



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 09:59 PM EDT

PDB ID : 7UNR / pdb_00007unr
EMDB ID : EMD-26630
Title : Pseudomonas aeruginosa 70S ribosome initiation complex bound to compact IF2-GDP (composite structure I-A)
Authors : Basu, R.S.; Sherman, M.B.; Gagnon, M.G.
Deposited on : 2022-04-11
Resolution : 2.90 Å (reported)
Based on initial models : 6SPG, 3JCJ

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:

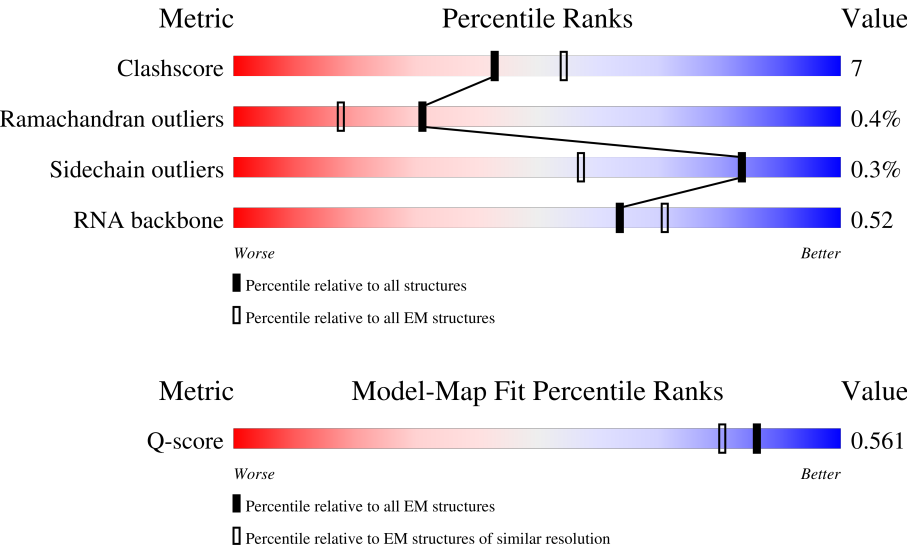
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.90 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	13054 (2.40 - 3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	1536	16% 58% 36% 6%
2	b	246	72% 20% 9%
3	c	228	71% 20% 9%

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Mol	Chain	Length	Quality of chain
4	d	206	
5	e	166	
6	f	139	
7	g	156	
8	h	130	
9	i	130	
10	j	103	
11	k	129	
12	l	123	
13	m	118	
14	n	101	
15	o	89	
16	p	83	
17	q	88	
18	r	76	
19	s	91	
20	t	91	
21	u	71	
22	v	77	
23	w	24	
24	x	840	
25	A	2891	
26	B	120	
27	C	273	
28	D	211	

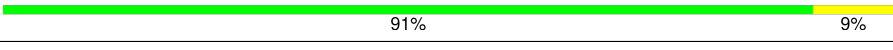
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Mol	Chain	Length	Quality of chain
29	E	200	
30	F	179	
31	G	177	
32	H	148	
33	I	166	
34	J	143	
35	L	142	
36	M	122	
37	N	144	
38	O	137	
39	P	129	
40	Q	116	
41	R	116	
42	S	118	
43	T	103	
44	U	110	
45	V	99	
46	W	104	
47	X	204	
48	Y	85	
49	Z	78	
50	1	63	
51	2	58	
52	3	71	
53	4	60	

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Mol	Chain	Length	Quality of chain
54	5	51	 92% 8%
55	6	44	 91% 9%
56	7	64	 83% 16%
57	8	38	 89% 11%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 149327 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 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1522	Total	C	N	O	P	0	0
			32675	14581	5999	10574	1521		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	224	Total	C	N	O	S	0	0
			1751	1104	320	317	10		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	208	Total	C	N	O	S	0	0
			1656	1047	313	291	5		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	205	Total	C	N	O	S	0	0
			1613	996	313	299	5		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	154	Total	C	N	O	S	0	0
			1134	711	210	207	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	106	Total	C	N	O	S	0	0
			857	534	159	158	6		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	152	Total	C	N	O	S	0	0
			1187	743	231	208	5		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	129	Total	C	N	O	S	0	0
			982	618	173	185	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	127	Total	C	N	O	S	0	0
			1010	625	203	181	1		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	99	Total	C	N	O	S	0	0
			793	496	150	146	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	119	Total	C	N	O	S	0	0
			879	545	171	161	2		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	122	Total	C	N	O	S	0	0
			959	588	198	169	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	114	Total	C	N	O	S	0	0
			892	544	182	162	4		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	100	Total	C	N	O	S	0	0
			800	494	167	136	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			703	434	139	129	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	81	Total	C	N	O	S	0	0
			636	397	125	113	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			645	404	124	115	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	62	Total	C	N	O	0	0
			480	307	85	88		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	83	Total	C	N	O	S	0	0
			663	422	129	109	3		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	87	Total	C	N	O	S	0	0
			671	414	138	117	2		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	62	Total	C	N	O	S	0	0
			506	316	103	86	1		

- Molecule 22 is a RNA chain called P-site initiator tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	v	76	Total	C	N	O	P	S	0	0
			1625	725	294	529	76	1		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	w	6	Total	C	N	O	P	0	0
			131	59	27	39	6		

- Molecule 24 is a protein called Translation initiation factor IF-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	x	486	Total	C	N	O	S	0	0
			3500	2195	643	649	13		

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	2884	Total	C	N	O	P	0	0
			61891	27621	11346	20041	2883		

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	117	Total	C	N	O	P	0	0
			2495	1114	448	816	117		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	272	Total	C	N	O	S	0	0
			2072	1276	426	364	6		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	D	211	Total	C	N	O	S	0	0
			1588	981	304	297	6		

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	E	200	Total	C	N	O	S	0	0
			1521	955	283	280	3		

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	176	Total	C	N	O	S	0	0
			1407	899	249	255	4		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	175	Total	C	N	O	S	0	0
			1323	834	244	243	2		

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	148	Total	C	N	O	S	0	0
			964	598	178	187	1		

- Molecule 33 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	I	117	Total	C	N	O	0	0
			668	414	128	126		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	J	134	Total	C	N	O	0	0
			718	432	141	145		

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L	142	Total	C	N	O	S	0	0
			1130	718	206	202	4		

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	N	144	Total	C	N	O	S	0	0
			1066	654	215	194	3		

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	O	137	Total	C	N	O	S	0	0
			1085	689	211	181	4		

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	P	120	Total	C	N	O	S	0	0
			959	600	192	162	5		

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Q	115	Total	C	N	O	S	0	0
			881	544	174	161	2		

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	114	Total	C	N	O	S	0	0
			902	568	171	162	1		

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	S	117	Total	C	N	O	0	0
			936	592	196	148		

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	T	103	Total	C	N	O	S	0	0
			822	521	156	143	2		

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	U	110	Total	C	N	O	S	0	0
			833	515	161	153	4		

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V	94	Total	C	N	O	S	0	0
			739	472	134	132	1		

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	W	103	Total	C	N	O	S	0	0
			786	494	150	141	1		

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	X	190	Total	C	N	O	S	0	0
			1445	915	262	265	3		

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	Y	76	Total	C	N	O	0	0
			575	364	111	100		

- Molecule 49 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Z	77	Total	C	N	O	S	0	0
			630	391	134	103	2		

- Molecule 50 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	61	Total	C	N	O	S	0	0
			490	301	96	91	2		

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2	57	Total	C	N	O	S	0	0
			445	277	87	79	2		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	47	Total	C	N	O	S	0	0
			356	222	60	68	6		

- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	55	Total	C	N	O	S	0	0
			440	264	93	82	1		

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	51	Total	C	N	O	S	0	0
			426	272	78	75	1		

- Molecule 55 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	6	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 56 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	7	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	8	38	Total	C	N	O	S	0	0
			307	186	69	48	4		

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

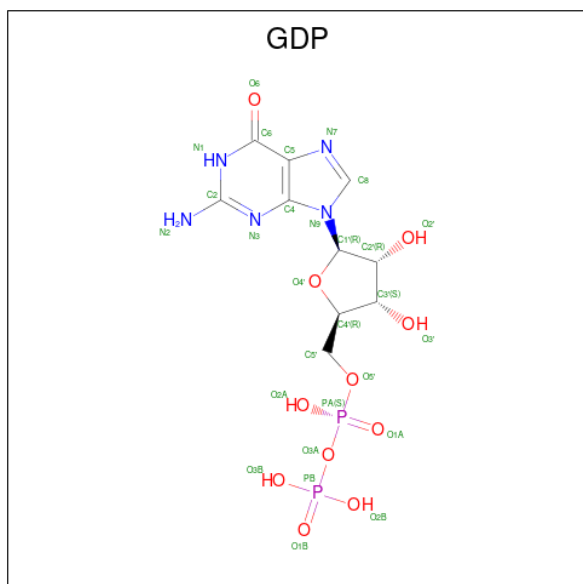
Mol	Chain	Residues	Atoms		AltConf
58	a	136	Total	Mg	0
			136	136	
58	t	1	Total	Mg	0
			1	1	
58	v	2	Total	Mg	0
			2	2	
58	A	471	Total	Mg	0
			471	471	
58	B	7	Total	Mg	0
			7	7	
58	C	2	Total	Mg	0
			2	2	
58	E	3	Total	Mg	0
			3	3	
58	N	1	Total	Mg	0
			1	1	
58	P	1	Total	Mg	0
			1	1	
58	S	2	Total	Mg	0
			2	2	
58	Y	1	Total	Mg	0
			1	1	
58	2	1	Total	Mg	0
			1	1	
58	4	1	Total	Mg	0
			1	1	
58	7	1	Total	Mg	0
			1	1	

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
59	v	1	10	6	1	2	1	0

- Molecule 60 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
60	x	1	28	10	5	11	2	0

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
61	3	1	Total 1	Zn 1	0
61	8	1	Total 1	Zn 1	0

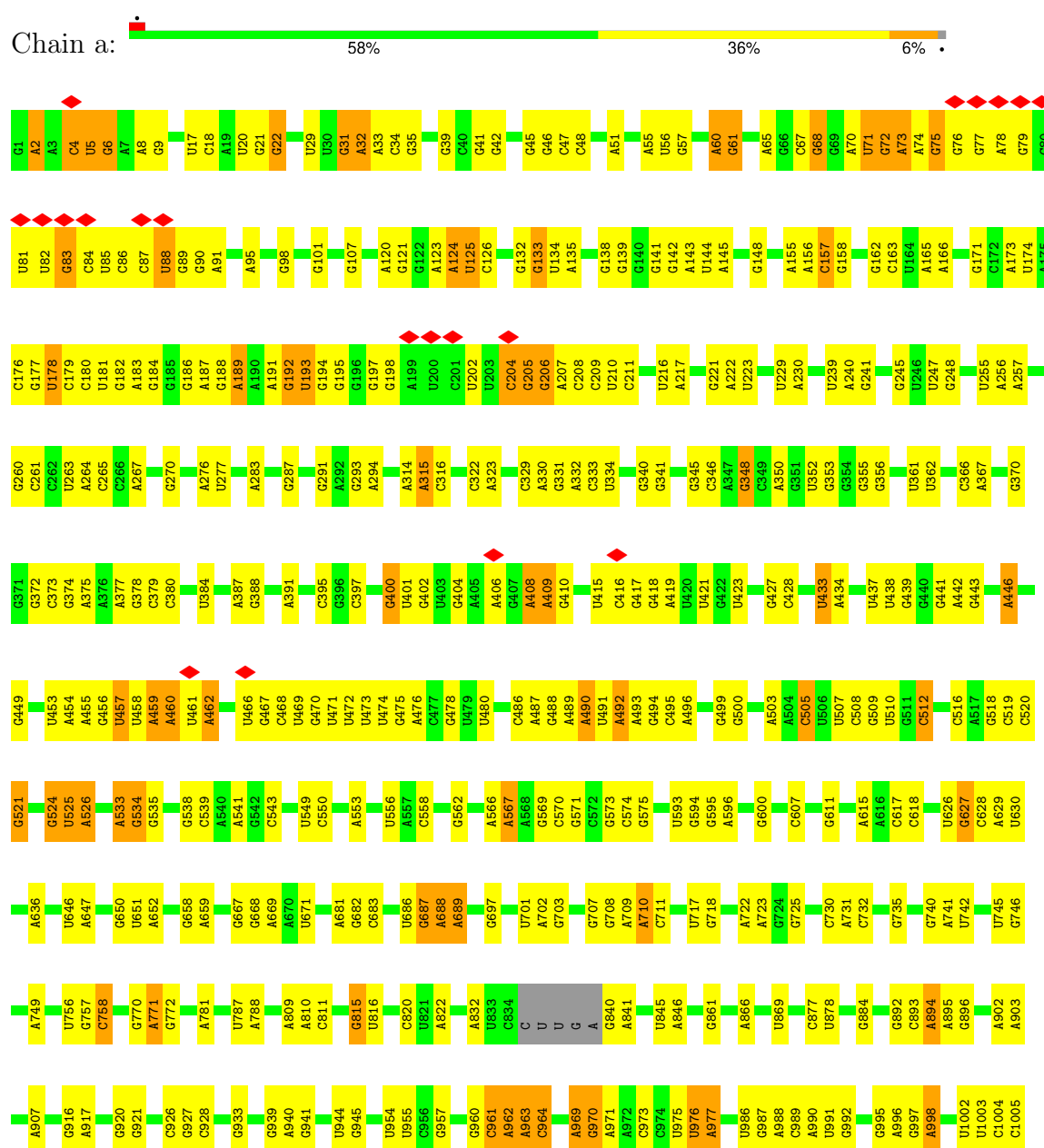
- Molecule 62 is water.

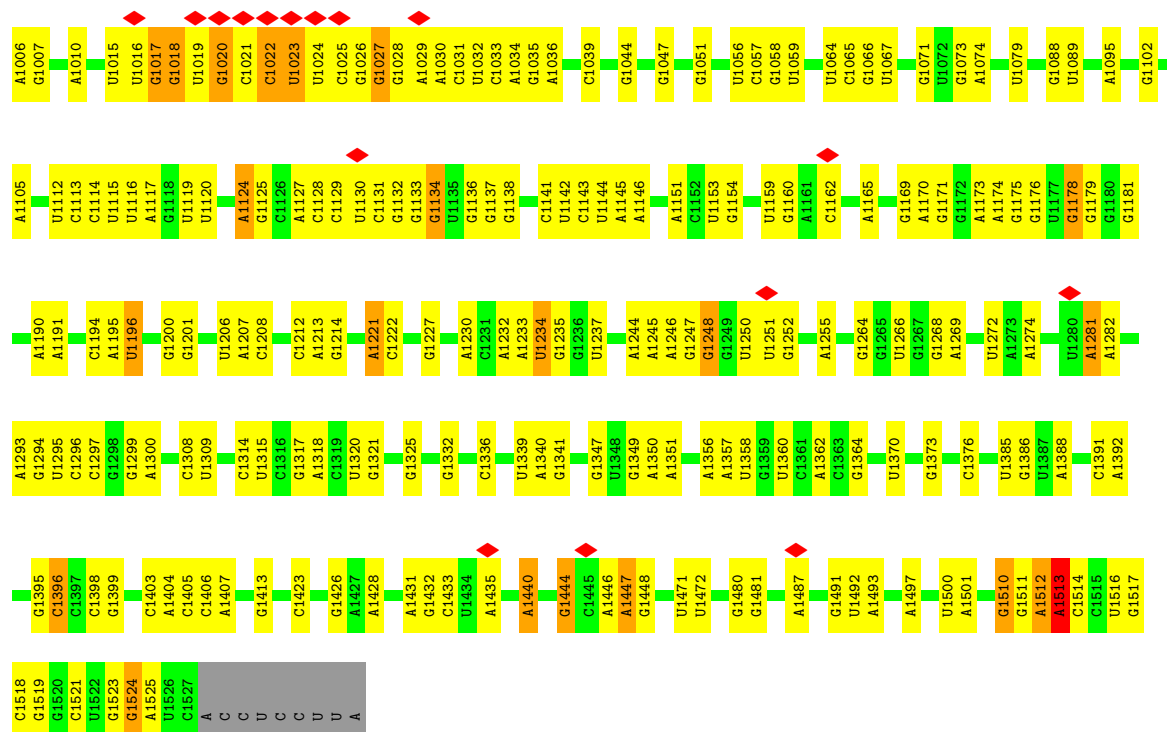
Mol	Chain	Residues	Atoms		AltConf
62	a	27	Total 27	O 27	0
62	w	1	Total 1	O 1	0
62	A	166	Total 166	O 166	0
62	C	1	Total 1	O 1	0
62	E	1	Total 1	O 1	0
62	P	1	Total 1	O 1	0
62	4	2	Total 2	O 2	0
62	6	1	Total 1	O 1	0

3 Residue-property plots

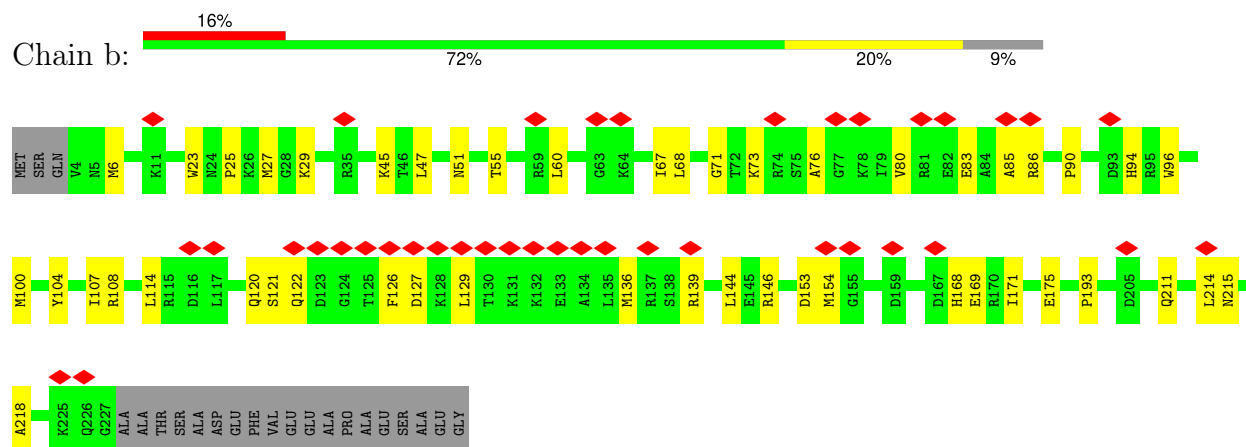
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S Ribosomal RNA

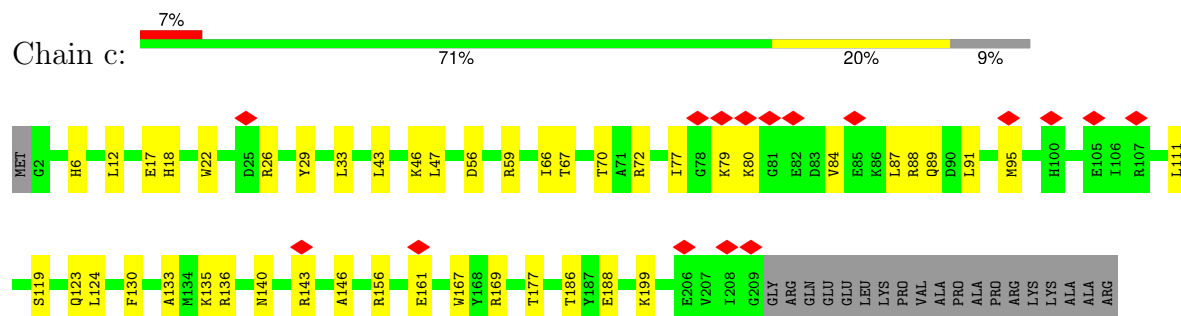




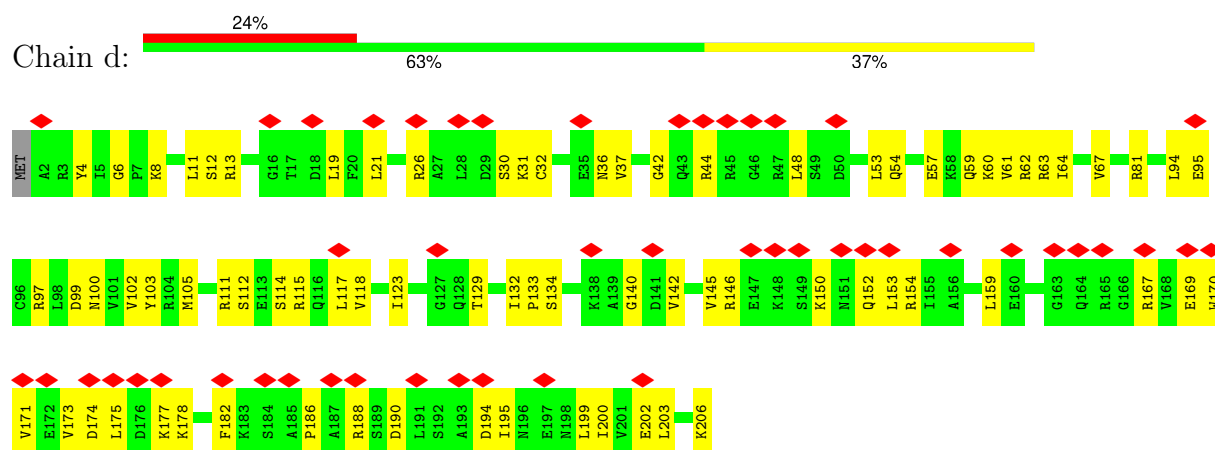
• Molecule 2: 30S ribosomal protein S2



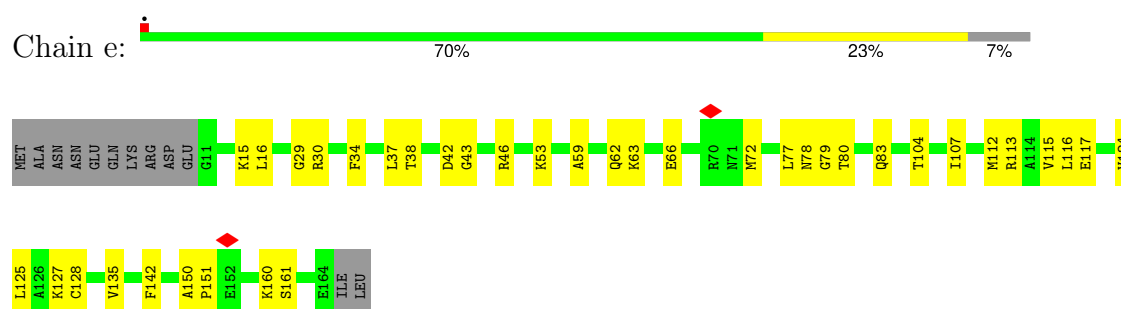
• Molecule 3: 30S ribosomal protein S3



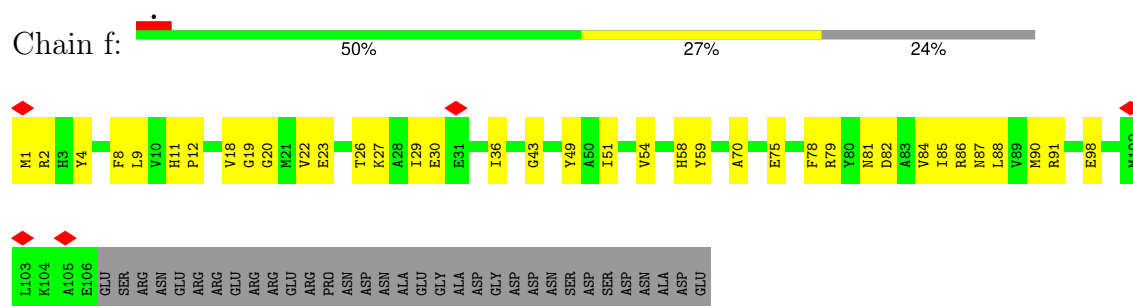
• Molecule 4: 30S ribosomal protein S4



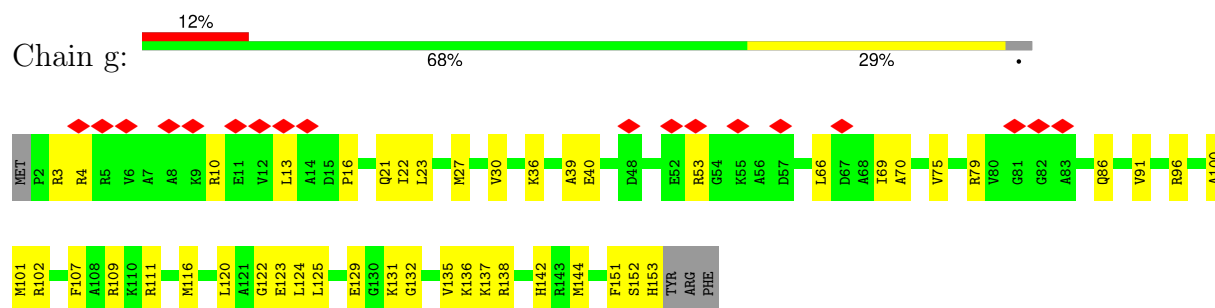
• Molecule 5: 30S ribosomal protein S5



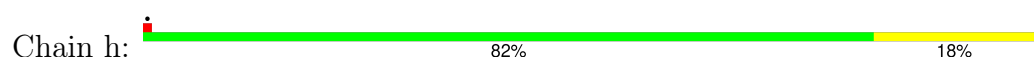
• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7

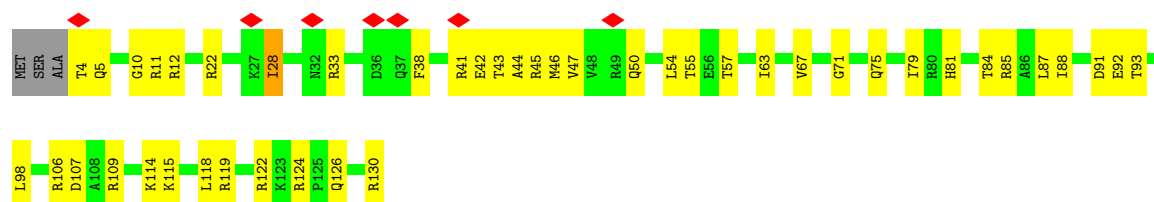


• Molecule 8: 30S ribosomal protein S8

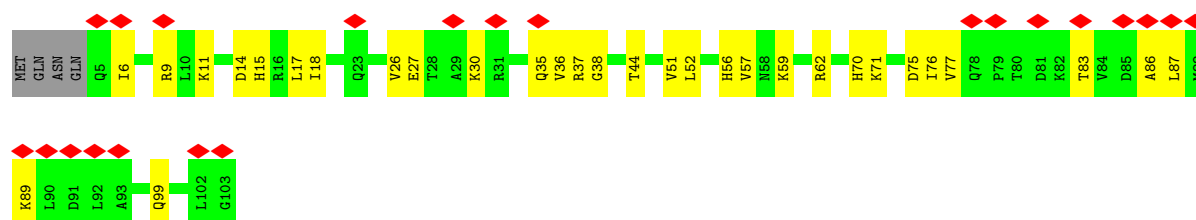




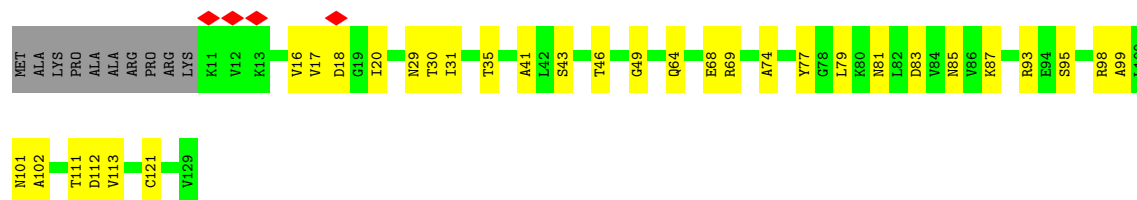
- Molecule 9: 30S ribosomal protein S9



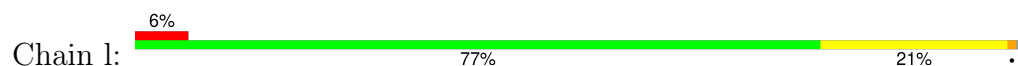
- Molecule 10: 30S ribosomal protein S10



- Molecule 11: 30S ribosomal protein S11

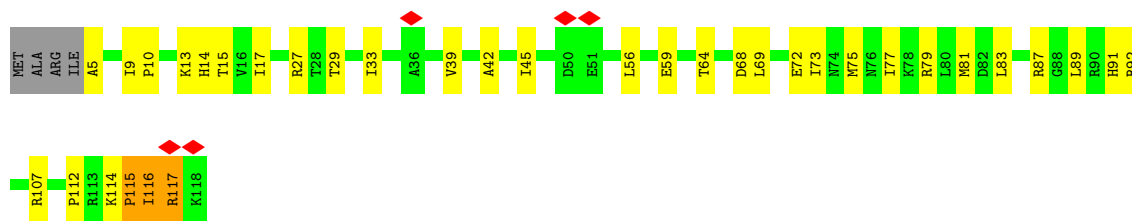


- Molecule 12: 30S ribosomal protein S12

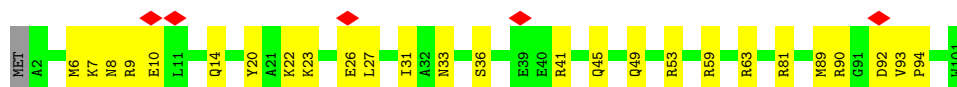
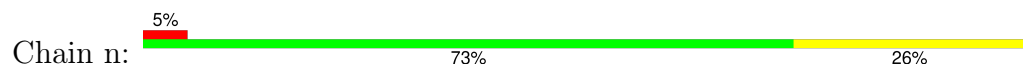


- Molecule 13: 30S ribosomal protein S13

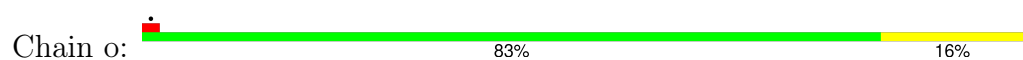




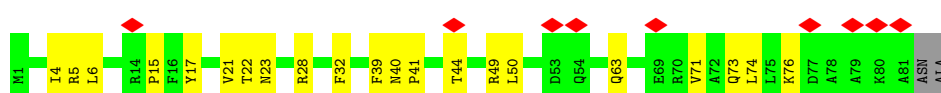
- Molecule 14: 30S ribosomal protein S14



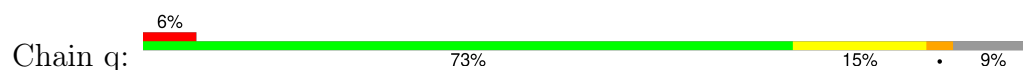
- Molecule 15: 30S ribosomal protein S15



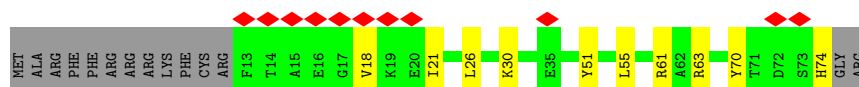
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17

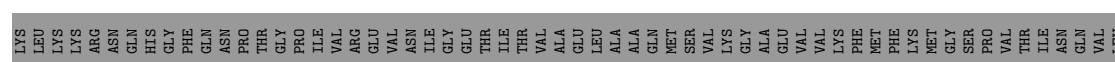


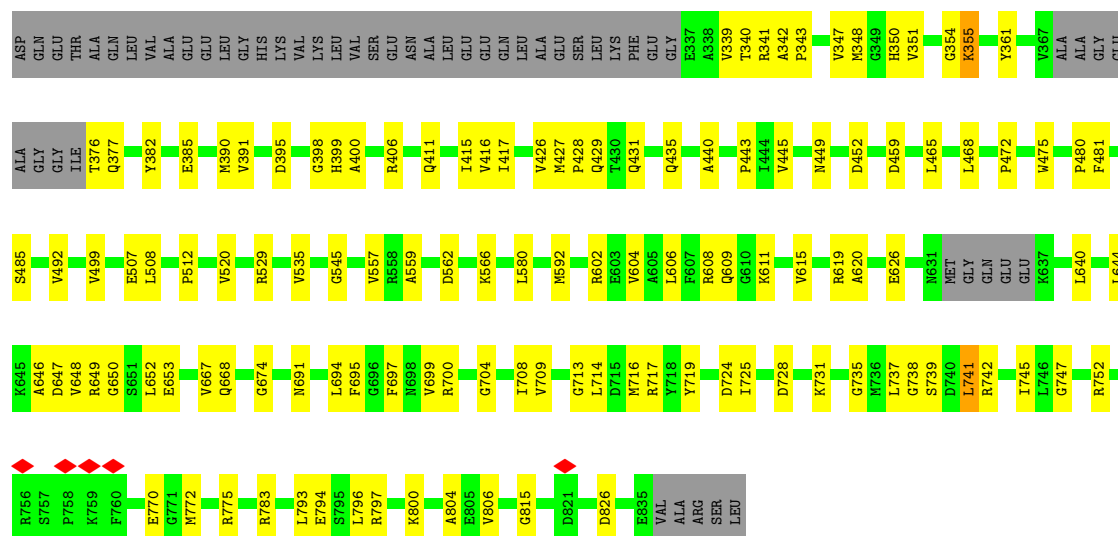
- Molecule 18: 30S ribosomal protein S18



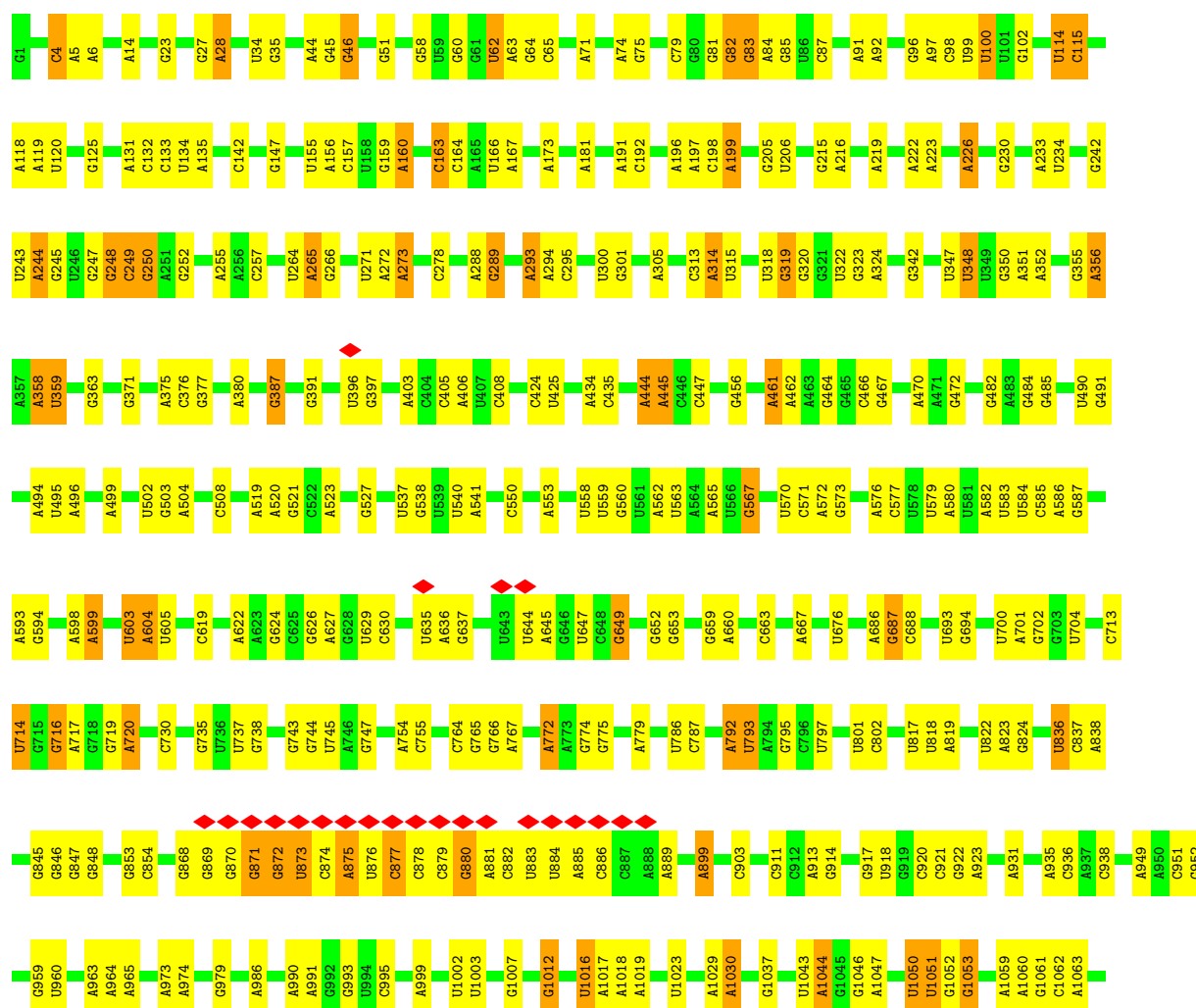
- Molecule 19: 30S ribosomal protein S19



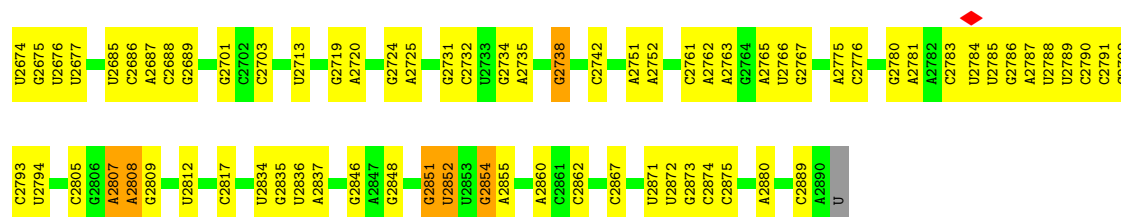




• Molecule 25: 23S Ribosomal RNA

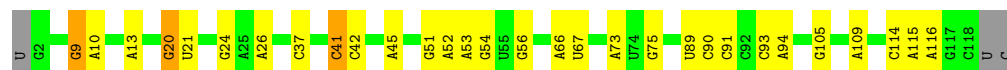






• Molecule 26: 5S Ribosomal RNA

Chain B: 72% 22%



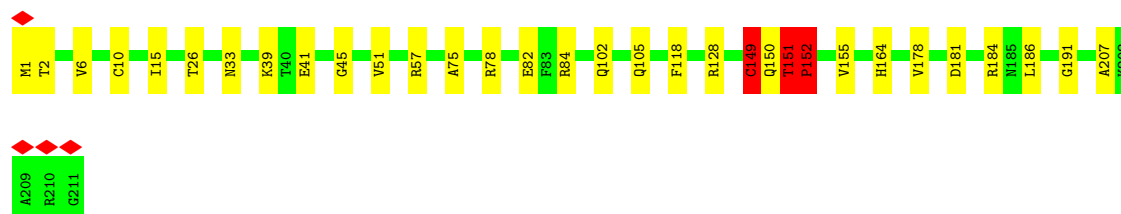
• Molecule 27: 50S ribosomal protein L2

Chain C: 90% 10%



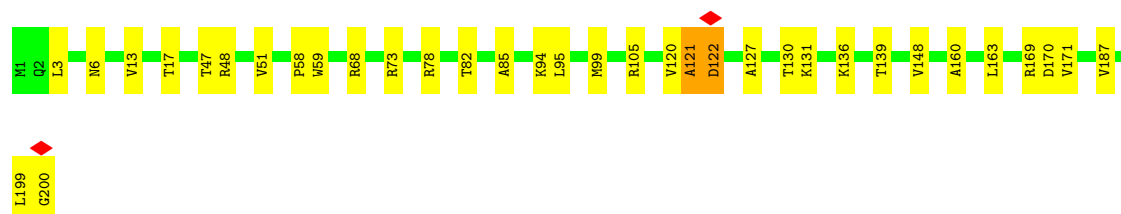
• Molecule 28: 50S ribosomal protein L3

Chain D: 85% 14%



• Molecule 29: 50S ribosomal protein L4

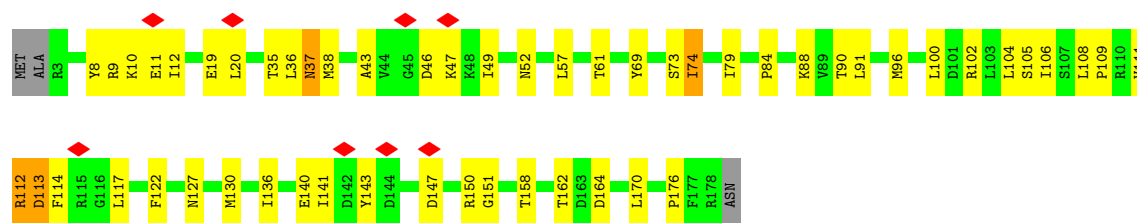
Chain E: 82% 16%



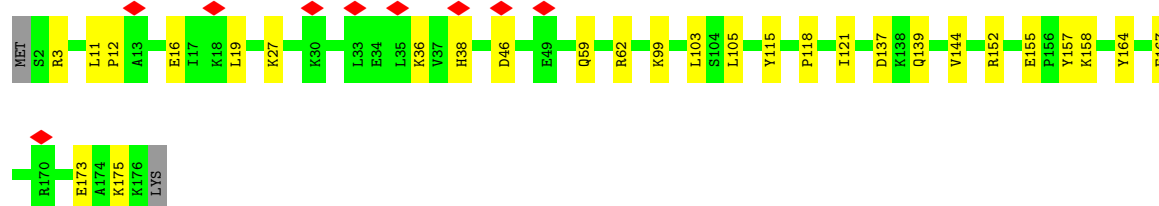
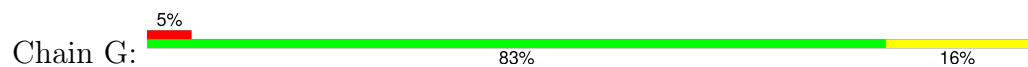
• Molecule 30: 50S ribosomal protein L5

Chain F: 68% 28%

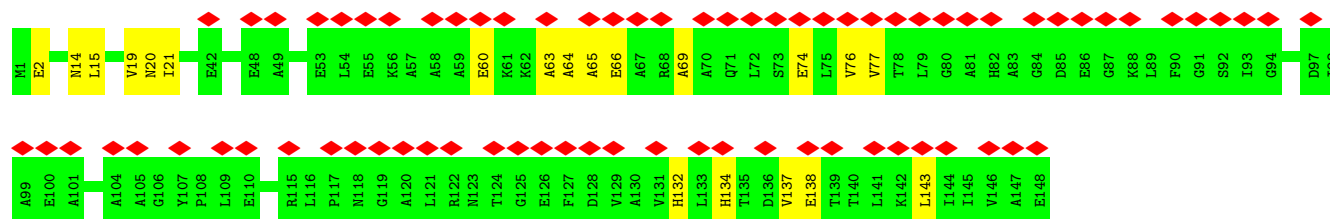
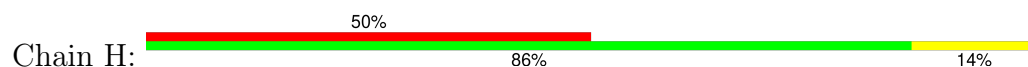




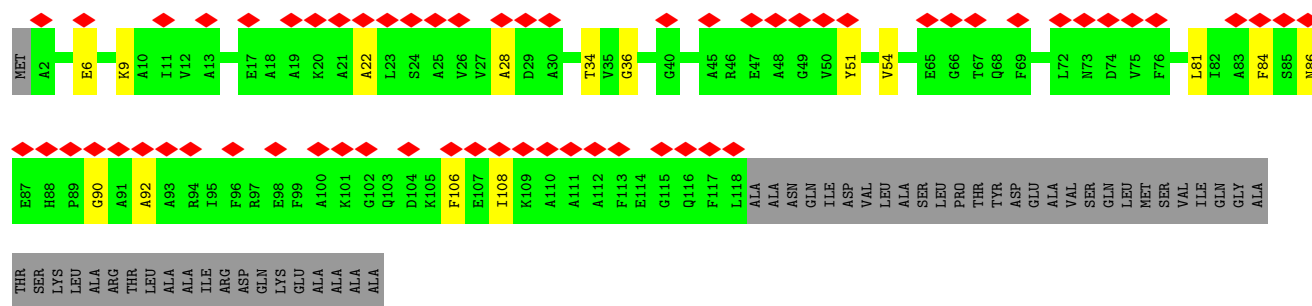
• Molecule 31: 50S ribosomal protein L6



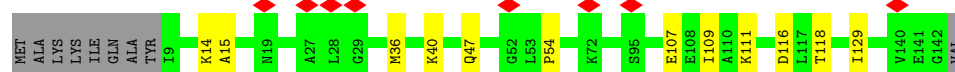
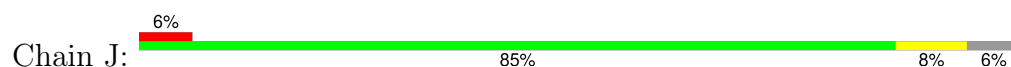
• Molecule 32: 50S ribosomal protein L9



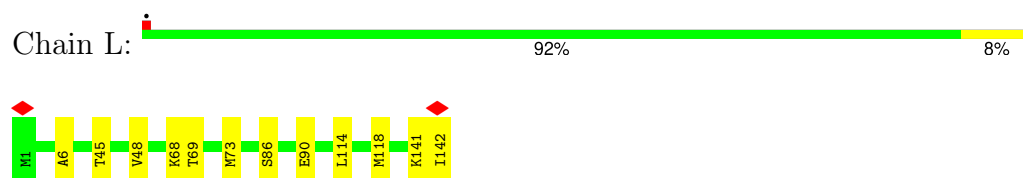
• Molecule 33: 50S ribosomal protein L10



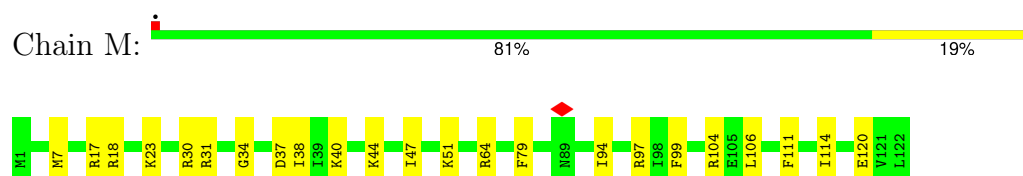
• Molecule 34: 50S ribosomal protein L11



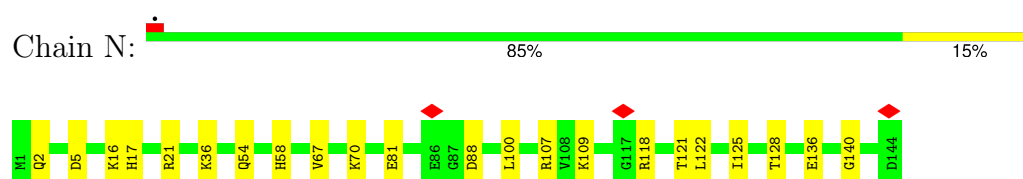
- Molecule 35: 50S ribosomal protein L13



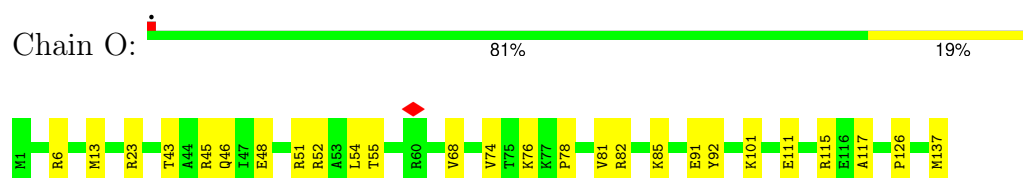
- Molecule 36: 50S ribosomal protein L14



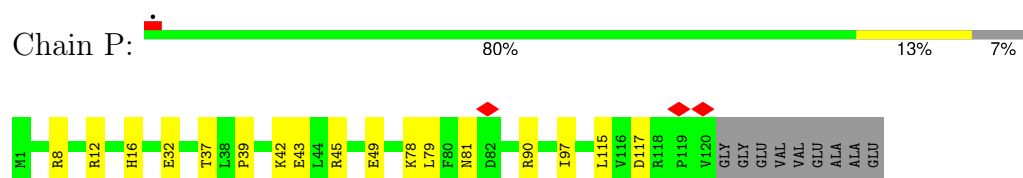
- Molecule 37: 50S ribosomal protein L15



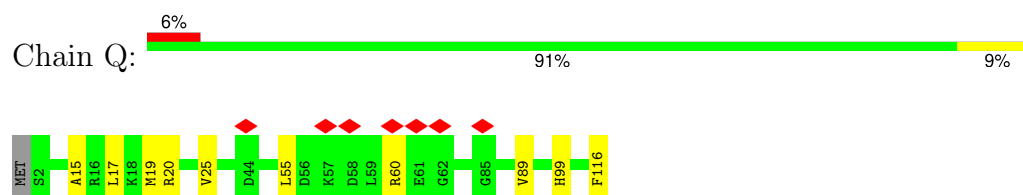
- Molecule 38: 50S ribosomal protein L16



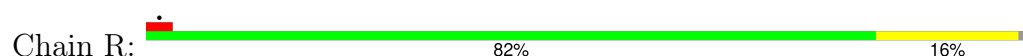
- Molecule 39: 50S ribosomal protein L17

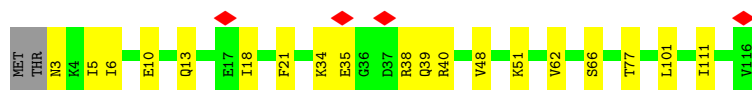


- Molecule 40: 50S ribosomal protein L18



- Molecule 41: 50S ribosomal protein L19

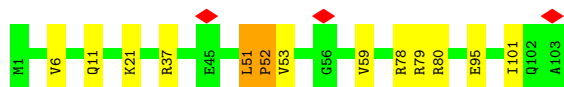




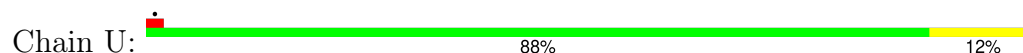
- Molecule 42: 50S ribosomal protein L20



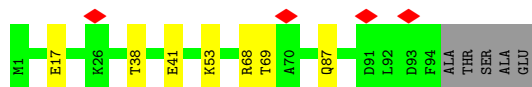
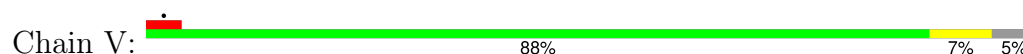
- Molecule 43: 50S ribosomal protein L21



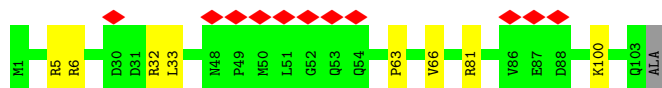
- Molecule 44: 50S ribosomal protein L22



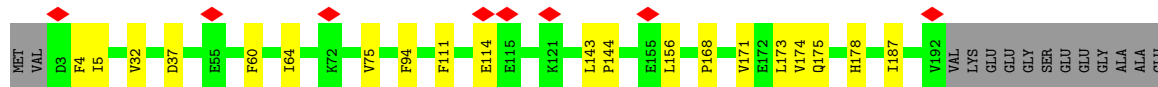
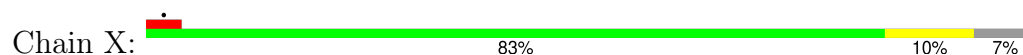
- Molecule 45: 50S ribosomal protein L23



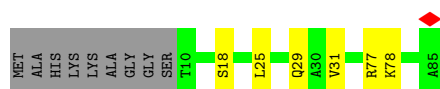
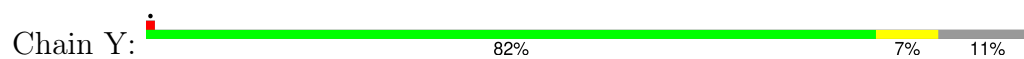
- Molecule 46: 50S ribosomal protein L24



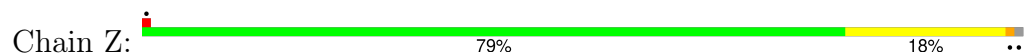
- Molecule 47: 50S ribosomal protein L25



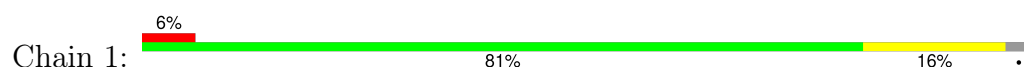
- Molecule 48: 50S ribosomal protein L27



- Molecule 49: 50S ribosomal protein L28



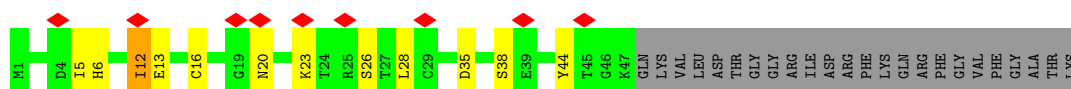
- Molecule 50: 50S ribosomal protein L29



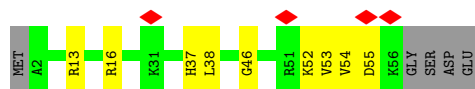
- Molecule 51: 50S ribosomal protein L30



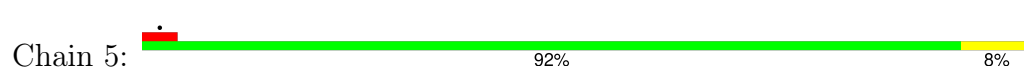
- Molecule 52: 50S ribosomal protein L31



- Molecule 53: 50S ribosomal protein L32

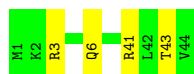


- Molecule 54: 50S ribosomal protein L33



- Molecule 55: 50S ribosomal protein L34

Chain 6:  91% 9%



- Molecule 56: 50S ribosomal protein L35

Chain 7:  83% 16%



- Molecule 57: 50S ribosomal protein L36

Chain 8:  89% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21480	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	31	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	29.428	Depositor
Minimum map value	-17.494	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	1.011	Depositor
Recommended contour level	3.3	Depositor
Map size (Å)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, 2MG, 1MG, 5MC, 4SU, 6MZ, 2MA, 4OC, OMU, OMC, MG, UR3, 5MU, FME, OMG, MA6, ZN, PSU, 7MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.17	0/36354	0.29	0/56707
2	b	0.15	0/1779	0.36	0/2392
3	c	0.14	0/1685	0.33	0/2270
4	d	0.14	0/1632	0.34	0/2184
5	e	0.18	0/1148	0.45	0/1544
6	f	0.20	0/871	0.51	0/1172
7	g	0.14	0/1204	0.35	0/1609
8	h	0.25	0/993	0.41	0/1332
9	i	0.17	0/1022	0.39	0/1365
10	j	0.15	0/803	0.40	0/1083
11	k	0.16	0/895	0.33	0/1209
12	l	0.19	0/973	0.41	0/1303
13	m	0.23	0/901	0.50	1/1209 (0.1%)
14	n	0.18	0/812	0.42	0/1082
15	o	0.15	0/710	0.25	0/947
16	p	0.12	0/647	0.37	0/870
17	q	0.29	0/653	0.52	0/881
18	r	0.19	0/488	0.38	0/660
19	s	0.14	0/678	0.34	0/912
20	t	0.18	0/678	0.37	0/904
21	u	0.13	0/513	0.28	0/680
22	v	0.25	0/1725	0.44	3/2689 (0.1%)
23	w	0.15	0/147	0.21	0/227
24	x	0.24	0/3541	0.45	0/4804
25	A	0.21	0/68977	0.32	3/107590 (0.0%)
26	B	0.19	0/2789	0.29	0/4345
27	C	0.20	0/2108	0.35	0/2831
28	D	0.28	0/1611	0.63	6/2167 (0.3%)
29	E	0.18	0/1541	0.36	2/2075 (0.1%)
30	F	0.18	0/1428	0.49	2/1918 (0.1%)
31	G	0.15	0/1341	0.31	0/1805

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
32	H	0.11	0/971	0.33	1/1324 (0.1%)
33	I	0.10	0/672	0.32	0/926
34	J	0.14	0/720	0.40	0/995
35	L	0.18	0/1156	0.33	0/1559
36	M	0.19	0/947	0.34	0/1268
37	N	0.18	0/1078	0.34	0/1436
38	O	0.18	0/1105	0.34	0/1476
39	P	0.18	0/975	0.30	0/1304
40	Q	0.14	0/888	0.28	0/1183
41	R	0.18	0/911	0.27	0/1218
42	S	0.19	0/946	0.28	0/1257
43	T	0.18	0/835	0.31	0/1117
44	U	0.17	0/837	0.27	0/1114
45	V	0.17	0/749	0.30	0/1002
46	W	0.15	0/794	0.31	0/1062
47	X	0.16	0/1468	0.32	0/1987
48	Y	0.18	0/583	0.31	0/774
49	Z	0.24	0/641	0.36	0/854
50	1	0.15	0/491	0.28	0/654
51	2	0.15	0/449	0.29	0/602
52	3	0.14	0/364	0.41	0/494
53	4	0.19	0/446	0.39	0/594
54	5	0.15	0/433	0.27	0/576
55	6	0.21	0/368	0.36	0/482
56	7	0.18	0/511	0.26	0/668
57	8	0.18	0/308	0.28	0/404
All	All	0.20	0/160293	0.33	18/239096 (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
28	D	0	1
30	F	0	2
43	T	0	1
All	All	0	4

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	v	75	C	OP1-P-O3'	-11.33	74.01	108.00
28	D	152	PRO	CA-N-CD	-11.16	96.38	112.00
28	D	152	PRO	CB-CA-C	9.61	127.42	111.56
25	A	1094	C	OP1-P-O3'	-9.06	80.82	108.00
22	v	75	C	OP2-P-O3'	8.76	134.27	108.00
28	D	151	THR	CB-CA-C	8.55	123.03	109.27
25	A	1016	U	C2'-C3'-O3'	8.50	126.45	113.70
25	A	1094	C	OP2-P-O3'	-8.02	83.95	108.00
22	v	76	A	O4'-C1'-N9	-6.71	98.13	108.20
30	F	113	ASP	CA-C-N	6.30	133.58	121.54
30	F	113	ASP	C-N-CA	6.30	133.58	121.54
13	m	117	ARG	CB-CA-C	-5.95	109.69	116.54
29	E	121	ALA	CA-C-N	5.64	132.31	121.54
29	E	121	ALA	C-N-CA	5.64	132.31	121.54
32	H	74	GLU	CB-CA-C	-5.25	110.09	117.23
28	D	151	THR	CA-C-O	-5.11	115.13	120.70
28	D	151	THR	CA-C-N	5.07	126.17	119.84
28	D	151	THR	C-N-CA	5.07	126.17	119.84

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
28	D	151	THR	Mainchain
30	F	105	SER	Peptide
30	F	112	ARG	Peptide
43	T	51	LEU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32675	0	16461	406	0
2	b	1751	0	1785	28	0
3	c	1656	0	1706	36	0
4	d	1613	0	1646	54	0
5	e	1134	0	1181	27	0
6	f	857	0	836	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	g	1187	0	1244	32	0
8	h	982	0	1036	11	0
9	i	1010	0	1052	38	0
10	j	793	0	833	27	0
11	k	879	0	896	21	0
12	l	959	0	1009	19	0
13	m	892	0	933	27	0
14	n	800	0	837	27	0
15	o	703	0	727	8	0
16	p	636	0	646	16	0
17	q	645	0	689	15	0
18	r	480	0	488	7	0
19	s	663	0	697	20	0
20	t	671	0	722	19	0
21	u	506	0	537	11	0
22	v	1625	0	828	5	0
23	w	131	0	66	0	0
24	x	3500	0	3506	83	0
25	A	61891	0	31143	475	0
26	B	2495	0	1263	8	0
27	C	2072	0	2152	18	0
28	D	1588	0	1603	28	0
29	E	1521	0	1581	23	0
30	F	1407	0	1470	37	0
31	G	1323	0	1386	19	0
32	H	964	0	886	11	0
33	I	668	0	513	7	0
34	J	718	0	458	7	0
35	L	1130	0	1160	9	0
36	M	938	0	1012	17	0
37	N	1066	0	1112	17	0
38	O	1085	0	1157	20	0
39	P	959	0	1005	10	0
40	Q	881	0	920	6	0
41	R	902	0	960	14	0
42	S	936	0	1025	7	0
43	T	822	0	858	11	0
44	U	833	0	897	9	0
45	V	739	0	788	6	0
46	W	786	0	836	5	0
47	X	1445	0	1486	13	0
48	Y	575	0	598	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	Z	630	0	653	9	0
50	1	490	0	520	6	0
51	2	445	0	472	3	0
52	3	356	0	342	8	0
53	4	440	0	437	8	0
54	5	426	0	457	2	0
55	6	365	0	409	2	0
56	7	506	0	569	6	0
57	8	307	0	342	2	0
58	2	1	0	0	0	0
58	4	1	0	0	0	0
58	7	1	0	0	0	0
58	A	471	0	0	0	0
58	B	7	0	0	0	0
58	C	2	0	0	0	0
58	E	3	0	0	0	0
58	N	1	0	0	0	0
58	P	1	0	0	0	0
58	S	2	0	0	0	0
58	Y	1	0	0	0	0
58	a	136	0	0	0	0
58	t	1	0	0	0	0
58	v	2	0	0	0	0
59	v	10	0	10	0	0
60	x	28	0	12	1	0
61	3	1	0	0	0	0
61	8	1	0	0	0	0
62	4	2	0	0	0	0
62	6	1	0	0	0	0
62	A	166	0	0	2	0
62	C	1	0	0	0	0
62	E	1	0	0	0	0
62	P	1	0	0	0	0
62	a	27	0	0	0	0
62	w	1	0	0	0	0
All	All	149327	0	100853	1614	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 7.

All (1614) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1221:A:N7	13:m:116:ILE:HD12	1.44	1.30
1:a:74:A:H62	1:a:89:G:H21	1.08	0.99
25:A:1834:A:HO2'	25:A:1835:A:H8	1.01	0.99
28:D:151:THR:HG23	28:D:152:PRO:HD2	1.46	0.97
1:a:74:A:H62	1:a:89:G:N2	1.63	0.97
1:a:174:U:H3	1:a:189:A:N6	1.64	0.95
24:x:719:TYR:HD1	24:x:725:ILE:HG12	1.33	0.94
28:D:151:THR:CG2	28:D:152:PRO:HD2	1.97	0.93
24:x:719:TYR:CD1	24:x:725:ILE:HG12	2.04	0.93
1:a:195:G:H1	1:a:210:U:H3	1.17	0.92
25:A:2087:G:H1	25:A:2176:U:H3	1.16	0.92
1:a:449:G:H1	1:a:471:U:H3	1.14	0.92
1:a:74:A:N6	1:a:89:G:H21	1.67	0.92
1:a:174:U:H3	1:a:189:A:H62	0.90	0.89
25:A:1070:C:H2'	25:A:1071:U:C6	2.09	0.86
1:a:1017:G:C6	1:a:1018:G:O6	2.29	0.85
1:a:75:G:H1	1:a:88:U:H3	0.88	0.83
25:A:2154:U:H3	25:A:2158:A:H62	1.26	0.83
1:a:1221:A:N7	13:m:116:ILE:CD1	2.36	0.83
17:q:64:ILE:HG13	17:q:76:TRP:HE3	1.44	0.83
1:a:1017:G:O6	1:a:1018:G:O6	1.98	0.82
6:f:9:LEU:HD21	6:f:86:ARG:HB3	1.62	0.81
10:j:52:LEU:HB2	14:n:81:ARG:HD2	1.62	0.81
30:F:111:VAL:HG23	30:F:112:ARG:H	1.47	0.80
25:A:871:G:N3	25:A:885:A:C8	2.51	0.79
3:c:140:ASN:HD22	3:c:143:ARG:HH12	1.27	0.79
3:c:70:THR:HG22	3:c:72:ARG:H	1.48	0.78
1:a:1117:A:H4'	10:j:38:GLY:HA3	1.66	0.77
31:G:16:GLU:HB3	31:G:27:LYS:HB2	1.64	0.77
25:A:1519:G:C6	25:A:1520:U:C4	2.73	0.77
3:c:46:LYS:HE2	3:c:87:LEU:HD11	1.67	0.76
13:m:114:LYS:O	13:m:115:PRO:O	2.02	0.76
24:x:606:LEU:HD13	24:x:609:GLN:HE22	1.48	0.76
1:a:969:A:H4'	1:a:970:G:H5''	1.66	0.76
45:V:68:ARG:NH1	45:V:69:THR:O	2.18	0.76
25:A:1519:G:C4	25:A:1520:U:C5	2.74	0.75
24:x:775:ARG:HD3	24:x:796:LEU:HD22	1.66	0.75
25:A:2151:C:H1'	25:A:2153:U:OP2	1.86	0.75
4:d:153:LEU:HD23	4:d:154:ARG:HH11	1.51	0.75
25:A:1587:A:H5''	25:A:1588:A:H5'	1.68	0.75
25:A:2154:U:H3	25:A:2158:A:N6	1.84	0.74
57:8:12:ARG:NH1	57:8:13:ASN:OD1	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1519:G:H1	25:A:1529:U:H3	1.32	0.74
4:d:202:GLU:OE2	5:e:113:ARG:NH1	2.21	0.74
20:t:28:VAL:O	20:t:32:ILE:HD12	1.88	0.74
29:E:170:ASP:OD1	29:E:171:VAL:N	2.21	0.74
1:a:174:U:O4	1:a:189:A:N7	2.21	0.73
17:q:64:ILE:HG13	17:q:76:TRP:CE3	2.22	0.73
3:c:33:LEU:HD11	14:n:93:VAL:HG22	1.71	0.73
4:d:13:ARG:HD2	4:d:32:CYS:HB2	1.70	0.73
1:a:1376:C:O2'	7:g:79:ARG:NH1	2.22	0.72
30:F:52:ASN:ND2	30:F:147:ASP:OD1	2.22	0.72
7:g:151:PHE:O	7:g:153:HIS:N	2.23	0.71
24:x:717:ARG:HD3	24:x:719:TYR:OH	1.90	0.71
1:a:204:C:OP2	1:a:205:G:N2	2.23	0.71
1:a:1019:U:H4'	1:a:1020:G:H5'	1.72	0.71
25:A:462:A:OP1	29:E:78:ARG:NH2	2.22	0.71
25:A:1050:U:H4'	25:A:1051:U:H5'	1.72	0.71
32:H:2:GLU:OE2	32:H:20:ASN:ND2	2.24	0.71
25:A:845:G:H2'	25:A:846:G:C8	2.26	0.71
1:a:526:A:N6	1:a:1200:G:O2'	2.24	0.70
1:a:178:U:O2	1:a:188:G:N2	2.24	0.70
25:A:2122:A:H4'	25:A:2147:C:H4'	1.74	0.69
39:P:37:THR:HG22	39:P:39:PRO:HD2	1.72	0.69
1:a:1145:A:H5''	10:j:44:THR:HG23	1.74	0.69
24:x:376:THR:OG1	24:x:377:GLN:N	2.23	0.69
25:A:871:G:N3	25:A:885:A:N7	2.40	0.69
25:A:1572:C:O2'	25:A:1573:U:OP1	2.11	0.69
25:A:2127:G:C6	25:A:2139:G:O6	2.45	0.69
27:C:261:ASN:ND2	27:C:264:THR:OG1	2.26	0.69
25:A:1983:C:OP1	36:M:31:ARG:NH1	2.25	0.68
25:A:1420:A:H2'	25:A:1421:A:C8	2.28	0.68
31:G:164:TYR:HB2	31:G:167:GLU:HB2	1.76	0.68
1:a:1360:U:OP1	9:i:119:ARG:NH1	2.27	0.68
25:A:2315:A:H2'	25:A:2316:A:C8	2.28	0.68
1:a:98:G:N7	20:t:9:LYS:NZ	2.34	0.68
12:l:29:GLN:HG3	12:l:81:LEU:HD21	1.76	0.68
1:a:1221:A:C8	13:m:116:ILE:HD12	2.25	0.68
53:4:53:VAL:HG23	53:4:54:VAL:HG13	1.74	0.68
51:2:5:LYS:HB2	51:2:57:GLU:HB2	1.75	0.68
1:a:1028:G:H2'	1:a:1029:A:H8	1.59	0.67
1:a:1524:G:N7	21:u:46:LYS:NZ	2.42	0.67
25:A:1519:G:H2'	25:A:1520:U:C6	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:211:GLN:NE2	2:b:215:ASN:OD1	2.27	0.67
25:A:2414:C:H5''	25:A:2416:G:H5'	1.76	0.67
52:3:38:SER:HA	52:3:44:TYR:HD2	1.60	0.67
30:F:37:ASN:HA	30:F:88:LYS:HA	1.77	0.67
1:a:1300:A:N6	1:a:1325:G:O2'	2.28	0.67
9:i:114:LYS:NZ	9:i:118:LEU:O	2.27	0.67
25:A:2098:U:H1'	25:A:2105:U:H4'	1.77	0.67
1:a:607:C:OP1	4:d:81:ARG:NH1	2.28	0.67
32:H:66:GLU:HA	32:H:69:ALA:HB3	1.75	0.67
33:I:28:ALA:O	33:I:81:LEU:N	2.28	0.67
30:F:43:ALA:HA	30:F:46:ASP:HB3	1.77	0.67
4:d:152:GLN:OE1	4:d:154:ARG:NH2	2.28	0.67
9:i:130:ARG:NH2	22:v:33:U:OP2	2.28	0.67
25:A:1521:C:H6	25:A:1521:C:O5'	1.78	0.67
16:p:22:THR:HG22	16:p:32:PHE:HB3	1.77	0.67
9:i:88:ILE:HD11	9:i:98:LEU:HD12	1.75	0.66
25:A:2138:C:O5'	25:A:2138:C:H6	1.78	0.66
25:A:2137:U:O5'	25:A:2137:U:H6	1.78	0.66
1:a:1141:C:O5'	1:a:1141:C:H6	1.78	0.66
1:a:1033:C:H2'	1:a:1034:A:H8	1.61	0.66
11:k:93:ARG:NH2	11:k:112:ASP:OD1	2.28	0.66
25:A:2122:A:H3'	25:A:2140:C:H42	1.60	0.66
13:m:107:ARG:NH1	13:m:112:PRO:O	2.28	0.66
16:p:6:LEU:HD22	16:p:17:TYR:HB3	1.77	0.66
21:u:61:GLN:OE1	21:u:62:ARG:NH2	2.29	0.66
1:a:61:G:N7	20:t:6:SER:OG	2.28	0.66
25:A:1845:A:H61	25:A:1871:G:H1'	1.59	0.66
9:i:84:THR:HG23	9:i:98:LEU:HD13	1.78	0.66
25:A:2152:C:H2'	25:A:2153:U:C6	2.31	0.66
35:L:45:THR:HG22	42:S:64:ARG:HH21	1.61	0.66
25:A:1789:A:H2'	25:A:1790:A:C8	2.32	0.65
25:A:28:A:N6	25:A:503:G:H1'	2.11	0.65
25:A:358:A:O2'	25:A:359:U:O2	2.11	0.65
25:A:1288:A:H2	25:A:1616:G:H21	1.44	0.65
49:Z:33:LEU:HA	49:Z:52:SER:HA	1.78	0.65
1:a:78:A:H2'	1:a:79:G:C8	2.32	0.65
25:A:1072:U:H6	25:A:1072:U:O5'	1.79	0.65
9:i:91:ASP:O	9:i:93:THR:N	2.29	0.65
21:u:58:LYS:O	21:u:62:ARG:NH1	2.29	0.65
24:x:604:VAL:HG12	24:x:608:ARG:HE	1.61	0.65
1:a:171:G:OP1	20:t:60:ARG:NH1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:x:350:HIS:CD2	24:x:351:VAL:H	2.14	0.65
25:A:1116:A:H4'	25:A:1117:A:H5''	1.78	0.65
30:F:140:GLU:HA	52:3:28:LEU:HD21	1.77	0.65
44:U:48:LYS:NZ	44:U:52:GLU:OE2	2.30	0.65
25:A:1070:C:H2'	25:A:1071:U:H6	1.58	0.65
10:j:26:VAL:HG23	10:j:36:VAL:HG11	1.79	0.65
16:p:4:ILE:HG12	16:p:21:VAL:HG22	1.76	0.65
20:t:43:ASP:OD2	20:t:46:LYS:NZ	2.27	0.65
24:x:700:ARG:HH21	24:x:745:ILE:HD11	1.60	0.65
24:x:728:ASP:OD2	24:x:742:ARG:NH1	2.31	0.64
25:A:288:A:O2'	25:A:289:G:O4'	2.15	0.64
26:B:75:G:H1'	47:X:32:VAL:HG21	1.78	0.64
1:a:1320:U:H2'	1:a:1321:G:H8	1.63	0.64
25:A:2152:C:O5'	25:A:2152:C:H6	1.80	0.64
1:a:223:U:O2'	16:p:23:ASN:ND2	2.31	0.64
1:a:370:G:H4'	16:p:5:ARG:HD2	1.80	0.64
9:i:55:THR:HG23	9:i:57:THR:HG22	1.78	0.64
25:A:1274:A:N1	25:A:1638:U:O2'	2.25	0.64
9:i:106:ARG:NH1	9:i:107:ASP:O	2.31	0.64
25:A:2186:A:N1	25:A:2213:C:N4	2.46	0.64
19:s:11:ILE:HD12	19:s:38:SER:HB3	1.80	0.64
36:M:104:ARG:NH2	41:R:34:LYS:O	2.30	0.64
9:i:5:GLN:OE1	9:i:22:ARG:NH1	2.31	0.64
25:A:461:A:OP1	29:E:73:ARG:NH2	2.25	0.64
25:A:1253:G:OP1	53:4:16:ARG:NH1	2.31	0.64
36:M:38:ILE:HD11	36:M:111:PHE:HZ	1.62	0.64
27:C:135:ILE:O	27:C:167:ARG:NH2	2.31	0.64
1:a:1250:U:H5'	3:c:26:ARG:HH21	1.62	0.64
6:f:29:ILE:HG22	6:f:70:ALA:HB1	1.80	0.64
21:u:30:ALA:HA	21:u:33:ARG:HH11	1.63	0.63
25:A:1251:G:OP1	53:4:16:ARG:NH2	2.23	0.63
33:I:22:ALA:HA	33:I:86:ASN:HA	1.80	0.63
1:a:209:C:H1'	1:a:459:A:H62	1.62	0.63
25:A:1518:C:H2'	25:A:1519:G:H8	1.63	0.63
25:A:2228:A:H2'	25:A:2229:G:C8	2.33	0.63
37:N:122:LEU:HG	37:N:125:ILE:HD11	1.80	0.63
51:2:5:LYS:NZ	51:2:36:GLU:OE1	2.23	0.63
5:e:59:ALA:O	5:e:63:LYS:HG3	1.98	0.63
9:i:67:VAL:HG22	9:i:79:ILE:HD11	1.81	0.63
24:x:415:ILE:HD13	24:x:443:PRO:HG2	1.79	0.63
1:a:516:C:H41	12:l:50:ARG:HH22	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:174:U:N3	1:a:189:A:N6	2.32	0.63
3:c:111:LEU:HD11	3:c:146:ALA:HB2	1.80	0.63
9:i:54:LEU:HD23	9:i:98:LEU:HD23	1.81	0.63
28:D:151:THR:HG22	28:D:152:PRO:HD2	1.79	0.63
1:a:248:G:H4'	17:q:23:THR:HG21	1.80	0.63
1:a:1007:G:N2	1:a:1010:A:OP2	2.24	0.63
1:a:197:G:N2	1:a:198:G:O6	2.32	0.62
1:a:1339:U:OP1	9:i:122:ARG:NH1	2.32	0.62
24:x:724:ASP:OD1	24:x:742:ARG:NH1	2.31	0.62
38:O:76:LYS:HB2	38:O:91:GLU:HG3	1.81	0.62
4:d:6:GLY:O	4:d:8:LYS:NZ	2.29	0.62
2:b:60:LEU:HD22	2:b:67:ILE:HD11	1.81	0.62
1:a:83:G:H2'	1:a:84:C:C6	2.34	0.62
1:a:179:C:H2'	1:a:180:C:C6	2.34	0.62
1:a:373:C:N4	1:a:374:G:O6	2.32	0.62
1:a:1295:U:O2'	1:a:1296:C:H5'	2.00	0.62
3:c:88:ARG:NH2	3:c:89:GLN:OE1	2.33	0.62
20:t:78:ARG:O	20:t:82:HIS:ND1	2.29	0.62
25:A:1572:C:O2'	25:A:1573:U:O4'	2.14	0.62
25:A:2127:G:H2'	25:A:2128:G:C8	2.35	0.62
1:a:73:A:H62	1:a:90:G:HO2'	1.47	0.62
1:a:400:G:N7	1:a:489:A:O2'	2.28	0.62
25:A:577:C:OP2	37:N:21:ARG:NH1	2.26	0.62
25:A:1519:G:C6	25:A:1520:U:O4	2.52	0.62
1:a:1350:A:H2'	1:a:1351:A:C8	2.34	0.62
13:m:81:MET:SD	13:m:92:ARG:HB3	2.40	0.62
14:n:90:ARG:NH1	14:n:92:ASP:OD2	2.32	0.62
25:A:1012:G:O6	35:L:68:LYS:NZ	2.26	0.62
25:A:2087:G:N2	25:A:2176:U:O2	2.26	0.62
25:A:2237:G:OP1	38:O:85:LYS:NZ	2.33	0.62
1:a:141:G:H2'	1:a:142:G:C8	2.35	0.62
1:a:350:A:N3	1:a:362:U:O2'	2.32	0.62
10:j:86:ALA:O	10:j:89:LYS:NZ	2.32	0.62
25:A:2337:C:OP2	56:7:44:ARG:NH1	2.32	0.61
34:J:109:ILE:HD11	34:J:129:ILE:HG21	1.80	0.61
1:a:600:G:N2	1:a:626:U:OP1	2.28	0.61
25:A:1519:G:H2'	25:A:1520:U:H6	1.64	0.61
16:p:73:GLN:HA	16:p:76:LYS:HE3	1.82	0.61
4:d:129:THR:OG1	4:d:146:ARG:NH2	2.33	0.61
4:d:159:LEU:HD21	4:d:175:LEU:HD12	1.81	0.61
7:g:138:ARG:HG3	7:g:142:HIS:CE1	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:882:C:H2'	25:A:883:U:C2	2.36	0.61
1:a:658:G:H22	1:a:735:G:H1	1.49	0.61
6:f:8:PHE:HE1	6:f:84:VAL:HG23	1.65	0.61
7:g:109:ARG:HG2	7:g:116:MET:HE1	1.83	0.61
25:A:244:A:H5''	37:N:67:VAL:HG11	1.82	0.61
25:A:466:C:O2	25:A:470:A:N6	2.33	0.61
25:A:1519:G:N2	25:A:1529:U:O2	2.27	0.61
25:A:2485:OMC:HM22	25:A:2486:C:H5'	1.83	0.61
43:T:51:LEU:O	43:T:53:VAL:N	2.34	0.61
10:j:56:HIS:ND1	10:j:57:VAL:HG22	2.16	0.61
25:A:1856:G:N2	25:A:1859:A:OP2	2.26	0.61
1:a:651:U:H2'	1:a:652:A:H8	1.66	0.60
1:a:709:A:H2'	1:a:710:A:C8	2.36	0.60
54:5:21:LYS:NZ	54:5:28:GLU:O	2.34	0.60
1:a:378:G:H2'	1:a:379:C:C6	2.37	0.60
4:d:97:ARG:NH2	4:d:99:ASP:OD2	2.34	0.60
25:A:1095:U:H2'	25:A:1096:A:H8	1.65	0.60
25:A:1237:G:H5''	42:S:6:ARG:HD3	1.83	0.60
29:E:148:VAL:HB	29:E:187:VAL:HG12	1.83	0.60
1:a:970:G:O2'	1:a:1356:A:N1	2.26	0.60
7:g:75:VAL:HG13	7:g:86:GLN:HB3	1.83	0.60
25:A:911:C:O2'	48:Y:29:GLN:NE2	2.35	0.60
25:A:1575:C:H3'	25:A:1576:A:H8	1.66	0.60
50:1:5:GLU:O	50:1:9:LYS:NZ	2.34	0.60
24:x:385:GLU:HA	24:x:390:MET:HA	1.82	0.60
29:E:105:ARG:NH1	29:E:199:LEU:O	2.32	0.60
13:m:89:LEU:HD13	13:m:92:ARG:HD3	1.83	0.60
25:A:1495:A:H4'	25:A:1496:A:H5'	1.83	0.60
49:Z:41:GLU:O	49:Z:44:LYS:NZ	2.34	0.60
1:a:176:C:OP2	1:a:177:G:N2	2.34	0.60
1:a:441:G:N1	1:a:480:U:OP1	2.31	0.60
1:a:707:G:H2'	1:a:708:G:C8	2.37	0.60
1:a:56:U:H2'	1:a:57:G:H8	1.67	0.60
25:A:686:A:HO2'	25:A:687:G:H8	1.49	0.60
5:e:83:GLN:NE2	5:e:150:ALA:HA	2.17	0.60
25:A:1519:G:C5	25:A:1520:U:C4	2.89	0.59
1:a:1151:A:N7	1:a:1174:A:N6	2.50	0.59
5:e:107:ILE:HB	5:e:125:LEU:HA	1.83	0.59
25:A:98:C:N4	25:A:99:U:O4	2.35	0.59
32:H:65:ALA:HB1	32:H:137:VAL:HG21	1.83	0.59
42:S:87:ALA:HB1	43:T:52:PRO:HD3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:k:112:ASP:HB3	21:u:2:PRO:HB2	1.84	0.59
1:a:1194:C:H5''	1:a:1195:A:H3'	1.83	0.59
25:A:155:U:H2'	25:A:156:A:C8	2.36	0.59
25:A:2114:G:H22	25:A:2148:C:H42	1.50	0.59
25:A:2118:U:HO2'	25:A:2144:G:HO2'	1.50	0.59
36:M:120:GLU:OE2	41:R:66:SER:OG	2.21	0.59
1:a:595:G:H2'	1:a:596:A:H8	1.68	0.59
4:d:59:GLN:OE1	4:d:62:ARG:NH1	2.36	0.59
16:p:5:ARG:HA	16:p:71:VAL:HG21	1.85	0.59
19:s:9:PRO:HA	19:s:39:MET:HE1	1.85	0.59
25:A:871:G:H2'	25:A:872:G:C8	2.38	0.59
26:B:42:C:H5	30:F:90:THR:HB	1.67	0.59
1:a:991:U:H2'	1:a:992:G:H8	1.67	0.59
3:c:156:ARG:NH2	3:c:161:GLU:OE2	2.35	0.59
4:d:11:LEU:HD23	4:d:63:ARG:HD2	1.85	0.59
25:A:1404:C:OP1	25:A:1577:G:N2	2.36	0.59
34:J:36:MET:O	34:J:40:LYS:N	2.34	0.59
39:P:90:ARG:NH2	39:P:117:ASP:OD2	2.36	0.59
1:a:340:G:OP1	41:R:40:ARG:NH1	2.34	0.59
9:i:55:THR:HG21	9:i:87:LEU:HD11	1.84	0.59
12:l:30:ARG:NH2	12:l:58:THR:OG1	2.35	0.59
6:f:26:THR:O	6:f:30:GLU:HG2	2.03	0.58
33:I:6:GLU:HA	33:I:9:LYS:HE2	1.85	0.58
5:e:62:GLN:O	5:e:66:GLU:HG3	2.02	0.58
25:A:653:G:H5''	37:N:17:HIS:NE2	2.18	0.58
25:A:2301:G:H5'	30:F:35:THR:HG21	1.84	0.58
30:F:147:ASP:OD2	30:F:150:ARG:NH1	2.36	0.58
1:a:708:G:H2'	1:a:709:A:C8	2.38	0.58
1:a:893:C:O2'	1:a:894:A:OP1	2.19	0.58
1:a:976:U:OP2	14:n:63:ARG:NH2	2.31	0.58
25:A:2087:G:H2'	25:A:2088:A:C8	2.37	0.58
1:a:486:C:H2'	1:a:487:A:C8	2.38	0.58
19:s:36:ARG:NH2	19:s:75:ALA:O	2.36	0.58
25:A:1635:G:H5''	25:A:1636:C:H5'	1.85	0.58
1:a:460:A:C6	1:a:462:A:C6	2.92	0.58
6:f:84:VAL:O	6:f:86:ARG:N	2.31	0.58
25:A:155:U:H2'	25:A:156:A:H8	1.68	0.58
25:A:491:G:N1	25:A:494:A:OP2	2.34	0.58
25:A:1302:C:O2'	25:A:1379:A:N3	2.36	0.58
10:j:35:GLN:HB3	10:j:77:VAL:HB	1.84	0.58
25:A:1120:U:C4	28:D:152:PRO:HD3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:132:HIS:ND1	32:H:138:GLU:OE2	2.27	0.58
1:a:75:G:O6	1:a:88:U:O4	2.21	0.58
3:c:22:TRP:CD1	3:c:59:ARG:HD2	2.39	0.58
4:d:188:ARG:O	4:d:188:ARG:NH1	2.33	0.58
25:A:1766:U:OP2	25:A:1771:A:N6	2.34	0.58
28:D:26:THR:OG1	28:D:191:GLY:O	2.22	0.58
3:c:43:LEU:HD11	3:c:91:LEU:HD11	1.86	0.58
10:j:27:GLU:HA	10:j:30:LYS:HE2	1.85	0.58
25:A:663:C:OP1	29:E:48:ARG:NH1	2.36	0.58
25:A:837:C:H2'	25:A:838:A:H8	1.68	0.58
1:a:1169:G:H2'	1:a:1170:A:H8	1.69	0.57
24:x:747:GLY:HA2	24:x:770:GLU:O	2.04	0.57
25:A:2109:U:H2'	25:A:2110:G:H8	1.70	0.57
16:p:50:LEU:HD13	16:p:74:LEU:HD12	1.86	0.57
25:A:2516:G:H4'	31:G:175:LYS:HD3	1.86	0.57
1:a:1360:U:O2'	10:j:62:ARG:NH2	2.37	0.57
1:a:1391:C:OP2	5:e:30:ARG:NH2	2.37	0.57
10:j:59:LYS:HE2	10:j:62:ARG:NH2	2.19	0.57
14:n:6:MET:SD	14:n:9:ARG:NH2	2.78	0.57
1:a:453:U:H2'	1:a:454:A:C8	2.39	0.57
9:i:46:MET:O	9:i:50:GLN:HG2	2.05	0.57
25:A:2364:A:O2'	40:Q:116:PHE:OXT	2.21	0.57
32:H:60:GLU:HA	32:H:63:ALA:HB3	1.85	0.57
1:a:132:G:C6	1:a:133:G:N7	2.73	0.57
1:a:1035:G:H2'	1:a:1036:A:C8	2.40	0.57
31:G:59:GLN:HG3	31:G:62:ARG:HH21	1.70	0.57
1:a:187:A:H2'	1:a:188:G:C8	2.39	0.57
1:a:418:G:H2'	1:a:419:A:H8	1.70	0.57
7:g:27:MET:HE3	7:g:40:GLU:HG2	1.86	0.57
17:q:50:HIS:NE2	17:q:52:GLU:OE1	2.35	0.57
30:F:162:THR:HG23	30:F:164:ASP:H	1.70	0.57
43:T:6:VAL:HG22	43:T:11:GLN:HG2	1.87	0.57
1:a:65:A:N7	1:a:375:A:N6	2.33	0.57
24:x:385:GLU:OE1	24:x:385:GLU:N	2.38	0.57
1:a:686:U:O2'	1:a:688:A:N7	2.32	0.57
1:a:740:G:H2'	1:a:741:A:C8	2.40	0.57
2:b:23:TRP:CZ3	2:b:25:PRO:HA	2.40	0.57
11:k:35:THR:HG22	11:k:41:ALA:HA	1.87	0.57
25:A:351:A:H2'	25:A:352:A:C8	2.40	0.57
25:A:2108:G:O6	25:A:2165:C:N4	2.38	0.57
1:a:1112:U:OP1	9:i:11:ARG:NH1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:u:30:ALA:HA	21:u:33:ARG:NH1	2.21	0.56
25:A:854:C:OP2	38:O:23:ARG:NH2	2.38	0.56
25:A:2732:C:O2	31:G:139:GLN:NE2	2.30	0.56
1:a:1113:C:OP1	9:i:85:ARG:NH2	2.38	0.56
1:a:1370:U:O4	7:g:10:ARG:NH1	2.38	0.56
5:e:46:ARG:HE	5:e:72:MET:HE3	1.70	0.56
6:f:29:ILE:HD11	6:f:36:ILE:HD11	1.87	0.56
36:M:106:LEU:HD11	36:M:114:ILE:HD11	1.87	0.56
1:a:998:A:N7	1:a:1020:G:H1'	2.20	0.56
3:c:133:ALA:HA	3:c:136:ARG:HG2	1.87	0.56
5:e:42:ASP:OD1	5:e:43:GLY:N	2.39	0.56
5:e:116:LEU:HD13	5:e:124:VAL:HG11	1.87	0.56
15:o:88:ARG:NH1	25:A:704:U:OP2	2.38	0.56
25:A:883:U:H3'	25:A:883:U:H6	1.70	0.56
25:A:1104:C:H2'	25:A:1105:G:C8	2.40	0.56
25:A:1572:C:H3'	25:A:1573:U:H5''	1.86	0.56
25:A:2131:G:N2	25:A:2133:C:O4'	2.38	0.56
28:D:6:VAL:H	28:D:33:ASN:HD21	1.53	0.56
41:R:35:GLU:OE2	41:R:38:ARG:NH1	2.38	0.56
1:a:1233:A:H4'	1:a:1234:U:O5'	2.03	0.56
1:a:75:G:H2'	1:a:76:G:C8	2.40	0.56
6:f:90:MET:SD	18:r:61:ARG:HD3	2.46	0.56
24:x:529:ARG:HD2	24:x:580:LEU:HD11	1.86	0.56
25:A:28:A:H61	25:A:503:G:H1'	1.68	0.56
25:A:1811:G:O2'	27:C:253:THR:HG21	2.04	0.56
25:A:2278:U:H2'	25:A:2279:G:C8	2.41	0.56
1:a:72:G:O2'	1:a:91:A:N6	2.37	0.56
1:a:73:A:N6	1:a:90:G:O2'	2.29	0.56
1:a:940:A:H2'	1:a:941:G:C8	2.40	0.56
33:I:90:GLY:O	33:I:92:ALA:N	2.37	0.56
2:b:68:LEU:HD13	2:b:90:PRO:HB2	1.87	0.56
22:v:24:U:O2'	25:A:1910:U:OP1	2.23	0.56
25:A:2127:G:C6	25:A:2139:G:C6	2.93	0.56
25:A:2278:U:OP1	25:A:2367:U:O2'	2.23	0.56
1:a:1512:MA6:H92	1:a:1513:MA6:N6	2.21	0.56
4:d:167:ARG:NH1	4:d:169:GLU:H	2.04	0.56
3:c:46:LYS:HE3	3:c:47:LEU:HD23	1.88	0.55
1:a:538:G:OP1	4:d:59:GLN:NE2	2.37	0.55
24:x:350:HIS:O	24:x:355:LYS:HE3	2.06	0.55
24:x:695:PHE:HE1	24:x:717:ARG:HD2	1.71	0.55
25:A:387:G:OP2	49:Z:10:LYS:NZ	2.30	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:229:U:H2'	1:a:230:A:H8	1.71	0.55
1:a:1022:C:H2'	1:a:1023:U:O4'	2.05	0.55
24:x:347:VAL:HG22	24:x:417:ILE:HD11	1.87	0.55
25:A:405:C:H2'	25:A:406:A:C8	2.41	0.55
25:A:2238:OMG:OP2	38:O:82:ARG:NH1	2.39	0.55
1:a:315:A:H2'	1:a:316:C:C6	2.41	0.55
1:a:683:C:OP1	11:k:29:ASN:ND2	2.37	0.55
5:e:115:VAL:HG13	5:e:142:PHE:HE1	1.71	0.55
25:A:2295:G:O2'	25:A:2296:A:O5'	2.24	0.55
1:a:446:A:O2'	16:p:73:GLN:OE1	2.20	0.55
25:A:1083:G:H21	25:A:1088:A:H62	1.53	0.55
38:O:111:GLU:OE2	38:O:115:ARG:NE	2.39	0.55
39:P:8:ARG:HD2	39:P:43:GLU:HG2	1.88	0.55
1:a:1221:A:H5''	19:s:83:HIS:HD2	1.72	0.55
1:a:1227:G:OP1	9:i:119:ARG:NH2	2.38	0.55
2:b:120:GLN:HE21	2:b:126:PHE:HD2	1.53	0.55
25:A:899:A:N7	38:O:13:MET:HG3	2.22	0.55
27:C:8:PRO:HB3	27:C:14:ARG:HG3	1.88	0.55
1:a:8:A:N6	4:d:202:GLU:O	2.39	0.55
1:a:162:G:H2'	1:a:163:C:C6	2.42	0.55
1:a:1221:A:C5	13:m:116:ILE:HD12	2.35	0.55
25:A:2087:G:H2'	25:A:2088:A:H8	1.72	0.55
25:A:2807:A:O2'	25:A:2808:A:OP1	2.24	0.55
1:a:509:G:H2'	1:a:510:U:H6	1.71	0.55
25:A:159:G:H21	25:A:167:A:H62	1.53	0.55
25:A:1672:G:H2'	25:A:1673:C:C6	2.42	0.55
25:A:2109:U:H2'	25:A:2110:G:C8	2.41	0.55
34:J:107:GLU:O	34:J:111:LYS:N	2.33	0.55
47:X:111:PHE:HB3	47:X:114:GLU:OE2	2.07	0.55
1:a:628:C:H2'	1:a:629:A:H8	1.72	0.55
25:A:5:A:H2'	25:A:6:A:H8	1.72	0.55
37:N:70:LYS:O	37:N:107:ARG:NH2	2.40	0.55
1:a:646:U:O4	1:a:746:G:O2'	2.22	0.54
2:b:51:ASN:O	2:b:55:THR:HG23	2.06	0.54
11:k:64:GLN:O	11:k:68:GLU:HG3	2.06	0.54
24:x:728:ASP:CG	24:x:742:ARG:HH12	2.14	0.54
25:A:219:A:N3	25:A:234:U:O2'	2.33	0.54
40:Q:55:LEU:HD12	40:Q:60:ARG:HH21	1.72	0.54
41:R:48:VAL:HG22	41:R:62:VAL:HG12	1.89	0.54
1:a:221:G:O2'	16:p:63:GLN:OE1	2.23	0.54
1:a:395:C:O2'	1:a:615:A:N3	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:499:G:H2'	1:a:500:G:C8	2.42	0.54
10:j:6:ILE:HG12	10:j:76:ILE:HG12	1.89	0.54
20:t:35:VAL:O	20:t:39:ILE:HD12	2.06	0.54
25:A:2300:C:O4'	30:F:37:ASN:ND2	2.40	0.54
31:G:118:PRO:HD2	31:G:121:ILE:HD11	1.89	0.54
42:S:89:GLU:OE2	43:T:37:ARG:NH2	2.35	0.54
16:p:5:ARG:NH1	16:p:22:THR:OG1	2.40	0.54
18:r:26:LEU:O	18:r:30:LYS:HG3	2.07	0.54
25:A:247:G:O6	56:7:12:LYS:NZ	2.38	0.54
36:M:64:ARG:NH2	36:M:99:PHE:O	2.41	0.54
8:h:5:ASP:HB2	8:h:81:PRO:HG3	1.88	0.54
1:a:291:G:N2	1:a:294:A:OP2	2.35	0.54
1:a:404:G:OP1	4:d:26:ARG:NH1	2.40	0.54
1:a:973:C:O2	14:n:59:ARG:NH1	2.40	0.54
25:A:1776:A:OP2	27:C:221:ARG:NH1	2.41	0.54
25:A:2154:U:N3	25:A:2158:A:N6	2.47	0.54
1:a:84:C:H2'	1:a:85:U:C6	2.43	0.54
1:a:438:U:H2'	1:a:439:G:H8	1.71	0.54
14:n:33:ASN:HB3	14:n:36:SER:HB3	1.89	0.54
25:A:1018:A:H2'	25:A:1019:A:C8	2.43	0.54
40:Q:17:LEU:HD23	40:Q:20:ARG:HH21	1.73	0.54
47:X:143:LEU:HD12	47:X:144:PRO:HD2	1.89	0.54
2:b:94:HIS:ND1	2:b:146:ARG:O	2.40	0.54
2:b:104:TYR:CE1	2:b:108:ARG:HD3	2.43	0.54
47:X:173:LEU:O	47:X:175:GLN:N	2.40	0.54
2:b:85:ALA:O	2:b:86:ARG:HB3	2.08	0.54
14:n:33:ASN:O	14:n:41:ARG:NH2	2.40	0.54
2:b:121:SER:OG	2:b:122:GLN:OE1	2.23	0.54
3:c:186:THR:HG22	3:c:199:LYS:HG2	1.89	0.54
9:i:28:ILE:HD13	9:i:63:ILE:HB	1.90	0.54
9:i:130:ARG:NH1	22:v:35:A:OP2	2.39	0.54
10:j:26:VAL:HG22	10:j:30:LYS:HZ3	1.73	0.54
25:A:872:G:C5	25:A:873:U:H1'	2.43	0.54
30:F:8:TYR:HA	30:F:12:ILE:HB	1.90	0.54
6:f:4:TYR:CE1	6:f:91:ARG:HB2	2.43	0.54
25:A:1741:A:O2'	25:A:1742:A:OP1	2.25	0.54
25:A:2099:G:H22	25:A:2106:A:H3'	1.73	0.54
30:F:100:LEU:O	30:F:104:LEU:N	2.36	0.54
32:H:60:GLU:O	32:H:64:ALA:N	2.38	0.54
2:b:136:MET:HA	2:b:139:ARG:HD3	1.89	0.53
1:a:315:A:H2'	1:a:316:C:H6	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:k:101:ASN:OD1	11:k:102:ALA:N	2.42	0.53
25:A:882:C:H2'	25:A:883:U:O2	2.08	0.53
25:A:1070:C:O2'	25:A:1071:U:H5'	2.09	0.53
1:a:533:A:H3'	1:a:534:G:H8	1.74	0.53
4:d:54:GLN:HG2	4:d:203:LEU:HB2	1.90	0.53
20:t:24:LEU:HB3	20:t:61:MET:CE	2.38	0.53
24:x:626:GLU:OE2	24:x:739:SER:N	2.41	0.53
25:A:314:A:N7	29:E:131:LYS:HE3	2.24	0.53
25:A:405:C:H2'	25:A:406:A:H8	1.73	0.53
50:1:48:ARG:HG3	50:1:48:ARG:HH11	1.73	0.53
4:d:115:ARG:HA	4:d:118:VAL:HG12	1.90	0.53
7:g:129:GLU:OE1	7:g:131:LYS:NZ	2.40	0.53
24:x:350:HIS:CD2	24:x:429:GLN:HB3	2.43	0.53
25:A:5:A:H2'	25:A:6:A:C8	2.43	0.53
25:A:1419:G:H2'	25:A:1420:A:C8	2.43	0.53
1:a:701:U:H2'	1:a:702:A:H8	1.74	0.53
25:A:2061:U:H2'	25:A:2062:U:C6	2.44	0.53
1:a:926:C:H5''	7:g:4:ARG:HH12	1.73	0.53
24:x:559:ALA:HB3	24:x:580:LEU:HD12	1.90	0.53
25:A:965:A:H5'	43:T:78:ARG:HH12	1.74	0.53
25:A:1043:U:H2'	25:A:1044:A:H5''	1.91	0.53
25:A:2119:U:H2'	25:A:2120:G:C8	2.44	0.53
25:A:2625:G:P	28:D:84:ARG:HH12	2.32	0.53
1:a:668:G:H2'	1:a:669:A:H8	1.72	0.53
1:a:1281:A:H2'	1:a:1282:A:C8	2.44	0.53
3:c:124:LEU:HD21	3:c:130:PHE:HB3	1.89	0.53
24:x:406:ARG:NE	24:x:440:ALA:HB2	2.23	0.53
24:x:602:ARG:O	24:x:606:LEU:HD23	2.09	0.53
25:A:744:G:H2'	25:A:745:U:C6	2.44	0.53
1:a:916:G:H2'	1:a:917:A:C8	2.43	0.53
22:v:8:4SU:H6	22:v:8:4SU:O5'	2.08	0.53
44:U:1:MET:HG2	44:U:109:ASP:H	1.74	0.53
1:a:1146:A:OP1	10:j:70:HIS:ND1	2.42	0.53
25:A:871:G:C4	25:A:885:A:N7	2.77	0.53
20:t:51:PHE:O	20:t:55:VAL:HG23	2.09	0.53
25:A:2098:U:H3'	25:A:2132:C:H2'	1.91	0.53
1:a:933:G:OP1	7:g:102:ARG:NH1	2.39	0.52
7:g:36:LYS:O	7:g:40:GLU:HG3	2.09	0.52
25:A:272:A:H2'	25:A:273:A:C8	2.44	0.52
36:M:7:MET:SD	36:M:18:ARG:NH1	2.83	0.52
1:a:1181:G:H5'	9:i:115:LYS:HE3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:o:8:LYS:HG2	15:o:31:LEU:HD22	1.91	0.52
27:C:72:ASP:OD1	27:C:189:ARG:NH2	2.43	0.52
1:a:181:U:N3	1:a:183:A:OP2	2.41	0.52
9:i:75:GLN:O	9:i:79:ILE:HG12	2.08	0.52
43:T:59:VAL:HG22	43:T:101:ILE:HG12	1.92	0.52
1:a:1247:G:H2'	1:a:1248:G:H8	1.73	0.52
24:x:343:PRO:HG2	24:x:391:VAL:HG23	1.91	0.52
24:x:545:GLY:H	24:x:557:VAL:HG23	1.74	0.52
24:x:606:LEU:HD13	24:x:609:GLN:NE2	2.21	0.52
25:A:2122:A:H3'	25:A:2140:C:N4	2.24	0.52
25:A:2645:C:OP1	31:G:158:LYS:NZ	2.38	0.52
33:I:34:THR:HG22	33:I:36:GLY:H	1.74	0.52
1:a:459:A:O2'	1:a:460:A:O5'	2.27	0.52
1:a:593:U:H2'	1:a:594:G:H8	1.75	0.52
6:f:75:GLU:O	6:f:79:ARG:HG2	2.10	0.52
10:j:26:VAL:C	10:j:30:LYS:HZ3	2.17	0.52
25:A:694:G:H1'	25:A:717:A:N6	2.24	0.52
30:F:111:VAL:HG23	30:F:112:ARG:N	2.22	0.52
39:P:32:GLU:HG3	39:P:115:LEU:HD12	1.92	0.52
1:a:331:G:H2'	1:a:332:A:C8	2.45	0.52
1:a:466:U:H3'	1:a:467:G:H21	1.74	0.52
1:a:1071:G:N2	1:a:1074:A:OP2	2.36	0.52
10:j:26:VAL:HG22	10:j:30:LYS:NZ	2.25	0.52
25:A:2095:U:O4	25:A:2169:G:N2	2.41	0.52
1:a:1308:C:OP2	19:s:4:SER:OG	2.23	0.52
24:x:535:VAL:HG21	24:x:592:MET:SD	2.50	0.52
33:I:51:TYR:O	33:I:84:PHE:N	2.42	0.52
1:a:78:A:H2'	1:a:79:G:H8	1.75	0.52
1:a:1237:U:O2'	13:m:27:ARG:NH2	2.41	0.52
11:k:85:ASN:ND2	11:k:111:THR:OG1	2.43	0.52
28:D:181:ASP:OD2	28:D:184:ARG:NH2	2.41	0.52
8:h:18:GLN:HE21	8:h:72:ILE:HB	1.74	0.52
24:x:647:ASP:OD1	24:x:648:VAL:N	2.43	0.52
25:A:694:G:H1'	25:A:717:A:H61	1.75	0.52
25:A:694:G:H2'	25:A:716:G:H22	1.73	0.52
25:A:2154:U:O4	25:A:2158:A:N7	2.43	0.52
25:A:2738:G:OP2	31:G:3:ARG:NH1	2.42	0.52
25:A:2775:A:H2'	25:A:2776:C:C6	2.45	0.52
35:L:45:THR:OG1	35:L:48:VAL:HG12	2.10	0.52
1:a:940:A:H2'	1:a:941:G:H8	1.74	0.52
9:i:10:GLY:HA2	9:i:81:HIS:HD2	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:2154:U:C2	25:A:2158:A:N6	2.78	0.52
28:D:118:PHE:HA	28:D:164:HIS:H	1.75	0.52
1:a:957:G:N2	10:j:57:VAL:HG11	2.25	0.51
3:c:167:TRP:HZ3	3:c:169:ARG:HD2	1.75	0.51
4:d:37:VAL:HG23	4:d:42:GLY:HA2	1.91	0.51
4:d:105:MET:HE1	4:d:171:VAL:HG21	1.91	0.51
8:h:113:ASP:OD1	8:h:114:ARG:N	2.43	0.51
25:A:2191:G:OP2	27:C:147:LYS:NZ	2.39	0.51
1:a:671:U:H3	1:a:707:G:H22	1.58	0.51
3:c:22:TRP:HB3	3:c:59:ARG:HB2	1.93	0.51
6:f:43:GLY:HA2	6:f:59:TYR:H	1.74	0.51
25:A:27:G:H1'	25:A:504:A:N6	2.24	0.51
25:A:1473:U:H3	25:A:1490:G:H1	1.58	0.51
25:A:1519:G:C5	25:A:1520:U:C5	2.98	0.51
25:A:1642:A:O2'	25:A:1643:G:OP1	2.26	0.51
25:A:1756:U:O2'	25:A:1945:C:OP1	2.28	0.51
25:A:2117:U:N3	25:A:2120:G:OP2	2.43	0.51
1:a:331:G:H2'	1:a:332:A:H8	1.75	0.51
6:f:98:GLU:O	6:f:98:GLU:HG2	2.10	0.51
24:x:694:LEU:HD23	24:x:714:LEU:HD13	1.93	0.51
25:A:467:G:N1	25:A:470:A:OP2	2.39	0.51
25:A:1460:U:H2'	25:A:1461:G:O4'	2.11	0.51
25:A:2230:U:H2'	25:A:2231:U:C6	2.45	0.51
25:A:2834:U:H2'	25:A:2835:G:O4'	2.09	0.51
32:H:63:ALA:HA	32:H:66:GLU:OE2	2.10	0.51
34:J:15:ALA:HB1	34:J:47:GLN:HA	1.91	0.51
1:a:60:A:N1	1:a:101:G:O2'	2.41	0.51
1:a:401:U:H2'	1:a:402:G:C8	2.44	0.51
1:a:667:G:H2'	1:a:668:G:C8	2.46	0.51
13:m:73:ILE:O	13:m:77:ILE:HG12	2.11	0.51
25:A:700:U:H2'	25:A:701:A:C8	2.46	0.51
25:A:871:G:C2	25:A:885:A:N7	2.78	0.51
1:a:77:G:H2'	1:a:78:A:H8	1.75	0.51
1:a:174:U:C2	1:a:189:A:N6	2.78	0.51
1:a:1143:C:O5'	1:a:1143:C:H6	1.93	0.51
1:a:1296:C:OP1	13:m:13:LYS:NZ	2.39	0.51
4:d:174:ASP:OD2	4:d:177:LYS:NZ	2.42	0.51
16:p:39:PHE:HB2	16:p:50:LEU:HD12	1.92	0.51
17:q:64:ILE:CG1	17:q:76:TRP:CE3	2.93	0.51
17:q:68:ARG:HG3	17:q:68:ARG:HH11	1.76	0.51
25:A:1522:U:H6	25:A:1522:U:O5'	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:617:C:H2'	1:a:618:C:H6	1.75	0.51
1:a:1341:G:O6	9:i:12:ARG:NH2	2.44	0.51
6:f:51:ILE:O	6:f:54:VAL:HG22	2.10	0.51
9:i:107:ASP:OD2	9:i:109:ARG:NE	2.39	0.51
25:A:2315:A:H2'	25:A:2316:A:H8	1.73	0.51
1:a:730:C:H2'	1:a:731:A:C8	2.46	0.51
1:a:1315:U:O2'	19:s:78:ARG:NH2	2.44	0.51
12:l:114:ARG:HB2	12:l:119:ALA:HB3	1.93	0.51
13:m:33:ILE:HG23	13:m:59:GLU:HB3	1.91	0.51
24:x:650:GLY:HA2	24:x:653:GLU:OE2	2.11	0.51
25:A:2605:G:H21	28:D:155:VAL:HG21	1.76	0.51
35:L:141:LYS:O	35:L:142:ILE:HG22	2.10	0.51
1:a:45:G:H2'	1:a:46:G:C8	2.46	0.51
1:a:518:G:H2'	1:a:519:C:C6	2.46	0.51
1:a:926:C:H5''	7:g:4:ARG:NH1	2.26	0.51
1:a:961:5MC:H2'	1:a:962:A:C2	2.45	0.51
1:a:1137:G:H2'	1:a:1138:G:H8	1.76	0.51
4:d:140:GLY:N	4:d:182:PHE:O	2.44	0.51
10:j:83:THR:O	10:j:87:LEU:N	2.44	0.51
12:l:74:LEU:HD21	12:l:104:THR:HG22	1.92	0.51
56:7:36:THR:HG22	56:7:38:LYS:H	1.75	0.51
1:a:216:U:H2'	1:a:217:A:H8	1.76	0.50
1:a:505:C:OP1	4:d:44:ARG:NH1	2.44	0.50
1:a:902:A:H2'	1:a:903:A:C8	2.46	0.50
2:b:29:LYS:O	2:b:45:LYS:NZ	2.29	0.50
3:c:77:ILE:HG12	3:c:84:VAL:HG11	1.93	0.50
25:A:2179:G:H2'	25:A:2180:G:H8	1.76	0.50
25:A:2536:G:O2'	25:A:2537:G:OP1	2.26	0.50
35:L:114:LEU:HG	35:L:118:MET:HE3	1.94	0.50
1:a:1031:C:H2'	1:a:1032:U:C6	2.46	0.50
1:a:1056:U:H2'	1:a:1057:C:C6	2.47	0.50
7:g:138:ARG:HG3	7:g:142:HIS:HE1	1.75	0.50
43:T:21:LYS:NZ	43:T:95:GLU:OE1	2.44	0.50
1:a:125:U:H2'	1:a:126:C:C6	2.47	0.50
4:d:117:LEU:HB3	4:d:123:ILE:HD11	1.92	0.50
25:A:191:A:H2'	25:A:192:C:C6	2.46	0.50
25:A:847:G:OP1	48:Y:78:LYS:NZ	2.42	0.50
49:Z:7:VAL:HG23	49:Z:8:THR:HG23	1.94	0.50
1:a:83:G:H2'	1:a:84:C:H6	1.75	0.50
1:a:524:G:H5'	1:a:525:U:H5'	1.92	0.50
3:c:56:ASP:HB2	3:c:67:THR:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:34:PHE:O	5:e:53:LYS:HA	2.11	0.50
10:j:11:LYS:HE2	10:j:71:LYS:HE2	1.93	0.50
24:x:694:LEU:HB3	24:x:716:MET:HG3	1.93	0.50
25:A:899:A:C5	38:O:13:MET:HG3	2.46	0.50
30:F:102:ARG:HG2	30:F:106:ILE:HD12	1.94	0.50
1:a:687:G:O2'	1:a:688:A:OP1	2.29	0.50
10:j:15:HIS:HA	10:j:18:ILE:HG22	1.92	0.50
24:x:417:ILE:HG22	24:x:445:VAL:HB	1.93	0.50
25:A:444:A:O2'	25:A:445:A:OP1	2.23	0.50
52:3:13:GLU:OE2	52:3:23:LYS:NZ	2.45	0.50
1:a:204:C:O2'	1:a:206:G:O6	2.29	0.50
1:a:668:G:H2'	1:a:669:A:C8	2.47	0.50
1:a:730:C:H2'	1:a:731:A:H8	1.77	0.50
25:A:823:A:H2'	25:A:824:G:C8	2.46	0.50
25:A:1518:C:H2'	25:A:1519:G:C8	2.43	0.50
25:A:2151:C:OP2	25:A:2158:A:O2'	2.30	0.50
25:A:2268:A:O2'	25:A:2269:G:H5'	2.11	0.50
30:F:43:ALA:HB2	30:F:49:ILE:HG12	1.93	0.50
57:8:30:GLU:HG3	57:8:32:ARG:H	1.77	0.50
1:a:1027:G:H2'	1:a:1028:G:O4'	2.12	0.50
9:i:114:LYS:NZ	9:i:115:LYS:O	2.43	0.50
16:p:15:PRO:HB2	16:p:41:PRO:HG2	1.94	0.50
28:D:15:ILE:HD11	28:D:178:VAL:HG11	1.93	0.50
36:M:34:GLY:N	36:M:37:ASP:OD1	2.44	0.50
45:V:68:ARG:HG3	45:V:68:ARG:HH11	1.77	0.50
1:a:944:U:H2'	1:a:945:G:C8	2.47	0.50
19:s:30:PRO:HA	19:s:48:THR:HG23	1.94	0.50
24:x:415:ILE:HG21	24:x:499:VAL:HG23	1.94	0.50
25:A:2124:C:H2'	25:A:2125:G:O4'	2.12	0.50
30:F:91:LEU:HB3	30:F:96:MET:HB3	1.92	0.50
1:a:65:A:H62	1:a:375:A:N6	2.10	0.50
1:a:418:G:H2'	1:a:419:A:C8	2.47	0.50
13:m:79:ARG:O	13:m:83:LEU:HG	2.12	0.50
25:A:508:C:OP1	53:A:13:ARG:NH2	2.45	0.50
25:A:1379:A:N6	45:V:17:GLU:OE2	2.35	0.50
25:A:1766:U:H5	25:A:1771:A:N7	2.10	0.50
25:A:2150:U:H5''	25:A:2150:U:H6	1.76	0.50
25:A:2173:G:C8	25:A:2174:C:H5	2.30	0.50
1:a:512:C:OP2	1:a:524:G:O2'	2.24	0.49
1:a:757:G:H2'	1:a:758:C:C6	2.47	0.49
1:a:1021:C:H2'	1:a:1022:C:C5	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:744:G:H2'	25:A:745:U:H6	1.76	0.49
25:A:2215:G:H2'	25:A:2216:U:C6	2.46	0.49
28:D:102:GLN:OE1	28:D:105:GLN:NE2	2.45	0.49
1:a:730:C:OP1	18:r:61:ARG:NH2	2.45	0.49
1:a:995:G:H2'	1:a:996:A:H8	1.77	0.49
1:a:1403:C:H2'	1:a:1404:A:H8	1.77	0.49
24:x:797:ARG:HH11	24:x:800:LYS:HA	1.76	0.49
25:A:1915:A:H2'	25:A:1916:G:O4'	2.12	0.49
27:C:130:MET:HE3	27:C:135:ILE:HG12	1.93	0.49
52:3:35:ASP:N	52:3:35:ASP:OD1	2.44	0.49
1:a:263:U:H2'	1:a:264:A:C8	2.46	0.49
4:d:12:SER:HA	4:d:19:LEU:HD23	1.95	0.49
5:e:77:LEU:HD13	5:e:80:THR:H	1.76	0.49
9:i:4:THR:O	9:i:5:GLN:HG2	2.12	0.49
25:A:882:C:H5''	25:A:883:U:OP2	2.12	0.49
25:A:1325:G:O2'	25:A:1380:A:N1	2.44	0.49
31:G:36:LYS:HE3	31:G:38:HIS:CE1	2.48	0.49
35:L:45:THR:HG22	42:S:64:ARG:NH2	2.25	0.49
7:g:22:ILE:HG23	7:g:101:MET:HE2	1.94	0.49
30:F:11:GLU:OE2	30:F:11:GLU:N	2.45	0.49
46:W:32:ARG:NH2	46:W:63:PRO:HG2	2.27	0.49
1:a:499:G:H2'	1:a:500:G:H8	1.76	0.49
1:a:1020:G:H1	1:a:1029:A:N6	2.11	0.49
1:a:1244:A:H2'	1:a:1245:A:C8	2.47	0.49
1:a:1308:C:H2'	1:a:1309:U:C6	2.47	0.49
13:m:92:ARG:NE	25:A:877:C:O2	2.46	0.49
25:A:191:A:H2'	25:A:192:C:H6	1.78	0.49
25:A:1673:C:H2'	25:A:1674:A:C8	2.47	0.49
28:D:2:THR:HA	28:D:84:ARG:O	2.12	0.49
49:Z:68:LEU:HA	49:Z:71:LEU:HD12	1.93	0.49
13:m:68:ASP:OD1	13:m:69:LEU:N	2.46	0.49
25:A:1537:U:H2'	25:A:1538:G:C8	2.47	0.49
25:A:2191:G:H4'	27:C:150:LYS:HD3	1.95	0.49
25:A:2391:U:H2'	25:A:2392:G:O4'	2.12	0.49
25:A:2524:U:H2'	25:A:2525:C:C6	2.48	0.49
1:a:446:A:H61	1:a:474:U:H3	1.60	0.49
12:l:100:GLY:N	12:l:104:THR:OG1	2.45	0.49
25:A:1420:A:H2'	25:A:1421:A:H8	1.77	0.49
36:M:7:MET:HE1	36:M:44:LYS:HD2	1.93	0.49
1:a:454:A:H2'	1:a:455:A:C8	2.48	0.49
1:a:1005:C:H2'	1:a:1006:A:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:649:G:H4'	29:E:94:LYS:HG2	1.95	0.49
25:A:1276:C:H2'	25:A:1277:A:C8	2.48	0.49
1:a:333:C:OP2	36:M:97:ARG:NH1	2.36	0.49
1:a:378:G:H2'	1:a:379:C:H6	1.76	0.49
25:A:801:U:H2'	37:N:21:ARG:HA	1.95	0.49
25:A:1575:C:H2'	25:A:1576:A:H5'	1.95	0.49
50:1:36:GLN:HG3	50:1:36:GLN:O	2.12	0.49
55:6:41:ARG:HD2	55:6:43:THR:H	1.77	0.49
1:a:65:A:C5	1:a:194:G:H1'	2.48	0.49
4:d:99:ASP:OD1	4:d:99:ASP:N	2.45	0.49
21:u:39:GLU:OE2	21:u:47:ARG:NE	2.39	0.49
25:A:570:U:H2'	25:A:571:C:H6	1.78	0.49
25:A:570:U:H2'	25:A:571:C:C6	2.48	0.49
25:A:2761:C:H2'	25:A:2762:A:O4'	2.13	0.49
36:M:17:ARG:HH21	36:M:47:ILE:HD11	1.77	0.49
56:7:30:HIS:ND1	56:7:31:ILE:HG13	2.28	0.49
7:g:69:ILE:HG23	7:g:100:ALA:HB1	1.95	0.48
9:i:115:LYS:HB2	9:i:118:LEU:HD12	1.94	0.48
11:k:49:GLY:O	11:k:69:ARG:NH1	2.44	0.48
25:A:579:U:H2'	25:A:580:A:C8	2.48	0.48
25:A:629:U:H2'	25:A:630:C:C6	2.48	0.48
25:A:1783:U:H2'	25:A:1784:C:C6	2.48	0.48
47:X:37:ASP:OD1	47:X:37:ASP:N	2.46	0.48
1:a:593:U:H2'	1:a:594:G:C8	2.48	0.48
1:a:1105:A:H61	3:c:177:THR:HG22	1.78	0.48
1:a:1245:A:H2'	1:a:1246:A:C8	2.47	0.48
25:A:1084:U:H1'	25:A:1087:U:H5	1.78	0.48
25:A:2100:U:H3'	25:A:2101:A:H8	1.77	0.48
25:A:2130:C:H3'	25:A:2131:G:C8	2.49	0.48
30:F:73:SER:O	30:F:79:ILE:HG13	2.13	0.48
1:a:73:A:H8	1:a:90:G:H21	1.61	0.48
1:a:107:G:H1'	1:a:348:G:H5'	1.95	0.48
1:a:208:C:C2	1:a:209:C:C5	3.00	0.48
1:a:488:G:H2'	1:a:490:A:H8	1.78	0.48
1:a:1221:A:H5''	19:s:83:HIS:CD2	2.47	0.48
5:e:83:GLN:NE2	5:e:151:PRO:HD3	2.27	0.48
25:A:4:C:H2'	25:A:5:A:H8	1.79	0.48
25:A:100:U:OP1	25:A:102:G:H5'	2.13	0.48
25:A:2088:A:H2'	25:A:2089:G:H8	1.78	0.48
25:A:2294:G:H1'	25:A:2298:A:H62	1.78	0.48
29:E:82:THR:HB	29:E:85:ALA:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:12:ILE:HD13	52:3:28:LEU:HB2	1.95	0.48
1:a:157:C:H2'	1:a:158:G:H8	1.77	0.48
3:c:17:GLU:N	3:c:17:GLU:OE1	2.45	0.48
4:d:57:GLU:OE2	4:d:199:LEU:HB3	2.13	0.48
5:e:78:ASN:HB2	5:e:83:GLN:OE1	2.13	0.48
7:g:53:ARG:HE	7:g:125:LEU:HD21	1.78	0.48
14:n:20:TYR:O	14:n:22:LYS:N	2.47	0.48
24:x:411:GLN:O	24:x:411:GLN:HG2	2.14	0.48
37:N:81:GLU:HB3	37:N:100:LEU:HD11	1.96	0.48
39:P:32:GLU:OE1	39:P:78:LYS:NZ	2.39	0.48
1:a:248:G:O6	1:a:267:A:N6	2.47	0.48
1:a:427:G:H2'	1:a:428:C:C6	2.49	0.48
2:b:127:ASP:OD1	2:b:127:ASP:N	2.46	0.48
4:d:54:GLN:HG3	4:d:199:LEU:HD23	1.95	0.48
25:A:295:C:OP2	46:W:81:ARG:NH2	2.47	0.48
25:A:1373:C:H2'	25:A:1374:A:C8	2.48	0.48
38:O:6:ARG:HG2	38:O:6:ARG:HH11	1.78	0.48
1:a:1137:G:H2'	1:a:1138:G:C8	2.48	0.48
5:e:15:LYS:NZ	5:e:117:GLU:OE2	2.43	0.48
25:A:1530:G:H2'	25:A:1531:A:C8	2.48	0.48
26:B:114:C:H2'	26:B:115:A:H8	1.78	0.48
30:F:102:ARG:HD3	52:3:26:SER:HB3	1.96	0.48
40:Q:25:VAL:HB	40:Q:89:VAL:HG12	1.94	0.48
14:n:36:SER:HG	14:n:41:ARG:HH21	1.56	0.48
25:A:1160:A:H2'	25:A:1161:C:C6	2.48	0.48
25:A:2051:C:H2'	25:A:2052:C:C6	2.48	0.48
31:G:137:ASP:OD2	31:G:137:ASP:N	2.47	0.48
46:W:33:LEU:HD11	46:W:66:VAL:HG23	1.96	0.48
1:a:120:A:H2'	1:a:121:G:O4'	2.13	0.48
1:a:157:C:H2'	1:a:158:G:C8	2.48	0.48
18:r:63:ARG:HD3	18:r:70:TYR:HA	1.94	0.48
21:u:58:LYS:O	21:u:62:ARG:HG2	2.14	0.48
25:A:2179:G:H2'	25:A:2180:G:C8	2.49	0.48
25:A:2258:G:OP1	48:Y:18:SER:HB3	2.14	0.48
25:A:2788:U:H2'	25:A:2789:U:C6	2.49	0.48
27:C:98:ASP:OD1	27:C:98:ASP:N	2.46	0.48
29:E:3:LEU:HD12	29:E:13:VAL:HG11	1.96	0.48
41:R:18:ILE:HD13	41:R:77:THR:HG22	1.96	0.48
1:a:438:U:H2'	1:a:439:G:C8	2.48	0.48
1:a:1124:A:H2'	1:a:1125:G:H8	1.79	0.48
6:f:49:TYR:HB3	18:r:74:HIS:ND1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:x:640:LEU:N	24:x:668:GLN:O	2.47	0.48
25:A:1352:A:OP1	49:Z:3:ARG:NH1	2.46	0.48
38:O:78:PRO:HG2	38:O:81:VAL:HG21	1.96	0.48
1:a:4:C:O2	1:a:5:U:O2'	2.23	0.48
1:a:437:U:H2'	1:a:438:U:C6	2.48	0.48
6:f:18:VAL:O	6:f:22:VAL:HG23	2.14	0.48
8:h:75:VAL:HG23	8:h:129:VAL:HG22	1.96	0.48
9:i:42:GLU:HG2	9:i:44:ALA:H	1.79	0.48
9:i:67:VAL:CG2	9:i:79:ILE:HD11	2.43	0.48
11:k:87:LYS:HB2	11:k:113:VAL:HG23	1.96	0.48
14:n:20:TYR:C	14:n:22:LYS:H	2.22	0.48
25:A:2273:G:H4'	25:A:2274:A:O5'	2.14	0.48
37:N:88:ASP:H	37:N:118:ARG:NH1	2.12	0.48
1:a:67:C:H2'	1:a:68:G:C8	2.49	0.47
1:a:124:A:N3	1:a:257:A:O2'	2.39	0.47
1:a:566:A:H5'	1:a:567:A:OP2	2.14	0.47
5:e:79:GLY:O	5:e:80:THR:OG1	2.31	0.47
7:g:107:PHE:CZ	7:g:137:LYS:HD2	2.49	0.47
13:m:87:ARG:O	13:m:91:HIS:HB2	2.14	0.47
25:A:371:G:H5'	49:Z:18:ILE:HD13	1.96	0.47
25:A:1490:G:H2'	25:A:1491:U:H6	1.78	0.47
25:A:2837:A:N7	25:A:2855:A:O2'	2.44	0.47
26:B:9:G:C2	26:B:10:A:C8	3.02	0.47
1:a:155:A:H2'	1:a:156:A:C8	2.50	0.47
1:a:995:G:H2'	1:a:996:A:C8	2.49	0.47
15:o:13:ASN:HA	15:o:16:LYS:HE3	1.96	0.47
25:A:1353:A:OP1	49:Z:2:SER:OG	2.32	0.47
29:E:169:ARG:HG3	29:E:170:ASP:H	1.80	0.47
1:a:179:C:C2	1:a:187:A:C2	3.02	0.47
1:a:574:C:H2'	1:a:575:G:O4'	2.14	0.47
7:g:91:VAL:O	7:g:96:ARG:NH2	2.34	0.47
11:k:29:ASN:OD1	11:k:30:THR:N	2.47	0.47
25:A:1407:U:O2'	25:A:1408:G:O5'	2.31	0.47
25:A:2292:U:C2	30:F:151:GLY:HA3	2.48	0.47
25:A:2817:C:H5''	28:D:57:ARG:HE	1.79	0.47
25:A:2835:G:O2'	25:A:2854:G:N2	2.40	0.47
37:N:88:ASP:O	37:N:121:THR:HG22	2.14	0.47
1:a:1308:C:H2'	1:a:1309:U:H6	1.79	0.47
11:k:20:ILE:CD1	11:k:83:ASP:HB3	2.45	0.47
25:A:2122:A:C8	25:A:2140:C:N4	2.83	0.47
38:O:48:GLU:OE2	38:O:52:ARG:NH1	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:4:52:LYS:HE3	53:4:55:ASP:HA	1.96	0.47
1:a:770:G:O2'	1:a:771:A:OP2	2.21	0.47
2:b:83:GLU:HG3	2:b:214:LEU:HB3	1.97	0.47
25:A:1781:A:H2'	25:A:1782:C:C6	2.50	0.47
29:E:58:PRO:HB2	29:E:59:TRP:CE3	2.50	0.47
30:F:113:ASP:O	30:F:114:PHE:CD1	2.67	0.47
1:a:1255:A:N6	1:a:1268:G:HI1'	2.29	0.47
1:a:1350:A:H2'	1:a:1351:A:H8	1.78	0.47
15:o:16:LYS:HD3	15:o:19:GLU:HA	1.96	0.47
25:A:652:G:H5'	37:N:16:LYS:HB2	1.97	0.47
30:F:47:LYS:HE3	30:F:84:PRO:HD2	1.95	0.47
1:a:77:G:H2'	1:a:78:A:C8	2.50	0.47
1:a:142:G:O2'	1:a:1440:A:N3	2.42	0.47
1:a:210:U:H2'	1:a:211:C:H6	1.80	0.47
1:a:455:A:N6	1:a:456:G:O6	2.48	0.47
1:a:495:C:H2'	1:a:496:A:H8	1.80	0.47
3:c:46:LYS:HD2	3:c:47:LEU:N	2.29	0.47
4:d:194:ASP:OD1	4:d:194:ASP:N	2.48	0.47
7:g:111:ARG:HD3	7:g:123:GLU:OE2	2.14	0.47
24:x:644:LEU:O	24:x:674:GLY:HA2	2.14	0.47
25:A:1298:G:OP2	25:A:1298:G:N2	2.28	0.47
25:A:2791:C:H2'	25:A:2792:C:C6	2.49	0.47
41:R:34:LYS:HD3	41:R:39:GLN:HB2	1.95	0.47
47:X:4:PHE:C	47:X:5:ILE:HD13	2.38	0.47
1:a:144:U:H2'	1:a:145:A:H8	1.80	0.47
1:a:995:G:O6	1:a:1034:A:N6	2.48	0.47
1:a:1510:2MG:N2	1:a:1513:MA6:OP2	2.45	0.47
14:n:41:ARG:HG2	19:s:7:LYS:HE2	1.96	0.47
24:x:445:VAL:HG13	24:x:480:PRO:HG2	1.96	0.47
25:A:264:U:O2'	25:A:265:A:OP2	2.31	0.47
25:A:579:U:H2'	25:A:580:A:H8	1.80	0.47
25:A:792:A:HO2'	25:A:793:U:P	2.36	0.47
25:A:1777:C:H2'	25:A:1778:A:C8	2.49	0.47
1:a:186:G:H2'	1:a:187:A:H8	1.80	0.47
1:a:372:G:N1	1:a:380:C:N3	2.63	0.47
15:o:26:GLU:HG2	15:o:81:LEU:HD22	1.97	0.47
24:x:520:VAL:HA	24:x:535:VAL:HA	1.96	0.47
25:A:817:U:O2'	25:A:2055:U:N3	2.48	0.47
25:A:2417:A:H2'	25:A:2417:A:N3	2.30	0.47
25:A:2471:G:OP1	38:O:45:ARG:NH2	2.48	0.47
25:A:2862:C:H4'	41:R:3:ASN:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:j:17:LEU:H	10:j:17:LEU:HD23	1.80	0.47
25:A:363:G:O2'	25:A:391:G:O6	2.33	0.47
28:D:186:LEU:HD21	41:R:5:ILE:HD12	1.96	0.47
1:a:595:G:H2'	1:a:596:A:C8	2.47	0.46
1:a:1516:U:H2'	1:a:1517:G:H8	1.80	0.46
2:b:96:TRP:NE1	2:b:175:GLU:OE1	2.41	0.46
7:g:111:ARG:HH12	7:g:122:GLY:C	2.22	0.46
24:x:728:ASP:OD1	24:x:742:ARG:NH2	2.35	0.46
25:A:567:G:O2'	25:A:1241:A:OP1	2.33	0.46
25:A:764:C:O2'	25:A:767:A:N3	2.47	0.46
25:A:837:C:H2'	25:A:838:A:C8	2.49	0.46
25:A:1711:A:H62	25:A:1723:G:H21	1.63	0.46
25:A:2102:G:N1	25:A:2106:A:OP2	2.34	0.46
25:A:2498:U:H5''	28:D:128:ARG:HG3	1.97	0.46
44:U:11:ARG:NH2	44:U:98:LYS:HB3	2.30	0.46
1:a:17:U:H2'	1:a:18:C:C6	2.50	0.46
1:a:387:A:C2	1:a:388:G:C8	3.03	0.46
1:a:722:A:H2'	1:a:723:A:C8	2.50	0.46
11:k:68:GLU:HG2	11:k:99:ALA:HB1	1.97	0.46
25:A:1340:A:H2'	25:A:1341:A:C8	2.50	0.46
25:A:2510:G:HO2'	25:A:2751:A:HO2'	1.62	0.46
27:C:146:LEU:HD21	27:C:154:ILE:HD11	1.97	0.46
1:a:73:A:N6	1:a:90:G:HO2'	2.12	0.46
1:a:1020:G:H1	1:a:1029:A:H61	1.63	0.46
1:a:1296:C:C4	13:m:17:ILE:HD11	2.50	0.46
2:b:136:MET:O	2:b:139:ARG:HG2	2.16	0.46
3:c:12:LEU:HD23	3:c:18:HIS:CE1	2.51	0.46
4:d:67:VAL:HG21	4:d:94:LEU:HD11	1.97	0.46
4:d:95:GLU:OE2	4:d:100:ASN:ND2	2.48	0.46
4:d:142:VAL:O	4:d:142:VAL:HG13	2.15	0.46
13:m:29:THR:O	13:m:33:ILE:HG12	2.16	0.46
17:q:79:VAL:HG23	17:q:80:ASP:OD1	2.15	0.46
30:F:19:GLU:OE1	30:F:20:LEU:HD22	2.15	0.46
1:a:471:U:H2'	1:a:472:U:C6	2.50	0.46
24:x:465:LEU:HD12	24:x:468:LEU:HD12	1.98	0.46
25:A:853:G:H2'	25:A:854:C:C6	2.50	0.46
1:a:270:G:H5'	17:q:20:MET:SD	2.56	0.46
1:a:367:A:N3	1:a:476:A:N6	2.64	0.46
1:a:469:U:H2'	1:a:470:G:C8	2.51	0.46
1:a:1480:G:H2'	1:a:1481:G:O4'	2.15	0.46
5:e:127:LYS:HG3	5:e:128:CYS:N	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:o:55:GLY:O	15:o:59:MET:HG3	2.16	0.46
25:A:1052:G:H2'	25:A:1053:G:H8	1.80	0.46
25:A:2034:C:H2'	25:A:2035:G:H8	1.80	0.46
25:A:2149:A:H4'	25:A:2150:U:OP1	2.12	0.46
1:a:70:A:HO2'	1:a:71:U:H6	1.61	0.46
1:a:1120:U:O4	10:j:9:ARG:NH1	2.49	0.46
1:a:1395:G:H2'	1:a:1396:4OC:O4'	2.16	0.46
1:a:1431:A:H2'	1:a:1432:G:H8	1.81	0.46
7:g:135:VAL:HG23	7:g:136:LYS:HE2	1.97	0.46
17:q:54:ASN:O	17:q:57:ARG:NH1	2.45	0.46
25:A:2320:A:OP1	48:Y:77:ARG:NH2	2.44	0.46
28:D:10:CYS:SG	41:R:5:ILE:HD11	2.56	0.46
37:N:2:GLN:H	37:N:5:ASP:HB3	1.81	0.46
1:a:8:A:N6	4:d:206:LYS:HB2	2.31	0.46
1:a:1127:A:H2'	1:a:1128:C:C6	2.51	0.46
11:k:31:ILE:HG12	11:k:46:THR:HG22	1.98	0.46
24:x:783:ARG:HB2	24:x:826:ASP:OD1	2.15	0.46
25:A:272:A:H2'	25:A:273:A:H8	1.80	0.46
25:A:1344:C:H2'	25:A:1345:G:O4'	2.15	0.46
25:A:2851:G:O2'	25:A:2852:U:OP1	2.33	0.46
38:O:137:MET:HE2	47:X:60:PHE:CD2	2.51	0.46
1:a:34:C:H2'	1:a:35:G:H8	1.80	0.46
1:a:352:U:H2'	1:a:353:G:H8	1.80	0.46
1:a:845:U:H2'	1:a:846:A:C8	2.51	0.46
1:a:1030:A:H2'	1:a:1031:C:C6	2.50	0.46
2:b:114:LEU:HD13	2:b:144:LEU:HB3	1.97	0.46
4:d:182:PHE:HZ	4:d:186:PRO:HD3	1.79	0.46
8:h:54:GLU:O	8:h:56:LYS:N	2.34	0.46
22:v:31:G:H3'	22:v:32:5MC:HM53	1.98	0.46
25:A:990:A:H2'	25:A:991:A:C8	2.50	0.46
25:A:1071:U:O2'	34:J:118:THR:O	2.33	0.46
25:A:1456:A:H2'	25:A:1457:A:C8	2.51	0.46
1:a:384:U:O2'	16:p:28:ARG:NH1	2.43	0.46
1:a:902:A:H2'	1:a:903:A:H8	1.81	0.46
1:a:963:A:O2'	1:a:964:C:OP1	2.34	0.46
1:a:1032:U:H2'	1:a:1033:C:C6	2.49	0.46
1:a:1141:C:H2'	1:a:1142:U:C6	2.50	0.46
7:g:75:VAL:CG1	7:g:86:GLN:HB3	2.46	0.46
24:x:361:TYR:CE2	24:x:492:VAL:HG21	2.51	0.46
24:x:709:VAL:HG22	24:x:714:LEU:HD11	1.98	0.46
25:A:619:C:O2	25:A:629:U:O2'	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:797:U:OP1	37:N:36:LYS:HE3	2.16	0.46
25:A:1783:U:H2'	25:A:1784:C:H6	1.80	0.46
25:A:2150:U:H5'	25:A:2152:C:H41	1.80	0.46
27:C:107:PRO:HD2	27:C:110:VAL:HG21	1.98	0.46
29:E:47:THR:O	29:E:51:VAL:HG23	2.15	0.46
30:F:136:ILE:HG12	30:F:143:TYR:HD1	1.81	0.46
44:U:11:ARG:HD2	44:U:11:ARG:HA	1.72	0.46
1:a:73:A:OP2	1:a:90:G:N2	2.41	0.46
1:a:1005:C:H2'	1:a:1006:A:C8	2.50	0.46
3:c:79:LYS:HD3	3:c:79:LYS:O	2.16	0.46
10:j:14:ASP:OD1	10:j:14:ASP:N	2.46	0.46
25:A:300:U:H2'	25:A:301:G:O4'	2.15	0.46
25:A:626:G:H5''	37:N:128:THR:HB	1.97	0.46
25:A:1430:C:H2'	25:A:1431:A:H8	1.81	0.46
25:A:2578:C:H2'	25:A:2579:G:C8	2.51	0.46
50:1:26:PHE:CE1	50:1:30:MET:HE3	2.51	0.46
1:a:991:U:H2'	1:a:992:G:C8	2.50	0.45
1:a:1112:U:H1'	1:a:1173:A:C5	2.51	0.45
12:l:36:ARG:HG2	12:l:38:TYR:HD1	1.81	0.45
19:s:25:LYS:O	19:s:28:ARG:NH1	2.49	0.45
25:A:1795:A:H3'	25:A:1796:A:C8	2.52	0.45
25:A:2292:U:O2	30:F:151:GLY:HA3	2.17	0.45
30:F:38:MET:HE3	30:F:57:LEU:HB2	1.98	0.45
30:F:117:LEU:N	30:F:176:PRO:O	2.43	0.45
35:L:69:THR:O	35:L:90:GLU:HG3	2.16	0.45
47:X:174:VAL:O	47:X:178:HIS:ND1	2.45	0.45
1:a:22:G:O2'	1:a:907:A:N1	2.43	0.45
1:a:229:U:H2'	1:a:230:A:C8	2.50	0.45
1:a:489:A:H4'	1:a:490:A:OP1	2.16	0.45
2:b:73:LYS:HB3	2:b:76:ALA:HB3	1.98	0.45
9:i:118:LEU:CD2	9:i:124:ARG:HG2	2.46	0.45
25:A:347:U:H5'	25:A:348:U:OP2	2.16	0.45
25:A:1018:A:N6	25:A:1115:G:H2'	2.31	0.45
25:A:1074:A:H1'	25:A:1095:U:O2'	2.17	0.45
25:A:1400:A:H2'	25:A:1401:C:C6	2.51	0.45
25:A:2300:C:H2'	25:A:2301:G:H8	1.81	0.45
25:A:2791:C:H2'	25:A:2792:C:H6	1.81	0.45
34:J:14:LYS:HA	34:J:54:PRO:HA	1.98	0.45
1:a:397:C:H5''	4:d:133:PRO:HD2	1.98	0.45
1:a:1212:C:H2'	1:a:1213:A:C8	2.51	0.45
4:d:61:VAL:HA	4:d:64:ILE:HG12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:150:LYS:HD2	4:d:178:LYS:HD3	1.97	0.45
5:e:37:LEU:HD22	5:e:135:VAL:HG22	1.98	0.45
7:g:75:VAL:HG21	7:g:144:MET:HG2	1.98	0.45
9:i:81:HIS:NE2	9:i:85:ARG:HD2	2.31	0.45
12:l:93:VAL:C	12:l:94:ARG:HG3	2.41	0.45
25:A:786:U:H2'	25:A:787:C:C6	2.51	0.45
25:A:917:G:H2'	25:A:918:U:C6	2.51	0.45
25:A:2578:C:H2'	25:A:2579:G:H8	1.81	0.45
1:a:611:G:O6	1:a:618:C:N4	2.49	0.45
1:a:1033:C:H2'	1:a:1034:A:C8	2.47	0.45
1:a:1247:G:H2'	1:a:1248:G:C8	2.51	0.45
4:d:4:TYR:HE2	4:d:11:LEU:HD21	1.81	0.45
25:A:1029:A:H2'	25:A:1030:A:O4'	2.17	0.45
25:A:1372:A:O2'	25:A:1383:U:O2	2.34	0.45
25:A:1453:U:O3'	25:A:1536:G:O2'	2.34	0.45
25:A:1497:G:O2'	25:A:1498:G:OP1	2.32	0.45
25:A:2233:G:H2'	25:A:2234:A:C8	2.52	0.45
44:U:29:VAL:HG21	44:U:69:LEU:HB2	1.98	0.45
1:a:401:U:H5''	4:d:112:SER:OG	2.17	0.45
1:a:732:C:OP1	6:f:2:ARG:NH1	2.50	0.45
6:f:87:ASN:OD1	6:f:88:LEU:N	2.50	0.45
25:A:1448:C:O2'	25:A:1449:C:OP1	2.33	0.45
54:5:27:PRO:O	54:5:29:LYS:NZ	2.50	0.45
1:a:401:U:H2'	1:a:402:G:H8	1.82	0.45
1:a:1115:U:H2'	1:a:1116:U:C6	2.52	0.45
7:g:30:VAL:HG13	7:g:39:ALA:HB1	1.99	0.45
14:n:20:TYR:HB3	14:n:23:LYS:HE2	1.99	0.45
18:r:51:TYR:O	18:r:55:LEU:HD23	2.16	0.45
25:A:293:A:N3	25:A:313:C:O2'	2.47	0.45
25:A:358:A:O2'	25:A:359:U:H5'	2.17	0.45
25:A:938:C:H1'	25:A:974:A:C8	2.51	0.45
25:A:2724:G:H2'	25:A:2725:A:C8	2.52	0.45
51:2:30:ARG:NH1	51:2:33:HIS:HB2	2.32	0.45
1:a:41:G:H2'	1:a:42:G:H8	1.80	0.45
1:a:939:G:C2	1:a:940:A:C8	3.05	0.45
5:e:160:LYS:HG3	5:e:161:SER:N	2.31	0.45
7:g:66:LEU:HA	7:g:69:ILE:HG22	1.97	0.45
12:l:43:LYS:HG2	12:l:44:LYS:H	1.81	0.45
25:A:198:C:H2'	25:A:199:A:H5''	1.98	0.45
25:A:2104:A:O2'	25:A:2105:U:H5'	2.17	0.45
25:A:2544:G:H2'	25:A:2545:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:O:6:ARG:HG2	38:O:6:ARG:NH1	2.31	0.45
39:P:42:LYS:HG2	39:P:45:ARG:HH12	1.82	0.45
1:a:88:U:H2'	1:a:89:G:O4'	2.17	0.45
1:a:549:U:H2'	1:a:550:C:C6	2.51	0.45
1:a:1031:C:H2'	1:a:1032:U:H6	1.81	0.45
2:b:71:GLY:HA3	2:b:80:VAL:HG21	1.98	0.45
4:d:103:TYR:CD1	4:d:111:ARG:HD2	2.51	0.45
24:x:699:VAL:O	24:x:700:ARG:HD2	2.17	0.45
25:A:4:C:H2'	25:A:5:A:C8	2.52	0.45
25:A:91:A:H1'	25:A:92:A:C8	2.51	0.45
25:A:1845:A:N6	25:A:1871:G:H1'	2.30	0.45
31:G:115:TYR:HE2	31:G:144:VAL:HG13	1.82	0.45
35:L:73:MET:HE3	35:L:86:SER:OG	2.17	0.45
1:a:34:C:H2'	1:a:35:G:C8	2.52	0.45
1:a:89:G:H3'	1:a:90:G:H8	1.82	0.45
1:a:636:A:C5	8:h:107:ASN:HA	2.52	0.45
3:c:46:LYS:NZ	3:c:87:LEU:HD21	2.32	0.45
14:n:45:GLN:O	14:n:49:GLN:HG3	2.17	0.45
25:A:571:C:H2'	25:A:572:A:H8	1.82	0.45
25:A:2084:U:H2'	25:A:2085:U:C6	2.52	0.45
25:A:2302:G:H2'	25:A:2303:U:H6	1.82	0.45
36:M:38:ILE:HD11	36:M:111:PHE:CZ	2.48	0.45
43:T:79:ARG:HD2	43:T:80:ARG:NH1	2.32	0.45
46:W:5:ARG:HG2	46:W:6:ARG:H	1.81	0.45
47:X:64:ILE:HB	47:X:75:VAL:HG23	1.99	0.45
1:a:20:U:H2'	1:a:21:G:O4'	2.17	0.45
1:a:472:U:H2'	1:a:473:U:C6	2.52	0.45
9:i:71:GLY:O	9:i:75:GLN:HG3	2.17	0.45
17:q:20:MET:HB2	17:q:23:THR:OG1	2.17	0.45
25:A:1276:C:H2'	25:A:1277:A:H8	1.82	0.45
25:A:1910:U:H2'	25:A:1911:C:C6	2.52	0.45
32:H:76:VAL:O	32:H:143:LEU:HA	2.17	0.45
39:P:12:ARG:HB3	39:P:16:HIS:HB3	1.99	0.45
1:a:437:U:H2'	1:a:438:U:H6	1.82	0.44
1:a:454:A:H2'	1:a:455:A:H8	1.81	0.44
2:b:6:MET:HE2	2:b:47:LEU:HD12	1.98	0.44
6:f:43:GLY:HA3	6:f:58:HIS:CD2	2.52	0.44
1:a:446:A:O3'	16:p:73:GLN:NE2	2.50	0.44
1:a:893:C:H2'	1:a:894:A:C8	2.52	0.44
1:a:1114:C:H2'	1:a:1115:U:C6	2.51	0.44
1:a:1214:G:OP1	14:n:53:ARG:NH1	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1349:G:H2'	1:a:1350:A:H8	1.82	0.44
24:x:620:ALA:HB2	24:x:713:GLY:HA3	1.98	0.44
25:A:1074:A:C4	33:I:54:VAL:HG21	2.51	0.44
25:A:2001:A:H2'	25:A:2002:A:C8	2.51	0.44
27:C:266:ASN:OD1	27:C:267:MET:HG2	2.18	0.44
1:a:628:C:H2'	1:a:629:A:C8	2.52	0.44
3:c:124:LEU:HD23	3:c:124:LEU:HA	1.79	0.44
4:d:60:LYS:HD3	4:d:195:ILE:HG21	1.99	0.44
24:x:794:GLU:N	24:x:815:GLY:O	2.48	0.44
25:A:818:U:H2'	25:A:819:A:C8	2.52	0.44
25:A:2102:G:H21	25:A:2158:A:H2	1.65	0.44
25:A:2129:A:H2'	25:A:2130:C:C6	2.53	0.44
25:A:2136:U:H2'	25:A:2137:U:C6	2.52	0.44
3:c:56:ASP:HB2	3:c:67:THR:CG2	2.47	0.44
8:h:48:ASP:OD1	8:h:49:PHE:N	2.49	0.44
24:x:341:ARG:HG3	24:x:342:ALA:H	1.83	0.44
25:A:114:U:O2'	25:A:115:C:OP1	2.32	0.44
25:A:248:G:H5'	25:A:250:G:N7	2.33	0.44
25:A:2029:A:O2'	25:A:2030:U:OP1	2.33	0.44
45:V:53:LYS:O	45:V:87:GLN:HG2	2.17	0.44
1:a:507:U:H2'	1:a:508:C:C6	2.53	0.44
1:a:1385:U:H2'	1:a:1386:G:C8	2.52	0.44
6:f:9:LEU:HA	6:f:58:HIS:O	2.17	0.44
6:f:81:ASN:OD1	6:f:82:ASP:N	2.50	0.44
13:m:39:VAL:HG11	13:m:56:LEU:HD11	2.00	0.44
25:A:883:U:C3'	25:A:883:U:C6	3.01	0.44
25:A:1095:U:H2'	25:A:1096:A:C8	2.49	0.44
25:A:1529:U:H2'	25:A:1530:G:C8	2.52	0.44
25:A:1673:C:H2'	25:A:1674:A:H8	1.81	0.44
50:l:10:SER:H	50:l:13:GLN:NE2	2.16	0.44
1:a:84:C:H2'	1:a:85:U:H6	1.82	0.44
1:a:125:U:O2'	1:a:256:A:N3	2.46	0.44
1:a:1051:G:O2'	3:c:188:GLU:OE1	2.28	0.44
1:a:1132:G:H2'	1:a:1134:G:H8	1.83	0.44
4:d:102:VAL:HG13	4:d:114:SER:HB2	1.99	0.44
6:f:22:VAL:O	6:f:26:THR:HG23	2.18	0.44
9:i:44:ALA:HA	9:i:47:VAL:HG12	1.99	0.44
11:k:18:ASP:HA	11:k:81:ASN:HB2	1.99	0.44
13:m:117:ARG:CZ	13:m:117:ARG:HB3	2.46	0.44
25:A:571:C:H2'	25:A:572:A:C8	2.53	0.44
25:A:598:A:H2'	25:A:599:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A:1561:A:H2'	25:A:1562:A:C8	2.52	0.44
52:3:5:ILE:HG13	52:3:6:HIS:CD2	2.53	0.44
1:a:134:U:H2'	1:a:135:A:C8	2.53	0.44
4:d:170:TRP:HZ3	4:d:190:ASP:HB3	1.82	0.44
8:h:29:SER:HB3	8:h:57:PRO:HG2	2.00	0.44
19:s:27:ASP:OD1	19:s:27:ASP:N	2.50	0.44
24:x:611:LYS:O	24:x:615:VAL:HG23	2.17	0.44
25:A:1657:G:O2'	25:A:1978:U:O4	2.28	0.44
25:A:2302:G:H2'	25:A:2303:U:C6	2.52	0.44
1:a:408:A:O2'	1:a:409:A:OP1	2.32	0.44
2:b:100:MET:HA	2:b:107:ILE:HD12	1.99	0.44
14:n:27:LEU:O	14:n:31:ILE:HG12	2.17	0.44
24:x:339:VAL:HG22	24:x:512:PRO:HD3	1.99	0.44
24:x:562:ASP:OD1	24:x:566:LYS:N	2.40	0.44
25:A:772:A:O2'	27:C:224:ALA:O	2.35	0.44
25:A:2534:A:H2'	25:A:2535:U:C6	2.53	0.44
29:E:121:ALA:O	29:E:122:ASP:OD1	2.35	0.44
38:O:54:LEU:HD12	38:O:117:ALA:HB1	2.00	0.44
1:a:1336:C:H4'	9:i:126:GLN:O	2.18	0.44
3:c:6:HIS:HB2	14:n:89:MET:HE3	1.99	0.44
7:g:13:LEU:HG	7:g:21:GLN:HG3	2.00	0.44
12:l:20:ASP:HB3	12:l:86:ARG:HH21	1.82	0.44
24:x:427:MET:HB3	24:x:428:PRO:HD2	1.99	0.44
25:A:527:G:OP2	62:A:3501:HOH:O	2.21	0.44
25:A:1050:U:C2	25:A:1052:G:H5'	2.52	0.44
25:A:1407:U:O2'	25:A:1408:G:H8	2.00	0.44
25:A:1517:U:H2'	25:A:1518:C:C6	2.53	0.44
25:A:2122:A:H8	25:A:2140:C:N4	2.16	0.44
25:A:2130:C:H3'	25:A:2131:G:H8	1.83	0.44
25:A:2559:A:N7	28:D:150:GLN:HG3	2.32	0.44
28:D:39:LYS:HD2	28:D:82:GLU:OE2	2.17	0.44
32:H:19:VAL:HG12	32:H:21:ILE:HG23	1.99	0.44
43:T:37:ARG:HD2	43:T:53:VAL:HG11	1.99	0.44
1:a:138:G:H2'	1:a:139:G:H8	1.82	0.43
1:a:495:C:H2'	1:a:496:A:C8	2.53	0.43
4:d:48:LEU:HD12	4:d:53:LEU:HD22	2.00	0.43
5:e:16:LEU:HA	5:e:38:THR:HG22	2.00	0.43
24:x:382:TYR:HE1	24:x:395:ASP:HB3	1.82	0.43
25:A:540:U:H2'	25:A:541:A:H8	1.83	0.43
25:A:1490:G:H2'	25:A:1491:U:C6	2.53	0.43
25:A:2098:U:O4	25:A:2135:G:N2	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:183:LYS:HE2	27:C:266:ASN:O	2.18	0.43
41:R:21:PHE:O	41:R:51:LYS:NZ	2.40	0.43
53:4:37:HIS:ND1	53:4:38:LEU:O	2.51	0.43
1:a:1320:U:H2'	1:a:1321:G:C8	2.48	0.43
24:x:646:ALA:HA	24:x:697:PHE:HB3	2.00	0.43
25:A:351:A:H2'	25:A:352:A:H8	1.82	0.43
25:A:603:U:H3'	25:A:604:A:H8	1.83	0.43
25:A:629:U:H2'	25:A:630:C:H6	1.82	0.43
25:A:882:C:C5'	25:A:883:U:OP2	2.66	0.43
25:A:1415:C:O2'	25:A:1559:A:OP2	2.30	0.43
25:A:2568:G:OP2	25:A:2568:G:N2	2.41	0.43
25:A:2789:U:H2'	25:A:2790:C:H6	1.83	0.43
26:B:37:C:O2	40:Q:99:HIS:NE2	2.41	0.43
36:M:17:ARG:NH2	36:M:47:ILE:HD11	2.33	0.43
1:a:8:A:C6	4:d:206:LYS:HB2	2.53	0.43
1:a:293:G:H2'	1:a:294:A:C8	2.54	0.43
1:a:741:A:H2'	1:a:742:U:C6	2.53	0.43
1:a:1021:C:N3	1:a:1022:C:N4	2.67	0.43
1:a:1066:G:H2'	1:a:1067:U:C6	2.52	0.43
6:f:9:LEU:H	6:f:9:LEU:HD23	1.84	0.43
6:f:23:GLU:O	6:f:27:LYS:HG2	2.17	0.43
10:j:51:VAL:HG13	14:n:81:ARG:HG3	1.99	0.43
19:s:19:VAL:O	19:s:23:VAL:HG13	2.17	0.43
19:s:40:ILE:HD12	19:s:40:ILE:H	1.83	0.43
25:A:132:C:H2'	25:A:133:C:C6	2.53	0.43
25:A:1456:A:H2'	25:A:1457:A:H8	1.83	0.43
25:A:2094:C:O2'	25:A:2095:U:O4'	2.35	0.43
25:A:2564:A:H2'	25:A:2601:A:N6	2.33	0.43
27:C:259:ARG:HD3	27:C:271:ARG:HH12	1.82	0.43
28:D:1:MET:O	28:D:2:THR:OG1	2.31	0.43
31:G:103:LEU:HD23	31:G:105:LEU:HD11	1.99	0.43
38:O:68:VAL:HG12	38:O:101:LYS:HE3	2.00	0.43
1:a:469:U:H2'	1:a:470:G:H8	1.82	0.43
1:a:1169:G:H2'	1:a:1170:A:C8	2.52	0.43
1:a:1433:C:OP1	20:t:33:LYS:HD2	2.17	0.43
25:A:1514:G:N1	25:A:1534:A:OP2	2.47	0.43
25:A:1905:A:O2'	25:A:1906:A:N7	2.47	0.43
25:A:2125:G:N1	25:A:2140:C:O2	2.50	0.43
1:a:516:C:H41	12:l:50:ARG:NH2	2.12	0.43
1:a:840:G:H2'	1:a:841:A:H8	1.82	0.43
1:a:1002:U:H1'	1:a:1016:U:C4	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1143:C:H2'	1:a:1144:U:C6	2.54	0.43
1:a:1175:G:H1'	1:a:1176:G:C4	2.54	0.43
3:c:119:SER:O	3:c:123:GLN:HG3	2.19	0.43
20:t:24:LEU:HB3	20:t:61:MET:HE1	2.00	0.43
25:A:1066:C:H2'	25:A:1067:A:O4'	2.19	0.43
25:A:1303:U:H2'	25:A:1304:G:H8	1.83	0.43
28:D:78:ARG:O	28:D:78:ARG:HG3	2.18	0.43
56:7:27:PHE:O	56:7:35:MET:HE1	2.17	0.43
1:a:630:U:H4'	17:q:9:ARG:HH21	1.83	0.43
1:a:702:A:H2'	1:a:703:G:H8	1.84	0.43
7:g:132:GLY:O	7:g:136:LYS:HG2	2.18	0.43
11:k:17:VAL:HA	11:k:79:LEU:HA	2.01	0.43
14:n:10:GLU:O	14:n:14:GLN:OE1	2.36	0.43
24:x:354:GLY:HA3	24:x:449:ASN:ND2	2.34	0.43
24:x:717:ARG:HD3	24:x:719:TYR:CZ	2.52	0.43
25:A:2260:A:H2'	25:A:2261:A:C8	2.53	0.43
25:A:2734:G:O6	25:A:2742:C:H5''	2.19	0.43
29:E:17:THR:OG1	29:E:200:GLY:O	2.36	0.43
1:a:132:G:N1	1:a:133:G:C5	2.87	0.43
3:c:79:LYS:O	3:c:80:LYS:HG2	2.19	0.43
4:d:13:ARG:HB3	4:d:36:ASN:O	2.19	0.43
5:e:29:GLY:C	5:e:30:ARG:HD2	2.44	0.43
10:j:36:VAL:HG22	10:j:76:ILE:HG22	2.01	0.43
18:r:21:ILE:HD12	18:r:21:ILE:H	1.83	0.43
25:A:45:G:H5'	25:A:46:G:OP1	2.18	0.43
25:A:871:G:H1'	25:A:885:A:H8	1.83	0.43
25:A:1574:U:H1'	25:A:1575:C:OP2	2.19	0.43
25:A:2632:G:OP2	25:A:2632:G:N2	2.32	0.43
30:F:74:ILE:O	30:F:74:ILE:HG13	2.17	0.43
30:F:141:ILE:HG13	30:F:141:ILE:O	2.19	0.43
31:G:173:GLU:OE2	31:G:173:GLU:N	2.52	0.43
47:X:4:PHE:O	47:X:5:ILE:HD13	2.19	0.43
1:a:6:G:N2	5:e:104:THR:OG1	2.42	0.43
1:a:995:G:C6	1:a:1034:A:C6	3.07	0.43
24:x:431:GLN:O	24:x:435:GLN:HG3	2.19	0.43
24:x:741:LEU:HG	24:x:742:ARG:HG3	2.01	0.43
25:A:502:U:H4'	25:A:1222:G:H4'	2.01	0.43
25:A:1434:U:H2'	25:A:1435:U:C6	2.54	0.43
25:A:1530:G:H2'	25:A:1531:A:H8	1.84	0.43
25:A:1535:A:H2'	25:A:1536:G:O4'	2.19	0.43
25:A:1720:U:HO2'	25:A:1721:C:H6	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:F:108:LEU:HD21	30:F:130:MET:HE1	2.00	0.43
35:L:6:ALA:H	35:L:45:THR:HG21	1.84	0.43
45:V:38:THR:OG1	45:V:41:GLU:HG3	2.18	0.43
1:a:494:G:H2'	1:a:495:C:C6	2.53	0.43
2:b:104:TYR:O	2:b:108:ARG:HG2	2.19	0.43
25:A:2025:G:H2'	25:A:2026:U:O4'	2.19	0.43
25:A:2687:A:H2'	25:A:2688:C:C6	2.54	0.43
30:F:9:ARG:HG3	30:F:10:LYS:HD3	2.00	0.43
36:M:64:ARG:HG2	36:M:79:PHE:CG	2.54	0.43
1:a:32:A:H2'	1:a:33:A:C8	2.54	0.43
1:a:247:U:O2'	17:q:20:MET:SD	2.76	0.43
1:a:1127:A:N6	1:a:1136:G:C6	2.87	0.43
1:a:1423:C:H4'	25:A:1693:G:O2'	2.18	0.43
4:d:30:SER:O	4:d:31:LYS:HD3	2.19	0.43
5:e:116:LEU:HD13	5:e:124:VAL:HG21	2.00	0.43
13:m:89:LEU:HA	13:m:92:ARG:HD3	2.01	0.43
20:t:43:ASP:OD1	20:t:44:LEU:N	2.52	0.43
24:x:704:GLY:O	24:x:708:ILE:HG12	2.19	0.43
25:A:160:A:N3	25:A:2195:C:O2'	2.43	0.43
25:A:1519:G:N1	25:A:1520:U:C4	2.86	0.43
25:A:1796:A:H2'	25:A:1797:A:C8	2.53	0.43
25:A:2509:U:O2'	25:A:2634:U:OP1	2.25	0.43
28:D:15:ILE:HA	41:R:13:GLN:HE22	1.84	0.43
29:E:163:LEU:HD12	29:E:163:LEU:HA	1.88	0.43
1:a:468:C:H2'	1:a:469:U:C6	2.54	0.42
1:a:757:G:H2'	1:a:758:C:H6	1.84	0.42
1:a:927:G:O6	7:g:3:ARG:NH2	2.52	0.42
5:e:115:VAL:HG13	5:e:142:PHE:CE1	2.51	0.42
9:i:88:ILE:O	9:i:92:GLU:HG2	2.19	0.42
11:k:43:SER:OG	11:k:74:ALA:HB2	2.19	0.42
14:n:31:ILE:HA	14:n:41:ARG:HG3	1.99	0.42
25:A:355:G:OP2	25:A:356:A:O2'	2.31	0.42
25:A:424:C:O2'	25:A:425:U:H5'	2.19	0.42
25:A:1425:U:H2'	25:A:1426:A:H8	1.82	0.42
25:A:1581:A:H2'	25:A:1582:C:C6	2.53	0.42
25:A:2674:U:H2'	25:A:2675:G:O4'	2.19	0.42
26:B:20:G:C6	26:B:21:U:C4	3.07	0.42
30:F:122:PHE:HZ	30:F:170:LEU:HD12	1.83	0.42
31:G:155:GLU:HG2	31:G:157:TYR:H	1.83	0.42
43:T:79:ARG:O	43:T:80:ARG:HG2	2.19	0.42
50:1:19:LEU:HD23	50:1:22:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:329:C:H2'	1:a:330:A:H8	1.84	0.42
1:a:453:U:H2'	1:a:454:A:H8	1.82	0.42
1:a:1444:G:H21	1:a:1447:A:H2	1.66	0.42
25:A:247:G:OP2	25:A:249:C:N4	2.44	0.42
25:A:562:A:OP2	43:T:80:ARG:NH2	2.43	0.42
25:A:1843:U:H2'	25:A:1844:G:O4'	2.18	0.42
25:A:1953:A:N3	25:A:2579:G:O2'	2.50	0.42
1:a:355:G:H2'	1:a:356:G:O4'	2.19	0.42
1:a:491:U:O2'	1:a:492:A:N7	2.48	0.42
1:a:701:U:H2'	1:a:702:A:C8	2.53	0.42
1:a:1113:C:H2'	1:a:1114:C:H6	1.84	0.42
1:a:1349:G:H2'	1:a:1350:A:C8	2.54	0.42
1:a:1403:C:H2'	1:a:1404:A:C8	2.55	0.42
1:a:1521:C:OP2	21:u:42:THR:HG22	2.18	0.42
2:b:168:HIS:HD2	2:b:169:GLU:OE2	2.02	0.42
6:f:19:GLY:O	6:f:23:GLU:OE1	2.37	0.42
13:m:14:HIS:CD2	13:m:42:ALA:HA	2.54	0.42
15:o:17:GLN:HB2	15:o:21:ASP:OD2	2.19	0.42
25:A:836:U:H5	25:A:923:A:N7	2.16	0.42
25:A:1425:U:H2'	25:A:1426:A:C8	2.55	0.42
25:A:2012:C:H2'	25:A:2013:U:C6	2.54	0.42
25:A:2172:U:H2'	25:A:2173:G:C4	2.54	0.42
25:A:2228:A:H2'	25:A:2229:G:H8	1.80	0.42
25:A:2351:C:H2'	25:A:2352:G:O4'	2.18	0.42
27:C:7:LYS:HA	27:C:8:PRO:HD3	1.90	0.42
29:E:160:ALA:HA	29:E:163:LEU:HB2	2.00	0.42
44:U:21:ALA:HB2	44:U:47:MET:HE1	2.01	0.42
47:X:168:PRO:HG2	47:X:171:VAL:HG21	2.00	0.42
1:a:165:A:H2'	1:a:166:A:C8	2.55	0.42
1:a:626:U:H3'	1:a:627:G:H5'	2.01	0.42
9:i:33:ARG:HH21	9:i:38:PHE:HA	1.84	0.42
11:k:16:VAL:HG12	11:k:77:TYR:HB3	2.00	0.42
14:n:36:SER:OG	14:n:41:ARG:NH2	2.40	0.42
25:A:1446:G:O2'	25:A:1447:U:H5'	2.19	0.42
25:A:2685:U:H2'	25:A:2686:C:C6	2.55	0.42
1:a:86:C:H2'	1:a:87:C:C6	2.54	0.42
1:a:507:U:H2'	1:a:508:C:H6	1.85	0.42
1:a:990:A:H2'	1:a:991:U:C6	2.55	0.42
4:d:57:GLU:OE2	4:d:200:ILE:HG12	2.19	0.42
6:f:30:GLU:OE2	6:f:30:GLU:HA	2.20	0.42
16:p:40:ASN:O	16:p:49:ARG:HD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:s:62:VAL:HA	19:s:66:MET:SD	2.60	0.42
24:x:619:ARG:NH2	24:x:691:ASN:OD1	2.42	0.42
25:A:1061:G:H2'	25:A:1062:C:C6	2.55	0.42
25:A:1268:G:H2'	25:A:1269:U:C6	2.54	0.42
25:A:1762:U:O4	25:A:1776:A:H2	2.02	0.42
25:A:2088:A:H2'	25:A:2089:G:C8	2.55	0.42
1:a:206:G:C4	1:a:207:A:C8	3.08	0.42
1:a:1128:C:H2'	1:a:1129:C:C6	2.55	0.42
13:m:64:THR:HG21	13:m:69:LEU:HD13	2.00	0.42
17:q:63:THR:O	17:q:79:VAL:HG22	2.18	0.42
21:u:28:VAL:O	21:u:32:VAL:HG23	2.19	0.42
24:x:340:THR:HA	24:x:508:LEU:O	2.19	0.42
25:A:1761:C:O2	25:A:1761:C:H2'	2.19	0.42
25:A:2472:G:O3'	38:O:126:PRO:HB3	2.18	0.42
36:M:51:LYS:HD2	36:M:94:ILE:HG22	2.00	0.42
41:R:6:ILE:O	41:R:10:GLU:HG3	2.20	0.42
45:V:68:ARG:NH1	45:V:68:ARG:HG3	2.34	0.42
1:a:457:U:H2'	1:a:458:U:C6	2.55	0.42
1:a:1406:C:H2'	1:a:1407:A:C8	2.55	0.42
3:c:66:ILE:HD12	3:c:91:LEU:HD23	2.01	0.42
4:d:8:LYS:HB3	4:d:21:LEU:HB3	2.02	0.42
4:d:132:ILE:C	4:d:134:SER:H	2.28	0.42
10:j:9:ARG:HB2	10:j:99:GLN:HB2	2.02	0.42
12:l:114:ARG:O	12:l:114:ARG:HG2	2.19	0.42
24:x:752:ARG:HA	24:x:752:ARG:HD2	1.90	0.42
24:x:772:MET:HG2	24:x:806:VAL:O	2.20	0.42
25:A:132:C:H2'	25:A:133:C:H6	1.85	0.42
25:A:244:A:H2'	25:A:245:G:O4'	2.20	0.42
25:A:314:A:H2'	29:E:130:THR:OG1	2.20	0.42
25:A:1424:C:H2'	25:A:1425:U:C6	2.54	0.42
25:A:1450:A:H2'	25:A:1451:A:C8	2.55	0.42
25:A:1672:G:H2'	25:A:1673:C:H6	1.85	0.42
25:A:2448:A:H2'	25:A:2449:C:C6	2.55	0.42
25:A:2874:C:H2'	25:A:2875:C:C6	2.55	0.42
46:W:100:LYS:HB3	46:W:100:LYS:HE2	1.76	0.42
1:a:87:C:HO2'	1:a:88:U:P	2.43	0.42
1:a:192:G:H2'	1:a:193:U:C6	2.55	0.42
1:a:617:C:H2'	1:a:618:C:C6	2.55	0.42
1:a:815:G:H2'	1:a:816:U:C6	2.55	0.42
1:a:1022:C:N3	1:a:1028:G:N2	2.67	0.42
1:a:1471:U:H2'	1:a:1472:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:171:ILE:O	2:b:175:GLU:HG2	2.20	0.42
7:g:70:ALA:HB1	7:g:96:ARG:HB2	2.00	0.42
14:n:33:ASN:O	14:n:36:SER:OG	2.34	0.42
19:s:40:ILE:HG23	19:s:44:MET:SD	2.60	0.42
20:t:84:LYS:HD3	20:t:84:LYS:HA	1.89	0.42
24:x:459:ASP:OD1	24:x:459:ASP:N	2.52	0.42
24:x:649:ARG:O	24:x:652:LEU:N	2.53	0.42
25:A:60:G:O2'	25:A:62:U:OP2	2.37	0.42
25:A:226:A:H5'	25:A:257:C:O2'	2.18	0.42
25:A:584:U:H2'	25:A:585:C:C6	2.55	0.42
25:A:1070:C:H2'	25:A:1071:U:C5	2.52	0.42
31:G:19:LEU:HD12	31:G:46:ASP:HB2	2.02	0.42
1:a:240:A:C2	1:a:276:A:C5	3.07	0.42
1:a:255:U:OP2	20:t:71:LYS:NZ	2.41	0.42
1:a:651:U:H2'	1:a:652:A:C8	2.50	0.42
1:a:745:U:H2'	1:a:746:G:O4'	2.20	0.42
3:c:91:LEU:O	3:c:95:MET:N	2.51	0.42
6:f:1:MET:HB3	6:f:2:ARG:H	1.76	0.42
10:j:15:HIS:HA	10:j:18:ILE:CG2	2.50	0.42
25:A:999:A:N3	25:A:1144:C:O2'	2.49	0.42
25:A:1076:A:H4'	25:A:1093:A:H2	1.84	0.42
25:A:1910:U:H2'	25:A:1911:C:H6	1.85	0.42
25:A:2478:U:H5''	25:A:2557:G:H5'	2.02	0.42
25:A:2817:C:H5''	28:D:57:ARG:NE	2.34	0.42
1:a:210:U:H2'	1:a:211:C:C6	2.55	0.42
1:a:1317:G:H2'	1:a:1318:A:C8	2.55	0.42
6:f:27:LYS:O	6:f:30:GLU:N	2.51	0.42
6:f:98:GLU:N	6:f:98:GLU:OE1	2.53	0.42
7:g:120:LEU:O	7:g:124:LEU:HD23	2.20	0.42
21:u:5:LYS:O	21:u:18:ARG:NH2	2.53	0.42
24:x:348:MET:HE2	24:x:416:VAL:HG11	2.02	0.42
25:A:586:A:H2'	25:A:587:G:C8	2.55	0.42
25:A:719:G:H5'	25:A:720:A:H5''	2.01	0.42
25:A:2415:G:N2	37:N:54:GLN:HE21	2.18	0.42
25:A:2661:G:H4'	36:M:30:ARG:HD2	2.02	0.42
26:B:93:C:H2'	26:B:94:A:H8	1.85	0.42
44:U:1:MET:HG3	44:U:2:GLU:H	1.85	0.42
1:a:31:G:O2'	1:a:32:A:O5'	2.32	0.41
1:a:55:A:C2	24:x:529:ARG:HG2	2.55	0.41
1:a:709:A:H2'	1:a:710:A:H8	1.82	0.41
1:a:976:U:H4'	1:a:977:A:O5'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:989:C:O4'	14:n:8:ASN:ND2	2.53	0.41
1:a:1116:U:O4	1:a:1117:A:N6	2.52	0.41
12:l:90:LEU:HD23	12:l:90:LEU:HA	1.89	0.41
13:m:15:THR:HA	13:m:45:ILE:HG23	2.02	0.41
13:m:72:GLU:HA	13:m:75:MET:HE2	2.02	0.41
20:t:24:LEU:HB3	20:t:61:MET:HE2	2.01	0.41
25:A:540:U:H2'	25:A:541:A:C8	2.55	0.41
25:A:1303:U:H2'	25:A:1304:G:C8	2.55	0.41
25:A:1643:G:OP1	25:A:2809:G:N2	2.39	0.41
28:D:151:THR:CG2	28:D:152:PRO:CD	2.85	0.41
40:Q:15:ALA:O	40:Q:19:MET:HG3	2.20	0.41
1:a:141:G:H2'	1:a:142:G:H8	1.79	0.41
1:a:143:A:H61	1:a:166:A:H62	1.68	0.41
1:a:772:G:H1'	11:k:121:CYS:HB3	2.01	0.41
1:a:1127:A:C5	1:a:1128:C:C4	3.08	0.41
6:f:78:PHE:O	6:f:84:VAL:HG11	2.20	0.41
12:l:107:VAL:HG13	12:l:110:ARG:HG3	2.02	0.41
24:x:361:TYR:CD2	24:x:492:VAL:HG21	2.55	0.41
24:x:475:TRP:N	24:x:475:TRP:CD1	2.84	0.41
25:A:1078:A:H2'	25:A:1078:A:N3	2.35	0.41
25:A:1161:C:H2'	25:A:1162:G:O4'	2.20	0.41
25:A:1461:G:H21	25:A:1504:A:H62	1.67	0.41
25:A:2120:G:O2'	25:A:2122:A:OP1	2.29	0.41
25:A:2432:2MG:OP1	29:E:68:ARG:NH1	2.44	0.41
1:a:208:C:H2'	1:a:209:C:H6	1.85	0.41
1:a:539:C:O2'	1:a:543:C:OP1	2.32	0.41
6:f:20:GLY:HA2	6:f:23:GLU:CD	2.44	0.41
14:n:7:LYS:O	14:n:10:GLU:HG3	2.19	0.41
19:s:39:MET:HE2	19:s:39:MET:HB3	1.84	0.41
25:A:484:G:O2'	44:U:7:LEU:HA	2.20	0.41
38:O:43:THR:HG22	38:O:46:GLN:HG3	2.02	0.41
56:7:16:LYS:NZ	56:7:17:THR:O	2.44	0.41
1:a:173:A:H2'	1:a:174:U:C6	2.55	0.41
1:a:421:U:OP1	4:d:13:ARG:NH1	2.44	0.41
1:a:1431:A:OP1	20:t:29:ARG:NH2	2.54	0.41
3:c:47:LEU:O	3:c:47:LEU:HD12	2.19	0.41
19:s:25:LYS:HE2	19:s:28:ARG:NE	2.35	0.41
24:x:737:LEU:HD23	24:x:738:GLY:N	2.36	0.41
25:A:134:U:H2'	25:A:135:A:H8	1.84	0.41
25:A:687:G:H2'	25:A:688:C:C6	2.55	0.41
25:A:2174:C:H2'	25:A:2175:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:59:GLN:HG3	31:G:62:ARG:NH2	2.35	0.41
53:4:46:GLY:HA3	53:4:54:VAL:HG22	2.02	0.41
1:a:247:U:H2'	1:a:248:G:C8	2.56	0.41
1:a:569:G:O2'	1:a:815:G:OP2	2.25	0.41
1:a:1112:U:H2'	1:a:1113:C:C6	2.55	0.41
1:a:1404:A:H2'	1:a:1405:C:C6	2.55	0.41
9:i:41:ARG:H	9:i:45:ARG:NH2	2.18	0.41
17:q:20:MET:HE3	17:q:23:THR:OG1	2.20	0.41
19:s:30:PRO:HA	19:s:48:THR:O	2.21	0.41
19:s:39:MET:HG3	19:s:69:HIS:O	2.21	0.41
25:A:64:G:H2'	25:A:65:C:C6	2.55	0.41
25:A:490:U:H2'	25:A:491:G:O4'	2.21	0.41
25:A:1105:G:H2'	25:A:1106:G:H8	1.84	0.41
25:A:2155:G:N1	25:A:2157:A:H5''	2.35	0.41
25:A:2269:G:H4'	25:A:2376:G:O2'	2.21	0.41
25:A:2316:A:H2'	25:A:2317:G:C8	2.56	0.41
28:D:149:CYS:HB3	28:D:150:GLN:H	1.64	0.41
44:U:88:ARG:HA	44:U:88:ARG:HD2	1.90	0.41
3:c:135:LYS:HE3	3:c:135:LYS:HB2	1.92	0.41
13:m:10:PRO:O	13:m:45:ILE:HD11	2.21	0.41
25:A:1052:G:H2'	25:A:1053:G:C8	2.56	0.41
25:A:1252:A:O2'	62:A:3502:HOH:O	2.22	0.41
25:A:1553:U:O2'	25:A:1554:C:H5'	2.20	0.41
29:E:136:LYS:HB2	29:E:136:LYS:HE2	1.78	0.41
30:F:61:THR:HG23	30:F:91:LEU:HD21	2.03	0.41
31:G:152:ARG:HD3	31:G:152:ARG:HA	1.87	0.41
1:a:2:A:H1'	1:a:607:C:O2'	2.21	0.41
1:a:4:C:H1'	1:a:5:U:H3'	2.02	0.41
1:a:87:C:O2'	1:a:88:U:P	2.79	0.41
1:a:467:G:H2'	1:a:468:C:O4'	2.21	0.41
1:a:1524:G:H2'	1:a:1525:A:H8	1.86	0.41
5:e:83:GLN:HE22	5:e:151:PRO:HD3	1.86	0.41
8:h:95:VAL:HG11	8:h:128:THR:OG1	2.20	0.41
24:x:472:PRO:HB3	24:x:481:PHE:CD1	2.56	0.41
25:A:156:A:H2'	25:A:157:C:C6	2.56	0.41
25:A:868:G:H2'	25:A:869:G:C8	2.56	0.41
25:A:1370:A:N3	25:A:1392:U:O2'	2.54	0.41
25:A:1373:C:H2'	25:A:1374:A:H8	1.84	0.41
25:A:1494:C:H2'	25:A:1495:A:C8	2.55	0.41
25:A:2123:G:C8	25:A:2124:C:H5	2.38	0.41
25:A:2182:U:H2'	25:A:2183:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:D:33:ASN:HD22	28:D:51:VAL:HG11	1.86	0.41
32:H:14:ASN:CG	32:H:15:LEU:H	2.28	0.41
49:Z:43:GLU:OE1	49:Z:45:ARG:NH2	2.54	0.41
1:a:973:C:O2	14:n:59:ARG:HG2	2.21	0.41
1:a:1518:C:H2'	1:a:1519:G:C8	2.55	0.41
2:b:129:LEU:HD23	2:b:129:LEU:H	1.85	0.41
25:A:572:A:H2'	25:A:573:G:C8	2.55	0.41
25:A:1185:U:H2'	25:A:1186:U:C6	2.55	0.41
25:A:1638:U:H6	25:A:1638:U:H5''	1.85	0.41
27:C:77:ILE:HD12	27:C:114:ASP:O	2.21	0.41
53:4:38:LEU:HD23	53:4:38:LEU:HA	1.96	0.41
1:a:314:A:H2'	1:a:315:A:C8	2.56	0.41
1:a:459:A:O2'	1:a:460:A:H8	2.04	0.41
1:a:1034:A:C2	1:a:1035:G:C5	3.09	0.41
1:a:1170:A:H2'	1:a:1171:G:C8	2.56	0.41
1:a:1178:G:C2	1:a:1179:G:C8	3.09	0.41
2:b:83:GLU:OE2	2:b:218:ALA:HB2	2.21	0.41
3:c:29:TYR:OH	14:n:94:PRO:O	2.38	0.41
3:c:88:ARG:HH11	3:c:88:ARG:HG2	1.86	0.41
4:d:54:GLN:HG3	4:d:199:LEU:CD2	2.51	0.41
4:d:173:VAL:HG12	4:d:175:LEU:HD22	2.03	0.41
5:e:112:MET:HE2	5:e:112:MET:HB3	1.91	0.41
7:g:16:PRO:HB3	9:i:43:THR:HG23	2.02	0.41
11:k:95:SER:HA	11:k:98:ARG:HG2	2.02	0.41
12:l:70:GLU:OE1	12:l:107:VAL:HG21	2.20	0.41
14:n:23:LYS:HA	14:n:26:GLU:OE2	2.20	0.41
20:t:37:LYS:HB3	20:t:37:LYS:HE2	1.86	0.41
24:x:399:HIS:O	24:x:399:HIS:CG	2.73	0.41
24:x:452:ASP:CG	60:x:901:GDP:HN1	2.29	0.41
25:A:822:U:H2'	25:A:823:A:H8	1.86	0.41
25:A:876:U:N3	25:A:880:G:N7	2.69	0.41
25:A:1433:C:H2'	25:A:1434:U:C6	2.55	0.41
25:A:2120:G:H1'	25:A:2147:C:O2	2.21	0.41
25:A:2273:G:N3	25:A:2273:G:H2'	2.35	0.41
25:A:2524:U:H2'	25:A:2525:C:H6	1.83	0.41
29:E:6:ASN:HB2	29:E:120:VAL:HG12	2.01	0.41
29:E:136:LYS:O	29:E:139:THR:HG22	2.21	0.41
31:G:99:LYS:HB3	31:G:99:LYS:HE3	1.92	0.41
32:H:134:HIS:HB3	32:H:137:VAL:HG22	2.02	0.41
36:M:23:LYS:HB3	36:M:40:LYS:HB3	2.03	0.41
47:X:75:VAL:HB	47:X:94:PHE:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:X:156:LEU:HD12	47:X:187:ILE:HG22	2.02	0.41
48:Y:25:LEU:HD22	48:Y:31:VAL:HG12	2.02	0.41
55:6:3:ARG:O	55:6:6:GLN:NE2	2.44	0.41
1:a:148:G:C6	1:a:162:G:C6	3.09	0.41
1:a:671:U:O2	1:a:771:A:O2'	2.32	0.41
2:b:153:ASP:O	2:b:154:MET:HG3	2.20	0.41
7:g:23:LEU:HD12	7:g:23:LEU:HA	1.86	0.41
10:j:37:ARG:HB2	10:j:75:ASP:OD1	2.21	0.41
11:k:64:GLN:HG3	11:k:99:ALA:HB2	2.03	0.41
12:l:87:VAL:HG12	12:l:90:LEU:H	1.86	0.41
24:x:697:PHE:O	24:x:699:VAL:HG13	2.21	0.41
25:A:163:C:H2'	25:A:164:C:H6	1.86	0.41
25:A:197:A:N6	25:A:2417:A:O2'	2.53	0.41
25:A:319:G:H2'	25:A:320:G:H8	1.86	0.41
25:A:883:U:H3'	25:A:883:U:C6	2.53	0.41
25:A:913:A:H2'	25:A:914:G:C8	2.56	0.41
25:A:1046:G:H5''	25:A:1047:A:H5'	2.03	0.41
25:A:1269:U:H2'	25:A:1270:G:O4'	2.21	0.41
25:A:1520:U:H2'	25:A:1521:C:C6	2.56	0.41
25:A:1562:A:H2'	25:A:1563:G:H8	1.86	0.41
30:F:36:LEU:O	30:F:37:ASN:OD1	2.39	0.41
30:F:127:ASN:ND2	30:F:158:THR:H	2.19	0.41
34:J:116:ASP:C	34:J:118:THR:H	2.29	0.41
37:N:58:HIS:CD2	37:N:58:HIS:H	2.39	0.41
1:a:1268:G:O2'	1:a:1269:A:H8	2.04	0.40
4:d:145:VAL:HG13	4:d:150:LYS:HG2	2.03	0.40
6:f:11:HIS:CG	6:f:12:PRO:HD2	2.56	0.40
12:l:71:GLY:O	12:l:99:ARG:NH2	2.35	0.40
19:s:12:ASP:OD2	19:s:14:HIS:NE2	2.54	0.40
24:x:485:SER:O	24:x:485:SER:OG	2.38	0.40
25:A:82:G:O2'	25:A:83:G:H5'	2.21	0.40
25:A:1902:UR3:H2'	25:A:1903:A:O4'	2.21	0.40
25:A:2121:A:H1'	25:A:2145:A:H2'	2.04	0.40
25:A:2134:A:H4'	25:A:2135:G:C8	2.56	0.40
38:O:43:THR:HG22	38:O:46:GLN:CD	2.47	0.40
42:S:61:TRP:O	42:S:65:ILE:HG13	2.22	0.40
42:S:100:VAL:O	42:S:103:LYS:NZ	2.53	0.40
52:3:16:CYS:HB3	52:3:20:ASN:HB3	2.03	0.40
1:a:34:C:O4'	12:l:29:GLN:NE2	2.55	0.40
1:a:686:U:H1'	1:a:689:A:N7	2.37	0.40
1:a:877:C:O2'	1:a:878:U:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:83:GLN:HE21	5:e:150:ALA:HA	1.86	0.40
8:h:21:GLU:HA	8:h:65:TYR:OH	2.21	0.40
12:l:107:VAL:HG12	12:l:117:TYR:HB3	2.03	0.40
20:t:9:LYS:O	20:t:13:GLN:HG3	2.21	0.40
24:x:716:MET:HE2	24:x:716:MET:HB3	1.86	0.40
25:A:2026:U:H2'	25:A:2027:G:C8	2.56	0.40
25:A:2051:C:H2'	25:A:2052:C:H6	1.86	0.40
26:B:41:C:N4	30:F:69:TYR:HE1	2.20	0.40
38:O:51:ARG:O	38:O:55:THR:HG23	2.21	0.40
39:P:79:LEU:C	39:P:81:ASN:H	2.28	0.40
1:a:433:U:H2'	1:a:434:A:O4'	2.22	0.40
1:a:892:G:N2	1:a:895:A:OP2	2.51	0.40
1:a:944:U:H2'	1:a:945:G:H8	1.84	0.40
1:a:1132:G:H2'	1:a:1134:G:C8	2.56	0.40
25:A:959:G:H2'	25:A:960:U:C6	2.57	0.40
25:A:1430:C:H2'	25:A:1431:A:C8	2.56	0.40
25:A:1781:A:H2'	25:A:1782:C:H6	1.87	0.40
29:E:95:LEU:HD12	29:E:99:MET:HE3	2.02	0.40
37:N:109:LYS:HE2	37:N:128:THR:HG22	2.02	0.40
37:N:136:GLU:HG3	37:N:140:GLY:O	2.22	0.40
38:O:74:VAL:HG21	38:O:92:TYR:CZ	2.56	0.40
39:P:45:ARG:O	39:P:49:GLU:HG3	2.22	0.40
41:R:101:LEU:HD11	41:R:111:ILE:HD11	2.02	0.40
1:a:1064:U:H2'	1:a:1065:C:C6	2.57	0.40
1:a:1398:C:H2'	1:a:1399:G:C8	2.57	0.40
2:b:27:MET:SD	2:b:193:PRO:HG3	2.62	0.40
13:m:5:ALA:O	13:m:9:ILE:HG22	2.22	0.40
17:q:68:ARG:HG3	17:q:68:ARG:NH1	2.36	0.40
24:x:507:GLU:HB3	24:x:508:LEU:H	1.59	0.40
24:x:793:LEU:HD23	24:x:793:LEU:HA	1.88	0.40
25:A:693:U:H2'	25:A:694:G:O4'	2.21	0.40
25:A:700:U:H2'	25:A:701:A:H8	1.85	0.40
25:A:713:C:H2'	25:A:714:U:O4'	2.20	0.40
25:A:1708:U:H2'	25:A:1709:G:O4'	2.21	0.40
25:A:1856:G:N2	25:A:1858:A:H3'	2.37	0.40
25:A:2223:U:H2'	25:A:2224:G:O4'	2.21	0.40
28:D:1:MET:HE3	28:D:207:ALA:HB2	2.02	0.40
28:D:41:GLU:HA	28:D:45:GLY:O	2.21	0.40
30:F:108:LEU:N	30:F:109:PRO:HD2	2.36	0.40
39:P:45:ARG:HD3	39:P:97:ILE:HD11	2.01	0.40
1:a:1142:U:H6	1:a:1142:U:O5'	2.05	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1159:U:H2'	1:a:1160:G:O4'	2.21	0.40
1:a:1195:A:H1'	1:a:1196:U:OP2	2.21	0.40
8:h:94:LYS:HD3	8:h:117:ARG:HH12	1.85	0.40
11:k:20:ILE:HD13	11:k:83:ASP:HB3	2.03	0.40
15:o:64:ARG:NH1	15:o:89:ARG:O	2.41	0.40
20:t:74:ARG:HG2	20:t:78:ARG:HD2	2.02	0.40
24:x:398:GLY:C	24:x:400:ALA:H	2.28	0.40
24:x:731:LYS:O	24:x:735:GLY:N	2.54	0.40
24:x:796:LEU:HD21	24:x:804:ALA:HA	2.03	0.40
25:A:874:C:C4	25:A:875:A:H1'	2.57	0.40
25:A:1400:A:H2'	25:A:1401:C:H6	1.86	0.40
25:A:2057:A:H2'	25:A:2058:A:C8	2.56	0.40
25:A:2274:A:O2'	25:A:2275:A:O5'	2.33	0.40
31:G:11:LEU:HA	31:G:12:PRO:HD3	1.95	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	222/246 (90%)	199 (90%)	23 (10%)	0	100	100
3	c	206/228 (90%)	189 (92%)	17 (8%)	0	100	100
4	d	203/206 (98%)	179 (88%)	24 (12%)	0	100	100
5	e	152/166 (92%)	138 (91%)	14 (9%)	0	100	100
6	f	104/139 (75%)	93 (89%)	10 (10%)	1 (1%)	12	39
7	g	150/156 (96%)	143 (95%)	6 (4%)	1 (1%)	18	48
8	h	127/130 (98%)	116 (91%)	9 (7%)	2 (2%)	7	27
9	i	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	44
10	j	97/103 (94%)	91 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	k	117/129 (91%)	110 (94%)	7 (6%)	0	100	100
12	l	120/123 (98%)	112 (93%)	7 (6%)	1 (1%)	16	44
13	m	112/118 (95%)	99 (88%)	12 (11%)	1 (1%)	14	41
14	n	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
15	o	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
16	p	79/83 (95%)	73 (92%)	5 (6%)	1 (1%)	9	32
17	q	78/88 (89%)	74 (95%)	4 (5%)	0	100	100
18	r	60/76 (79%)	57 (95%)	2 (3%)	1 (2%)	7	26
19	s	81/91 (89%)	73 (90%)	8 (10%)	0	100	100
20	t	85/91 (93%)	85 (100%)	0	0	100	100
21	u	60/71 (84%)	58 (97%)	2 (3%)	0	100	100
24	x	480/840 (57%)	422 (88%)	55 (12%)	3 (1%)	21	51
27	C	270/273 (99%)	250 (93%)	19 (7%)	1 (0%)	30	59
28	D	209/211 (99%)	186 (89%)	20 (10%)	3 (1%)	9	30
29	E	198/200 (99%)	189 (96%)	7 (4%)	2 (1%)	12	39
30	F	174/179 (97%)	156 (90%)	16 (9%)	2 (1%)	11	36
31	G	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
32	H	146/148 (99%)	133 (91%)	12 (8%)	1 (1%)	18	48
33	I	115/166 (69%)	105 (91%)	8 (7%)	2 (2%)	7	26
34	J	132/143 (92%)	108 (82%)	24 (18%)	0	100	100
35	L	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
36	M	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
37	N	142/144 (99%)	128 (90%)	14 (10%)	0	100	100
38	O	135/137 (98%)	129 (96%)	6 (4%)	0	100	100
39	P	118/129 (92%)	112 (95%)	6 (5%)	0	100	100
40	Q	113/116 (97%)	104 (92%)	9 (8%)	0	100	100
41	R	112/116 (97%)	104 (93%)	8 (7%)	0	100	100
42	S	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
43	T	101/103 (98%)	98 (97%)	2 (2%)	1 (1%)	12	39
44	U	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
45	V	92/99 (93%)	86 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	W	101/104 (97%)	92 (91%)	9 (9%)	0	100	100
47	X	188/204 (92%)	175 (93%)	13 (7%)	0	100	100
48	Y	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
49	Z	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
50	1	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
51	2	55/58 (95%)	55 (100%)	0	0	100	100
52	3	45/71 (63%)	39 (87%)	5 (11%)	1 (2%)	5	20
53	4	53/60 (88%)	51 (96%)	2 (4%)	0	100	100
54	5	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
55	6	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
56	7	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
57	8	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
All	All	6393/7157 (89%)	5909 (92%)	459 (7%)	25 (0%)	31	59

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	g	152	SER
12	l	77	HIS
13	m	115	PRO
24	x	667	VAL
24	x	741	LEU
28	D	152	PRO
29	E	122	ASP
30	F	37	ASN
30	F	74	ILE
33	I	106	PHE
43	T	52	PRO
52	3	12	ILE
28	D	149	CYS
6	f	85	ILE
33	I	108	ILE
8	h	55	VAL
28	D	75	ALA
9	i	28	ILE
16	p	44	THR
27	C	114	ASP
29	E	127	ALA

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Mol	Chain	Res	Type
32	H	77	VAL
8	h	66	PHE
24	x	426	VAL
18	r	18	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	b	184/202 (91%)	184 (100%)	0	100	100
3	c	170/187 (91%)	170 (100%)	0	100	100
4	d	170/174 (98%)	170 (100%)	0	100	100
5	e	113/124 (91%)	113 (100%)	0	100	100
6	f	88/119 (74%)	88 (100%)	0	100	100
7	g	118/122 (97%)	118 (100%)	0	100	100
8	h	108/109 (99%)	108 (100%)	0	100	100
9	i	104/106 (98%)	104 (100%)	0	100	100
10	j	88/92 (96%)	88 (100%)	0	100	100
11	k	90/98 (92%)	90 (100%)	0	100	100
12	l	106/107 (99%)	105 (99%)	1 (1%)	70	90
13	m	95/99 (96%)	94 (99%)	1 (1%)	65	88
14	n	80/82 (98%)	80 (100%)	0	100	100
15	o	74/75 (99%)	74 (100%)	0	100	100
16	p	64/65 (98%)	64 (100%)	0	100	100
17	q	73/79 (92%)	67 (92%)	6 (8%)	10	32
18	r	48/64 (75%)	48 (100%)	0	100	100
19	s	72/78 (92%)	72 (100%)	0	100	100
20	t	69/70 (99%)	69 (100%)	0	100	100
21	u	51/60 (85%)	51 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	x	342/668 (51%)	341 (100%)	1 (0%)	86	96
27	C	212/213 (100%)	212 (100%)	0	100	100
28	D	162/162 (100%)	160 (99%)	2 (1%)	63	86
29	E	157/158 (99%)	157 (100%)	0	100	100
30	F	150/153 (98%)	150 (100%)	0	100	100
31	G	138/141 (98%)	138 (100%)	0	100	100
32	H	72/107 (67%)	72 (100%)	0	100	100
33	I	28/122 (23%)	28 (100%)	0	100	100
34	J	19/110 (17%)	19 (100%)	0	100	100
35	L	119/119 (100%)	119 (100%)	0	100	100
36	M	102/102 (100%)	102 (100%)	0	100	100
37	N	106/106 (100%)	106 (100%)	0	100	100
38	O	110/110 (100%)	110 (100%)	0	100	100
39	P	99/104 (95%)	99 (100%)	0	100	100
40	Q	86/87 (99%)	86 (100%)	0	100	100
41	R	96/98 (98%)	96 (100%)	0	100	100
42	S	87/88 (99%)	87 (100%)	0	100	100
43	T	86/86 (100%)	86 (100%)	0	100	100
44	U	87/87 (100%)	87 (100%)	0	100	100
45	V	79/82 (96%)	79 (100%)	0	100	100
46	W	84/88 (96%)	84 (100%)	0	100	100
47	X	154/164 (94%)	154 (100%)	0	100	100
48	Y	56/61 (92%)	56 (100%)	0	100	100
49	Z	66/67 (98%)	64 (97%)	2 (3%)	36	70
50	1	54/55 (98%)	54 (100%)	0	100	100
51	2	48/49 (98%)	48 (100%)	0	100	100
52	3	41/61 (67%)	41 (100%)	0	100	100
53	4	48/52 (92%)	48 (100%)	0	100	100
54	5	47/47 (100%)	47 (100%)	0	100	100
55	6	37/37 (100%)	37 (100%)	0	100	100
56	7	54/55 (98%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	8	34/34 (100%)	34 (100%)	0	100	100
All	All	5025/5785 (87%)	5012 (100%)	13 (0%)	84	96

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	l	94	ARG
13	m	116	ILE
17	q	9	ARG
17	q	10	THR
17	q	11	LEU
17	q	62	VAL
17	q	63	THR
17	q	64	ILE
24	x	355	LYS
28	D	149	CYS
28	D	151	THR
49	Z	2	SER
49	Z	4	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (98) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	5	ASN
2	b	15	HIS
2	b	51	ASN
2	b	168	HIS
2	b	177	ASN
3	c	18	HIS
3	c	122	GLN
3	c	123	GLN
3	c	140	ASN
3	c	190	HIS
4	d	116	GLN
4	d	120	HIS
4	d	196	ASN
5	e	20	ASN
5	e	83	GLN
5	e	133	ASN
5	e	147	ASN
5	e	149	GLN

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Mol	Chain	Res	Type
6	f	14	GLN
6	f	55	HIS
7	g	28	ASN
7	g	148	ASN
8	h	18	GLN
8	h	58	GLN
10	j	58	ASN
11	k	72	GLN
11	k	85	ASN
12	l	5	ASN
12	l	6	GLN
12	l	59	ASN
12	l	72	HIS
13	m	14	HIS
13	m	76	ASN
13	m	91	HIS
14	n	49	GLN
15	o	37	ASN
15	o	40	GLN
15	o	46	ASN
15	o	61	ASN
16	p	23	ASN
17	q	48	HIS
18	r	52	GLN
19	s	69	HIS
24	x	350	HIS
24	x	399	HIS
24	x	609	GLN
24	x	641	ASN
27	C	53	HIS
27	C	163	GLN
27	C	261	ASN
28	D	33	ASN
28	D	37	GLN
28	D	65	GLN
28	D	89	GLN
28	D	105	GLN
28	D	185	ASN
29	E	45	GLN
29	E	91	HIS
29	E	155	ASN
29	E	165	HIS

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Mol	Chain	Res	Type
30	F	127	ASN
31	G	22	GLN
32	H	20	ASN
35	L	58	ASN
36	M	29	HIS
36	M	67	HIS
37	N	55	GLN
37	N	58	HIS
37	N	93	GLN
39	P	3	HIS
39	P	9	HIS
39	P	16	HIS
40	Q	34	GLN
41	R	7	GLN
41	R	8	GLN
41	R	13	GLN
41	R	15	ASN
41	R	67	ASN
41	R	76	GLN
42	S	44	GLN
42	S	71	GLN
43	T	66	HIS
44	U	23	GLN
44	U	60	HIS
45	V	77	ASN
46	W	65	HIS
46	W	99	GLN
46	W	103	GLN
47	X	25	ASN
47	X	106	HIS
47	X	110	HIS
48	Y	46	HIS
49	Z	16	ASN
49	Z	22	HIS
50	1	39	GLN
51	2	13	ASN
52	3	33	HIS
55	6	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1520/1536 (98%)	249 (16%)	0
22	v	75/77 (97%)	9 (12%)	0
23	w	5/24 (20%)	0	0
25	A	2881/2891 (99%)	526 (18%)	41 (1%)
26	B	116/120 (96%)	19 (16%)	2 (1%)
All	All	4597/4648 (98%)	803 (17%)	43 (0%)

All (803) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	2	A
1	a	4	C
1	a	5	U
1	a	6	G
1	a	9	G
1	a	22	G
1	a	29	U
1	a	31	G
1	a	32	A
1	a	39	G
1	a	47	C
1	a	48	C
1	a	51	A
1	a	60	A
1	a	61	G
1	a	68	G
1	a	71	U
1	a	72	G
1	a	73	A
1	a	75	G
1	a	81	U
1	a	82	U
1	a	83	G
1	a	88	U
1	a	95	A
1	a	123	A
1	a	124	A
1	a	125	U
1	a	133	G
1	a	157	C
1	a	178	U
1	a	182	G
1	a	184	G

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Mol	Chain	Res	Type
1	a	189	A
1	a	191	A
1	a	192	G
1	a	193	U
1	a	202	U
1	a	204	C
1	a	205	G
1	a	206	G
1	a	222	A
1	a	239	U
1	a	241	G
1	a	245	G
1	a	260	G
1	a	261	C
1	a	265	C
1	a	277	U
1	a	283	A
1	a	287	G
1	a	315	A
1	a	322	C
1	a	323	A
1	a	334	U
1	a	341	G
1	a	345	G
1	a	346	C
1	a	348	G
1	a	361	U
1	a	366	C
1	a	377	A
1	a	391	A
1	a	400	G
1	a	406	A
1	a	408	A
1	a	409	A
1	a	410	G
1	a	415	U
1	a	416	C
1	a	417	G
1	a	423	U
1	a	433	U
1	a	442	A
1	a	443	G

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Mol	Chain	Res	Type
1	a	446	A
1	a	457	U
1	a	459	A
1	a	460	A
1	a	461	U
1	a	462	A
1	a	475	G
1	a	478	G
1	a	490	A
1	a	492	A
1	a	493	A
1	a	503	A
1	a	505	C
1	a	512	C
1	a	520	C
1	a	521	7MG
1	a	524	G
1	a	525	U
1	a	526	A
1	a	533	A
1	a	534	G
1	a	535	G
1	a	541	A
1	a	553	A
1	a	556	U
1	a	558	C
1	a	562	G
1	a	567	A
1	a	570	C
1	a	571	G
1	a	573	G
1	a	627	G
1	a	647	A
1	a	650	G
1	a	659	A
1	a	681	A
1	a	682	G
1	a	687	G
1	a	688	A
1	a	689	A
1	a	697	G
1	a	710	A

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Mol	Chain	Res	Type
1	a	711	C
1	a	717	U
1	a	718	G
1	a	725	G
1	a	749	A
1	a	756	U
1	a	758	C
1	a	771	A
1	a	781	A
1	a	787	U
1	a	788	A
1	a	809	A
1	a	810	A
1	a	811	C
1	a	815	G
1	a	820	C
1	a	822	A
1	a	832	A
1	a	861	G
1	a	866	A
1	a	869	U
1	a	884	G
1	a	894	A
1	a	896	G
1	a	920	G
1	a	921	G
1	a	928	C
1	a	954	U
1	a	955	U
1	a	962	A
1	a	963	A
1	a	964	C
1	a	969	A
1	a	970	G
1	a	971	A
1	a	975	U
1	a	976	U
1	a	977	A
1	a	986	U
1	a	987	G
1	a	988	A
1	a	997	G

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Mol	Chain	Res	Type
1	a	998	A
1	a	1003	U
1	a	1004	C
1	a	1015	U
1	a	1017	G
1	a	1018	G
1	a	1020	G
1	a	1022	C
1	a	1023	U
1	a	1024	U
1	a	1025	C
1	a	1026	G
1	a	1027	G
1	a	1039	C
1	a	1044	G
1	a	1047	G
1	a	1058	G
1	a	1059	U
1	a	1073	G
1	a	1079	U
1	a	1088	G
1	a	1089	U
1	a	1095	A
1	a	1102	G
1	a	1119	U
1	a	1124	A
1	a	1130	U
1	a	1131	C
1	a	1133	G
1	a	1134	G
1	a	1153	U
1	a	1154	G
1	a	1162	C
1	a	1165	A
1	a	1178	G
1	a	1190	A
1	a	1191	A
1	a	1196	U
1	a	1206	U
1	a	1207	A
1	a	1208	C
1	a	1221	A

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Mol	Chain	Res	Type
1	a	1222	C
1	a	1230	A
1	a	1232	A
1	a	1234	U
1	a	1235	G
1	a	1248	G
1	a	1251	U
1	a	1252	G
1	a	1264	G
1	a	1266	U
1	a	1272	U
1	a	1274	A
1	a	1281	A
1	a	1293	A
1	a	1294	G
1	a	1297	C
1	a	1299	G
1	a	1314	C
1	a	1332	G
1	a	1340	A
1	a	1347	G
1	a	1357	A
1	a	1358	U
1	a	1362	A
1	a	1364	G
1	a	1373	G
1	a	1388	A
1	a	1392	A
1	a	1413	G
1	a	1426	G
1	a	1428	A
1	a	1435	A
1	a	1440	A
1	a	1444	G
1	a	1446	A
1	a	1447	A
1	a	1448	G
1	a	1487	A
1	a	1491	G
1	a	1493	A
1	a	1497	A
1	a	1500	U

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Mol	Chain	Res	Type
1	a	1501	A
1	a	1511	G
1	a	1513	MA6
1	a	1514	C
1	a	1523	G
1	a	1524	G
22	v	9	G
22	v	20	U
22	v	21	A
22	v	47	U
22	v	49	G
22	v	61	C
22	v	68	C
22	v	71	C
22	v	76	A
25	A	14	A
25	A	23	G
25	A	28	A
25	A	34	U
25	A	35	G
25	A	44	A
25	A	46	G
25	A	51	G
25	A	58	G
25	A	62	U
25	A	63	A
25	A	71	A
25	A	74	A
25	A	75	G
25	A	79	C
25	A	82	G
25	A	83	G
25	A	84	A
25	A	85	G
25	A	96	G
25	A	97	A
25	A	100	U
25	A	114	U
25	A	115	C
25	A	118	A
25	A	119	A
25	A	120	U

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Mol	Chain	Res	Type
25	A	125	G
25	A	131	A
25	A	142	C
25	A	147	G
25	A	160	A
25	A	163	C
25	A	166	U
25	A	173	A
25	A	181	A
25	A	196	A
25	A	199	A
25	A	205	G
25	A	206	U
25	A	215	G
25	A	216	A
25	A	222	A
25	A	223	A
25	A	226	A
25	A	230	G
25	A	233	A
25	A	242	G
25	A	243	U
25	A	244	A
25	A	248	G
25	A	249	C
25	A	250	G
25	A	252	G
25	A	255	A
25	A	265	A
25	A	266	G
25	A	271	U
25	A	273	A
25	A	278	C
25	A	289	G
25	A	293	A
25	A	294	A
25	A	305	A
25	A	315	U
25	A	318	U
25	A	319	G
25	A	322	U
25	A	323	G

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Mol	Chain	Res	Type
25	A	324	A
25	A	342	G
25	A	348	U
25	A	350	G
25	A	356	A
25	A	358	A
25	A	359	U
25	A	375	A
25	A	376	C
25	A	377	G
25	A	380	A
25	A	387	G
25	A	396	U
25	A	397	G
25	A	403	A
25	A	408	C
25	A	435	C
25	A	445	A
25	A	447	C
25	A	456	G
25	A	461	A
25	A	464	G
25	A	472	G
25	A	482	G
25	A	485	G
25	A	495	U
25	A	496	A
25	A	499	A
25	A	519	A
25	A	520	A
25	A	521	G
25	A	523	A
25	A	537	U
25	A	538	G
25	A	550	C
25	A	553	A
25	A	558	U
25	A	559	U
25	A	560	G
25	A	563	U
25	A	565	A
25	A	567	G

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Mol	Chain	Res	Type
25	A	576	A
25	A	582	A
25	A	583	U
25	A	593	A
25	A	594	G
25	A	599	A
25	A	603	U
25	A	604	A
25	A	605	U
25	A	622	A
25	A	624	G
25	A	627	A
25	A	635	U
25	A	636	A
25	A	637	G
25	A	644	U
25	A	645	A
25	A	647	U
25	A	649	G
25	A	659	G
25	A	660	A
25	A	667	A
25	A	676	U
25	A	687	G
25	A	702	G
25	A	714	U
25	A	716	G
25	A	720	A
25	A	730	C
25	A	737	U
25	A	738	G
25	A	743	G
25	A	747	G
25	A	754	A
25	A	755	C
25	A	765	G
25	A	766	G
25	A	772	A
25	A	774	G
25	A	775	G
25	A	779	A
25	A	793	U

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Mol	Chain	Res	Type
25	A	795	G
25	A	802	C
25	A	836	U
25	A	848	G
25	A	870	G
25	A	871	G
25	A	872	G
25	A	873	U
25	A	875	A
25	A	877	C
25	A	878	C
25	A	879	C
25	A	880	G
25	A	881	A
25	A	884	U
25	A	886	C
25	A	889	A
25	A	899	A
25	A	903	C
25	A	921	C
25	A	922	G
25	A	931	A
25	A	935	A
25	A	936	C
25	A	949	A
25	A	951	C
25	A	952	G
25	A	963	A
25	A	964	A
25	A	973	A
25	A	979	G
25	A	986	A
25	A	993	G
25	A	995	C
25	A	1002	U
25	A	1003	U
25	A	1007	G
25	A	1012	G
25	A	1016	U
25	A	1017	A
25	A	1023	U
25	A	1030	A

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Mol	Chain	Res	Type
25	A	1037	G
25	A	1044	A
25	A	1050	U
25	A	1051	U
25	A	1053	G
25	A	1059	A
25	A	1060	A
25	A	1063	A
25	A	1067	A
25	A	1078	A
25	A	1102	G
25	A	1114	G
25	A	1117	A
25	A	1119	A
25	A	1122	U
25	A	1123	A
25	A	1124	A
25	A	1125	C
25	A	1129	G
25	A	1133	A
25	A	1146	A
25	A	1147	A
25	A	1148	G
25	A	1162	G
25	A	1168	G
25	A	1169	A
25	A	1170	C
25	A	1193	G
25	A	1199	G
25	A	1211	A
25	A	1214	A
25	A	1223	G
25	A	1225	G
25	A	1234	A
25	A	1237	G
25	A	1240	A
25	A	1242	U
25	A	1243	G
25	A	1253	G
25	A	1255	A
25	A	1258	G
25	A	1259	A

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Mol	Chain	Res	Type
25	A	1260	C
25	A	1261	A
25	A	1263	U
25	A	1276	C
25	A	1287	A
25	A	1288	A
25	A	1308	A
25	A	1316	U
25	A	1339	U
25	A	1352	A
25	A	1353	A
25	A	1355	A
25	A	1365	A
25	A	1366	U
25	A	1371	A
25	A	1372	A
25	A	1373	C
25	A	1403	G
25	A	1404	C
25	A	1408	G
25	A	1410	A
25	A	1415	C
25	A	1422	G
25	A	1429	C
25	A	1439	G
25	A	1447	U
25	A	1448	C
25	A	1449	C
25	A	1454	U
25	A	1469	G
25	A	1480	U
25	A	1498	G
25	A	1508	G
25	A	1509	A
25	A	1511	G
25	A	1512	A
25	A	1527	G
25	A	1545	G
25	A	1556	A
25	A	1558	G
25	A	1559	A
25	A	1560	A

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Mol	Chain	Res	Type
25	A	1568	U
25	A	1571	G
25	A	1573	U
25	A	1574	U
25	A	1575	C
25	A	1576	A
25	A	1585	G
25	A	1597	C
25	A	1598	A
25	A	1624	A
25	A	1628	C
25	A	1629	C
25	A	1634	C
25	A	1637	U
25	A	1638	U
25	A	1639	G
25	A	1641	G
25	A	1643	G
25	A	1653	G
25	A	1664	G
25	A	1665	C
25	A	1673	C
25	A	1686	G
25	A	1690	A
25	A	1716	U
25	A	1720	U
25	A	1721	C
25	A	1732	G
25	A	1735	U
25	A	1736	G
25	A	1742	A
25	A	1743	G
25	A	1745	U
25	A	1746	A
25	A	1750	G
25	A	1751	G
25	A	1760	A
25	A	1769	U
25	A	1771	A
25	A	1787	C
25	A	1788	A
25	A	1789	A

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Mol	Chain	Res	Type
25	A	1795	A
25	A	1797	A
25	A	1798	G
25	A	1803	C
25	A	1816	A
25	A	1841	A
25	A	1861	C
25	A	1893	G
25	A	1897	G
25	A	1899	A
25	A	1900	A
25	A	1906	A
25	A	1916	G
25	A	1917	G
25	A	1923	A
25	A	1924	A
25	A	1925	A
25	A	1942	U
25	A	1954	C
25	A	1957	A
25	A	1958	U
25	A	1959	G
25	A	1978	U
25	A	1980	U
25	A	1984	C
25	A	2010	C
25	A	2018	A
25	A	2020	A
25	A	2023	C
25	A	2030	U
25	A	2042	C
25	A	2043	G
25	A	2047	A
25	A	2048	G
25	A	2049	A
25	A	2055	U
25	A	2056	7MG
25	A	2067	G
25	A	2068	U
25	A	2080	G
25	A	2094	C
25	A	2097	G

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Mol	Chain	Res	Type
25	A	2098	U
25	A	2099	G
25	A	2103	G
25	A	2104	A
25	A	2105	U
25	A	2106	A
25	A	2110	G
25	A	2114	G
25	A	2115	G
25	A	2116	C
25	A	2118	U
25	A	2119	U
25	A	2121	A
25	A	2122	A
25	A	2127	G
25	A	2129	A
25	A	2132	C
25	A	2133	C
25	A	2134	A
25	A	2135	G
25	A	2138	C
25	A	2140	C
25	A	2141	G
25	A	2143	G
25	A	2144	G
25	A	2145	A
25	A	2146	G
25	A	2147	C
25	A	2148	C
25	A	2150	U
25	A	2151	C
25	A	2152	C
25	A	2153	U
25	A	2156	A
25	A	2157	A
25	A	2163	A
25	A	2169	G
25	A	2171	A
25	A	2173	G
25	A	2174	C
25	A	2185	A
25	A	2187	C

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Mol	Chain	Res	Type
25	A	2191	G
25	A	2194	C
25	A	2199	A
25	A	2200	U
25	A	2212	A
25	A	2225	G
25	A	2226	G
25	A	2229	G
25	A	2238	OMG
25	A	2255	A
25	A	2265	A
25	A	2270	U
25	A	2274	A
25	A	2275	A
25	A	2292	U
25	A	2293	C
25	A	2294	G
25	A	2296	A
25	A	2306	C
25	A	2308	G
25	A	2309	A
25	A	2312	A
25	A	2313	U
25	A	2314	A
25	A	2323	A
25	A	2330	U
25	A	2332	G
25	A	2334	C
25	A	2337	C
25	A	2357	G
25	A	2358	G
25	A	2359	U
25	A	2365	A
25	A	2366	G
25	A	2370	G
25	A	2372	C
25	A	2378	G
25	A	2389	U
25	A	2393	U
25	A	2410	U
25	A	2412	A
25	A	2414	C

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Mol	Chain	Res	Type
25	A	2416	G
25	A	2417	A
25	A	2428	U
25	A	2434	G
25	A	2435	A
25	A	2446	A
25	A	2457	G
25	A	2462	C
25	A	2467	C
25	A	2474	G
25	A	2478	U
25	A	2481	G
25	A	2485	OMC
25	A	2489	G
25	A	2492	G
25	A	2493	U
25	A	2505	A
25	A	2506	U
25	A	2516	G
25	A	2522	G
25	A	2534	A
25	A	2537	G
25	A	2553	A
25	A	2554	G
25	A	2560	C
25	A	2565	G
25	A	2569	G
25	A	2586	G
25	A	2589	A
25	A	2595	G
25	A	2596	U
25	A	2600	U
25	A	2602	U
25	A	2616	U
25	A	2633	C
25	A	2648	G
25	A	2650	G
25	A	2651	G
25	A	2672	G
25	A	2676	U
25	A	2677	U
25	A	2689	G

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Mol	Chain	Res	Type
25	A	2701	G
25	A	2703	C
25	A	2713	U
25	A	2719	G
25	A	2720	A
25	A	2731	G
25	A	2735	A
25	A	2738	G
25	A	2752	A
25	A	2763	A
25	A	2765	A
25	A	2766	U
25	A	2767	G
25	A	2780	G
25	A	2781	A
25	A	2783	C
25	A	2784	U
25	A	2785	U
25	A	2786	G
25	A	2787	A
25	A	2794	U
25	A	2805	C
25	A	2807	A
25	A	2808	A
25	A	2812	U
25	A	2836	U
25	A	2846	G
25	A	2848	G
25	A	2852	U
25	A	2854	G
25	A	2860	A
25	A	2867	C
25	A	2871	U
25	A	2872	U
25	A	2873	G
25	A	2880	A
25	A	2889	C
26	B	9	G
26	B	13	A
26	B	20	G
26	B	24	G
26	B	26	A

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Mol	Chain	Res	Type
26	B	41	C
26	B	45	A
26	B	52	A
26	B	53	A
26	B	54	G
26	B	56	G
26	B	67	U
26	B	73	A
26	B	89	U
26	B	90	C
26	B	91	C
26	B	105	G
26	B	109	A
26	B	116	A

All (43) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	4	C
25	A	34	U
25	A	81	G
25	A	83	G
25	A	87	C
25	A	114	U
25	A	243	U
25	A	265	A
25	A	314	A
25	A	434	A
25	A	444	A
25	A	687	G
25	A	774	G
25	A	792	A
25	A	920	C
25	A	963	A
25	A	1016	U
25	A	1169	A
25	A	1233	A
25	A	1391	C
25	A	1407	U
25	A	1448	C
25	A	1497	G
25	A	1574	U

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Mol	Chain	Res	Type
25	A	1627	A
25	A	1642	A
25	A	1672	G
25	A	1715	U
25	A	1741	A
25	A	2029	A
25	A	2149	A
25	A	2228	A
25	A	2273	G
25	A	2274	A
25	A	2295	G
25	A	2392	G
25	A	2461	U
25	A	2536	G
25	A	2783	C
25	A	2793	C
25	A	2851	G
26	B	51	G
26	B	66	A

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

26 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
25	5MC	A	1949	25	19,22,23	1.43	3 (15%)	26,32,35	1.12	2 (7%)
1	4OC	a	1396	1	20,23,24	0.76	0	25,32,35	0.91	1 (4%)
1	5MC	a	961	1	19,22,23	1.58	3 (15%)	26,32,35	1.09	3 (11%)
25	OMU	A	2539	25	19,22,23	1.29	3 (15%)	25,31,34	1.88	5 (20%)
25	2MG	A	2432	25,58	23,26,27	1.28	3 (13%)	33,38,41	2.22	6 (18%)
25	UR3	A	1902	25	19,22,23	1.02	1 (5%)	26,32,35	1.75	4 (15%)
1	MA6	a	1512	1	23,26,27	1.48	5 (21%)	33,38,41	2.40	13 (39%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	5MC	v	32	22	19,22,23	1.44	3 (15%)	26,32,35	1.30	3 (11%)
1	2MG	a	1510	1	23,26,27	1.25	3 (13%)	33,38,41	2.25	8 (24%)
25	OMG	A	2238	22,25,58	23,26,27	1.20	3 (13%)	32,38,41	1.99	6 (18%)
1	UR3	a	1492	1	19,22,23	0.95	0	26,32,35	1.77	2 (7%)
25	1MG	A	735	25	23,26,27	1.17	3 (13%)	33,39,42	1.73	5 (15%)
25	5MU	A	1926	25	19,22,23	1.39	5 (26%)	27,32,35	2.17	6 (22%)
1	2MG	a	960	1	23,26,27	1.25	4 (17%)	33,38,41	2.18	7 (21%)
25	6MZ	A	2017	25	22,25,26	1.87	6 (27%)	29,36,39	3.47	11 (37%)
1	7MG	a	521	1	23,26,27	1.30	3 (13%)	27,39,42	2.67	7 (25%)
25	2MG	A	1822	25	23,26,27	1.24	3 (13%)	33,38,41	2.31	10 (30%)
25	6MZ	A	1608	25	22,25,26	1.87	6 (27%)	29,36,39	3.43	10 (34%)
22	5MU	v	54	22	19,22,23	1.37	6 (31%)	27,32,35	2.14	6 (22%)
1	2MG	a	1201	1	23,26,27	1.25	4 (17%)	33,38,41	2.21	6 (18%)
22	PSU	v	55	22	18,21,22	1.37	2 (11%)	21,30,33	2.08	4 (19%)
25	7MG	A	2056	25,58	23,26,27	1.31	3 (13%)	27,39,42	2.66	7 (25%)
25	2MA	A	2490	25,58	22,25,26	1.46	5 (22%)	32,37,40	2.31	9 (28%)
25	OMC	A	2485	25,58	19,22,23	0.80	0	25,31,34	0.94	1 (4%)
1	MA6	a	1513	1	23,26,27	1.46	5 (21%)	33,38,41	2.41	14 (42%)
22	4SU	v	8	22	18,21,22	2.04	6 (33%)	25,30,33	1.63	5 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	5MC	A	1949	25	-	0/7/25/26	0/2/2/2
1	4OC	a	1396	1	-	1/9/29/30	0/2/2/2
1	5MC	a	961	1	-	0/7/25/26	0/2/2/2
25	OMU	A	2539	25	-	0/9/27/28	0/2/2/2
25	2MG	A	2432	25,58	-	1/9/27/28	0/3/3/3
25	UR3	A	1902	25	-	0/7/25/26	0/2/2/2
1	MA6	a	1512	1	-	1/11/29/30	0/3/3/3
22	5MC	v	32	22	-	0/7/25/26	0/2/2/2
1	2MG	a	1510	1	-	0/9/27/28	0/3/3/3
25	OMG	A	2238	22,25,58	-	2/9/27/28	0/3/3/3
1	UR3	a	1492	1	-	0/7/25/26	0/2/2/2
25	1MG	A	735	25	-	0/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	5MU	A	1926	25	-	0/7/25/26	0/2/2/2
1	2MG	a	960	1	-	0/9/27/28	0/3/3/3
25	6MZ	A	2017	25	-	2/9/27/28	0/3/3/3
1	7MG	a	521	1	-	2/7/37/38	0/3/3/3
25	2MG	A	1822	25	-	0/9/27/28	0/3/3/3
25	6MZ	A	1608	25	-	0/9/27/28	0/3/3/3
22	5MU	v	54	22	-	0/7/25/26	0/2/2/2
1	2MG	a	1201	1	-	0/9/27/28	0/3/3/3
22	PSU	v	55	22	-	0/7/25/26	0/2/2/2
25	7MG	A	2056	25,58	-	2/7/37/38	0/3/3/3
25	2MA	A	2490	25,58	-	0/7/25/26	0/3/3/3
25	OMC	A	2485	25,58	-	2/9/27/28	0/2/2/2
1	MA6	a	1513	1	-	4/11/29/30	0/3/3/3
22	4SU	v	8	22	-	0/7/25/26	0/2/2/2

All (88) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	961	5MC	C5-C4	5.58	1.48	1.44
25	A	2017	6MZ	C6-N6	5.51	1.40	1.34
25	A	1608	6MZ	C6-N6	5.44	1.40	1.34
22	v	8	4SU	C4-S4	-4.96	1.59	1.68
25	A	1949	5MC	C5-C4	4.91	1.47	1.44
22	v	32	5MC	C5-C4	4.85	1.47	1.44
1	a	1512	MA6	C5-C4	4.50	1.47	1.39
25	A	1608	6MZ	C5-C4	4.38	1.46	1.39
25	A	2490	2MA	C5-C4	4.35	1.46	1.39
1	a	1513	MA6	C5-C4	4.31	1.46	1.39
22	v	8	4SU	C4-N3	-4.19	1.33	1.37
25	A	2017	6MZ	C5-C4	4.15	1.46	1.39
22	v	8	4SU	C5-C4	-3.43	1.38	1.42
25	A	2056	7MG	C4-N9	-3.38	1.33	1.37
22	v	55	PSU	C6-C5	3.35	1.39	1.35
1	a	521	7MG	C5-C4	3.21	1.47	1.37
25	A	735	1MG	C5-C4	3.09	1.47	1.38
1	a	1201	2MG	C5-C4	3.09	1.47	1.38
25	A	2539	OMU	C4-N3	-3.03	1.33	1.38
1	a	960	2MG	C5-C4	3.01	1.47	1.38
25	A	2056	7MG	C5-C4	3.01	1.46	1.37
25	A	2238	OMG	C5-C4	2.94	1.46	1.38
1	a	521	7MG	C4-N9	-2.92	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	2432	2MG	C5-C4	2.91	1.46	1.38
1	a	1510	2MG	C5-C4	2.90	1.46	1.38
25	A	1926	5MU	C4-N3	-2.89	1.33	1.38
25	A	1822	2MG	C5-C4	2.86	1.46	1.38
1	a	961	5MC	C6-C5	2.83	1.39	1.34
25	A	2432	2MG	C6-N1	-2.81	1.33	1.38
1	a	1513	MA6	C5-C6	2.78	1.48	1.41
25	A	1822	2MG	C6-N1	-2.74	1.33	1.38
25	A	2017	6MZ	C5-C6	2.74	1.48	1.41
25	A	2238	OMG	C6-N1	-2.70	1.33	1.38
25	A	1608	6MZ	C5-C6	2.68	1.48	1.41
22	v	55	PSU	C4-N3	-2.68	1.33	1.38
25	A	1926	5MU	C6-C5	2.68	1.39	1.34
1	a	1512	MA6	C5-C6	2.67	1.48	1.41
1	a	1510	2MG	C6-N1	-2.63	1.33	1.38
25	A	2539	OMU	C2-N3	-2.61	1.33	1.38
25	A	2056	7MG	C6-N1	-2.61	1.34	1.38
22	v	54	5MU	C4-N3	-2.60	1.34	1.38
1	a	1201	2MG	C6-N1	-2.59	1.34	1.38
22	v	32	5MC	C6-N1	-2.57	1.33	1.38
25	A	2490	2MA	C5-C6	2.55	1.48	1.41
25	A	1949	5MC	C6-C5	2.53	1.38	1.34
1	a	960	2MG	C6-N1	-2.51	1.34	1.38
22	v	8	4SU	C2-N3	-2.51	1.33	1.38
25	A	2017	6MZ	C5-N7	-2.49	1.34	1.39
22	v	54	5MU	C6-C5	2.49	1.38	1.34
25	A	1926	5MU	C6-N1	-2.49	1.33	1.38
1	a	521	7MG	C6-N1	-2.49	1.34	1.38
25	A	2490	2MA	C5-N7	-2.45	1.34	1.39
25	A	1949	5MC	C6-N1	-2.45	1.33	1.38
1	a	1512	MA6	C5-N7	-2.43	1.34	1.39
22	v	32	5MC	C6-C5	2.41	1.38	1.34
25	A	1608	6MZ	C5-N7	-2.40	1.34	1.39
25	A	1926	5MU	C2-N3	-2.38	1.33	1.38
1	a	1513	MA6	C5-N7	-2.35	1.34	1.39
22	v	54	5MU	C6-N1	-2.34	1.34	1.38
25	A	2238	OMG	C5-N7	-2.32	1.34	1.39
1	a	1513	MA6	C8-N7	2.31	1.36	1.31
25	A	2432	2MG	C5-N7	-2.27	1.34	1.39
25	A	1902	UR3	C2-N1	2.25	1.41	1.38
22	v	54	5MU	C2-N1	2.24	1.42	1.38
25	A	735	1MG	C5-N7	-2.24	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	2017	6MZ	C4-N9	-2.23	1.33	1.37
1	a	961	5MC	C6-N1	-2.23	1.34	1.38
1	a	1201	2MG	C2-N3	2.22	1.36	1.32
1	a	960	2MG	C5-N7	-2.21	1.34	1.39
22	v	54	5MU	C4-C5	2.21	1.48	1.44
25	A	1608	6MZ	C8-N7	2.20	1.35	1.31
25	A	2539	OMU	C5-C4	-2.19	1.38	1.43
25	A	2490	2MA	C8-N7	2.19	1.35	1.31
25	A	1822	2MG	C5-N7	-2.19	1.34	1.39
25	A	2017	6MZ	C8-N7	2.15	1.35	1.31
1	a	1510	2MG	C5-N7	-2.15	1.34	1.39
22	v	8	4SU	O2-C2	2.14	1.26	1.23
1	a	1513	MA6	C4-N9	-2.13	1.33	1.37
1	a	1512	MA6	C8-N7	2.09	1.35	1.31
1	a	960	2MG	C2-N3	2.08	1.35	1.32
22	v	8	4SU	C2-N1	2.07	1.41	1.38
1	a	1201	2MG	C5-N7	-2.06	1.34	1.39
1	a	1512	MA6	C4-N9	-2.05	1.33	1.37
25	A	2490	2MA	C4-N9	-2.04	1.33	1.37
25	A	735	1MG	C2-N1	2.03	1.41	1.37
25	A	1926	5MU	C4-C5	2.02	1.48	1.44
25	A	1608	6MZ	C4-N9	-2.01	1.33	1.37
22	v	54	5MU	C2-N3	-2.01	1.34	1.38

All (161) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2017	6MZ	C9-N6-C6	-14.79	109.13	122.85
25	A	1608	6MZ	C9-N6-C6	-14.43	109.47	122.85
1	a	521	7MG	N9-C4-N3	9.30	139.09	125.46
25	A	2056	7MG	N9-C4-N3	8.93	138.55	125.46
25	A	2490	2MA	C5-C4-N3	-8.11	118.64	127.18
25	A	1822	2MG	C2-N3-C4	7.57	121.47	112.00
1	a	1201	2MG	C2-N3-C4	7.29	121.12	112.00
1	a	1510	2MG	C2-N3-C4	7.29	121.11	112.00
25	A	2432	2MG	C2-N3-C4	7.24	121.05	112.00
1	a	960	2MG	C2-N3-C4	7.07	120.85	112.00
1	a	1492	UR3	C4-N3-C2	-7.01	118.94	124.58
25	A	1902	UR3	C4-N3-C2	-6.69	119.19	124.58
22	v	55	PSU	N1-C2-N3	6.45	121.97	115.17
1	a	1201	2MG	C5-C4-N3	-6.36	118.27	128.39
25	A	1822	2MG	C5-C4-N3	-6.36	118.27	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2238	OMG	C5-C4-N3	-6.33	118.31	128.39
25	A	2490	2MA	N3-C4-N9	6.29	134.97	126.99
25	A	2432	2MG	C5-C4-N3	-6.20	118.52	128.39
1	a	960	2MG	C5-C4-N3	-6.03	118.79	128.39
1	a	1510	2MG	C5-C4-N3	-6.03	118.79	128.39
25	A	1608	6MZ	C5-C4-N3	-5.81	118.72	126.72
1	a	1512	MA6	C5-C4-N3	-5.77	118.77	126.72
1	a	521	7MG	C5-C4-N3	-5.64	117.54	128.13
1	a	1513	MA6	C5-C4-N3	-5.59	119.01	126.72
25	A	2017	6MZ	C5-C4-N3	-5.57	119.04	126.72
25	A	2056	7MG	N9-C8-N7	-5.56	95.51	103.37
25	A	735	1MG	C5-C4-N3	-5.39	119.81	128.39
25	A	2056	7MG	C5-C4-N3	-5.38	118.03	128.13
25	A	1926	5MU	C4-N3-C2	-5.35	120.33	127.34
22	v	54	5MU	C4-N3-C2	-5.23	120.48	127.34
25	A	1926	5MU	N3-C2-N1	5.23	121.70	114.89
1	a	521	7MG	N9-C8-N7	-5.23	95.97	103.37
25	A	2539	OMU	C4-N3-C2	-5.13	120.24	126.61
25	A	2238	OMG	C2-N3-C4	5.11	121.10	112.30
22	v	54	5MU	N3-C2-N1	4.93	121.30	114.89
22	v	8	4SU	C5-C4-N3	4.74	119.16	114.75
1	a	1201	2MG	N9-C4-N3	4.73	135.41	125.95
25	A	2238	OMG	N9-C4-N3	4.67	135.30	125.95
25	A	2432	2MG	N9-C4-N3	4.67	135.30	125.95
1	a	1513	MA6	C10-N6-C6	-4.64	108.72	120.52
25	A	1822	2MG	N9-C4-N3	4.56	135.08	125.95
1	a	1512	MA6	N3-C4-N9	4.56	134.92	127.17
25	A	1608	6MZ	N3-C4-N9	4.56	134.92	127.17
25	A	2539	OMU	N3-C2-N1	4.53	120.79	114.89
25	A	1926	5MU	C5-C4-N3	4.53	119.26	115.32
1	a	1512	MA6	C10-N6-C6	-4.53	109.00	120.52
1	a	960	2MG	N9-C4-N3	4.52	134.99	125.95
1	a	521	7MG	C2-N3-C4	4.51	120.06	112.30
22	v	54	5MU	C5-C4-N3	4.50	119.23	115.32
25	A	2056	7MG	C2-N3-C4	4.45	119.97	112.30
25	A	735	1MG	C2-N3-C4	4.39	121.86	111.98
1	a	1510	2MG	N9-C4-N3	4.29	134.53	125.95
22	v	55	PSU	C4-N3-C2	-4.25	120.52	126.37
25	A	1926	5MU	O4-C4-C5	-4.16	120.16	124.92
1	a	1513	MA6	C2-N1-C6	4.14	121.94	111.83
1	a	1512	MA6	C2-N1-C6	4.13	121.92	111.83
25	A	2017	6MZ	N3-C4-N9	4.11	134.16	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	v	54	5MU	O4-C4-C5	-4.11	120.22	124.92
1	a	1513	MA6	N3-C4-N9	4.08	134.10	127.17
25	A	2539	OMU	C5-C4-N3	4.04	120.46	114.80
1	a	1513	MA6	C9-N6-C6	-4.03	110.28	120.52
25	A	735	1MG	N9-C4-N3	4.02	133.99	125.95
25	A	1926	5MU	C5-C6-N1	-3.97	119.00	123.31
25	A	2017	6MZ	C6-C5-N7	3.93	136.72	132.43
1	a	1513	MA6	C4-C5-N7	-3.92	106.10	110.58
25	A	2017	6MZ	C4-C5-N7	-3.83	106.20	110.58
1	a	1512	MA6	C9-N6-C6	-3.78	110.89	120.52
25	A	1608	6MZ	C2-N3-C4	3.76	121.02	111.83
1	a	1513	MA6	C2-N3-C4	3.71	120.90	111.83
25	A	1608	6MZ	C6-C5-N7	3.70	136.47	132.43
22	v	55	PSU	O2-C2-N1	-3.68	118.99	122.79
25	A	2017	6MZ	C2-N3-C4	3.68	120.81	111.83
1	a	1512	MA6	C2-N3-C4	3.68	120.81	111.83
25	A	2490	2MA	C4-C5-N7	-3.59	106.47	110.58
25	A	1608	6MZ	C4-C5-N7	-3.58	106.49	110.58
1	a	1512	MA6	C4-C5-N7	-3.55	106.52	110.58
1	a	1510	2MG	C6-C5-N7	3.54	136.73	130.29
22	v	54	5MU	C5-C6-N1	-3.52	119.49	123.31
1	a	1492	UR3	C5-C4-N3	3.50	119.65	115.04
25	A	1902	UR3	C5-C4-N3	3.38	119.49	115.04
1	a	1512	MA6	N1-C6-N6	3.36	120.95	116.86
22	v	32	5MC	C5-C4-N3	-3.32	118.35	121.75
25	A	1949	5MC	C5-C6-N1	-3.32	119.70	123.31
25	A	1822	2MG	C6-C5-N7	3.32	136.32	130.29
25	A	1608	6MZ	N1-C2-N3	-3.31	123.57	128.58
1	a	1513	MA6	N1-C2-N3	-3.27	123.64	128.58
1	a	961	5MC	C5-C6-N1	-3.26	119.78	123.31
22	v	32	5MC	C5-C6-N1	-3.25	119.78	123.31
25	A	2432	2MG	C6-C5-N7	3.25	136.21	130.29
25	A	2017	6MZ	N1-C2-N3	-3.24	123.67	128.58
1	a	1512	MA6	N1-C2-N3	-3.23	123.70	128.58
22	v	8	4SU	C1'-N1-C2	3.17	123.29	117.59
1	a	960	2MG	C6-C5-N7	3.15	136.02	130.29
1	a	1201	2MG	C6-C5-N7	3.09	135.91	130.29
25	A	2539	OMU	O4-C4-C5	-3.04	119.91	125.16
25	A	2238	OMG	C6-C5-N7	3.02	135.78	130.29
25	A	1926	5MU	O2-C2-N1	-3.01	118.88	122.80
22	v	8	4SU	C4-N3-C2	-2.91	124.52	127.31
22	v	8	4SU	C5-C4-S4	-2.88	121.02	124.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2490	2MA	N6-C6-N1	2.82	120.83	117.03
25	A	2056	7MG	C5-C6-N1	2.78	115.83	110.94
25	A	1608	6MZ	C4-N9-C8	2.77	108.65	105.74
25	A	2490	2MA	C4-N9-C8	2.77	108.65	105.74
25	A	1822	2MG	N1-C2-N2	2.76	119.38	116.56
1	a	1513	MA6	C5-N7-C8	2.74	107.75	103.45
1	a	1510	2MG	C4-C5-N7	-2.74	106.34	110.67
1	a	521	7MG	C5-C6-N1	2.72	115.72	110.94
25	A	735	1MG	C6-C5-N7	2.71	135.38	129.36
25	A	2490	2MA	C2-N1-C6	2.71	122.26	118.10
1	a	961	5MC	C5-C4-N3	-2.70	118.98	121.75
1	a	1513	MA6	C10-N6-C9	-2.70	107.50	116.18
1	a	1513	MA6	N1-C6-N6	2.69	120.13	116.86
25	A	2017	6MZ	C5-N7-C8	2.68	107.67	103.45
22	v	32	5MC	O2-C2-N3	-2.68	118.11	122.33
1	a	1512	MA6	C4-N9-C8	2.66	108.54	105.74
25	A	2490	2MA	C5-N7-C8	2.66	107.63	103.45
25	A	735	1MG	C4-C5-N7	-2.63	106.51	110.67
25	A	1822	2MG	C4-C5-N7	-2.63	106.51	110.67
25	A	1608	6MZ	C5-N7-C8	2.61	107.56	103.45
25	A	2017	6MZ	C4-N9-C8	2.57	108.43	105.74
1	a	1513	MA6	C4-N9-C8	2.56	108.43	105.74
25	A	1949	5MC	C5-C4-N3	-2.54	119.15	121.75
1	a	1512	MA6	C5-N7-C8	2.53	107.43	103.45
1	a	1201	2MG	C4-C5-N7	-2.51	106.70	110.67
25	A	2432	2MG	C4-C5-N7	-2.50	106.70	110.67
1	a	1510	2MG	N1-C2-N2	2.48	119.09	116.56
1	a	960	2MG	C4-C5-N7	-2.43	106.82	110.67
25	A	2238	OMG	C4-C5-N7	-2.42	106.83	110.67
1	a	1512	MA6	C10-N6-C9	-2.40	108.47	116.18
1	a	1512	MA6	C5-C6-N6	-2.38	121.56	125.33
25	A	1902	UR3	C6-N1-C2	-2.37	119.86	121.80
25	A	2539	OMU	O2-C2-N1	-2.33	119.77	122.80
1	a	521	7MG	C5-C4-N9	-2.32	103.36	106.33
25	A	2485	OMC	O2-C2-N3	-2.31	118.68	122.33
25	A	2056	7MG	C5-C4-N9	-2.28	103.41	106.33
25	A	2490	2MA	C6-C5-N7	2.28	136.49	132.09
22	v	54	5MU	O2-C2-N1	-2.28	119.83	122.80
22	v	8	4SU	C6-C5-C4	-2.27	117.98	119.95
1	a	960	2MG	O6-C6-C5	-2.26	120.58	126.53
1	a	1513	MA6	C6-C5-N7	2.23	136.99	133.43
25	A	1822	2MG	O6-C6-C5	-2.22	120.66	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2432	2MG	O6-C6-C5	-2.22	120.67	126.53
25	A	2238	OMG	O6-C6-C5	-2.21	120.69	126.53
25	A	1822	2MG	C2-N1-C6	-2.19	121.90	124.55
1	a	1513	MA6	N9-C8-N7	-2.19	110.83	113.94
22	v	55	PSU	C5-C6-N1	-2.18	119.11	122.14
25	A	1902	UR3	C1'-N1-C2	2.18	120.61	117.04
25	A	2490	2MA	N9-C8-N7	-2.17	110.86	113.94
25	A	2056	7MG	O6-C6-C5	-2.17	122.30	127.62
1	a	1396	4OC	C6-C5-C4	2.15	119.59	117.00
25	A	2017	6MZ	N9-C8-N7	-2.14	110.89	113.94
25	A	1822	2MG	N2-C2-N3	-2.13	117.80	120.51
25	A	1608	6MZ	N9-C8-N7	-2.11	110.94	113.94
1	a	1201	2MG	O6-C6-C5	-2.11	120.97	126.53
1	a	960	2MG	N1-C2-N2	2.09	118.70	116.56
1	a	521	7MG	O6-C6-C5	-2.08	122.52	127.62
1	a	1510	2MG	O6-C6-C5	-2.06	121.08	126.53
1	a	1510	2MG	CM2-N2-C2	-2.05	119.25	123.65
1	a	961	5MC	O2-C2-N3	-2.01	119.16	122.33
25	A	1822	2MG	C5-C6-N1	2.01	118.37	113.25
25	A	2017	6MZ	C2-N1-C6	2.00	121.88	115.24

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	A	2238	OMG	O4'-C4'-C5'-O5'
1	a	1513	MA6	O4'-C4'-C5'-O5'
25	A	2238	OMG	C3'-C4'-C5'-O5'
1	a	521	7MG	C3'-C4'-C5'-O5'
1	a	521	7MG	O4'-C4'-C5'-O5'
25	A	2056	7MG	O4'-C4'-C5'-O5'
1	a	1513	MA6	C3'-C4'-C5'-O5'
25	A	2056	7MG	C3'-C4'-C5'-O5'
25	A	2017	6MZ	O4'-C4'-C5'-O5'
25	A	2017	6MZ	C3'-C4'-C5'-O5'
1	a	1512	MA6	C5-C6-N6-C9
1	a	1513	MA6	C5-C6-N6-C9
25	A	2485	OMC	O4'-C4'-C5'-O5'
25	A	2485	OMC	C3'-C2'-O2'-CM2
1	a	1513	MA6	N1-C6-N6-C9
1	a	1396	4OC	C3'-C2'-O2'-CM2
25	A	2432	2MG	C3'-C4'-C5'-O5'

There are no ring outliers.

11 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	a	1396	4OC	1	0
1	a	961	5MC	1	0
25	A	2432	2MG	1	0
25	A	1902	UR3	1	0
1	a	1512	MA6	1	0
22	v	32	5MC	1	0
1	a	1510	2MG	1	0
25	A	2238	OMG	1	0
25	A	2485	OMC	1	0
1	a	1513	MA6	2	0
22	v	8	4SU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 634 ligands modelled in this entry, 632 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	FME	v	103	22	8,9,10	0.41	0	8,9,11	1.23	0
60	GDP	x	901	-	29,30,30	1.17	3 (10%)	45,47,47	1.77	7 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	FME	v	103	22	-	4/7/9/11	-
60	GDP	x	901	-	-	1/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	x	901	GDP	C5-C4	2.86	1.46	1.38
60	x	901	GDP	C6-N1	-2.71	1.33	1.38
60	x	901	GDP	C5-N7	-2.35	1.34	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	x	901	GDP	C5-C4-N3	-5.95	118.92	128.39
60	x	901	GDP	C2-N3-C4	4.87	120.68	112.30
60	x	901	GDP	N9-C4-N3	4.34	134.63	125.95
60	x	901	GDP	C6-C5-N7	3.23	136.18	130.29
60	x	901	GDP	C4-C5-N7	-2.54	106.64	110.67
60	x	901	GDP	C3'-C2'-C1'	2.07	105.38	101.46
60	x	901	GDP	O6-C6-C5	-2.06	121.10	126.53

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	v	103	FME	O1-CN-N-CA
59	v	103	FME	CB-CA-N-CN
59	v	103	FME	N-CA-CB-CG
59	v	103	FME	C-CA-CB-CG
60	x	901	GDP	C5'-O5'-PA-O1A

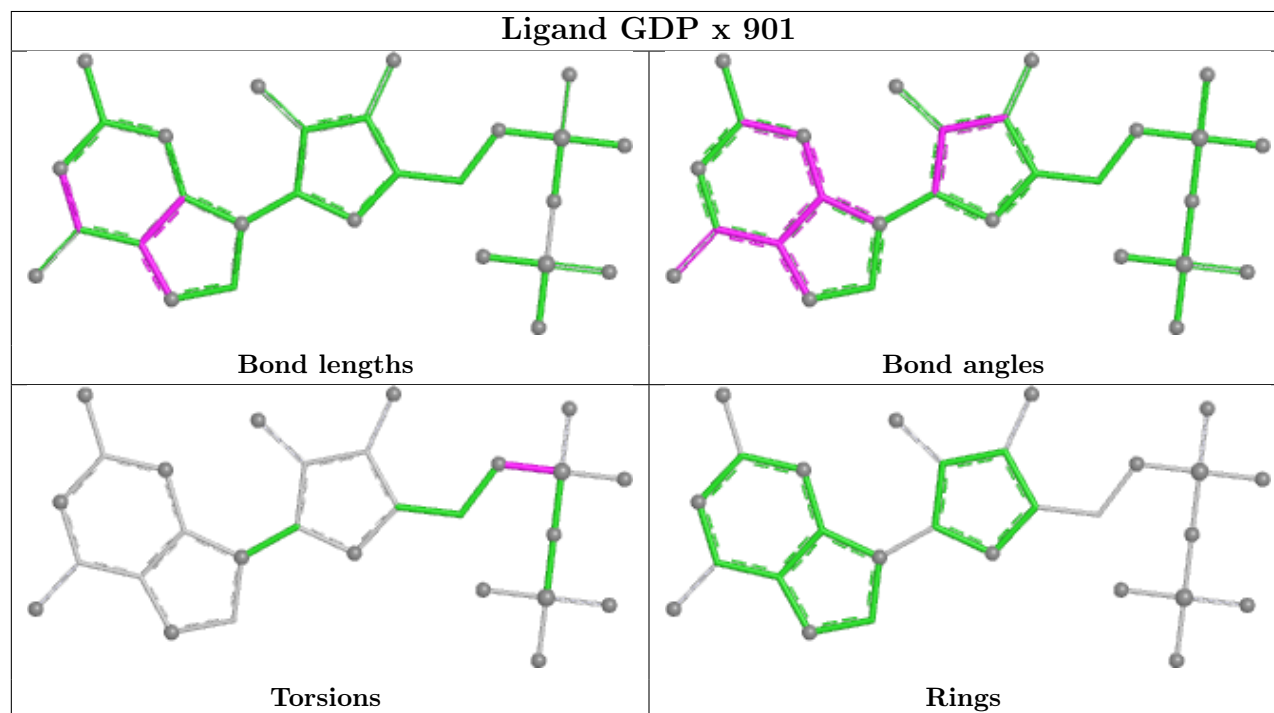
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	x	901	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

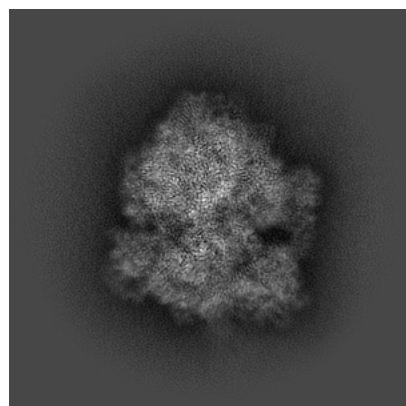
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26630. These allow visual inspection of the internal detail of the map and identification of artifacts.

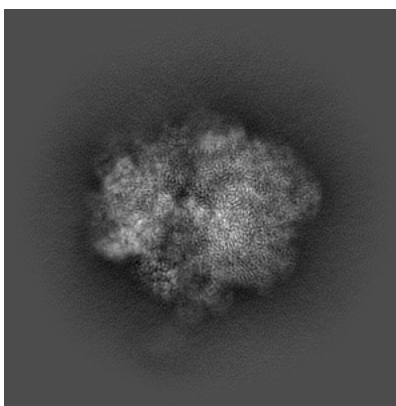
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

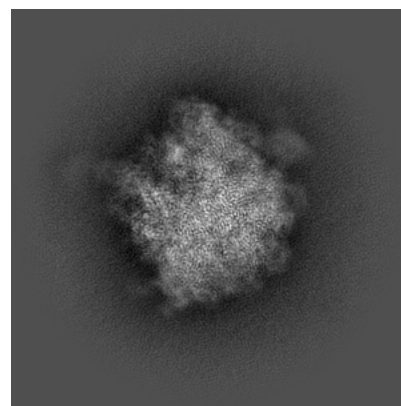
6.1.1 Primary map



X

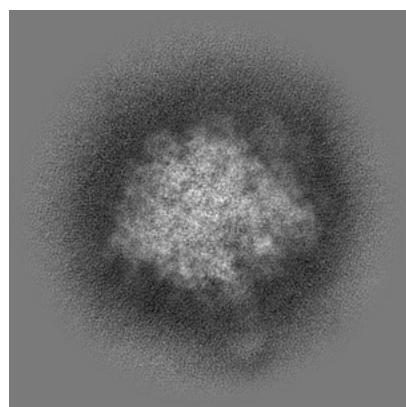


Y

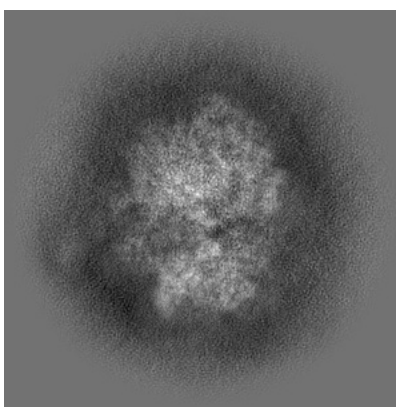


Z

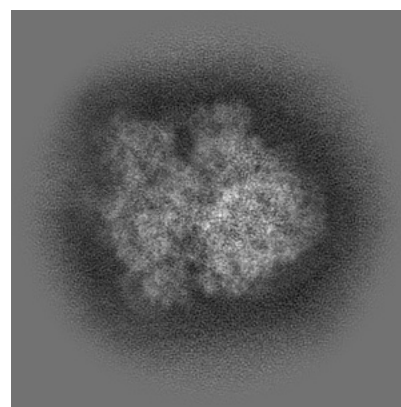
6.1.2 Raw map



X



Y

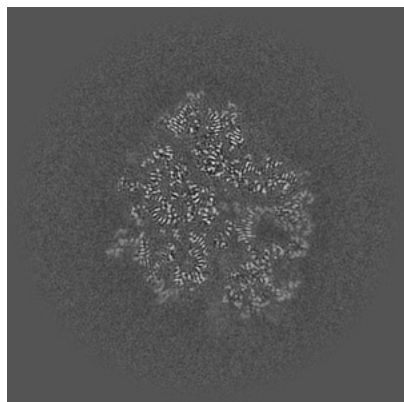


Z

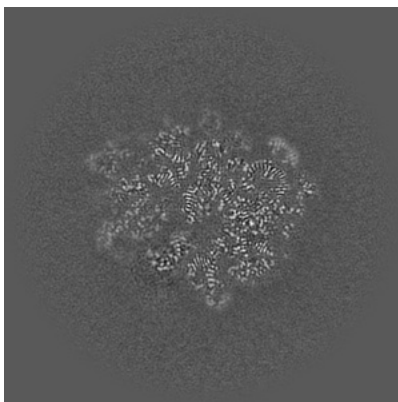
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

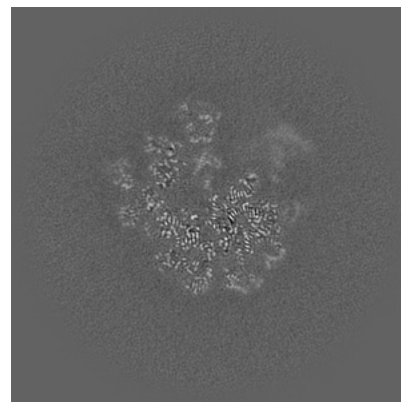
6.2.1 Primary map



X Index: 256

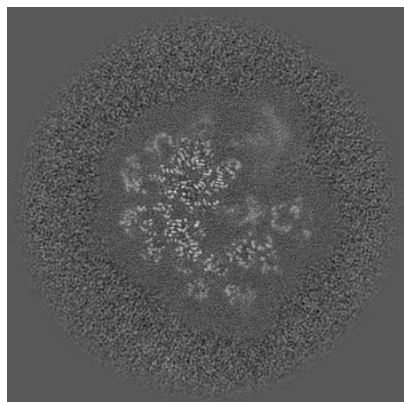


Y Index: 256

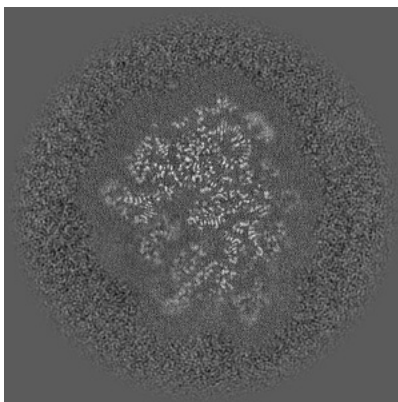


Z Index: 256

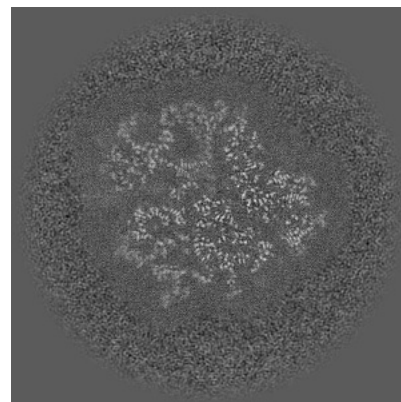
6.2.2 Raw map



X Index: 256



Y Index: 256

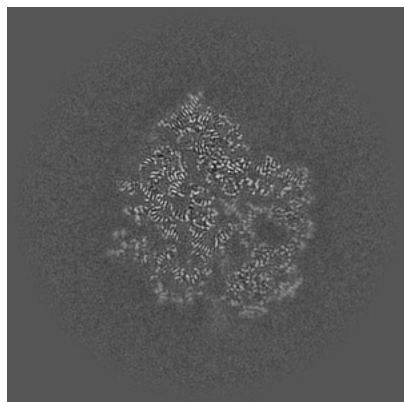


Z Index: 256

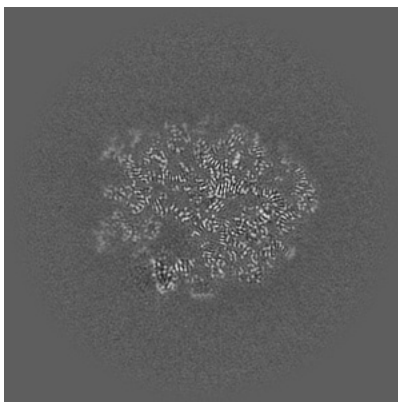
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

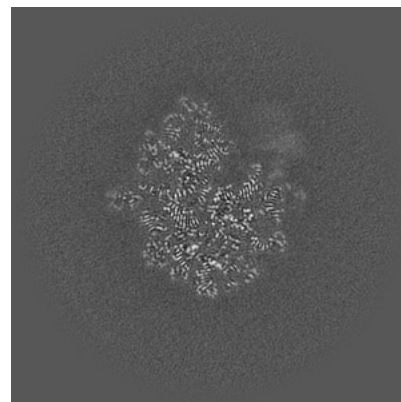
6.3.1 Primary map



X Index: 252

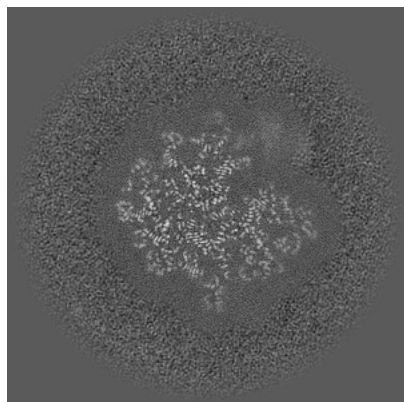


Y Index: 243

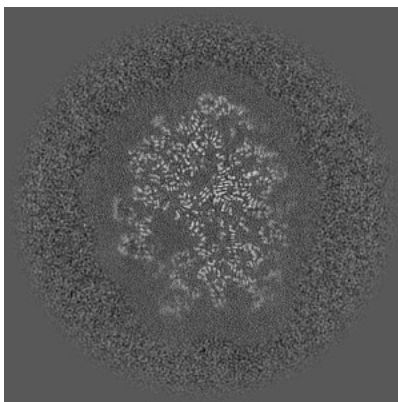


Z Index: 278

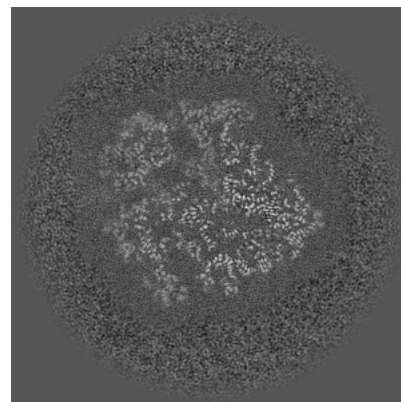
6.3.2 Raw map



X Index: 278



Y Index: 243

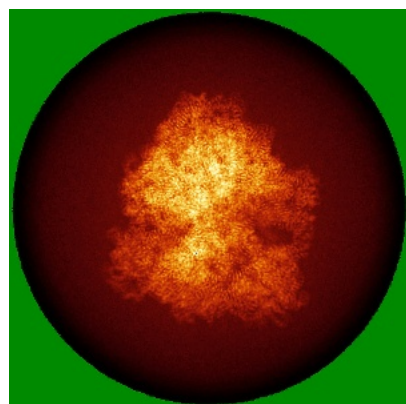


Z Index: 248

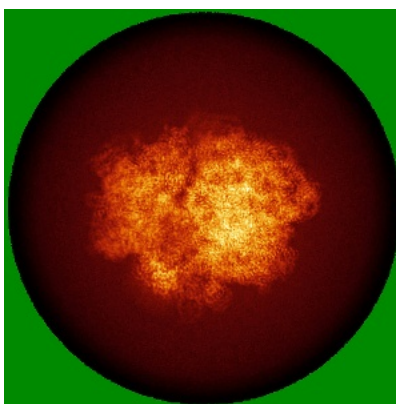
The images above show the largest variance slices of the map in three orthogonal directions.

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

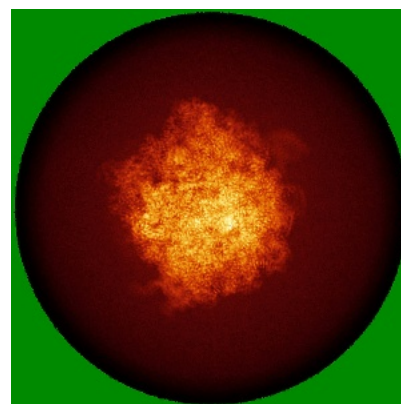
6.4.1 Primary map



X

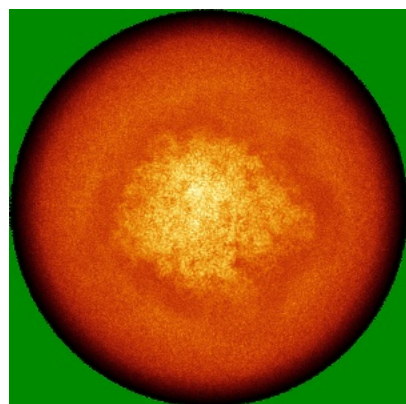


Y

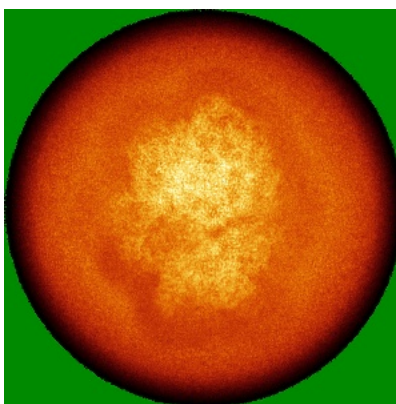


Z

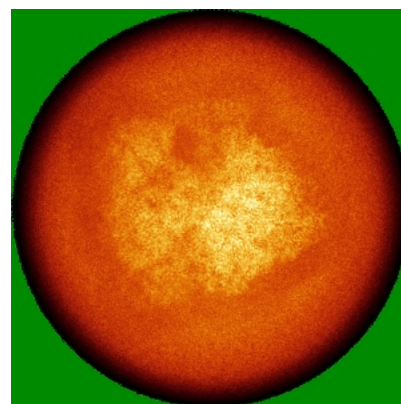
6.4.2 Raw map



X



Y

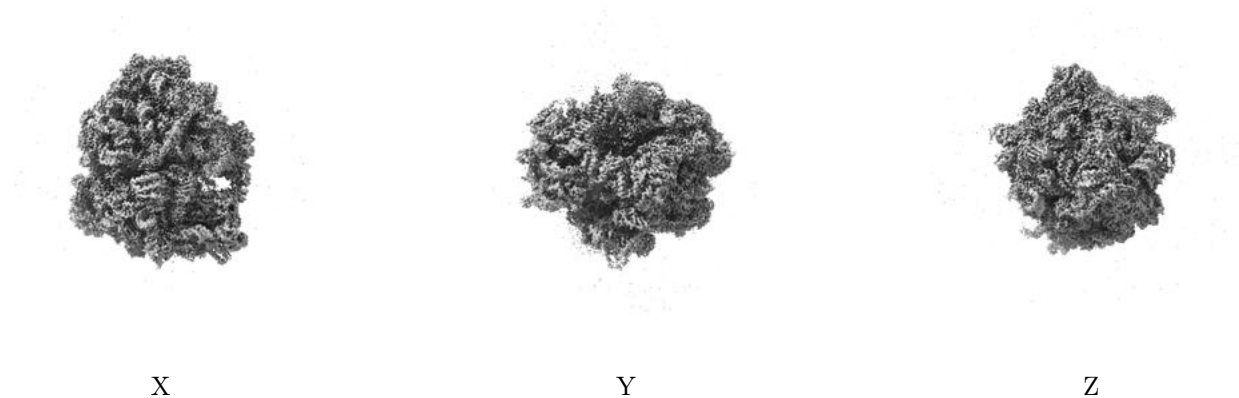


Z

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.

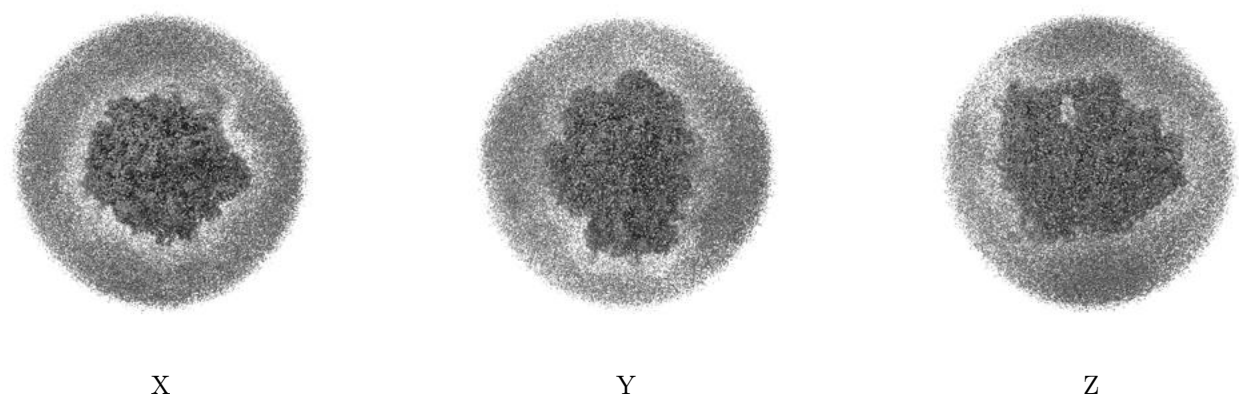
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.3. 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.

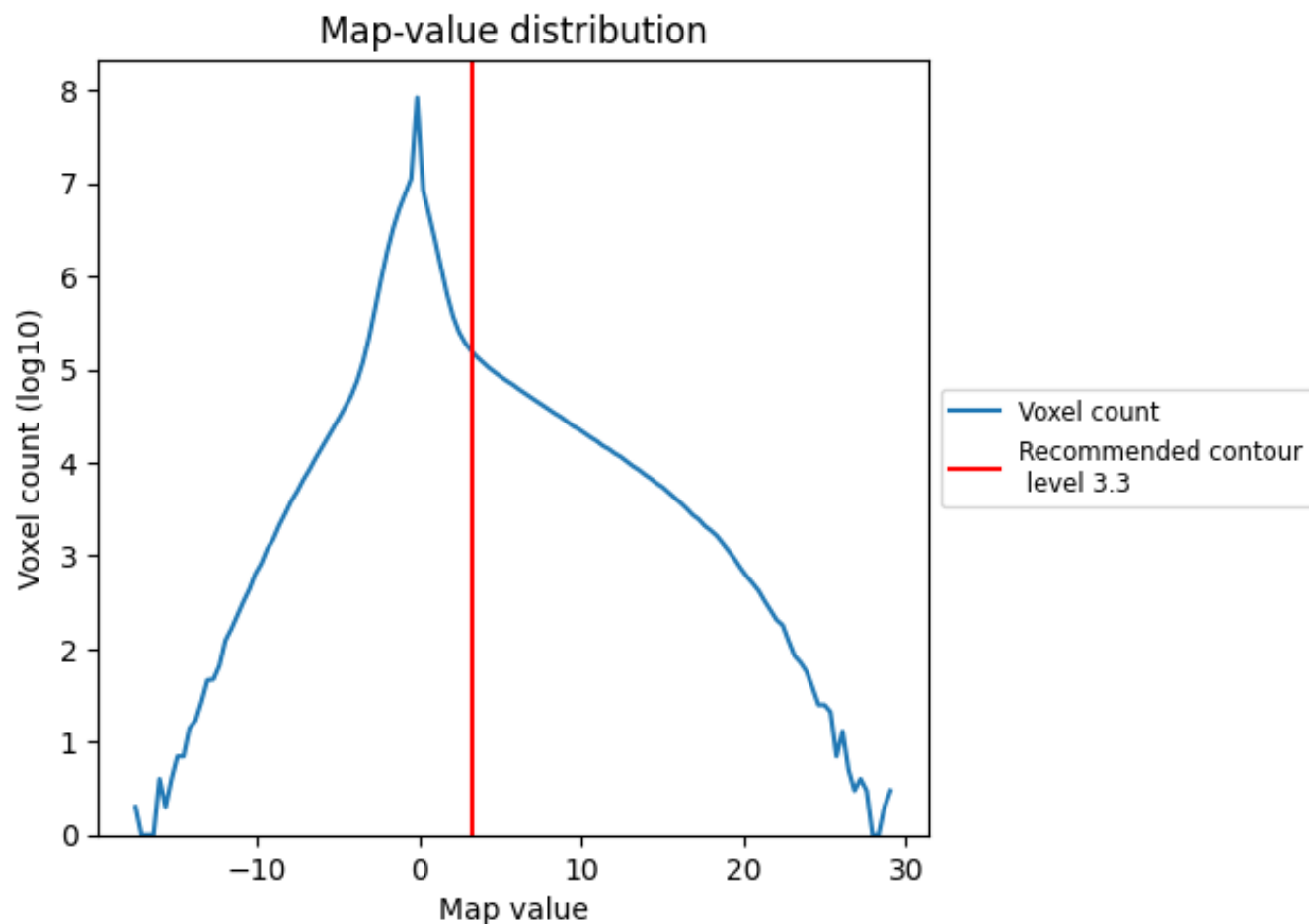
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

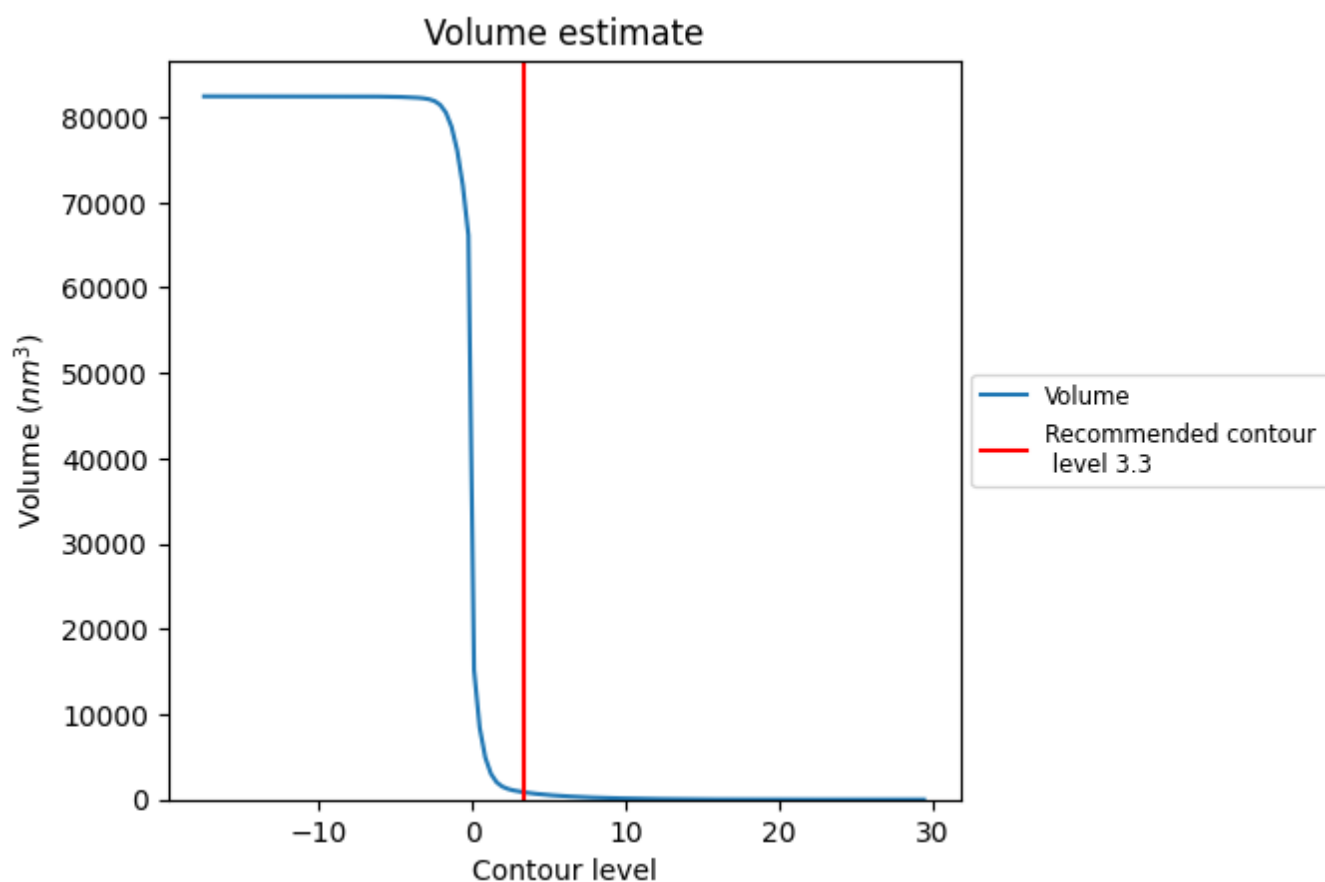
This section contains the results of statistical analysis of the map.

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.

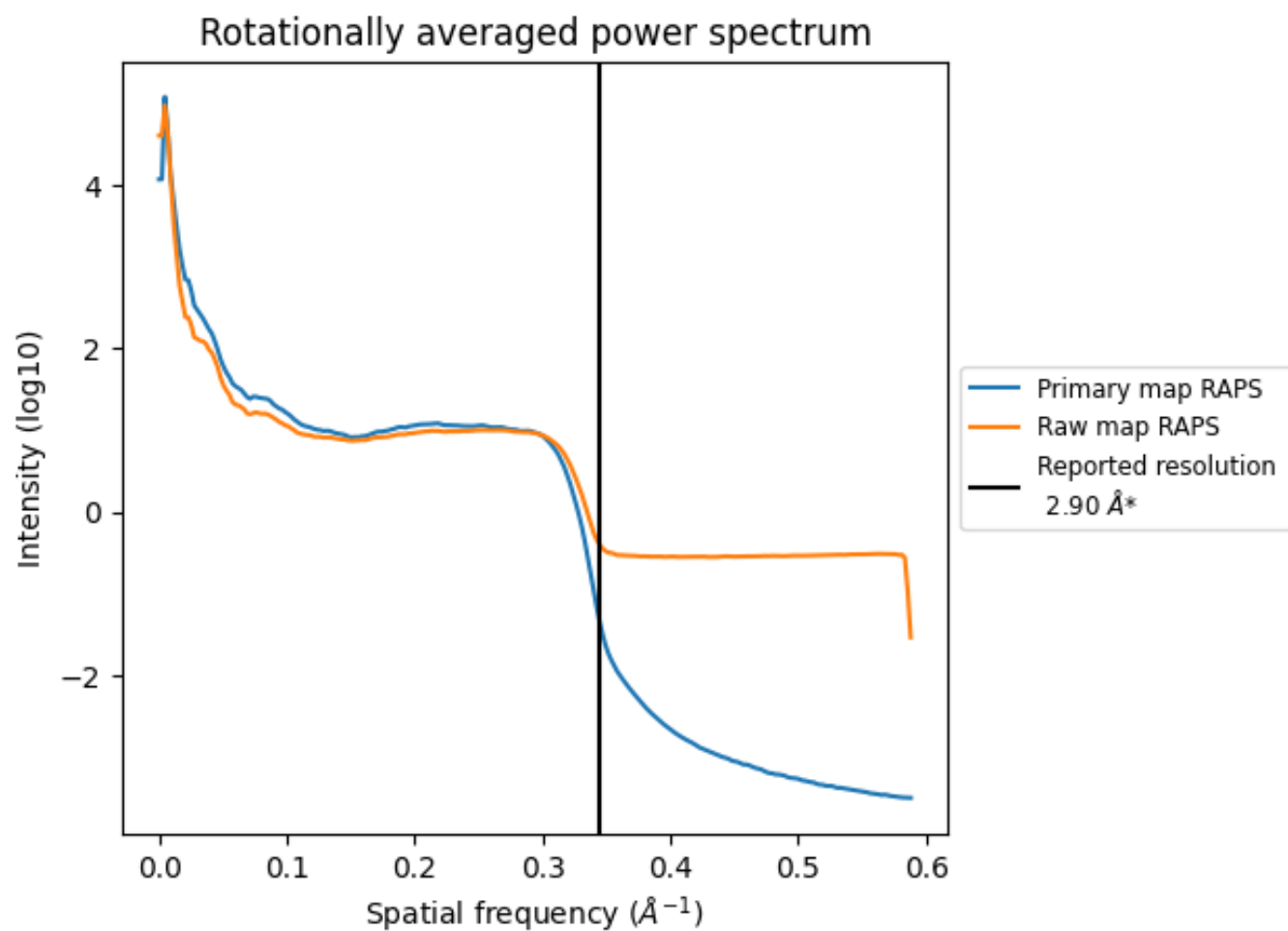
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 869 nm³; this corresponds to an approximate mass of 785 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 ⓘ

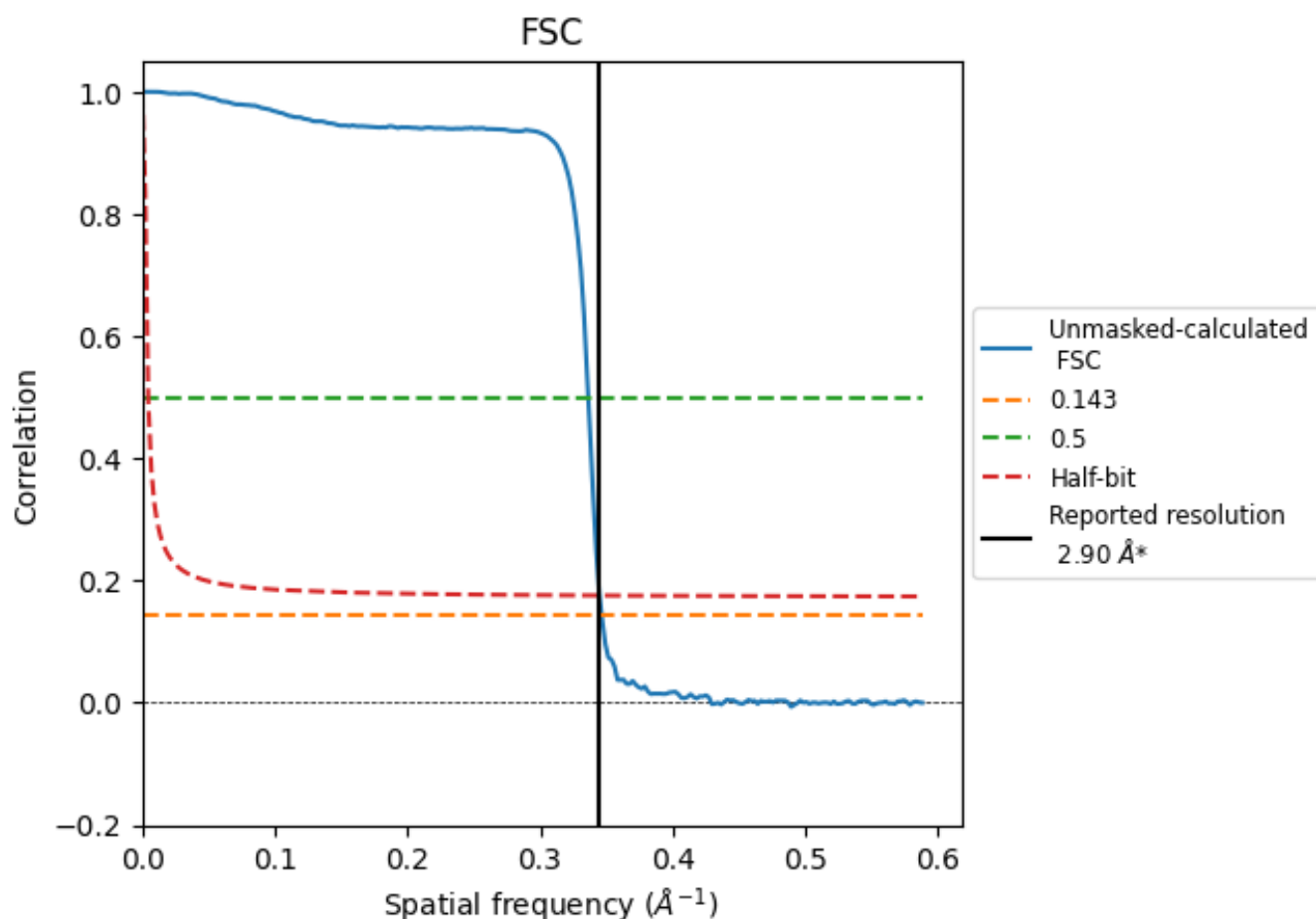


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

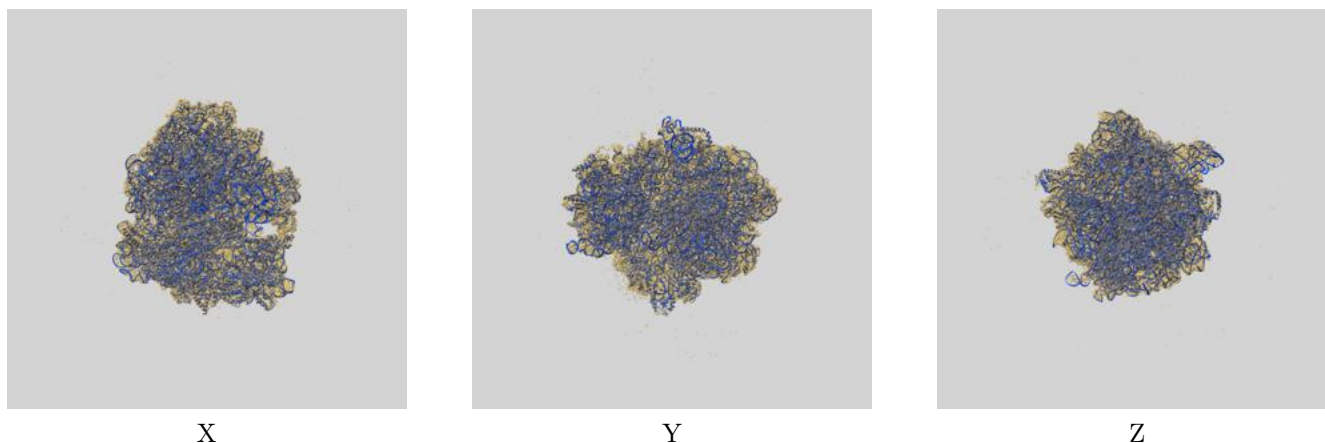
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.89	2.97	2.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

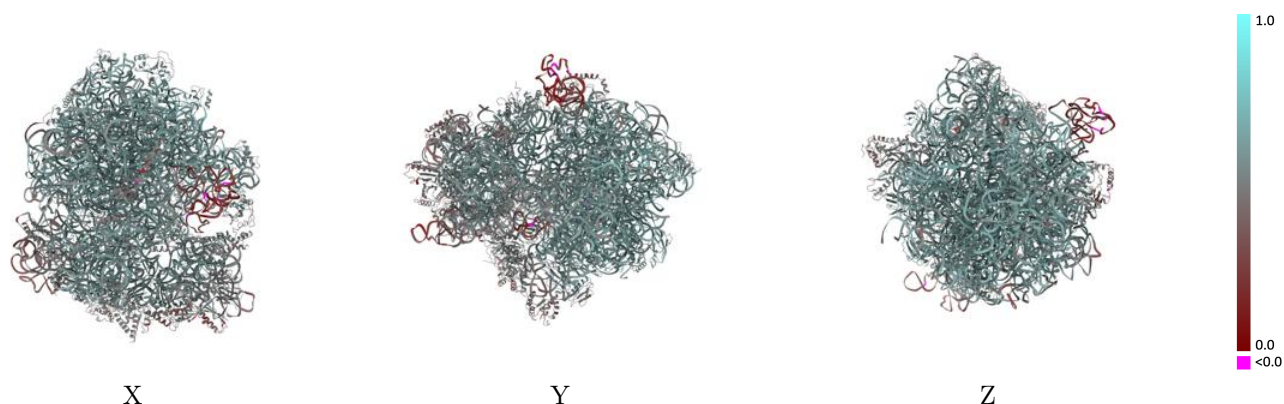
This section contains information regarding the fit between EMDB map EMD-26630 and PDB model 7UNR. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



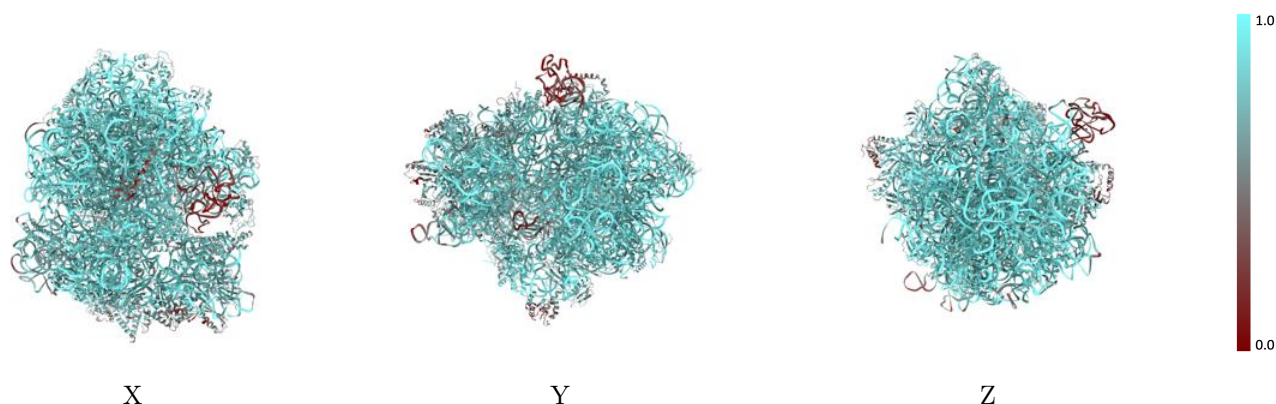
The images above show the 3D surface view of the map at the recommended contour level 3.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



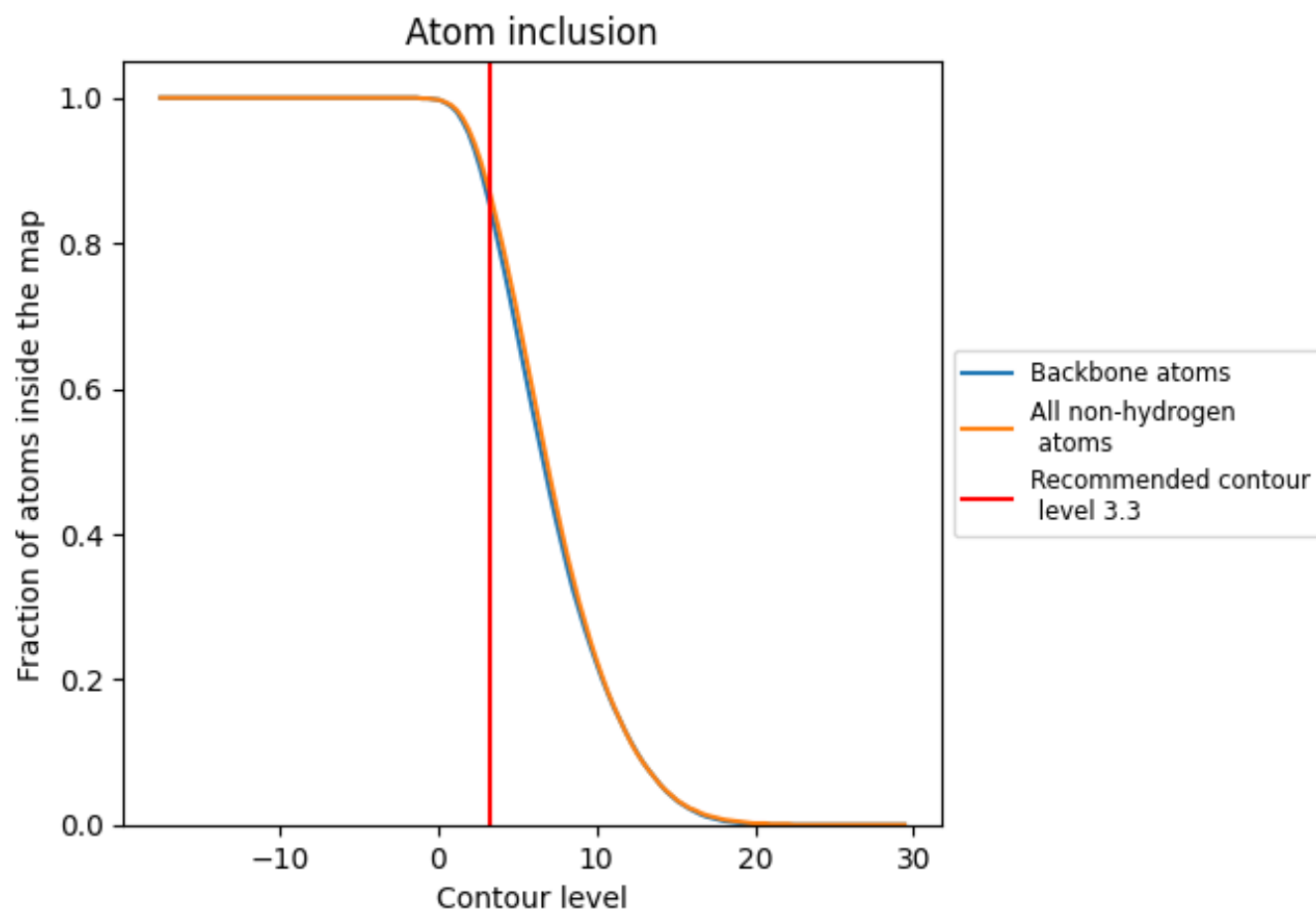
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 87% 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 (3.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8680	 0.5610
1	 0.8060	 0.5580
2	 0.8250	 0.6050
3	 0.6350	 0.4570
4	 0.8570	 0.5950
5	 0.8340	 0.5850
6	 0.9040	 0.6240
7	 0.9290	 0.6210
8	 0.9050	 0.6070
A	 0.9290	 0.5890
B	 0.9110	 0.5750
C	 0.8950	 0.6110
D	 0.8620	 0.5930
E	 0.8390	 0.5900
F	 0.7370	 0.5200
G	 0.7350	 0.5340
H	 0.4720	 0.4490
I	 0.4220	 0.4160
J	 0.8500	 0.4240
L	 0.8850	 0.6070
M	 0.8580	 0.5970
N	 0.8600	 0.5920
O	 0.8750	 0.6030
P	 0.8880	 0.6060
Q	 0.7500	 0.5540
R	 0.8380	 0.5890
S	 0.9000	 0.6120
T	 0.8400	 0.5880
U	 0.8800	 0.6060
V	 0.8360	 0.5850
W	 0.7200	 0.5430
X	 0.7400	 0.5670
Y	 0.8720	 0.6080
Z	 0.8680	 0.5990
a	 0.8920	 0.5370



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Chain	Atom inclusion	Q-score
b	 0.6320	 0.4640
c	 0.6950	 0.5140
d	 0.5800	 0.4320
e	 0.7940	 0.5580
f	 0.7430	 0.5100
g	 0.6470	 0.4860
h	 0.8010	 0.5620
i	 0.7230	 0.5020
j	 0.6040	 0.4580
k	 0.7900	 0.5540
l	 0.7210	 0.5310
m	 0.7160	 0.4940
n	 0.7360	 0.5100
o	 0.8260	 0.5680
p	 0.7190	 0.4920
q	 0.7360	 0.5130
r	 0.7220	 0.5450
s	 0.7020	 0.4790
t	 0.7690	 0.5010
u	 0.6390	 0.5100
v	 0.8300	 0.5460
w	 0.8400	 0.5610
x	 0.8940	 0.5150