277	U
2	P	279	U
2	P	369	G
2	P	370	U
2	P	376	U
2	P	377	U
2	P	383	U
2	P	564	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

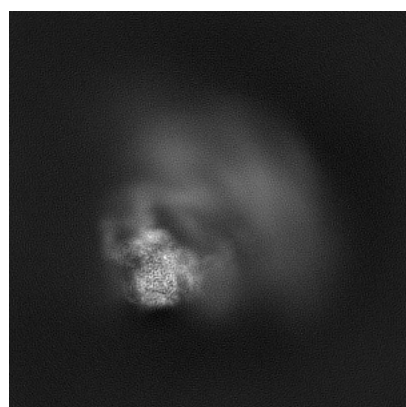
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6973. These allow visual inspection of the internal detail of the map and identification of artifacts.

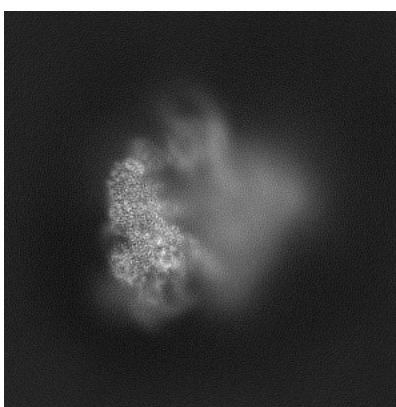
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

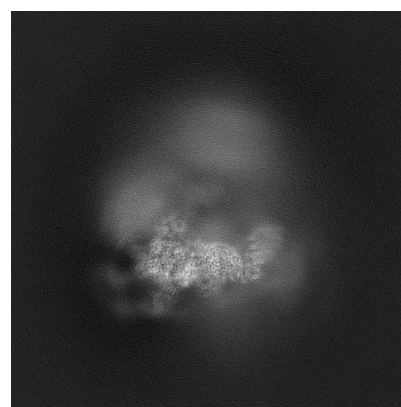
6.1.1 Primary map



X



Y

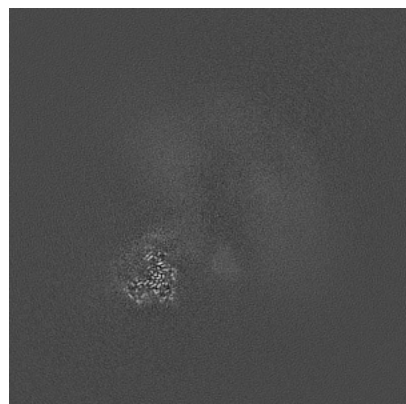


Z

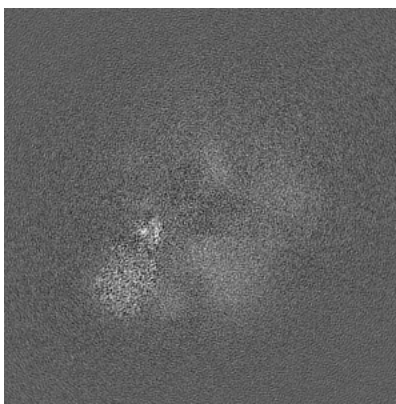
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

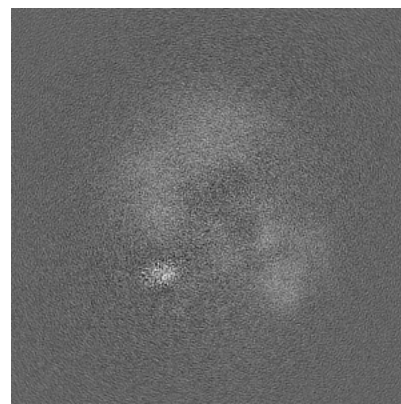
6.2.1 Primary map



X Index: 200



Y Index: 200

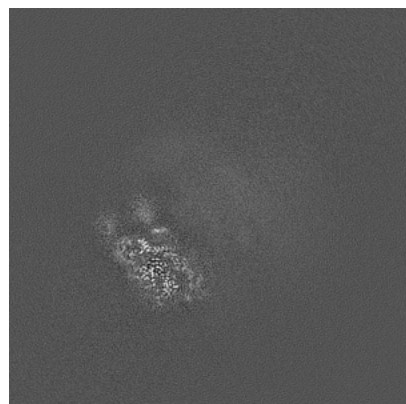


Z Index: 200

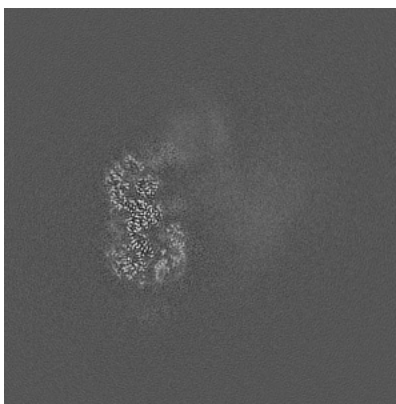
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

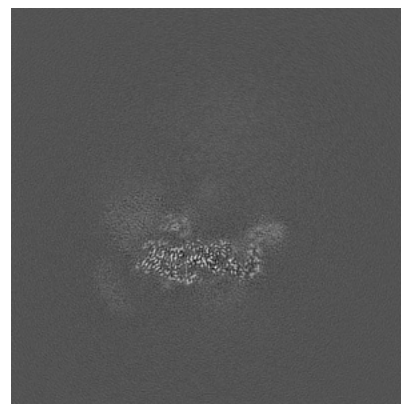
6.3.1 Primary map



X Index: 156



Y Index: 149

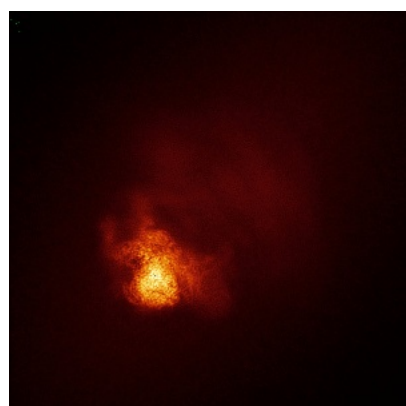


Z Index: 132

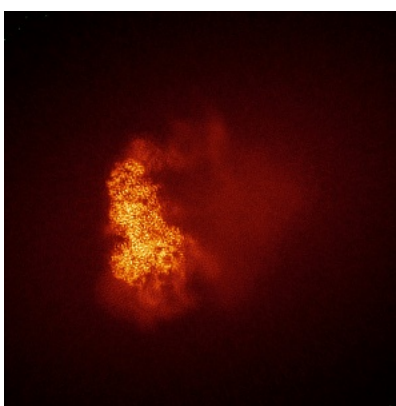
The images above show the largest variance slices of the map in three orthogonal directions.

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

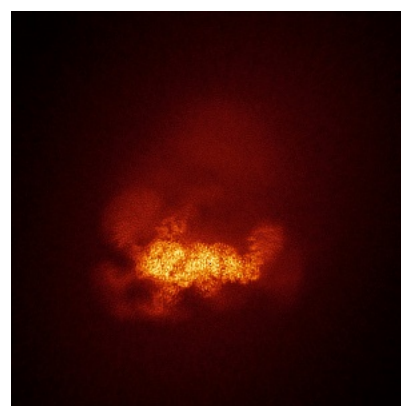
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

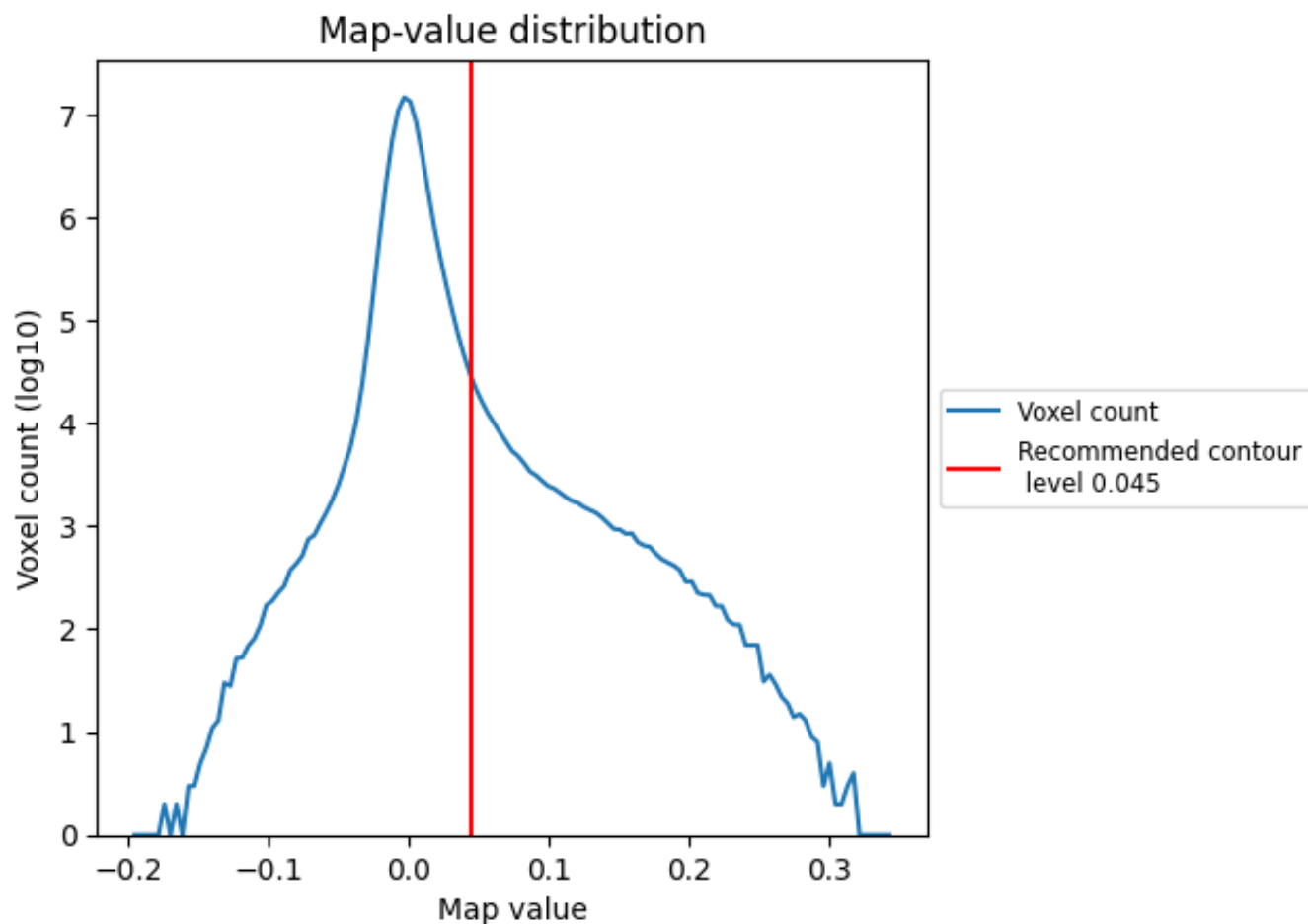
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

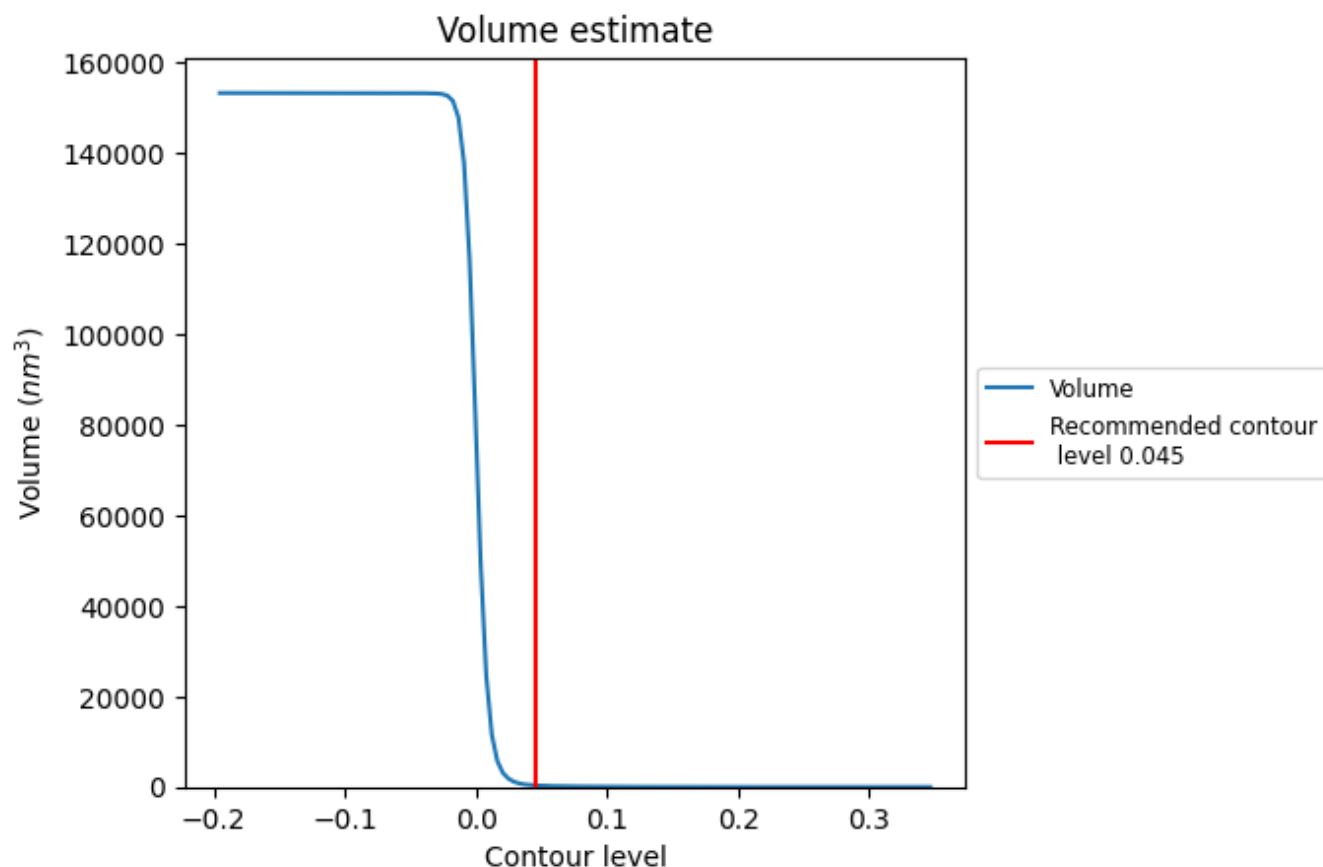
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

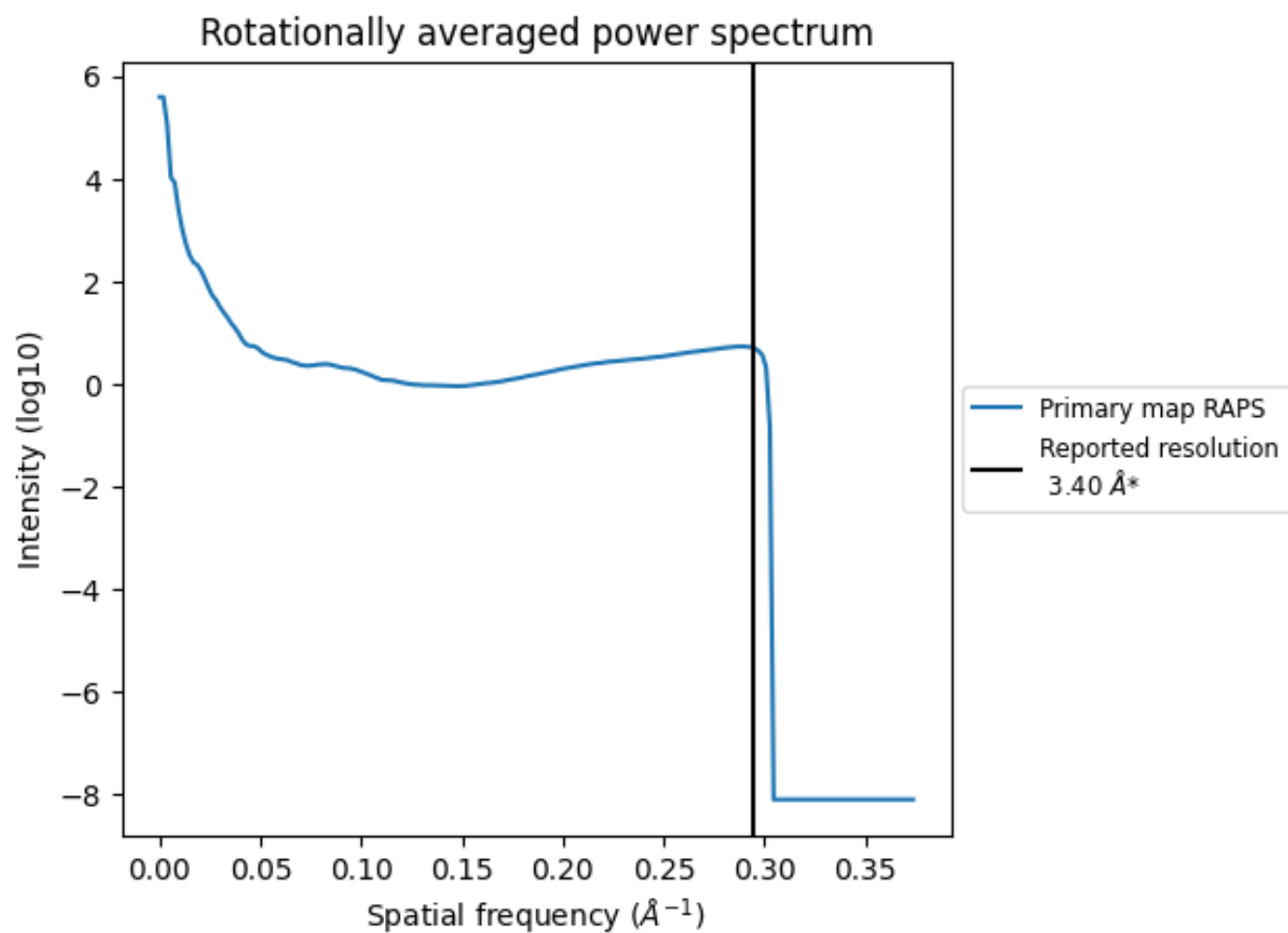
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 352 nm³; this corresponds to an approximate mass of 318 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

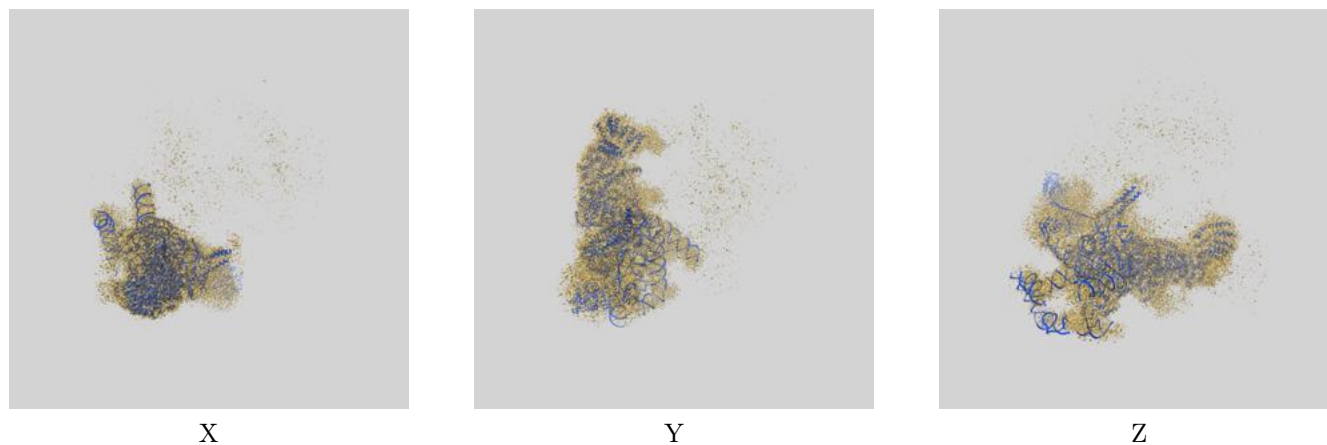
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

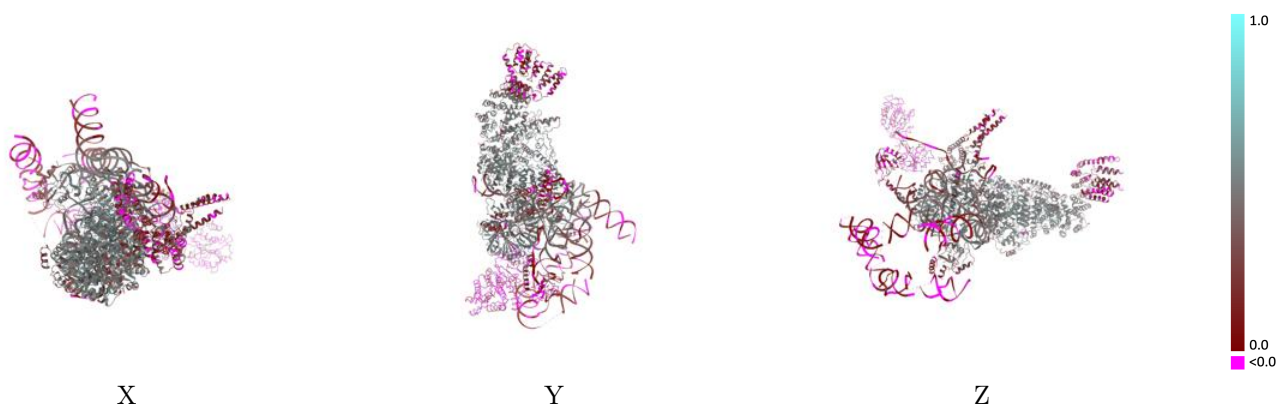
This section contains information regarding the fit between EMDB map EMD-6973 and PDB model 5ZWN. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



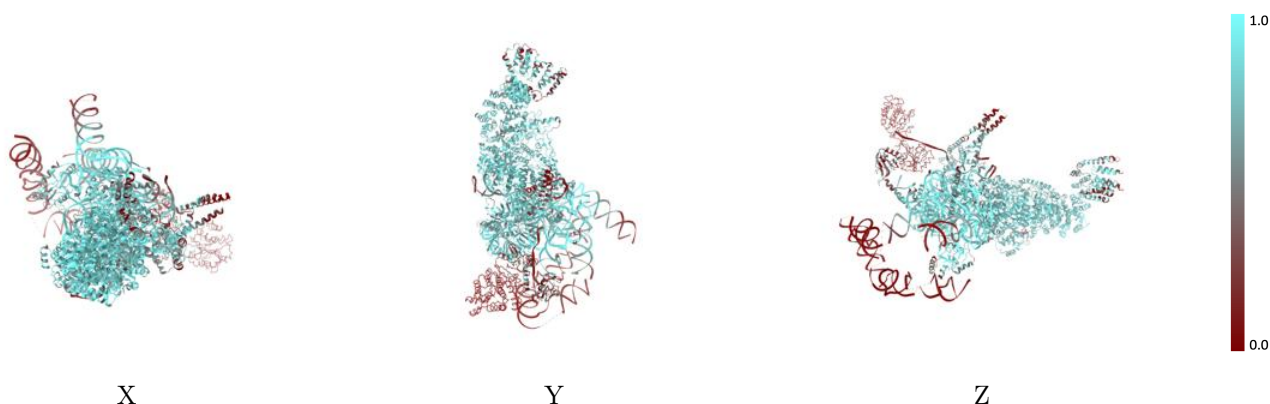
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



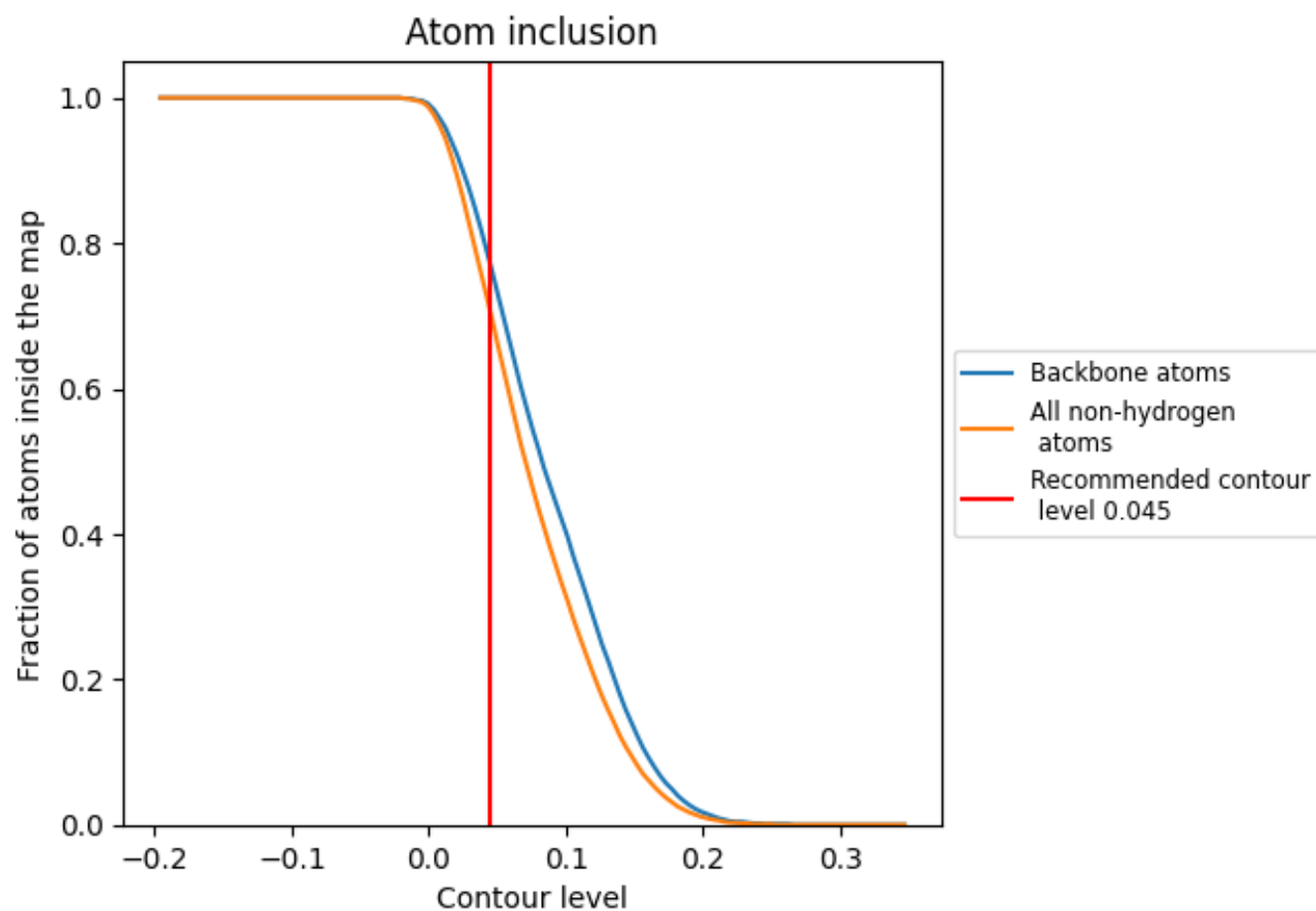
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 70% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7050	 0.3560
G	 0.3920	 0.1480
P	 0.5770	 0.2450
Q	 0.5660	 0.2580
R	 0.7850	 0.4510
S	 0.6590	 0.2830
T	 0.8670	 0.5010
U	 0.7550	 0.3460
V	 0.8010	 0.4510
W	 0.8170	 0.4520
X	 0.8180	 0.4560
Y	 0.6070	 0.2700
a	 0.7800	 0.4500
b	 0.8010	 0.4510
c	 0.8840	 0.4770
d	 0.8570	 0.5130
e	 0.8780	 0.4940
f	 0.9150	 0.5100
g	 0.8290	 0.4790
x	 0.5920	 0.2520
y	 0.0380	 -0.0240

