



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 01:49 AM UTC

PDB ID : 5X8P / pdb_00005x8p
EMDB ID : EMD-6709
Title : Structure of the 70S chloroplast ribosome from spinach
Authors : Ahmed, T.; Shi, J.; Bhushan, S.
Deposited on : 2017-03-03
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

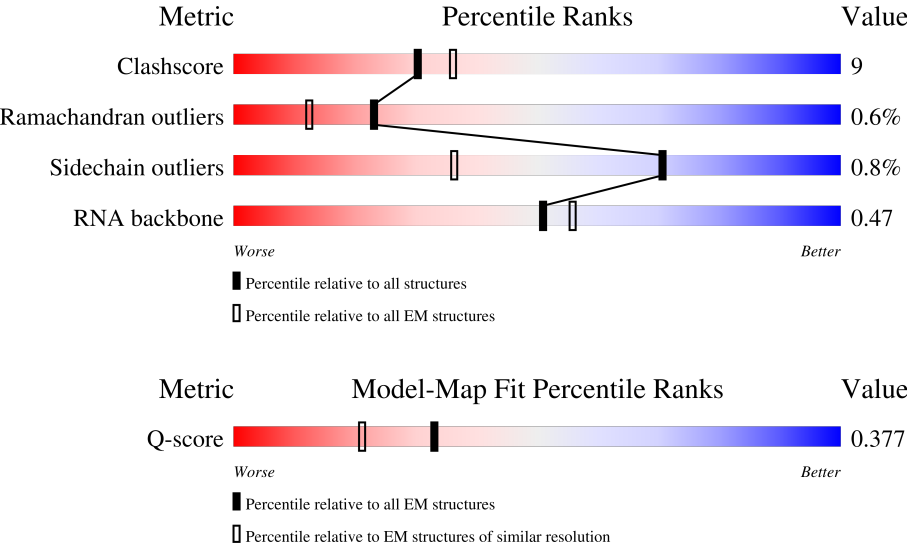
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



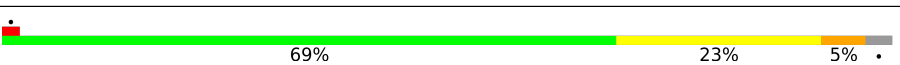
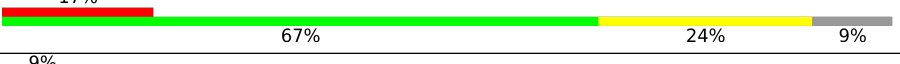
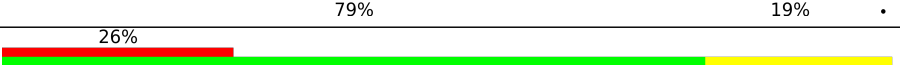
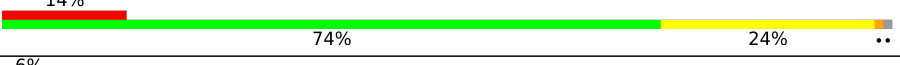
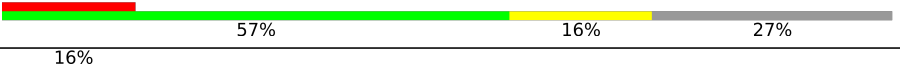
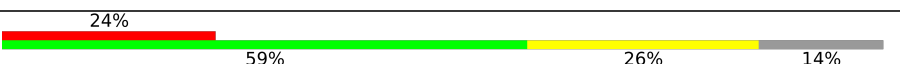
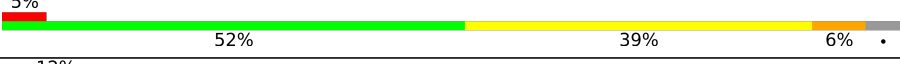
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	1	56	7% 70% 12% 18%
2	2	65	26% 57% 22% 22%
3	3	61	7% 74% 20% 7%

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Mol	Chain	Length	Quality of chain
4	4	73	
5	5	37	
6	6	142	
7	7	116	
8	B	121	
9	C	271	
10	D	221	
11	E	243	
12	F	220	
13	G	182	
14	H	155	
15	K	197	
16	L	121	
17	M	192	
18	N	135	
19	O	116	
20	P	123	
21	Q	156	
22	R	127	
23	S	201	
24	T	199	
25	U	122	
26	V	145	
27	W	106	
28	X	137	

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Mol	Chain	Length	Quality of chain
29	Y	77	
30	Z	109	
31	A	2810	
32	0	94	
33	b	236	
34	c	218	
35	e	253	
36	f	146	
37	g	155	
38	h	134	
39	i	157	
40	j	122	
41	k	138	
42	l	123	
43	m	126	
44	o	90	
45	p	88	
46	q	108	
47	r	101	
48	s	92	
49	t	108	
50	u	137	
51	y	236	
52	a	1491	
53	w	121	

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Mol	Chain	Length	Quality of chain
54	d	201	
55	v	198	
56	n	100	
57	x	47	
58	8	370	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 147126 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	46	Total	C	N	O	0	0
			378	250	70	58		

- Molecule 2 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	51	Total	C	N	O	S	0	0
			415	258	83	70	4		

- Molecule 3 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	57	Total	C	N	O	S	0	0
			445	268	103	71	3		

- Molecule 4 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	69	Total	C	N	O	S	0	0
			563	353	119	90	1		

- Molecule 5 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	37	Total	C	N	O	S	0	0
			304	186	70	44	4		

- Molecule 6 is a protein called protein cL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	49	Total	C	N	O	S	0	0
			422	268	92	57	5		

- Molecule 7 is a protein called protein cL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	46	Total	C	N	O	S	0	0
			368	237	71	59	1		

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	117	Total	C	N	O	P	0	0
			2500	1116	452	815	117		

- Molecule 9 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	247	Total	C	N	O	S	0	0
			1904	1181	390	327	6		

- Molecule 10 is a protein called protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	212	Total	C	N	O	S	0	0
			1620	1025	295	289	11		

- Molecule 11 is a protein called 50S ribosomal protein L4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	210	Total	C	N	O	S	0	0
			1655	1052	308	292	3		

- Molecule 12 is a protein called 50S ribosomal protein L5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	175	Total	C	N	O	S	0	0
			1351	862	233	248	8		

- Molecule 13 is a protein called protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	173	Total	C	N	O	S	0	0
			1353	855	249	245	4		

- Molecule 14 is a protein called protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	53	Total	C	N	O	S	0	0
			423	280	74	68	1		

- Molecule 15 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	193	Total	C	N	O	S	0	0
			1568	1000	289	274	5		

- Molecule 16 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	121	Total	C	N	O	S	0	0
			942	588	179	170	5		

- Molecule 17 is a protein called protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	177	Total	C	N	O	S	0	0
			1342	836	264	236	6		

- Molecule 18 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	134	Total	C	N	O	S	0	0
			1067	672	217	173	5		

- Molecule 19 is a protein called protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	116	Total	C	N	O	S	0	0
			944	592	193	155	4		

- Molecule 20 is a protein called protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	120	Total	C	N	O	S	0	0
			947	589	183	170	5		

- Molecule 21 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	118	Total	C	N	O	S	0	0
			953	610	186	156	1		

- Molecule 22 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	115	Total	C	N	O	S	0	0
			996	633	208	153	2		

- Molecule 23 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	147	Total	C	N	O		0	0
			1171	759	202	210			

- Molecule 24 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	144	Total	C	N	O	S	0	0
			1149	731	210	200	8		

- Molecule 25 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	92	Total	C	N	O	S	0	0
			740	477	129	132	2		

- Molecule 26 is a protein called 50S ribosomal protein L24, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	124	Total	C	N	O	S	0	0
			993	624	187	180	2		

- Molecule 27 is a RNA chain called 4.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	102	Total	C	N	O	P	0	0
			2187	977	403	705	102		

- Molecule 28 is a protein called protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	X	100	Total	C	N	O		
			810	511	159	140	0	0

- Molecule 29 is a protein called protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	74	Total	C	N	O	S		
			605	385	121	98	1	0	0

- Molecule 30 is a protein called protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	90	Total	C	N	O	S		
			754	470	150	131	3	0	0

- Molecule 31 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	2809	Total	C	N	O	P		
			60324	26912	11166	19437	2809	0	0

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	0	64	Total	C	N	O	S		
			521	330	89	100	2	0	0

- Molecule 33 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	227	Total	C	N	O	S		
			1787	1127	326	321	13	0	0

- Molecule 34 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	213	Total	C	N	O	S		
			1719	1099	310	304	6	0	0

- Molecule 35 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	171	Total	C	N	O	S	0	0
			1292	806	250	230	6		

- Molecule 36 is a protein called 30S ribosomal protein S6 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	111	Total	C	N	O	S	0	0
			886	566	145	171	4		

- Molecule 37 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	149	Total	C	N	O	S	0	0
			1161	723	231	204	3		

- Molecule 38 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	134	Total	C	N	O	S	0	0
			1088	684	211	187	6		

- Molecule 39 is a protein called 30S ribosomal protein S9, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	133	Total	C	N	O	S	0	0
			1020	650	191	178	1		

- Molecule 40 is a protein called protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	98	Total	C	N	O	S	0	0
			796	512	142	137	5		

- Molecule 41 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	118	Total	C	N	O	S	0	0
			887	549	182	151	5		

- Molecule 42 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	123	Total	C	N	O	S	0	0
			967	604	198	162	3		

- Molecule 43 is a protein called 30S ribosomal protein S13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	110	Total	C	N	O	S	0	0
			898	559	183	153	3		

- Molecule 44 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	62	Total	C	N	O	S	0	0
			525	339	100	85	1		

- Molecule 45 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 46 is a protein called protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	78	Total	C	N	O	S	0	0
			635	399	124	108	4		

- Molecule 47 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	64	Total	C	N	O	S	0	0
			518	326	101	90	1		

- Molecule 48 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	78	Total	C	N	O	S	0	0
			627	403	118	104	2		

- Molecule 49 is a protein called protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	105	Total	C	N	O	S	0	0
			832	514	169	148	1		

- Molecule 50 is a protein called protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	44	Total	C	N	O	S	0	0
			393	238	87	66	2		

- Molecule 51 is a protein called protein plastid pY.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	108	Total	C	N	O	S	0	0
			845	521	164	159	1		

- Molecule 52 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	1480	Total	C	N	O	P	0	0
			31777	14168	5863	10266	1480		

- Molecule 53 is a protein called protein cS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	84	Total	C	N	O	S	0	0
			689	454	115	118	2		

- Molecule 54 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	d	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 55 is a protein called protein cS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	190	Total	C	N	O	S	0	0
			1464	908	255	298	3		

- Molecule 56 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	n	99	Total	C	N	O	S	0	0
			819	507	174	135	3		

- Molecule 57 is a protein called protein bTHXc.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	x	37	Total	C	N	O	0	0
			289	179	65	45		

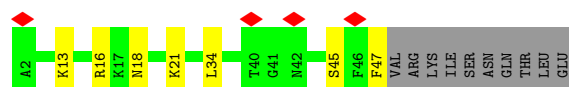
- Molecule 58 is a protein called 30S ribosomal protein S1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	154	Total	C	N	O	S	0	0
			1201	744	222	227	8		

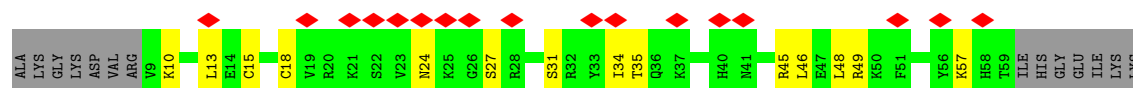
3 Residue-property plots [i](#)

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.

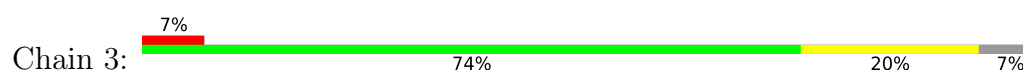
- Molecule 1: 50S ribosomal protein L32, chloroplastic



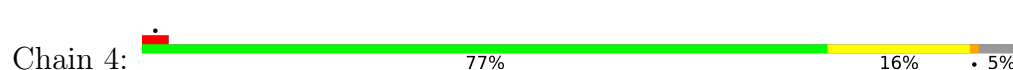
- Molecule 2: 50S ribosomal protein L33, chloroplastic



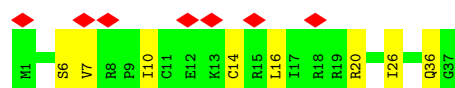
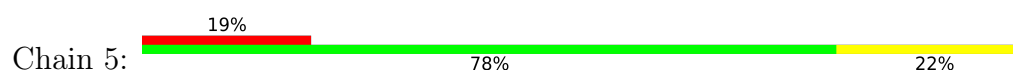
- Molecule 3: 50S ribosomal protein L34, chloroplastic

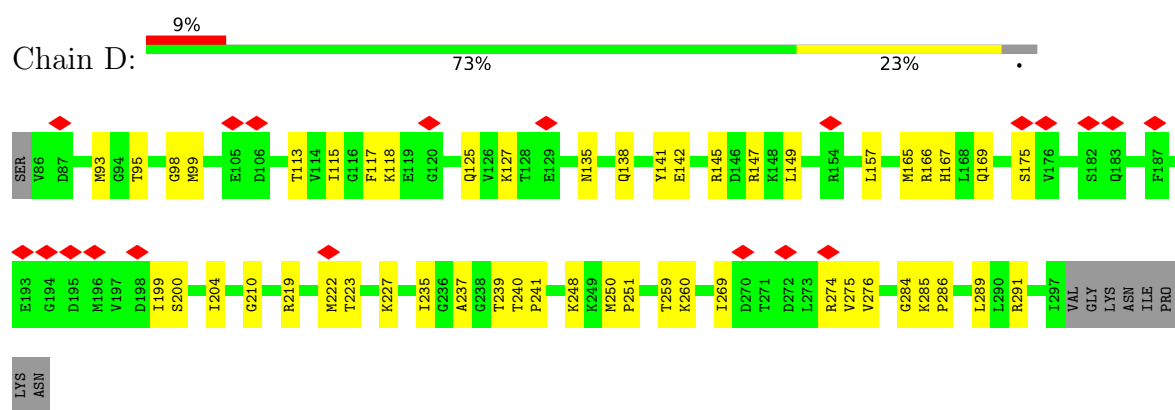


- Molecule 4: 50S ribosomal protein L35, chloroplastic

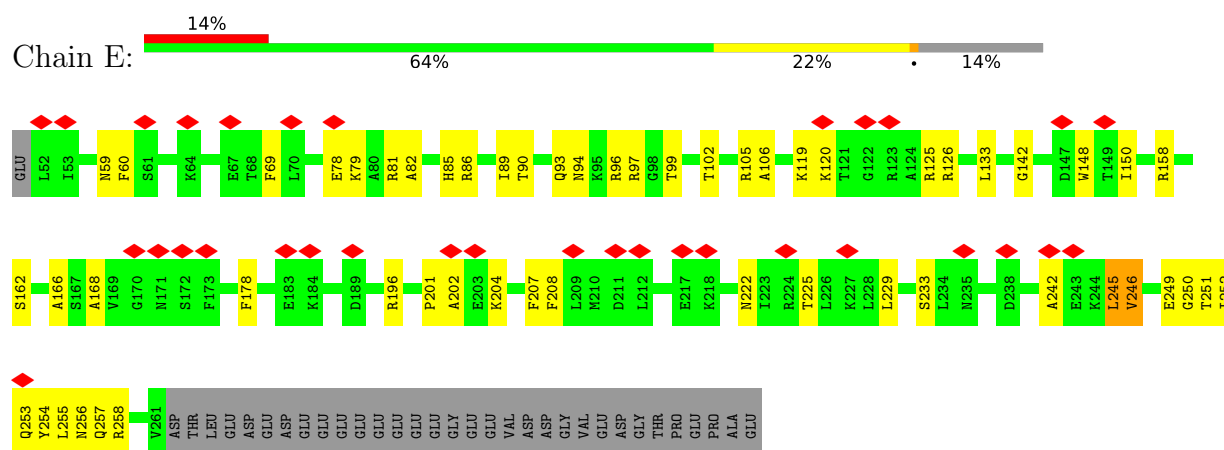


- Molecule 5: 50S ribosomal protein L36, chloroplastic

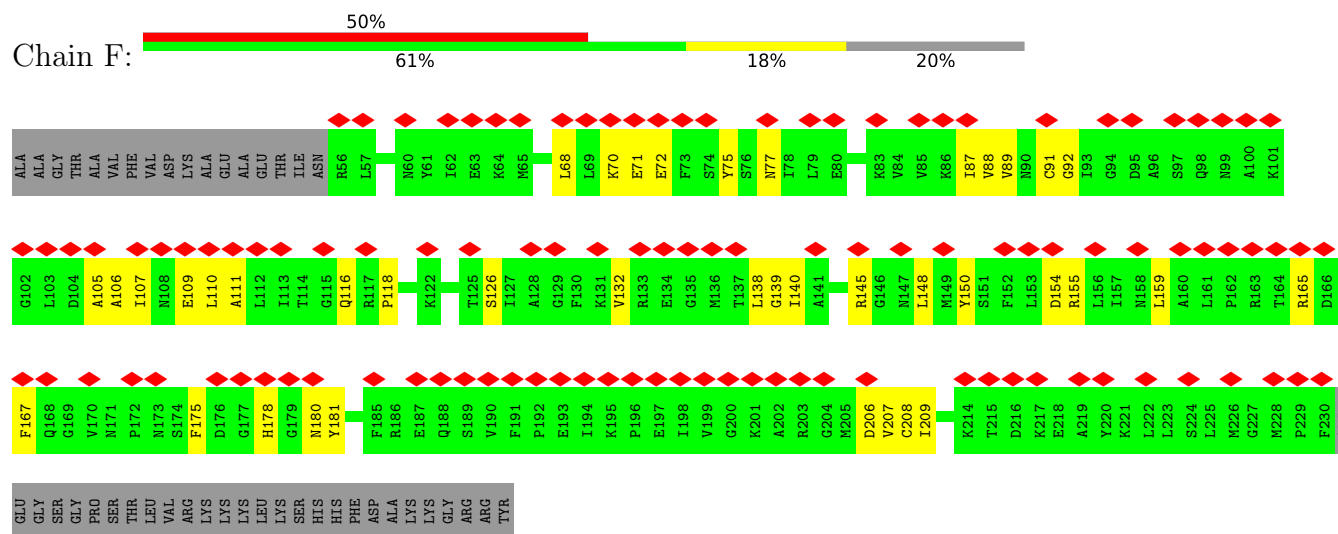




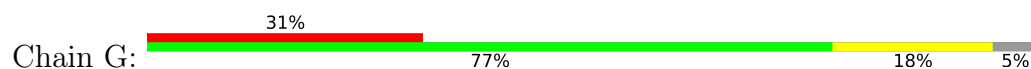
- Molecule 11: 50S ribosomal protein L4, chloroplastic

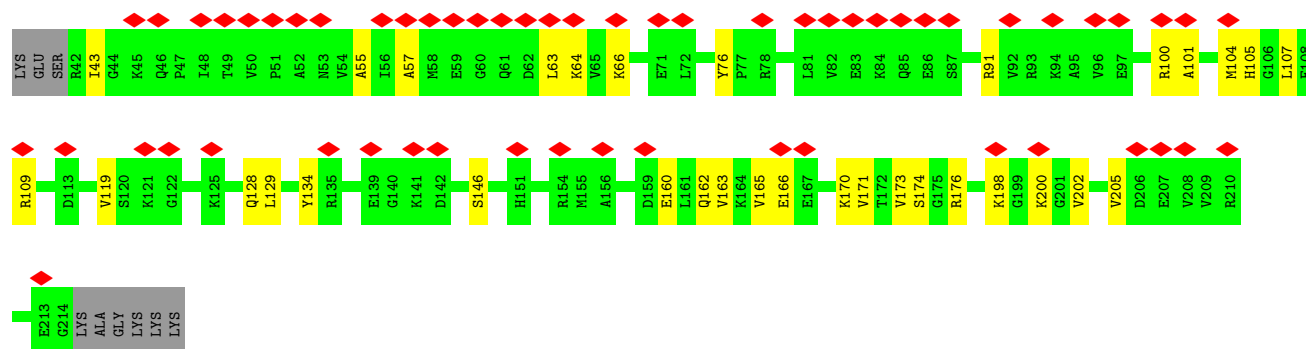


- Molecule 12: 50S ribosomal protein L5, chloroplastic

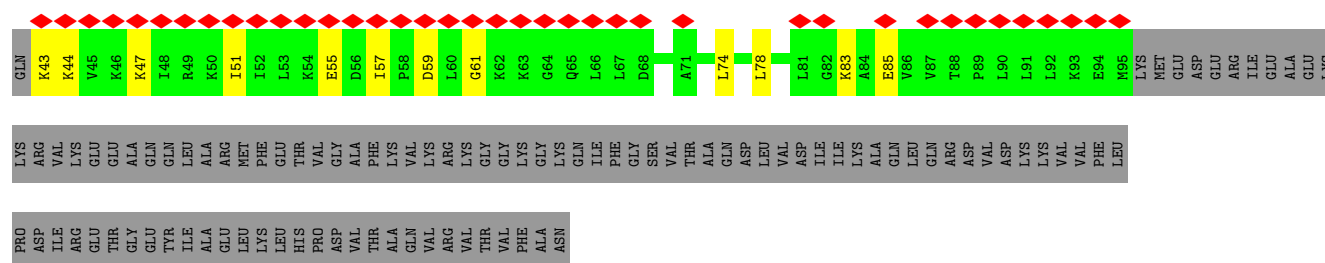


- Molecule 13: protein L6

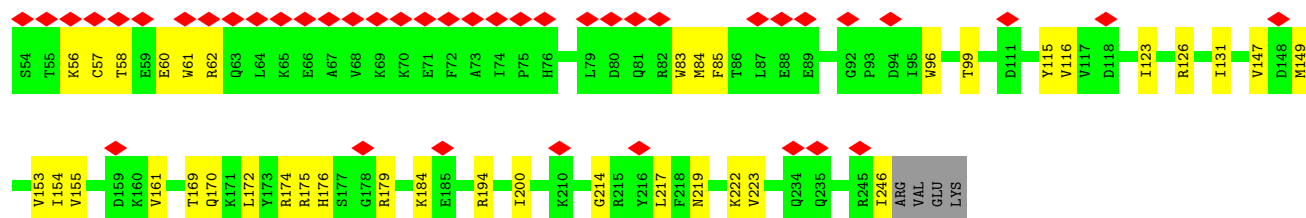
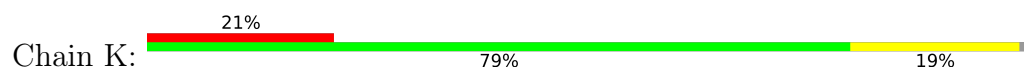




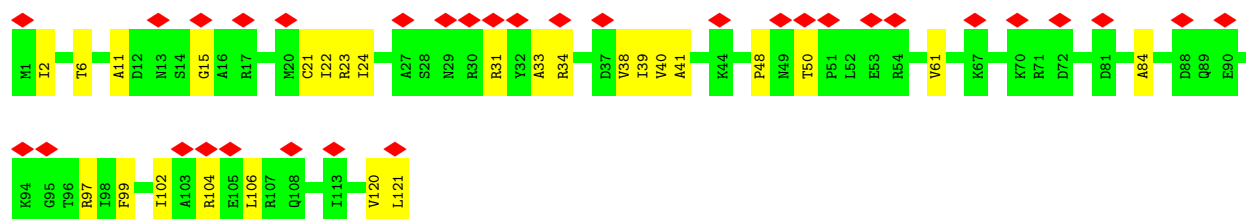
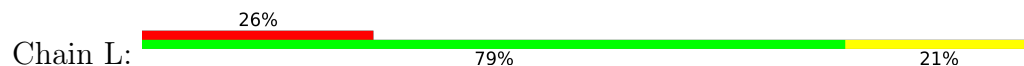
• Molecule 14: protein L9



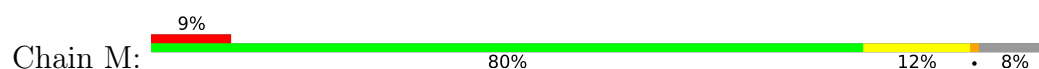
• Molecule 15: 50S ribosomal protein L13, chloroplastic

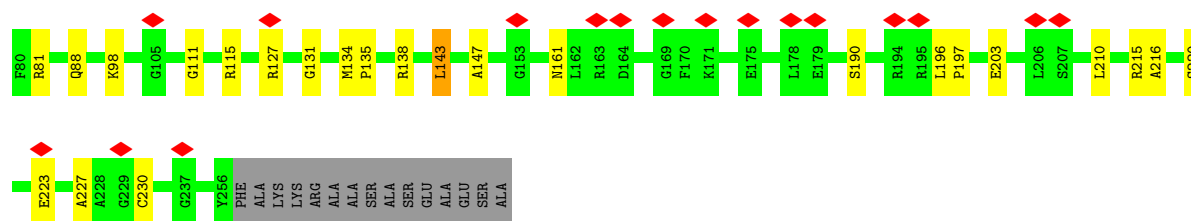


• Molecule 16: 50S ribosomal protein L14, chloroplastic

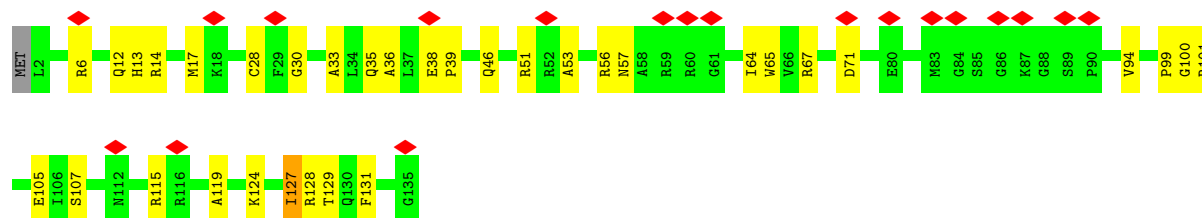
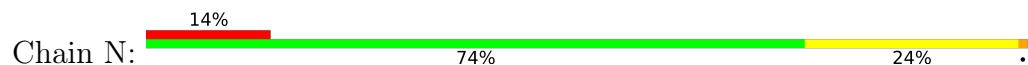


• Molecule 17: protein L15

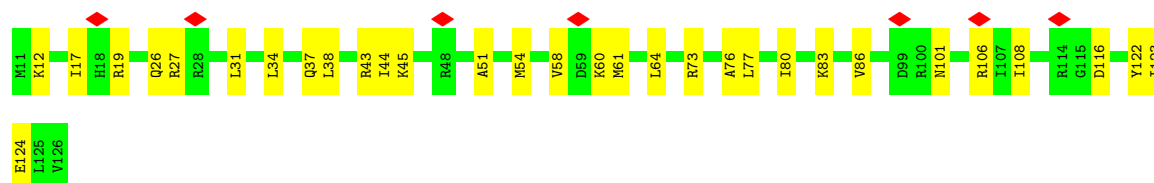




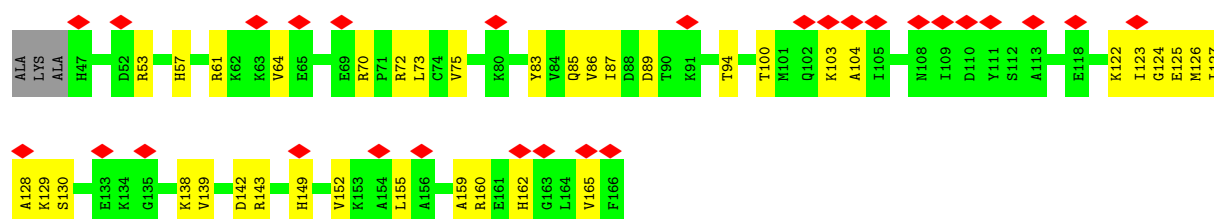
- Molecule 18: 50S ribosomal protein L16, chloroplastic



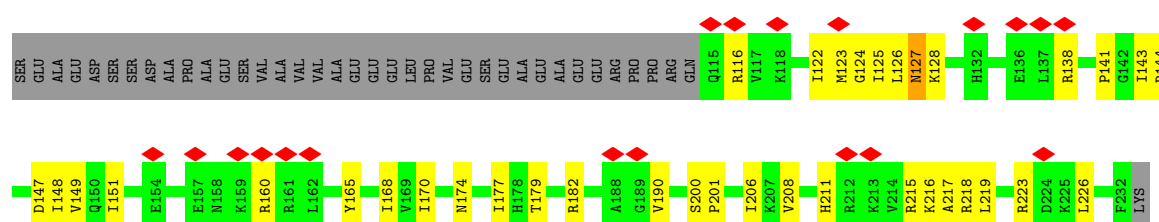
- Molecule 19: protein L17



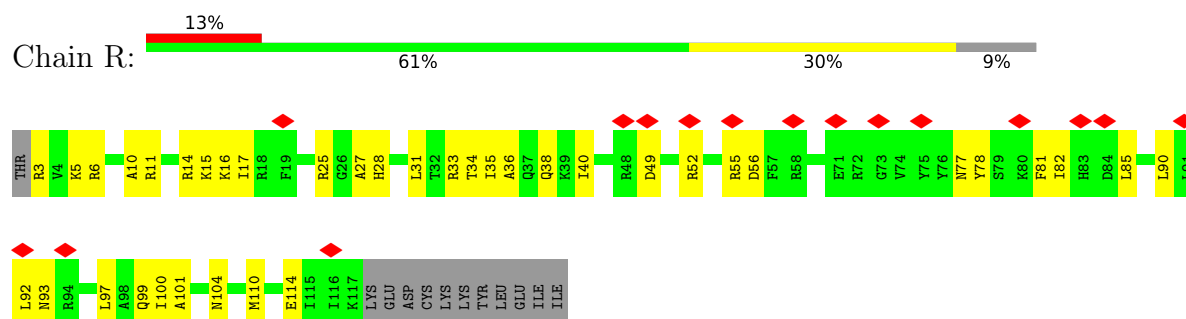
- Molecule 20: protein L18



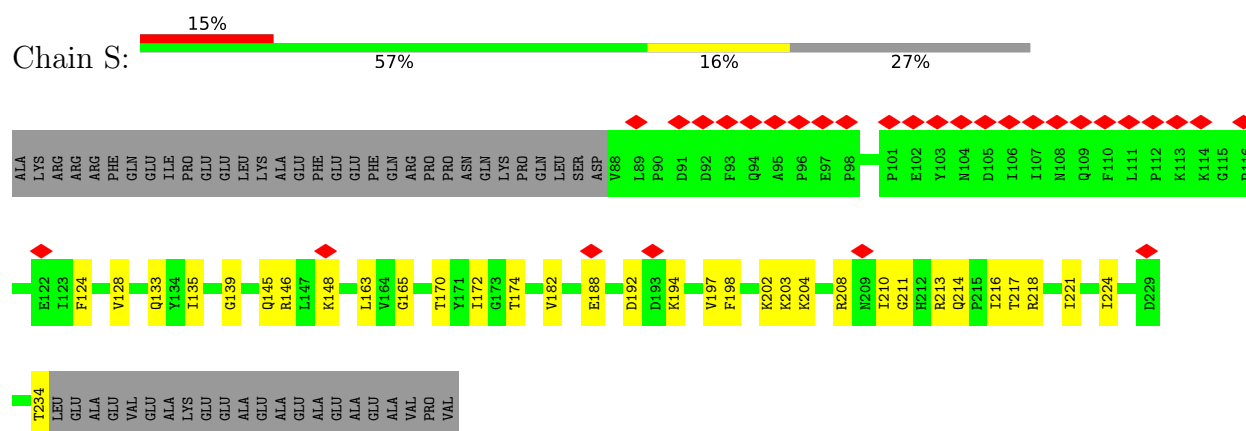
- Molecule 21: 50S ribosomal protein L19, chloroplastic



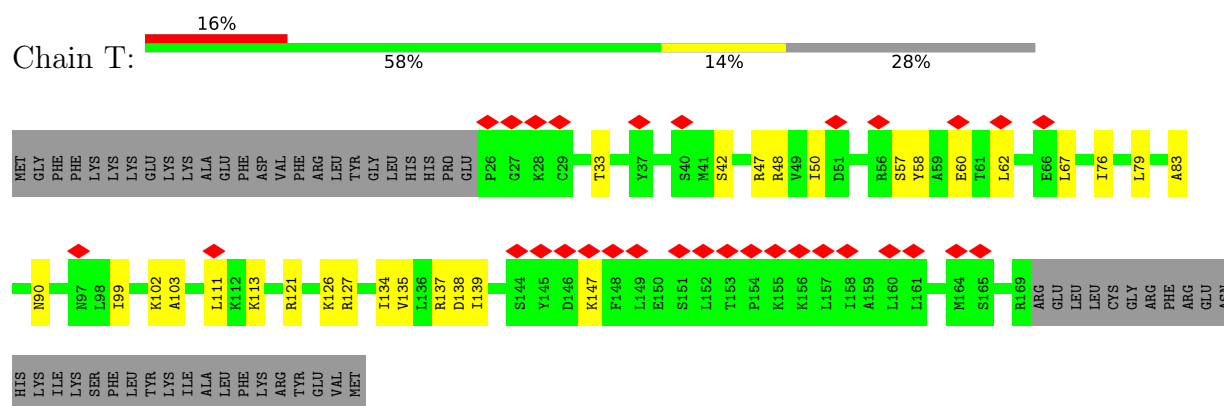
- Molecule 22: 50S ribosomal protein L20, chloroplastic



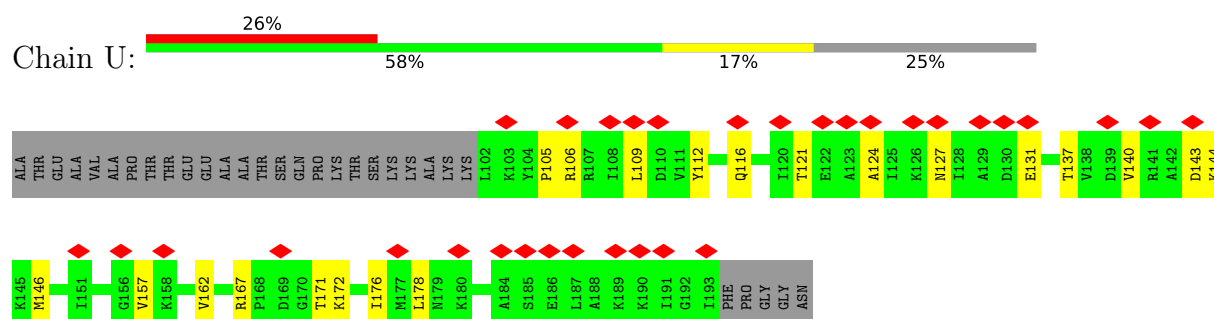
- Molecule 23: 50S ribosomal protein L21, chloroplastic



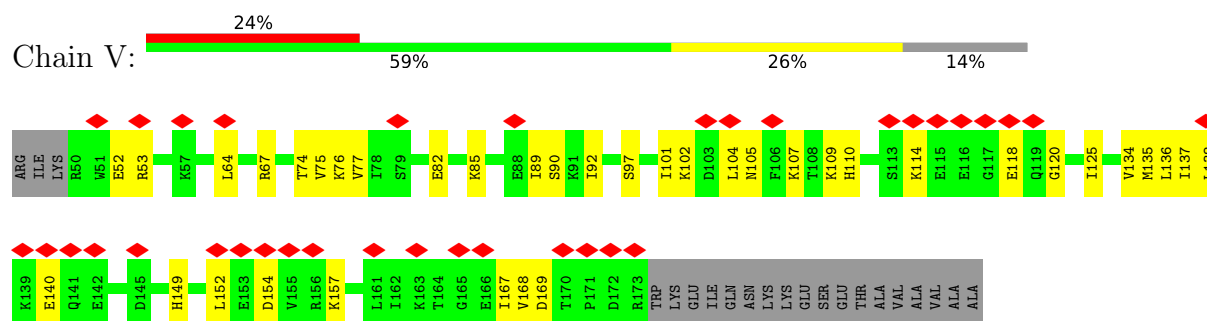
- Molecule 24: 50S ribosomal protein L22, chloroplastic



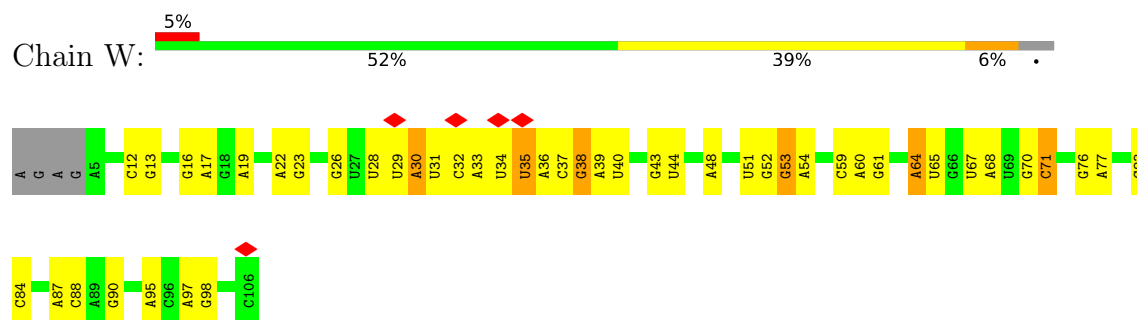
- Molecule 25: 50S ribosomal protein L23, chloroplastic



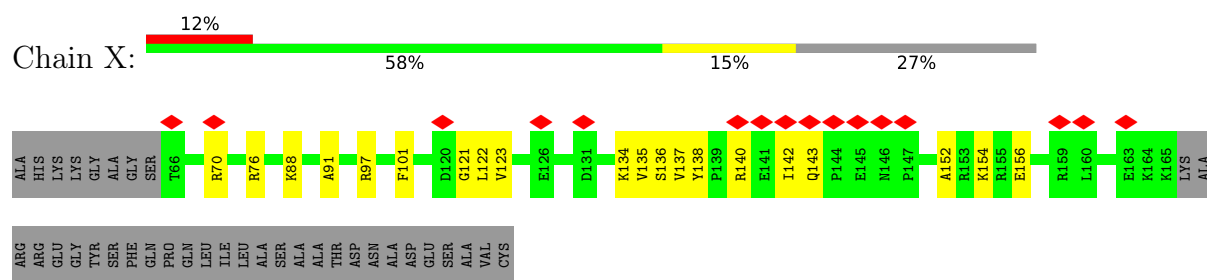
- Molecule 26: 50S ribosomal protein L24, chloroplastic



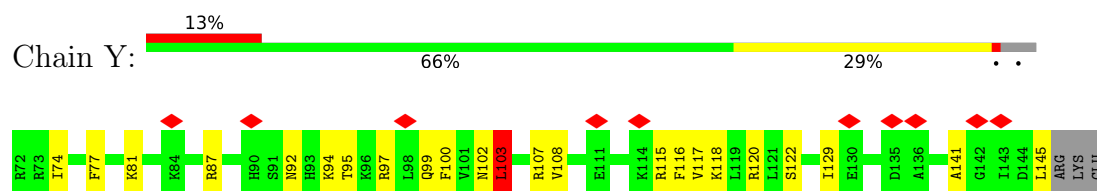
- Molecule 27: 4.8S rRNA



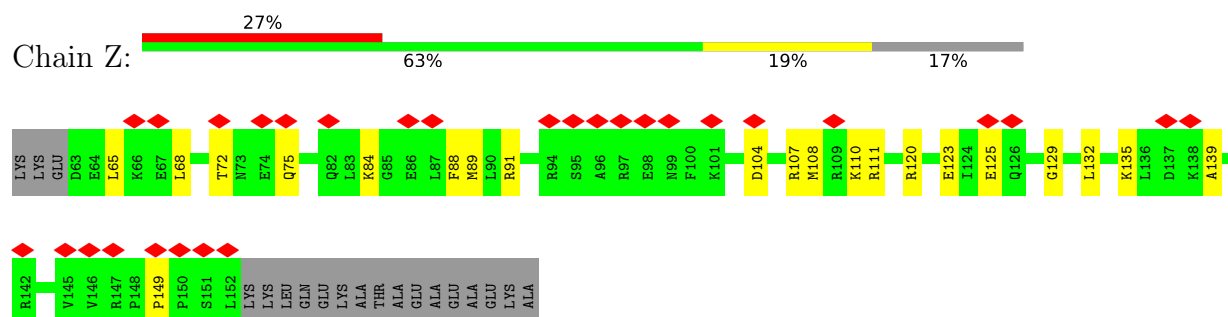
- Molecule 28: protein L27



- Molecule 29: protein L28



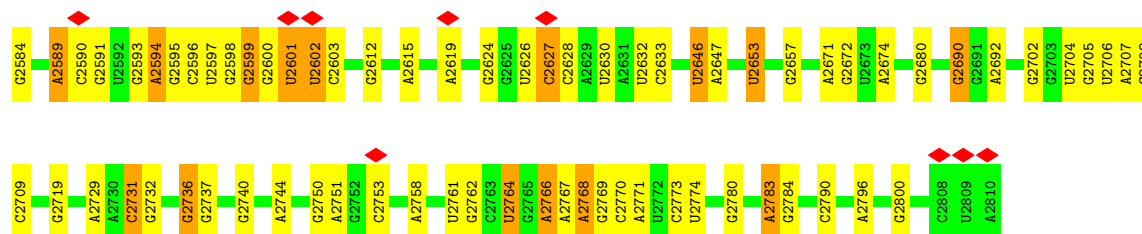
- Molecule 30: protein L29



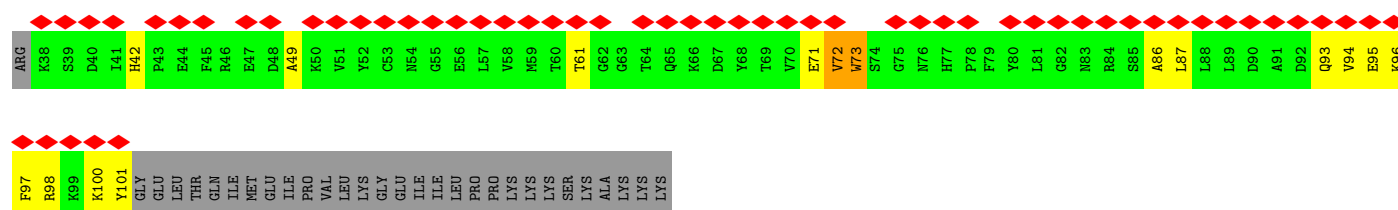
Chain A: 100% 63% 32% 5%

The diagram illustrates a network structure with nodes and connections. The nodes are labeled with IDs, and the connections are color-coded based on a percentage scale: 100% (green), 63% (orange), 32% (red), and 5% (grey). The network is organized into a grid-like structure, with nodes arranged in rows and columns. The connections between nodes are represented by lines, and the color of the line indicates the percentage value. The diagram shows a complex web of relationships, with some nodes having multiple connections and others having only one. The overall structure suggests a hierarchical or flow-based system, possibly representing a supply chain or a data network. The nodes are labeled with IDs, and the connections are color-coded based on a percentage scale: 100% (green), 63% (orange), 32% (red), and 5% (grey).

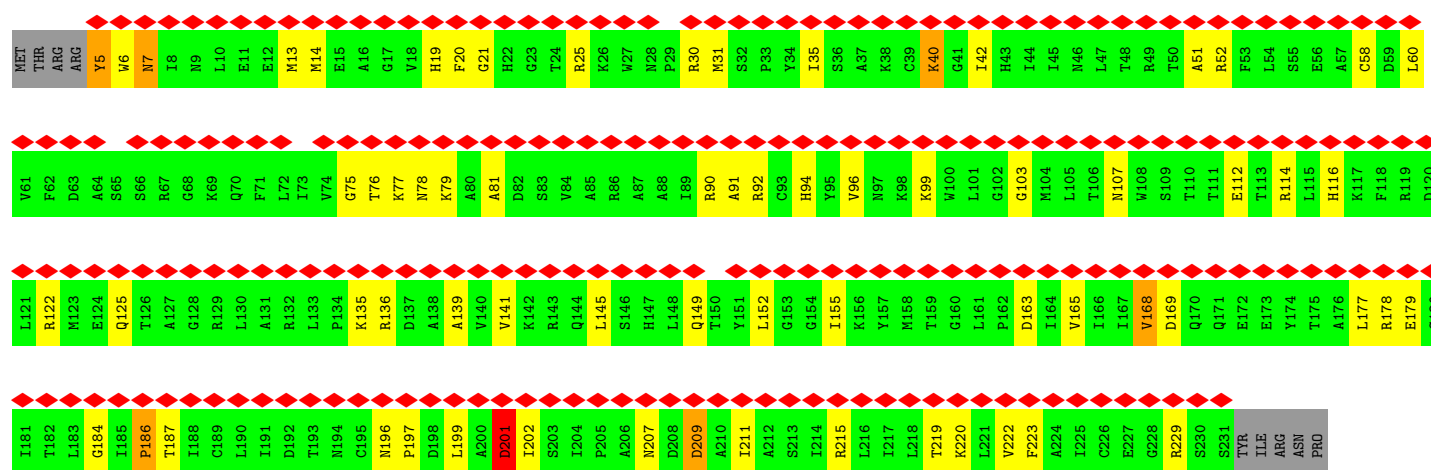




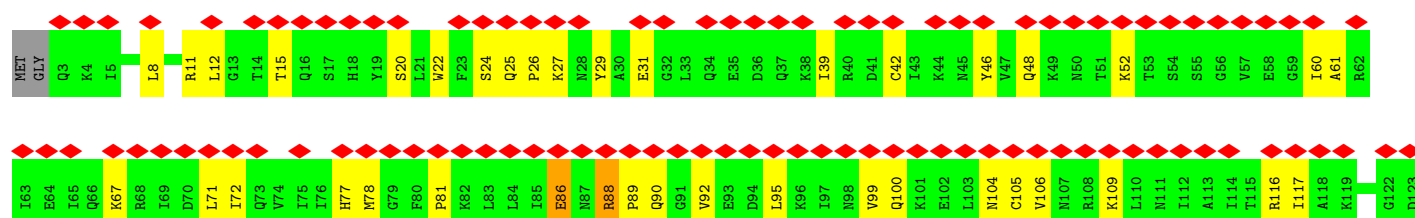
• Molecule 32: 50S ribosomal protein L31

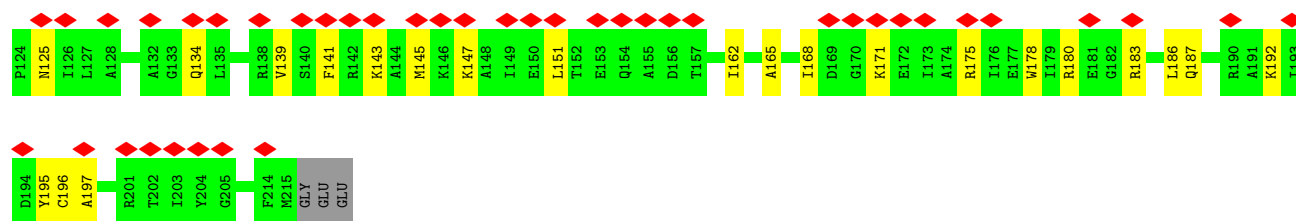


• Molecule 33: 30S ribosomal protein S2, chloroplactic

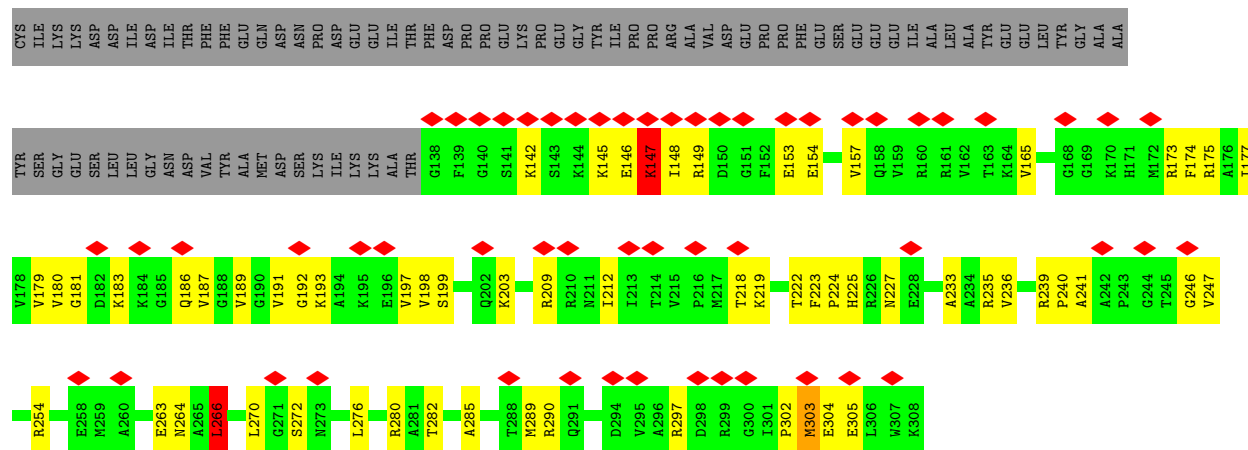


• Molecule 34: 30S ribosomal protein S3, chloroplactic

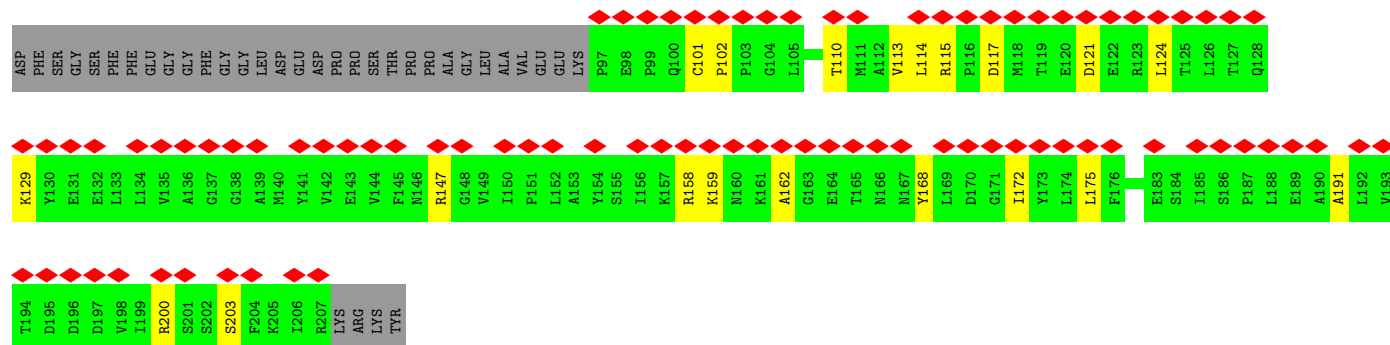




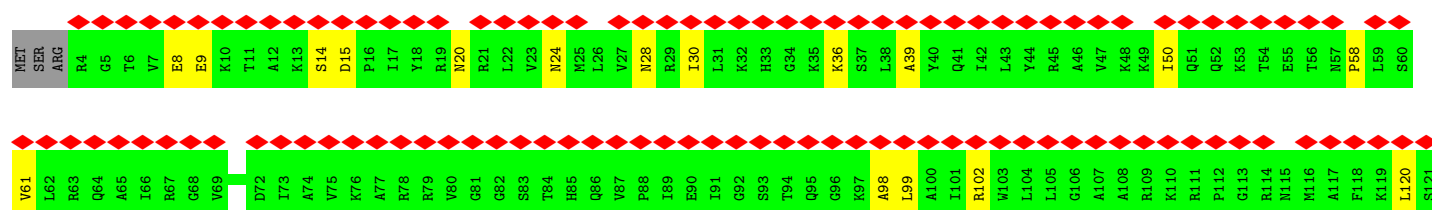
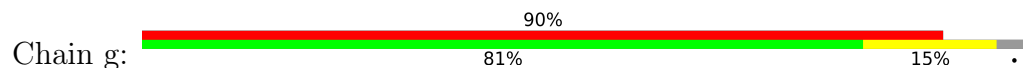
• Molecule 35: 30S ribosomal protein S5, chloroplastic



• Molecule 36: 30S ribosomal protein S6 alpha, chloroplastic

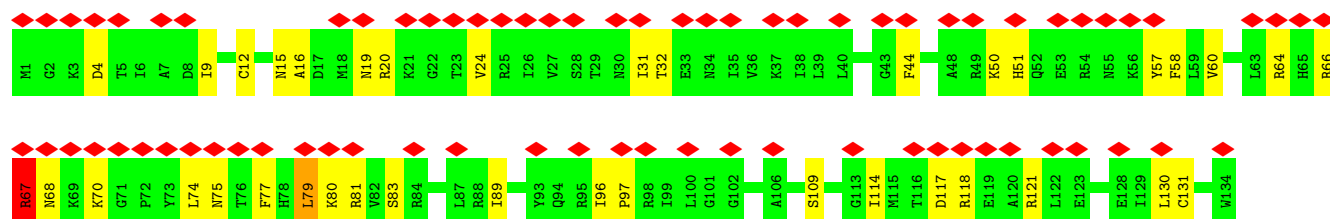


• Molecule 37: 30S ribosomal protein S7, chloroplastic

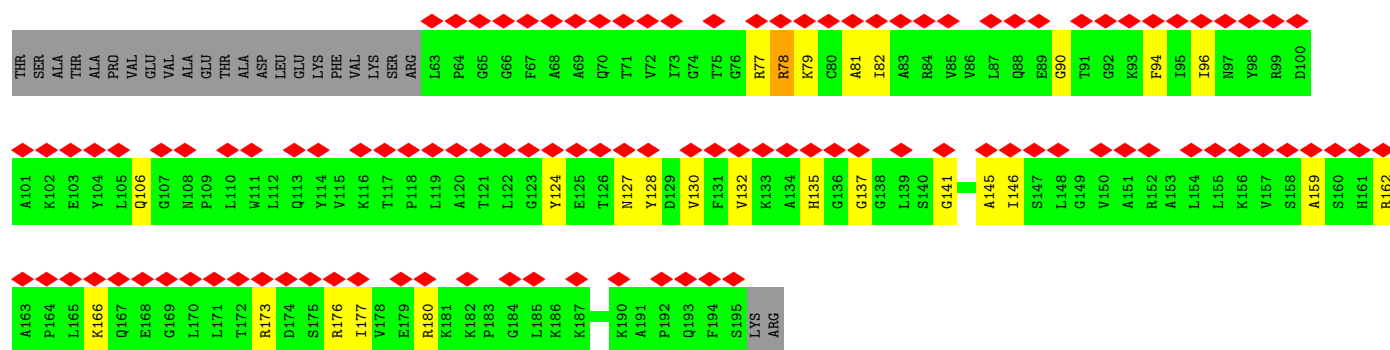




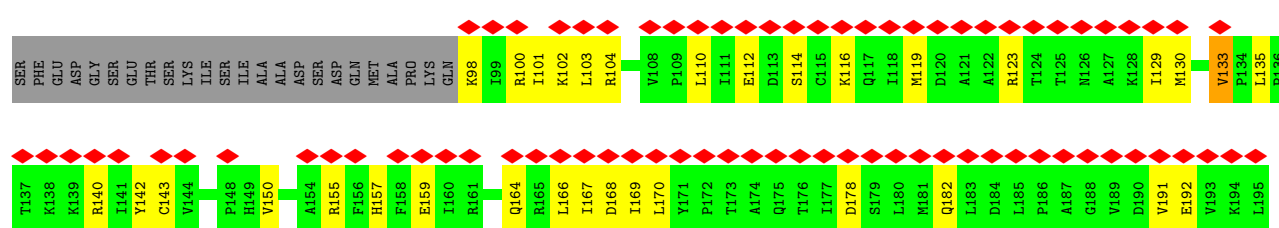
- Molecule 38: 30S ribosomal protein S8, chloroplastic



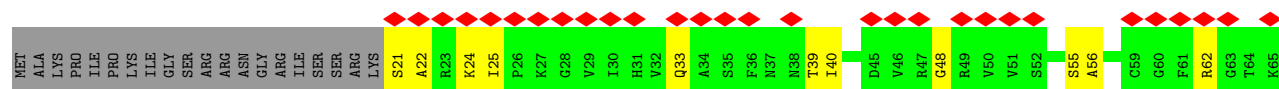
- Molecule 39: 30S ribosomal protein S9, chloroplastic

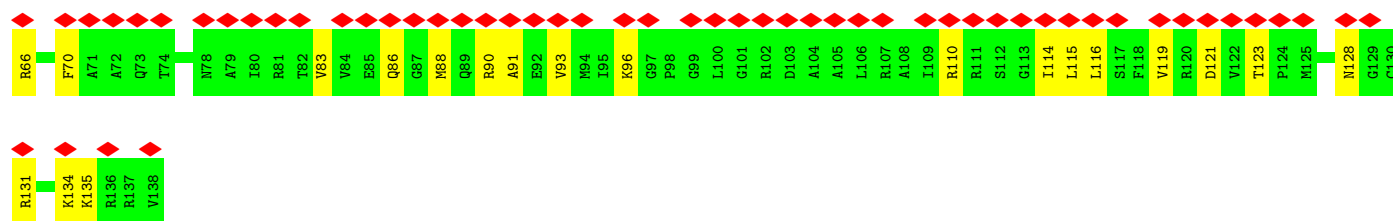


- Molecule 40: protein S10

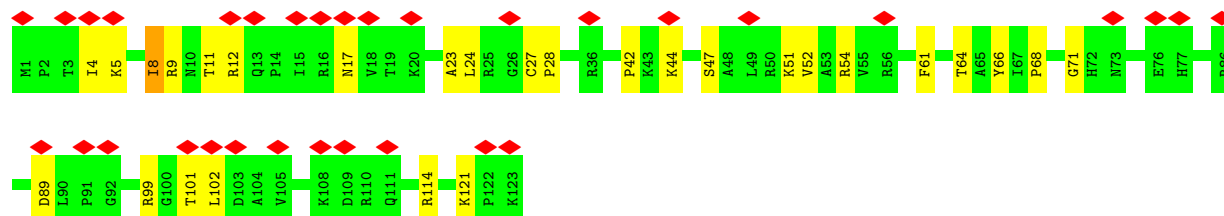
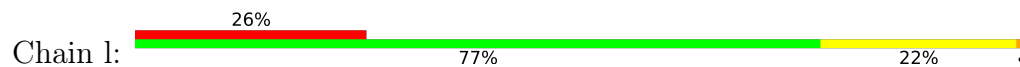


- Molecule 41: 30S ribosomal protein S11, chloroplastic

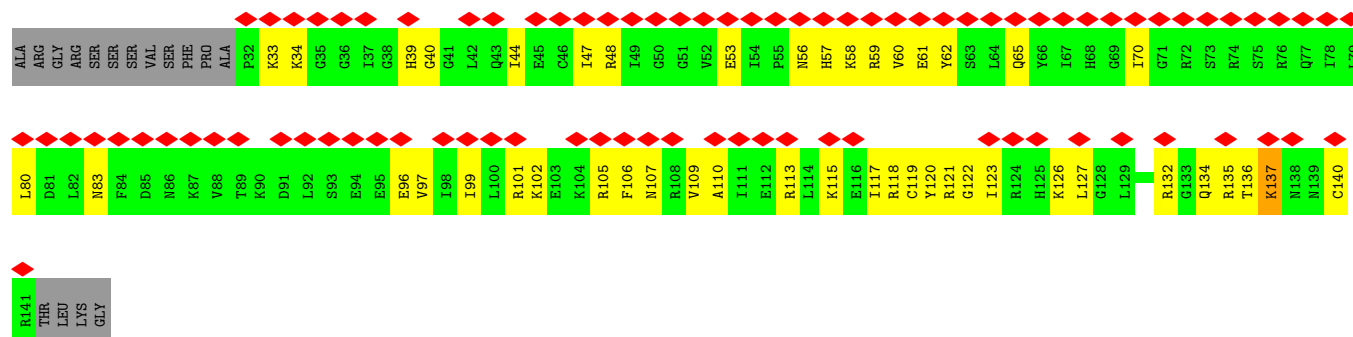




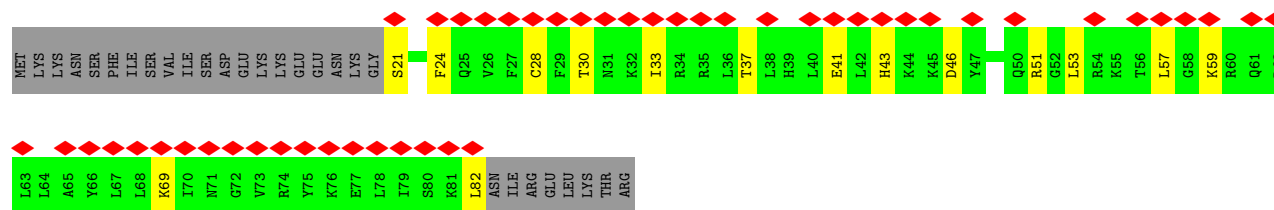
- Molecule 42: 30S ribosomal protein S12, chloroplactic



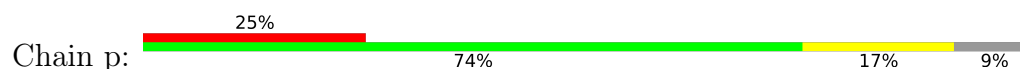
- Molecule 43: 30S ribosomal protein S13, chloroplactic

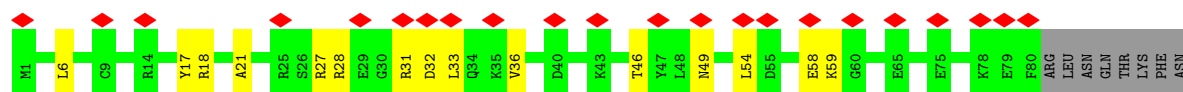


- Molecule 44: 30S ribosomal protein S15, chloroplactic

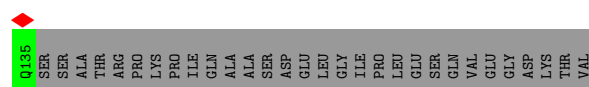
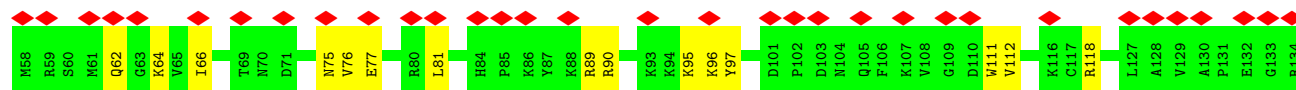


- Molecule 45: 30S ribosomal protein S16, chloroplactic

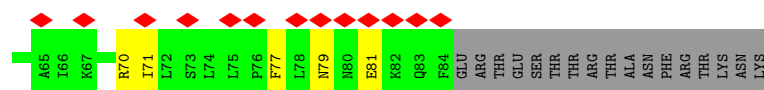
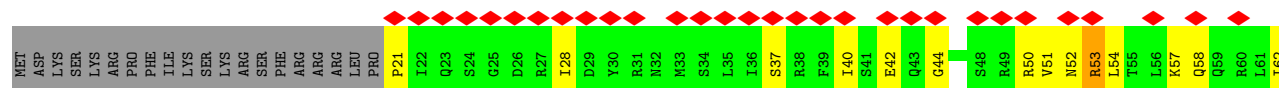
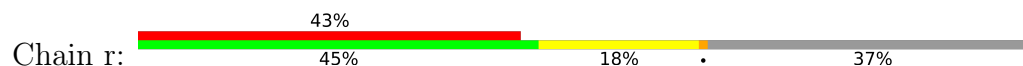




- Molecule 46: protein S17



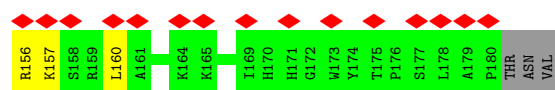
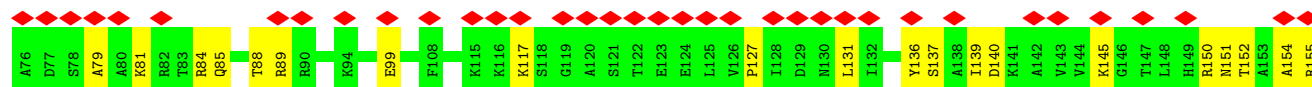
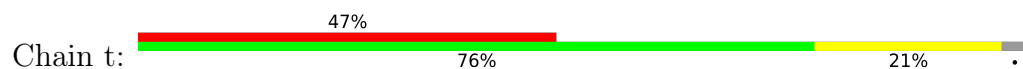
- Molecule 47: 30S ribosomal protein S18, chloroplastic



- Molecule 48: 30S ribosomal protein S19 alpha, chloroplastic

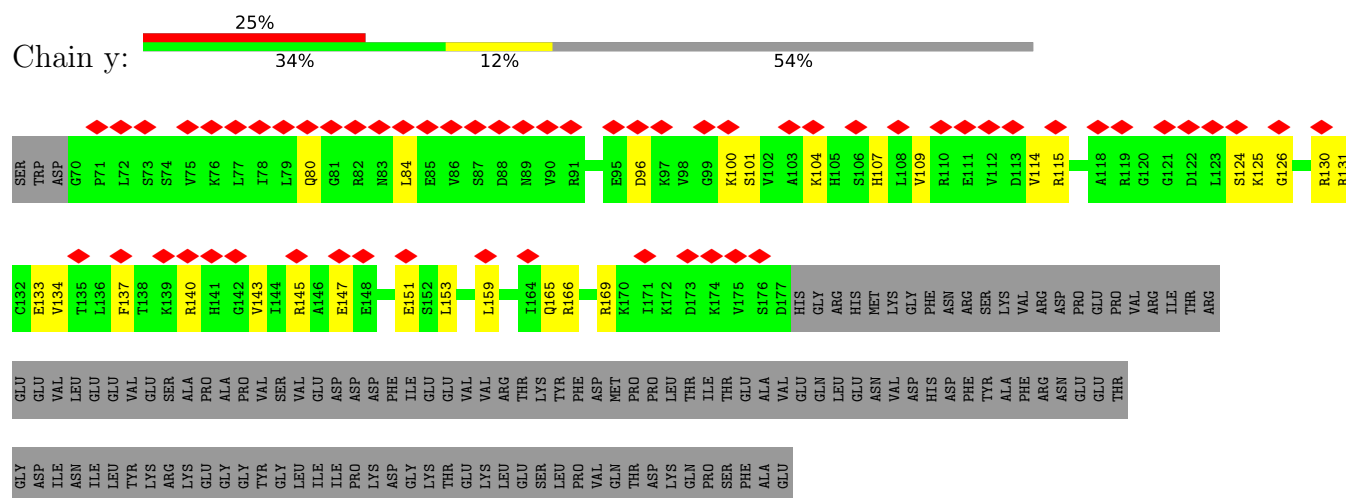


- Molecule 49: protein S20

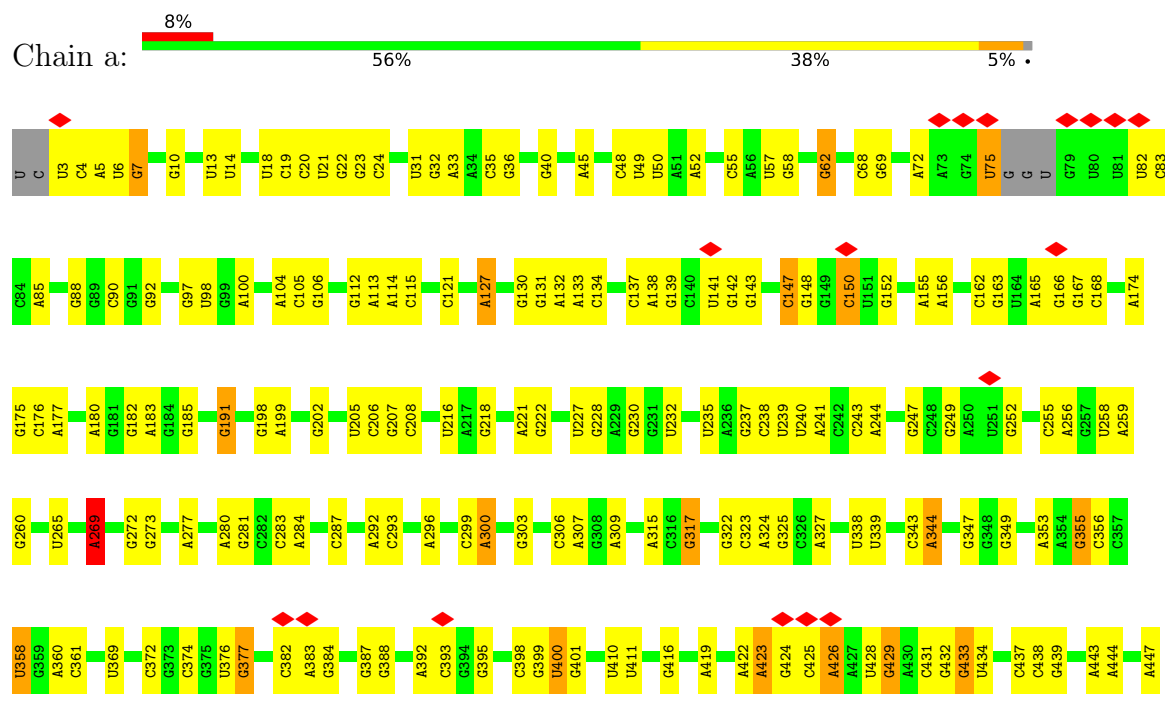


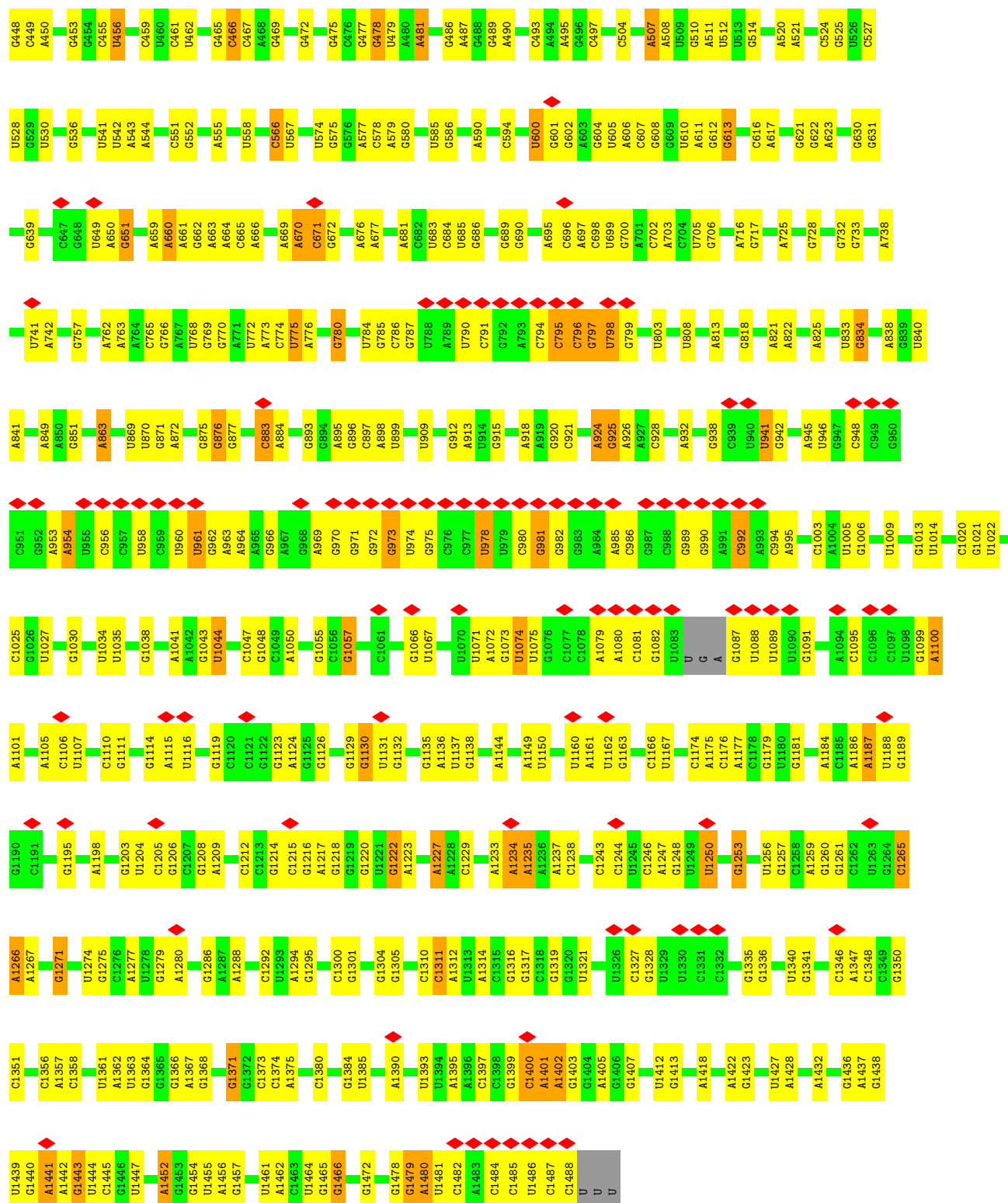
- Molecule 50: protein S21

- Molecule 51: protein plastid pY

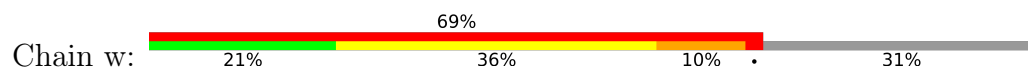


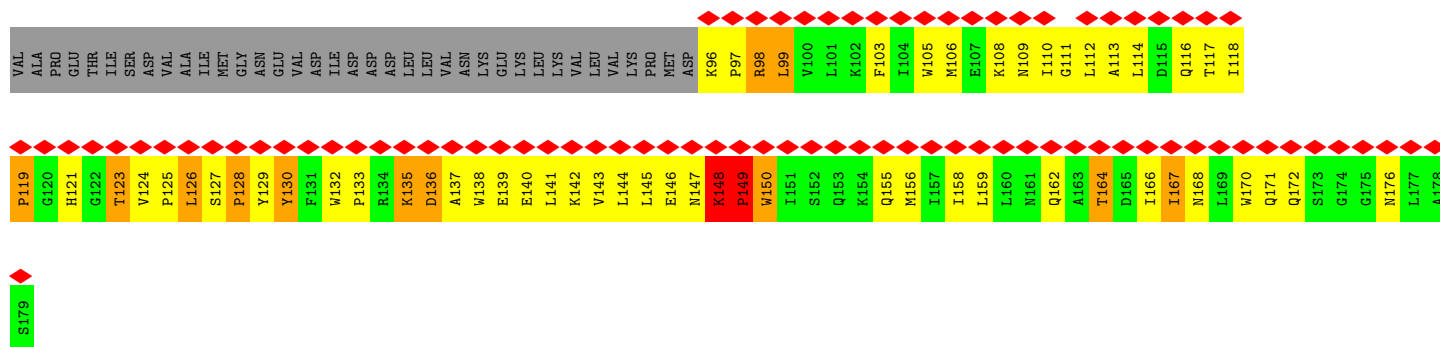
- Molecule 52: 16S rRNA



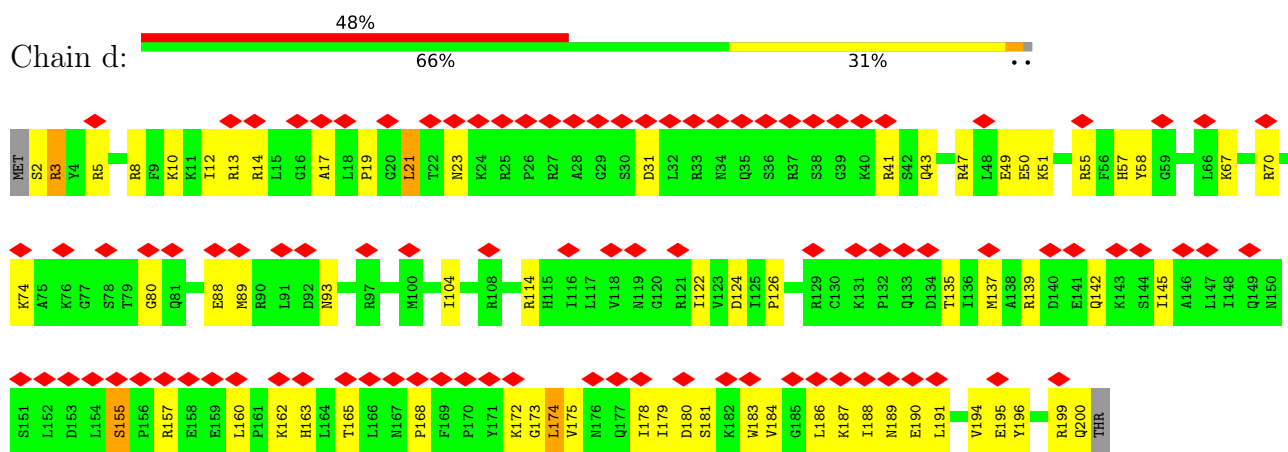


• Molecule 53: protein cS23

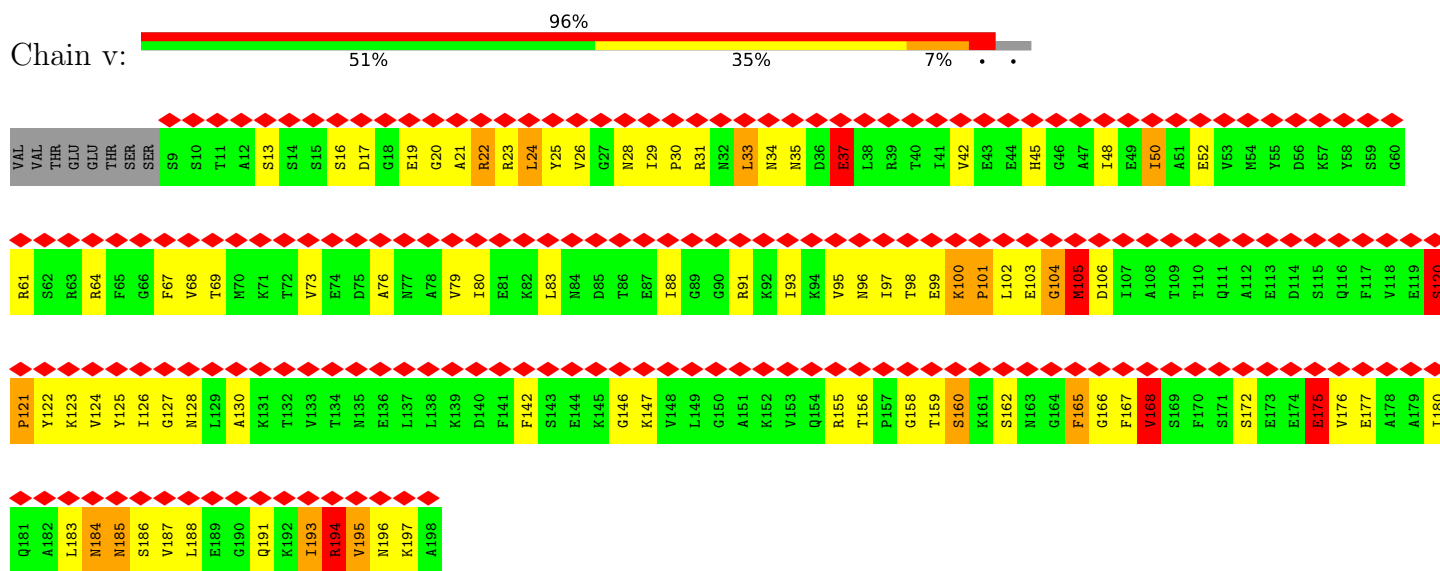




- Molecule 54: 30S ribosomal protein S4, chloroplastic

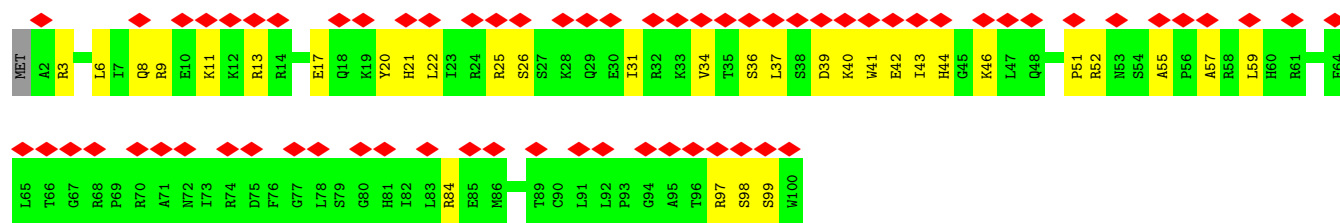


- Molecule 55: protein cS22

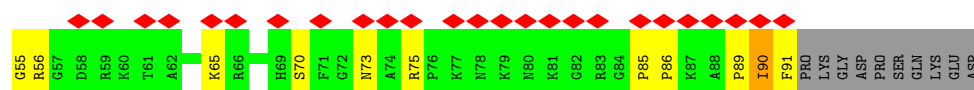


- Molecule 56: 30S ribosomal protein S14, chloroplastic

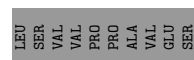
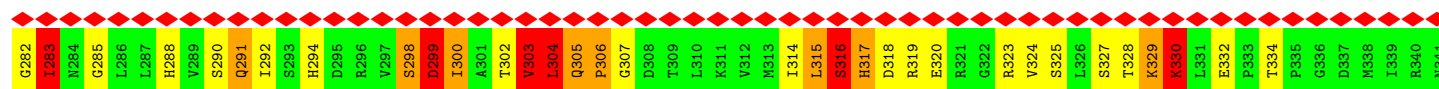
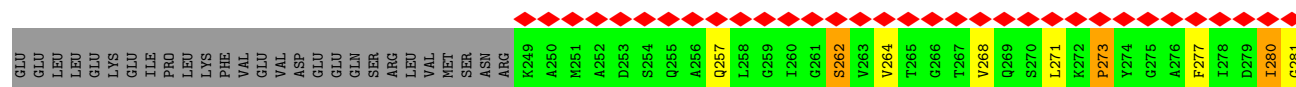
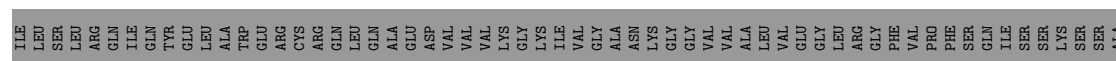
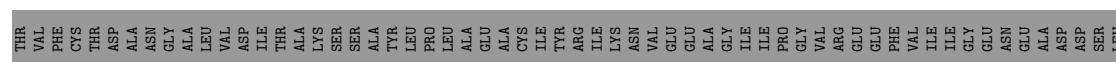




• Molecule 57: protein bTHXc



• Molecule 58: 30S ribosomal protein S1, chloroplastic



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81305	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3700	Depositor
Magnification	133333	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.475	Depositor
Minimum map value	-0.303	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.20	0/387	0.53	0/513
2	2	0.30	0/422	0.81	0/564
3	3	0.22	0/447	0.57	0/588
4	4	0.24	0/569	0.64	0/752
5	5	0.26	0/306	0.69	0/403
6	6	0.20	0/425	0.50	0/551
7	7	0.23	0/382	0.66	2/520 (0.4%)
8	B	0.16	0/2796	0.36	0/4357
9	C	0.24	0/1938	0.64	0/2603
10	D	0.26	0/1646	0.63	0/2201
11	E	0.25	0/1687	0.68	0/2271
12	F	0.21	0/1372	0.55	0/1848
13	G	0.19	0/1374	0.55	2/1849 (0.1%)
14	H	0.20	0/427	0.60	0/568
15	K	0.20	0/1608	0.50	0/2174
16	L	0.24	0/951	0.55	0/1282
17	M	0.21	0/1361	0.53	0/1806
18	N	0.27	0/1089	0.68	0/1461
19	O	0.24	0/959	0.61	0/1280
20	P	0.21	0/963	0.54	0/1293
21	Q	0.29	0/967	0.73	2/1300 (0.2%)
22	R	0.32	0/1013	0.69	0/1351
23	S	0.25	0/1199	0.65	0/1633
24	T	0.21	0/1168	0.55	0/1566
25	U	0.20	0/749	0.53	0/1006
26	V	0.21	0/1006	0.66	0/1343
27	W	0.19	0/2449	0.43	0/3817
28	X	0.24	0/825	0.60	1/1099 (0.1%)
29	Y	0.22	0/615	0.60	1/819 (0.1%)
30	Z	0.20	0/762	0.56	0/1012
31	A	0.18	0/67572	0.35	0/105421
32	0	0.26	0/533	0.75	0/718
33	b	0.74	8/1819 (0.4%)	0.92	8/2458 (0.3%)
34	c	0.45	0/1746	0.71	0/2348

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	e	0.59	1/1307 (0.1%)	0.82	5/1754 (0.3%)
36	f	0.37	0/904	0.71	1/1225 (0.1%)
37	g	0.32	0/1175	0.65	0/1574
38	h	0.87	6/1103 (0.5%)	1.18	6/1477 (0.4%)
39	i	0.40	0/1038	0.75	0/1397
40	j	0.45	0/813	0.72	0/1099
41	k	0.37	0/901	0.64	0/1214
42	l	0.60	0/983	0.85	1/1323 (0.1%)
43	m	0.44	0/909	0.81	0/1209
44	o	0.34	0/532	0.66	0/707
45	p	0.48	0/674	0.74	0/902
46	q	0.44	0/647	0.70	0/867
47	r	0.49	0/522	0.78	2/697 (0.3%)
48	s	0.44	0/642	0.81	2/866 (0.2%)
49	t	0.46	0/842	0.80	0/1127
50	u	0.85	3/396 (0.8%)	0.96	2/518 (0.4%)
51	y	0.42	0/852	0.72	0/1139
52	a	0.52	0/35582	0.50	1/55510 (0.0%)
53	w	0.92	2/709 (0.3%)	1.39	14/965 (1.5%)
54	d	0.39	0/1661	0.84	2/2230 (0.1%)
55	v	1.19	13/1481 (0.9%)	1.40	14/1991 (0.7%)
56	n	0.36	0/835	0.75	1/1116 (0.1%)
57	x	0.55	0/296	0.89	0/390
58	8	0.94	0/1216	1.86	41/1631 (2.5%)
All	All	0.38	33/159552 (0.0%)	0.55	108/237703 (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
17	M	0	1
21	Q	0	1
23	S	0	1
32	0	0	1
33	b	0	2
34	c	0	3
35	e	0	1
36	f	0	1
37	g	0	1
39	i	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
40	j	0	1
42	l	0	3
43	m	0	2
50	u	0	1
53	w	0	7
54	d	0	2
55	v	0	15
58	8	0	17
All	All	0	62

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	h	67	ARG	CZ-NH2	-15.64	1.13	1.33
38	h	67	ARG	CB-CG	-13.10	1.13	1.52
55	v	142	PHE	CE1-CZ	-12.45	1.01	1.38
55	v	142	PHE	CE2-CZ	-11.74	1.03	1.38
33	b	7	ASN	CG-ND2	-11.62	1.08	1.33
55	v	142	PHE	CG-CD2	-11.40	1.15	1.38
55	v	194	ARG	CG-CD	-10.85	1.19	1.52
55	v	142	PHE	CG-CD1	-10.60	1.16	1.38
55	v	165	PHE	CE2-CZ	-9.90	1.08	1.38
55	v	168	VAL	CB-CG1	-9.03	1.22	1.52
33	b	209	ASP	CG-OD2	-8.71	1.08	1.25
55	v	195	VAL	CB-CG2	-8.44	1.24	1.52
38	h	67	ARG	CA-CB	-7.92	1.40	1.53
55	v	165	PHE	CG-CD2	-7.80	1.22	1.38
50	u	103	PHE	CD1-CE1	-7.64	1.15	1.38
53	w	149	PRO	CG-CD	-7.51	1.25	1.50
33	b	201	ASP	CB-CG	7.47	1.70	1.52
53	w	164	THR	CB-CG2	-6.88	1.29	1.52
50	u	103	PHE	CD2-CE2	-6.87	1.18	1.38
38	h	67	ARG	CZ-NH1	-6.76	1.23	1.32
50	u	103	PHE	CB-CG	-6.44	1.35	1.50
55	v	26	VAL	CB-CG1	-6.24	1.31	1.52
55	v	193	ILE	CB-CG2	-6.17	1.32	1.52
33	b	201	ASP	CG-OD1	-5.62	1.14	1.25
33	b	201	ASP	CG-OD2	5.58	1.35	1.25
35	e	303	MET	CB-CG	-5.57	1.35	1.52
55	v	142	PHE	CD2-CE2	5.53	1.55	1.38
33	b	186	PRO	CA-CB	-5.47	1.46	1.53
38	h	67	ARG	CD-NE	-5.44	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	v	142	PHE	CD1-CE1	5.35	1.54	1.38
38	h	67	ARG	CG-CD	-5.31	1.36	1.52
33	b	7	ASN	CG-OD1	-5.14	1.13	1.23
33	b	7	ASN	CB-CG	-5.09	1.39	1.52

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	h	67	ARG	NE-CZ-NH1	24.07	145.57	121.50
33	b	201	ASP	CA-CB-CG	14.19	126.79	112.60
38	h	67	ARG	NH1-CZ-NH2	-13.91	101.21	119.30
38	h	67	ARG	CD-NE-CZ	13.84	143.78	124.40
38	h	67	ARG	CB-CG-CD	13.80	143.04	111.30
58	8	72	MET	N-CA-C	-11.99	85.27	110.80
58	8	316	SER	CA-C-N	11.08	138.64	122.36
58	8	316	SER	C-N-CA	11.08	138.64	122.36
58	8	73	GLU	N-CA-C	-10.99	87.39	110.80
58	8	299	ASP	N-CA-C	-10.18	89.11	110.80
58	8	362	GLN	N-CA-C	10.02	122.28	111.36
33	b	201	ASP	N-CA-CB	9.44	123.14	110.59
58	8	360	ILE	N-CA-C	-9.09	90.42	109.34
58	8	368	ARG	CB-CG-CD	9.05	132.11	111.30
58	8	69	ASN	N-CA-C	8.61	127.73	114.64
55	v	160	SER	N-CA-C	8.24	123.45	112.25
58	8	367	ALA	CA-C-N	8.08	136.97	121.54
58	8	367	ALA	C-N-CA	8.08	136.97	121.54
33	b	201	ASP	CB-CG-OD2	8.04	136.90	118.40
33	b	201	ASP	N-CA-C	-7.77	104.33	113.88
58	8	303	VAL	N-CA-C	7.63	125.21	109.34
55	v	185	ASN	CB-CA-C	-7.50	102.40	109.83
58	8	73	GLU	CB-CA-C	7.49	125.33	110.42
38	h	67	ARG	NE-CZ-NH2	-7.31	112.62	119.20
55	v	142	PHE	CD1-CG-CD2	-7.26	107.71	118.60
53	w	133	PRO	CA-N-CD	-7.04	102.15	112.00
58	8	280	ILE	CB-CA-C	7.00	122.77	111.29
47	r	53	ARG	CA-CB-CG	-6.96	100.19	114.10
58	8	304	LEU	CA-CB-CG	6.83	140.21	116.30
47	r	21	PRO	N-CA-CB	6.77	110.44	103.00
33	b	201	ASP	OD1-CG-OD2	-6.72	106.77	122.90
55	v	96	ASN	N-CA-C	-6.71	99.63	109.63
53	w	124	VAL	N-CA-C	6.56	114.64	108.15
58	8	273	PRO	CA-C-N	6.50	133.96	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	8	273	PRO	C-N-CA	6.50	133.96	121.54
58	8	367	ALA	N-CA-CB	6.47	121.43	110.49
58	8	300	ILE	N-CA-C	-6.44	95.94	109.34
53	w	99	LEU	N-CA-C	6.27	119.41	109.81
53	w	148	LYS	CA-C-N	6.26	127.67	119.84
53	w	148	LYS	C-N-CA	6.26	127.67	119.84
53	w	149	PRO	N-CA-C	6.16	125.17	112.47
55	v	22	ARG	CA-C-N	6.14	129.84	121.05
55	v	22	ARG	C-N-CA	6.14	129.84	121.05
53	w	149	PRO	CB-CA-C	-6.13	101.45	111.56
50	u	98	ARG	CA-CB-CG	6.12	126.34	114.10
33	b	5	TYR	CA-C-N	6.11	133.21	121.54
33	b	5	TYR	C-N-CA	6.11	133.21	121.54
33	b	40	LYS	CD-CE-NZ	-6.10	92.39	111.90
58	8	330	LYS	N-CA-CB	6.10	120.79	110.49
58	8	65	GLU	CA-C-N	6.10	133.07	122.95
58	8	65	GLU	C-N-CA	6.10	133.07	122.95
58	8	73	GLU	CB-CG-CD	6.05	122.89	112.60
58	8	344	LEU	CB-CG-CD2	-6.04	92.59	110.70
38	h	67	ARG	N-CA-CB	-5.97	99.27	110.07
35	e	157	VAL	N-CA-C	-5.95	108.06	113.71
53	w	123	THR	CA-C-N	-5.92	116.74	123.25
53	w	123	THR	C-N-CA	-5.92	116.74	123.25
53	w	135	LYS	CA-C-N	5.89	129.12	120.82
53	w	135	LYS	C-N-CA	5.89	129.12	120.82
36	f	101	CYS	N-CA-C	5.88	122.81	109.81
55	v	99	GLU	CA-CB-CG	-5.87	102.36	114.10
54	d	3	ARG	CA-C-N	5.86	132.74	121.54
54	d	3	ARG	C-N-CA	5.86	132.74	121.54
42	l	28	PRO	N-CA-C	5.83	121.52	113.65
55	v	177	GLU	CA-CB-CG	-5.82	102.47	114.10
58	8	73	GLU	CA-CB-CG	5.76	125.63	114.10
58	8	346	PHE	N-CA-CB	5.75	119.19	110.28
53	w	128	PRO	N-CA-C	5.73	120.23	110.95
58	8	262	SER	N-CA-C	5.72	122.99	110.80
21	Q	223	ARG	CA-C-N	5.68	134.94	124.82
21	Q	223	ARG	C-N-CA	5.68	134.94	124.82
7	7	55	GLY	CA-C-N	5.60	132.23	121.54
7	7	55	GLY	C-N-CA	5.60	132.23	121.54
28	X	134	LYS	N-CA-C	5.58	117.44	110.91
48	s	8	ASN	CA-C-N	-5.56	114.03	119.76
48	s	8	ASN	C-N-CA	-5.56	114.03	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	v	37	GLU	CB-CG-CD	5.47	121.90	112.60
13	G	205	VAL	CA-C-N	5.47	130.17	122.46
13	G	205	VAL	C-N-CA	5.47	130.17	122.46
58	8	280	ILE	CA-CB-CG1	5.41	119.59	110.40
58	8	317	HIS	N-CA-C	5.41	119.29	111.56
58	8	363	ALA	N-CA-C	5.40	117.89	109.52
35	e	266	LEU	CA-CB-CG	5.37	135.08	116.30
58	8	70	ALA	N-CA-CB	5.36	119.92	110.37
58	8	328	THR	CA-C-N	5.36	131.77	121.54
58	8	328	THR	C-N-CA	5.36	131.77	121.54
53	w	148	LYS	C-N-CD	-5.34	103.10	125.00
53	w	136	ASP	N-CA-CB	-5.34	101.52	109.69
55	v	105	MET	N-CA-C	5.32	122.12	110.80
58	8	303	VAL	CB-CA-C	-5.32	102.57	111.29
58	8	370	ASP	CA-C-N	5.31	131.68	121.54
58	8	370	ASP	C-N-CA	5.31	131.68	121.54
35	e	303	MET	CB-CG-SD	5.30	128.59	112.70
58	8	283	ILE	CA-CB-CG1	5.30	119.41	110.40
58	8	298	SER	CA-C-N	5.30	131.66	121.54
58	8	298	SER	C-N-CA	5.30	131.66	121.54
52	a	269	A	N9-C1'-C2'	5.27	119.90	112.00
56	n	39	ASP	N-CA-C	5.23	116.98	111.28
58	8	368	ARG	N-CA-CB	-5.21	101.68	110.49
35	e	147	LYS	CA-C-N	5.21	131.34	121.97
35	e	147	LYS	C-N-CA	5.21	131.34	121.97
58	8	291	GLN	CG-CD-NE2	-5.21	108.59	116.40
55	v	175	GLU	CA-CB-CG	-5.19	103.72	114.10
55	v	50	ILE	N-CA-C	5.09	114.98	107.75
50	u	98	ARG	N-CA-CB	-5.08	102.50	109.97
55	v	165	PHE	CA-C-N	-5.08	112.64	120.86
55	v	165	PHE	C-N-CA	-5.08	112.64	120.86
29	Y	103	LEU	CA-CB-CG	5.05	133.98	116.30

There are no chirality outliers.

All (62) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	0	73	TRP	Peptide
58	8	273	PRO	Peptide
58	8	277	PHE	Peptide
58	8	298	SER	Peptide
58	8	299	ASP	Peptide

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Mol	Chain	Res	Type	Group
58	8	302	THR	Peptide
58	8	303	VAL	Peptide
58	8	304	LEU	Peptide
58	8	315	LEU	Peptide
58	8	329	LYS	Peptide
58	8	346	PHE	Sidechain
58	8	359	ARG	Peptide
58	8	366	MET	Mainchain
58	8	369	ALA	Peptide
58	8	370	ASP	Peptide
58	8	69	ASN	Peptide
58	8	71	PRO	Peptide
58	8	72	MET	Peptide
17	M	143	LEU	Peptide
21	Q	190	VAL	Peptide
23	S	174	THR	Peptide
33	b	168	VAL	Peptide
33	b	201	ASP	Sidechain
34	c	168	ILE	Peptide
34	c	86	GLU	Peptide
34	c	88	ARG	Peptide
54	d	155	SER	Peptide
54	d	23	ASN	Peptide
35	e	147	LYS	Peptide
36	f	102	PRO	Peptide
37	g	8	GLU	Peptide
39	i	78	ARG	Peptide
39	i	96	ILE	Peptide
40	j	135	LEU	Peptide
42	l	24	LEU	Peptide
42	l	27	CYS	Peptide
42	l	8	ILE	Peptide
43	m	137	LYS	Peptide
43	m	34	LYS	Peptide
50	u	103	PHE	Sidechain
55	v	100	LYS	Peptide
55	v	101	PRO	Peptide
55	v	104	GLY	Peptide
55	v	120	SER	Mainchain
55	v	147	LYS	Peptide
55	v	158	GLY	Peptide
55	v	159	THR	Peptide

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Mol	Chain	Res	Type	Group
55	v	165	PHE	Sidechain
55	v	168	VAL	Peptide
55	v	184	ASN	Peptide
55	v	185	ASN	Peptide
55	v	187	VAL	Peptide
55	v	188	LEU	Peptide
55	v	194	ARG	Sidechain
55	v	33	LEU	Peptide
53	w	108	LYS	Peptide
53	w	110	ILE	Peptide
53	w	126	LEU	Peptide
53	w	130	TYR	Peptide
53	w	148	LYS	Peptide
53	w	176	ASN	Peptide
53	w	98	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	378	0	415	7	0
2	2	415	0	434	8	0
3	3	445	0	501	12	0
4	4	563	0	623	9	0
5	5	304	0	345	7	0
6	6	422	0	508	8	0
7	7	368	0	386	7	0
8	B	2500	0	1263	15	0
9	C	1904	0	1985	59	0
10	D	1620	0	1699	36	0
11	E	1655	0	1725	43	0
12	F	1351	0	1407	41	0
13	G	1353	0	1416	19	0
14	H	423	0	490	7	0
15	K	1568	0	1595	26	0
16	L	942	0	995	22	0
17	M	1342	0	1417	20	0
18	N	1067	0	1122	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	O	944	0	1004	28	0
20	P	947	0	966	29	0
21	Q	953	0	1042	40	0
22	R	996	0	1062	37	0
23	S	1171	0	1216	24	0
24	T	1149	0	1220	22	0
25	U	740	0	795	15	0
26	V	993	0	1055	25	0
27	W	2187	0	1102	18	0
28	X	810	0	847	13	0
29	Y	605	0	652	17	0
30	Z	754	0	808	13	0
31	A	60324	0	30373	529	0
32	0	521	0	498	49	0
33	b	1787	0	1828	107	0
34	c	1719	0	1807	34	0
35	e	1292	0	1355	52	0
36	f	886	0	888	22	0
37	g	1161	0	1237	13	0
38	h	1088	0	1149	59	0
39	i	1020	0	1072	17	0
40	j	796	0	841	25	0
41	k	887	0	933	25	0
42	l	967	0	1046	17	0
43	m	898	0	949	89	0
44	o	525	0	572	25	0
45	p	664	0	703	12	0
46	q	635	0	667	13	0
47	r	518	0	544	36	0
48	s	627	0	653	36	0
49	t	832	0	883	20	0
50	u	393	0	406	91	0
51	y	845	0	892	17	0
52	a	31777	0	16003	380	0
53	w	689	0	706	152	0
54	d	1633	0	1727	117	0
55	v	1464	0	1456	93	0
56	n	819	0	858	41	0
57	x	289	0	301	20	0
58	8	1201	0	1220	147	0
All	All	147126	0	101662	2192	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 9.

All (2192) 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)
54:d:162:LYS:HB2	54:d:183:TRP:CH2	1.20	1.62
54:d:162:LYS:HB2	54:d:183:TRP:CZ2	1.41	1.54
54:d:137:MET:SD	54:d:172:LYS:HE3	1.48	1.52
50:u:103:PHE:CD1	53:w:138:TRP:CD1	1.98	1.52
54:d:162:LYS:CB	54:d:183:TRP:CH2	1.92	1.51
54:d:89:MET:CE	54:d:178:ILE:HA	1.42	1.46
32:0:87:LEU:HB2	43:m:105:ARG:NH2	1.15	1.44
47:r:51:VAL:O	53:w:149:PRO:CD	1.64	1.43
32:0:87:LEU:CB	43:m:105:ARG:NH2	1.80	1.42
31:A:1933:A:N1	52:a:1444:U:O2'	1.58	1.37
35:e:247:VAL:N	54:d:195:GLU:OE1	1.60	1.34
32:0:87:LEU:HB2	43:m:105:ARG:CZ	1.57	1.32
32:0:93:GLN:HG3	48:s:67:VAL:O	1.35	1.25
55:v:123:LYS:HE2	55:v:167:PHE:CD2	1.72	1.24
31:A:1934:C:OP1	52:a:1466:G:C8	1.89	1.24
50:u:103:PHE:CZ	53:w:138:TRP:HB3	1.74	1.20
54:d:50:GLU:OE1	54:d:188:ILE:CG2	1.90	1.20
38:h:67:ARG:HH11	58:8:68:ARG:N	1.39	1.20
50:u:106:GLU:HB2	53:w:138:TRP:CZ2	1.78	1.19
50:u:103:PHE:CE1	53:w:138:TRP:HB3	1.80	1.17
9:C:133:LEU:CD2	36:f:159:LYS:HE2	1.74	1.16
43:m:65:GLN:NE2	57:x:86:PRO:HD2	1.58	1.15
50:u:106:GLU:N	53:w:138:TRP:CH2	2.14	1.15
9:C:133:LEU:HD21	36:f:159:LYS:HE2	1.26	1.15
21:Q:160:ARG:HH12	52:a:317:G:H1'	1.04	1.14
38:h:67:ARG:NH1	58:8:68:ARG:H	1.43	1.14
38:h:67:ARG:CD	58:8:71:PRO:HD2	1.77	1.13
53:w:136:ASP:CB	53:w:139:GLU:OE2	1.95	1.13
54:d:137:MET:SD	54:d:172:LYS:CE	2.36	1.12
50:u:100:LEU:HD11	53:w:168:ASN:ND2	1.63	1.11
50:u:103:PHE:HA	53:w:138:TRP:NE1	1.51	1.11
21:Q:160:ARG:HH22	52:a:317:G:C1'	1.63	1.10
33:b:201:ASP:CB	58:8:66:ARG:HD3	1.82	1.10
38:h:67:ARG:HD2	58:8:71:PRO:HD2	1.27	1.10
47:r:51:VAL:O	53:w:149:PRO:HD3	0.92	1.10
21:Q:160:ARG:NH1	52:a:317:G:H1'	1.66	1.10
54:d:137:MET:HG2	54:d:172:LYS:HG2	1.30	1.10
55:v:128:ASN:HB3	55:v:193:ILE:HA	1.23	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:727:A:N3	44:o:41:GLU:OE2	1.84	1.09
50:u:106:GLU:HB3	53:w:139:GLU:OE1	1.53	1.09
50:u:107:VAL:HG23	53:w:138:TRP:HZ3	1.14	1.08
54:d:89:MET:HE1	54:d:178:ILE:HA	1.34	1.08
31:A:726:G:H21	44:o:37:THR:HG23	1.13	1.07
54:d:50:GLU:OE1	54:d:188:ILE:HG23	1.51	1.07
54:d:162:LYS:CB	54:d:183:TRP:CZ2	2.24	1.07
31:A:897:A:N6	43:m:119:CYS:SG	2.26	1.07
31:A:897:A:O2'	43:m:122:GLY:O	1.73	1.07
54:d:89:MET:HE3	54:d:178:ILE:HA	1.12	1.07
47:r:51:VAL:O	53:w:149:PRO:CG	2.04	1.06
50:u:107:VAL:HG23	53:w:138:TRP:CZ3	1.89	1.06
54:d:162:LYS:C	54:d:183:TRP:CZ3	2.35	1.05
53:w:136:ASP:HB2	53:w:139:GLU:OE2	1.56	1.04
50:u:103:PHE:CD1	53:w:138:TRP:HD1	1.54	1.04
52:a:75:U:H5''	55:v:194:ARG:CD	1.87	1.04
53:w:136:ASP:HB3	53:w:139:GLU:HG2	1.37	1.04
54:d:190:GLU:OE1	54:d:190:GLU:N	1.90	1.04
32:0:96:LYS:HG2	52:a:1259:A:H5''	1.38	1.04
57:x:90:ILE:HG22	57:x:91:PHE:H	1.15	1.03
9:C:163:LYS:HE2	36:f:162:ALA:HB2	1.41	1.03
12:F:167:PHE:CD2	43:m:101:ARG:NH2	2.26	1.03
9:C:133:LEU:CG	36:f:159:LYS:HE2	1.90	1.02
21:Q:160:ARG:NH2	52:a:317:G:C8	2.27	1.02
50:u:106:GLU:N	53:w:138:TRP:CZ2	2.27	1.02
54:d:163:HIS:CB	54:d:175:VAL:HG13	1.86	1.02
54:d:89:MET:CE	54:d:178:ILE:CA	2.36	1.02
53:w:136:ASP:CG	53:w:139:GLU:OE2	2.00	1.02
54:d:19:PRO:CG	54:d:186:LEU:HD13	1.89	1.01
31:A:63:A:H61	31:A:89:A:N6	1.59	1.01
32:0:101:TYR:CD1	48:s:7:LYS:O	2.13	1.01
54:d:163:HIS:O	54:d:175:VAL:HA	1.59	1.01
50:u:100:LEU:HD11	53:w:168:ASN:HD21	0.85	1.01
53:w:136:ASP:OD1	53:w:139:GLU:OE2	1.79	1.00
54:d:181:SER:O	54:d:184:VAL:HG22	1.59	1.00
31:A:897:A:N3	43:m:123:ILE:HD11	1.76	1.00
52:a:75:U:H5''	55:v:194:ARG:HD3	1.44	1.00
54:d:163:HIS:HB2	54:d:175:VAL:CG1	1.90	0.99
31:A:293:G:H21	31:A:365:A:N6	1.62	0.98
32:0:86:ALA:C	43:m:105:ARG:HH22	1.61	0.98
50:u:100:LEU:HD21	53:w:164:THR:HG21	1.44	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:293:G:N2	31:A:365:A:H62	1.61	0.98
50:u:103:PHE:CE1	53:w:138:TRP:CD1	2.51	0.98
33:b:201:ASP:HB2	58:8:66:ARG:HD3	1.45	0.98
31:A:1505:C:H42	31:A:1515:G:H1	1.09	0.98
57:x:90:ILE:HG22	57:x:91:PHE:N	1.79	0.97
31:A:2118:U:H3	31:A:2199:G:H1	1.08	0.97
31:A:727:A:C2	44:o:41:GLU:OE2	2.18	0.97
31:A:313:A:H2	31:A:323:G:H1	1.02	0.97
47:r:51:VAL:HG13	53:w:146:GLU:C	1.90	0.97
50:u:106:GLU:N	53:w:138:TRP:HH2	1.59	0.97
52:a:611:A:H61	52:a:690:G:H1	1.02	0.96
32:0:96:LYS:CG	52:a:1259:A:H5''	1.75	0.96
31:A:63:A:H61	31:A:89:A:H61	0.98	0.96
54:d:162:LYS:HB2	54:d:183:TRP:CZ3	1.99	0.96
50:u:107:VAL:CG2	53:w:138:TRP:HZ3	1.77	0.96
50:u:106:GLU:CB	53:w:138:TRP:CZ2	2.48	0.95
47:r:51:VAL:HG22	53:w:147:ASN:OD1	1.64	0.95
9:C:163:LYS:HE2	36:f:162:ALA:CB	1.96	0.95
50:u:106:GLU:H	53:w:138:TRP:HZ2	1.10	0.95
48:s:8:ASN:OD1	56:n:42:GLU:OE2	1.83	0.94
58:8:317:HIS:HA	58:8:324:VAL:HA	1.47	0.94
50:u:103:PHE:HD1	53:w:138:TRP:CD1	1.83	0.94
21:Q:160:ARG:NH2	52:a:317:G:N9	2.16	0.94
54:d:51:LYS:HD2	54:d:196:TYR:CE1	2.03	0.94
31:A:1084:G:H21	31:A:1131:A:N6	1.65	0.93
31:A:1121:G:H21	31:A:1126:A:H62	1.09	0.93
47:r:51:VAL:HG13	53:w:146:GLU:O	1.68	0.93
54:d:173:GLY:C	54:d:174:LEU:HD12	1.92	0.92
56:n:36:SER:C	56:n:37:LEU:HD12	1.95	0.92
50:u:107:VAL:N	53:w:138:TRP:CH2	2.38	0.92
31:A:63:A:N6	31:A:89:A:H61	1.66	0.92
54:d:162:LYS:HB3	54:d:183:TRP:CH2	2.01	0.92
12:F:167:PHE:CE2	43:m:101:ARG:NH2	2.37	0.92
31:A:726:G:N2	44:o:37:THR:HG23	1.84	0.92
31:A:1084:G:N2	31:A:1131:A:H62	1.67	0.92
50:u:103:PHE:CE1	53:w:167:ILE:HD12	2.05	0.91
47:r:51:VAL:O	53:w:149:PRO:HG3	1.68	0.91
47:r:51:VAL:HA	53:w:147:ASN:HA	1.53	0.91
50:u:103:PHE:CG	53:w:138:TRP:CD1	2.58	0.91
43:m:65:GLN:NE2	57:x:86:PRO:CD	2.33	0.91
9:C:163:LYS:CE	36:f:162:ALA:HB2	1.99	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:r:53:ARG:NH2	53:w:150:TRP:CH2	2.39	0.91
31:A:897:A:C2	43:m:123:ILE:HD11	2.06	0.90
47:r:53:ARG:HG3	53:w:149:PRO:HD2	1.52	0.90
31:A:726:G:H21	44:o:37:THR:CG2	1.84	0.90
50:u:106:GLU:CA	53:w:138:TRP:CH2	2.55	0.90
54:d:163:HIS:HB2	54:d:175:VAL:HG13	0.94	0.90
12:F:106:ALA:O	12:F:110:LEU:HB3	1.72	0.90
33:b:77:LYS:HE3	33:b:79:LYS:HD2	1.54	0.90
50:u:103:PHE:CA	53:w:138:TRP:NE1	2.35	0.90
55:v:124:VAL:CG1	55:v:195:VAL:CG2	2.50	0.90
16:L:48:PRO:CB	52:a:1371:G:O5'	2.20	0.89
21:Q:160:ARG:NH2	52:a:317:G:C1'	2.35	0.89
54:d:163:HIS:N	54:d:183:TRP:HZ3	1.70	0.89
50:u:98:ARG:HE	53:w:168:ASN:HB3	1.35	0.88
50:u:103:PHE:CD1	53:w:138:TRP:CG	2.60	0.88
20:P:73:LEU:HA	20:P:85:GLN:O	1.73	0.88
54:d:89:MET:HE3	54:d:178:ILE:CA	2.00	0.88
54:d:50:GLU:OE1	54:d:188:ILE:HG21	1.71	0.87
51:y:96:ASP:O	51:y:100:LYS:HB2	1.74	0.87
53:w:136:ASP:HB3	53:w:139:GLU:CG	2.04	0.87
31:A:1926:A:H2	52:a:1356:C:O2	1.58	0.86
50:u:103:PHE:CE1	53:w:138:TRP:CB	2.58	0.86
31:A:1933:A:C2	52:a:1444:U:O2'	2.28	0.86
31:A:1235:A:H62	31:A:1256:G:H21	1.24	0.86
31:A:1084:G:H21	31:A:1131:A:H62	0.88	0.86
50:u:100:LEU:CD2	53:w:164:THR:HG21	2.06	0.86
31:A:898:G:H1	43:m:121:ARG:HB3	1.41	0.86
9:C:133:LEU:HG	36:f:159:LYS:CE	2.05	0.86
12:F:165:ARG:O	43:m:101:ARG:NH2	2.07	0.86
33:b:201:ASP:CG	58:8:66:ARG:HD3	2.00	0.85
35:e:263:GLU:HB3	54:d:191:LEU:CD1	2.06	0.85
54:d:89:MET:HE1	54:d:178:ILE:CA	2.02	0.85
31:A:1196:A:H61	31:A:1201:A:H61	1.25	0.85
50:u:107:VAL:N	53:w:138:TRP:HH2	1.75	0.85
56:n:43:ILE:O	56:n:46:LYS:HB3	1.76	0.84
52:a:611:A:N6	52:a:690:G:H1	1.75	0.84
54:d:137:MET:CG	54:d:172:LYS:HG2	2.06	0.84
48:s:50:ALA:HA	48:s:58:LEU:O	1.78	0.84
50:u:100:LEU:CD1	53:w:168:ASN:HD21	1.81	0.84
13:G:57:ALA:HB3	13:G:64:LYS:O	1.77	0.84
54:d:19:PRO:HG3	54:d:186:LEU:HD13	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:0:87:LEU:HB2	43:m:105:ARG:NE	1.93	0.83
31:A:726:G:C2	44:o:53:LEU:HD21	2.13	0.83
33:b:7:ASN:ND2	58:8:345:VAL:O	2.11	0.83
54:d:19:PRO:HG3	54:d:186:LEU:CD1	2.07	0.83
43:m:65:GLN:CD	57:x:86:PRO:HD2	2.03	0.83
31:A:313:A:C2	31:A:323:G:N1	2.45	0.83
16:L:48:PRO:HB3	52:a:1371:G:P	2.18	0.83
31:A:897:A:C2'	43:m:122:GLY:O	2.26	0.83
53:w:136:ASP:CB	53:w:139:GLU:CD	2.51	0.83
54:d:163:HIS:N	54:d:183:TRP:CZ3	2.45	0.83
31:A:1926:A:C2	52:a:1356:C:O2	2.31	0.83
50:u:126:GLN:O	50:u:130:LYS:HB2	1.78	0.83
58:8:63:ALA:O	58:8:66:ARG:C	2.22	0.83
58:8:291:GLN:HB3	58:8:327:SER:HA	1.60	0.83
58:8:342:PRO:HA	58:8:345:VAL:HB	1.61	0.83
32:0:87:LEU:CB	43:m:105:ARG:CZ	2.14	0.83
31:A:313:A:H2	31:A:323:G:N1	1.77	0.82
16:L:48:PRO:HB3	52:a:1371:G:OP1	1.79	0.82
50:u:107:VAL:H	53:w:138:TRP:HH2	1.26	0.82
52:a:954:A:N6	52:a:973:G:H21	1.78	0.82
32:0:49:ALA:HB3	32:0:61:THR:O	1.79	0.82
56:n:34:VAL:HG12	56:n:41:TRP:HZ3	1.45	0.81
54:d:57:HIS:CD2	54:d:186:LEU:HD22	2.16	0.81
12:F:105:ALA:O	12:F:109:GLU:HB2	1.80	0.81
54:d:180:ASP:OD1	54:d:181:SER:N	2.14	0.81
56:n:34:VAL:HG12	56:n:41:TRP:CZ3	2.15	0.81
50:u:103:PHE:HA	53:w:138:TRP:HE1	1.45	0.80
35:e:246:GLY:HA3	54:d:195:GLU:HG3	1.60	0.80
38:h:67:ARG:CZ	58:8:69:ASN:H	1.94	0.80
34:c:71:LEU:HA	34:c:109:LYS:O	1.81	0.80
21:Q:226:LEU:HD21	52:a:1380:C:H4'	1.63	0.80
52:a:75:U:H5''	55:v:194:ARG:HD2	1.60	0.80
32:0:86:ALA:C	43:m:105:ARG:NH2	2.28	0.80
33:b:60:LEU:HD13	58:8:65:GLU:HB3	1.63	0.80
31:A:1505:C:N4	31:A:1515:G:H1	1.78	0.80
32:0:87:LEU:HB2	43:m:105:ARG:HH21	1.01	0.80
38:h:67:ARG:CG	58:8:71:PRO:HD2	2.11	0.80
50:u:103:PHE:CE1	53:w:138:TRP:HD1	1.97	0.80
32:0:87:LEU:CA	43:m:105:ARG:NH2	2.29	0.79
35:e:263:GLU:HB3	54:d:191:LEU:HD11	1.62	0.79
54:d:162:LYS:C	54:d:183:TRP:HZ3	1.89	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:898:G:N1	43:m:121:ARG:HB3	1.95	0.79
13:G:101:ALA:O	13:G:105:HIS:HB2	1.82	0.79
33:b:201:ASP:HB2	58:8:66:ARG:CD	2.12	0.79
52:a:612:G:H22	52:a:689:G:H1	1.28	0.79
53:w:136:ASP:OD1	53:w:139:GLU:CD	2.24	0.79
31:A:892:C:O2'	31:A:893:C:H5'	1.82	0.79
56:n:43:ILE:O	56:n:46:LYS:CB	2.31	0.78
32:0:87:LEU:HB3	43:m:105:ARG:NH2	1.94	0.78
35:e:174:PHE:O	35:e:193:LYS:HA	1.82	0.78
31:A:726:G:H1'	44:o:33:ILE:HG21	1.65	0.78
38:h:24:VAL:O	38:h:60:VAL:HA	1.83	0.78
12:F:167:PHE:CE2	43:m:101:ARG:NH1	2.52	0.77
55:v:128:ASN:HB3	55:v:193:ILE:CA	2.11	0.77
34:c:26:PRO:HG3	40:j:140:ARG:HH22	1.48	0.77
9:C:133:LEU:CG	36:f:159:LYS:CE	2.61	0.77
54:d:19:PRO:CG	54:d:186:LEU:CD1	2.63	0.77
13:G:162:GLN:O	13:G:174:SER:HB2	1.85	0.77
31:A:2764:U:O4	31:A:2774:U:C4	2.38	0.77
50:u:98:ARG:HB2	53:w:168:ASN:CG	2.10	0.77
33:b:14:MET:SD	58:8:334:THR:OG1	2.43	0.77
53:w:130:TYR:CD2	53:w:140:GLU:OE2	2.37	0.77
50:u:106:GLU:C	53:w:138:TRP:CH2	2.62	0.76
56:n:37:LEU:HB2	56:n:41:TRP:CZ2	2.20	0.76
52:a:1358:C:O2	52:a:1440:G:N2	2.17	0.76
56:n:43:ILE:O	56:n:46:LYS:N	2.18	0.76
50:u:98:ARG:HD3	53:w:168:ASN:ND2	1.99	0.76
53:w:106:MET:HE3	53:w:109:ASN:HD21	1.50	0.76
33:b:7:ASN:HD22	58:8:345:VAL:HA	1.49	0.76
31:A:1926:A:O2'	52:a:1444:U:H5'	1.86	0.76
32:0:101:TYR:HB2	48:s:7:LYS:O	1.86	0.76
31:A:293:G:H21	31:A:365:A:H62	0.83	0.75
32:0:93:GLN:CG	48:s:67:VAL:O	2.27	0.75
38:h:67:ARG:HD2	58:8:71:PRO:CD	2.11	0.75
31:A:897:A:N3	43:m:123:ILE:CD1	2.49	0.75
50:u:100:LEU:HD21	53:w:164:THR:CG2	2.16	0.75
54:d:162:LYS:CA	54:d:183:TRP:CH2	2.69	0.75
47:r:53:ARG:NH2	53:w:150:TRP:CZ2	2.54	0.75
47:r:53:ARG:NH2	53:w:150:TRP:CZ3	2.55	0.75
55:v:50:ILE:HG22	55:v:69:THR:HB	1.68	0.75
31:A:721:U:H3	31:A:732:A:H61	1.33	0.74
32:0:101:TYR:HD1	48:s:7:LYS:O	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:t:84:ARG:NH1	52:a:88:G:N7	2.35	0.74
55:v:30:PRO:HG3	55:v:91:ARG:HB2	1.68	0.74
56:n:36:SER:O	56:n:37:LEU:HD12	1.86	0.74
58:8:365:ALA:O	58:8:366:MET:O	2.03	0.74
31:A:1121:G:N2	31:A:1126:A:H62	1.86	0.74
31:A:2107:G:H1	31:A:2210:C:H42	1.34	0.74
54:d:162:LYS:C	54:d:183:TRP:CH2	2.63	0.74
11:E:251:THR:O	11:E:255:LEU:HB2	1.88	0.73
21:Q:160:ARG:CZ	52:a:317:G:H1'	2.17	0.73
22:R:81:PHE:O	22:R:85:LEU:HB2	1.86	0.73
33:b:211:ILE:HG13	58:8:317:HIS:CE1	2.23	0.73
58:8:354:GLN:OE1	58:8:357:ARG:NH1	2.18	0.73
31:A:726:G:H1'	44:o:33:ILE:CG2	2.17	0.73
31:A:901:C:H2'	31:A:902:G:H5''	1.70	0.73
52:a:75:U:O3'	55:v:196:ASN:ND2	2.22	0.73
33:b:90:ARG:HH22	58:8:359:ARG:HB2	1.53	0.73
31:A:722:G:H1	31:A:731:U:H3	1.37	0.73
33:b:79:LYS:HD3	58:8:317:HIS:HB2	1.69	0.73
40:j:101:ILE:HA	40:j:192:GLU:O	1.87	0.73
16:L:48:PRO:HB2	52:a:1371:G:O5'	1.89	0.72
38:h:67:ARG:HG2	58:8:67:CYS:HA	1.69	0.72
52:a:75:U:C5'	55:v:194:ARG:HD2	2.18	0.72
55:v:21:ALA:HA	55:v:23:ARG:HG2	1.71	0.72
55:v:123:LYS:HE2	55:v:167:PHE:CG	2.24	0.72
58:8:64:TYR:HA	58:8:67:CYS:HB2	1.72	0.72
53:w:98:ARG:HG2	53:w:155:GLN:HE21	1.54	0.72
52:a:954:A:H62	52:a:973:G:N2	1.88	0.72
33:b:52:ARG:HD2	58:8:73:GLU:HG3	1.71	0.72
39:i:79:LYS:HE2	39:i:177:ILE:HG13	1.71	0.72
10:D:260:LYS:HD2	31:A:2790:C:H5''	1.72	0.71
50:u:98:ARG:NE	53:w:168:ASN:HB3	2.03	0.71
53:w:135:LYS:HG2	53:w:140:GLU:OE1	1.89	0.71
50:u:103:PHE:HA	53:w:138:TRP:CD1	2.25	0.71
52:a:954:A:H62	52:a:973:G:H21	1.37	0.71
32:0:96:LYS:HG2	52:a:1259:A:C5'	2.17	0.71
33:b:79:LYS:HZ3	58:8:317:HIS:C	1.98	0.71
54:d:89:MET:HE1	54:d:178:ILE:HG12	1.73	0.71
32:0:100:LYS:HD3	52:a:1260:G:C5'	2.20	0.71
46:q:64:LYS:HD3	46:q:111:TRP:HB3	1.73	0.71
50:u:96:GLU:HB3	53:w:172:GLN:CD	2.16	0.71
31:A:1462:G:H1	31:A:1584:C:H42	1.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:127:GLY:O	55:v:193:ILE:HA	1.91	0.71
54:d:162:LYS:CA	54:d:183:TRP:CZ3	2.73	0.70
31:A:2112:U:H3	31:A:2205:G:H1	1.39	0.70
54:d:162:LYS:CB	54:d:183:TRP:HH2	1.97	0.70
53:w:112:LEU:HD11	53:w:167:ILE:HD11	1.73	0.70
54:d:179:ILE:HG23	54:d:183:TRP:HB3	1.73	0.70
19:O:31:LEU:HA	19:O:54:MET:HE1	1.73	0.70
51:y:166:ARG:NH1	52:a:1350:G:OP2	2.25	0.70
9:C:133:LEU:HD21	36:f:159:LYS:CE	2.15	0.70
31:A:2764:U:O4	31:A:2774:U:C5	2.45	0.70
10:D:127:LYS:O	10:D:135:ASN:HA	1.92	0.69
55:v:67:PHE:HB3	55:v:101:PRO:HB3	1.73	0.69
43:m:56:ASN:HD22	43:m:59:ARG:HD2	1.57	0.69
55:v:146:GLY:HA3	55:v:175:GLU:HG2	1.74	0.69
54:d:174:LEU:HD12	54:d:174:LEU:N	2.06	0.69
53:w:136:ASP:CB	53:w:139:GLU:CG	2.70	0.69
52:a:75:U:C5'	55:v:194:ARG:CD	2.68	0.69
33:b:58:CYS:SG	33:b:220:LYS:NZ	2.66	0.69
55:v:13:SER:HB3	55:v:103:GLU:HG3	1.75	0.69
32:0:100:LYS:HB3	52:a:1260:G:H5'	1.74	0.69
53:w:136:ASP:O	53:w:140:GLU:CD	2.36	0.69
31:A:55:G:H1	31:A:112:C:H42	1.42	0.69
14:H:51:ILE:HA	14:H:85:GLU:O	1.93	0.68
43:m:126:LYS:O	43:m:132:ARG:NH2	2.26	0.68
52:a:1442:A:H2'	52:a:1443:G:H5'	1.75	0.68
34:c:162:ILE:O	34:c:178:TRP:HA	1.93	0.68
50:u:103:PHE:CE1	53:w:138:TRP:CG	2.78	0.68
53:w:126:LEU:HB2	53:w:128:PRO:HD3	1.76	0.68
55:v:42:VAL:HA	55:v:45:HIS:HD2	1.57	0.68
58:8:318:ASP:HB3	58:8:323:ARG:HB2	1.74	0.68
16:L:22:ILE:HB	16:L:40:VAL:O	1.94	0.68
31:A:897:A:H2'	43:m:122:GLY:CA	2.23	0.68
35:e:247:VAL:CA	54:d:195:GLU:OE1	2.42	0.68
55:v:124:VAL:CG1	55:v:195:VAL:HG21	2.22	0.68
14:H:57:ILE:HG22	14:H:59:ASP:H	1.58	0.68
58:8:359:ARG:HG3	58:8:360:ILE:HG13	1.75	0.68
31:A:2707:A:H62	31:A:2737:G:N2	1.92	0.68
32:0:101:TYR:HD1	48:s:7:LYS:C	2.02	0.68
9:C:167:SER:HA	9:C:180:ILE:O	1.93	0.67
32:0:87:LEU:CB	43:m:105:ARG:NE	2.55	0.67
50:u:106:GLU:CD	53:w:136:ASP:OD1	2.37	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:124:VAL:HB	55:v:168:VAL:CG1	2.24	0.67
16:L:48:PRO:HB3	52:a:1371:G:O5'	1.91	0.67
33:b:75:GLY:H	33:b:96:VAL:HB	1.59	0.67
12:F:167:PHE:HD2	43:m:101:ARG:NH2	1.85	0.67
55:v:123:LYS:CE	55:v:167:PHE:CD2	2.66	0.67
58:8:257:GLN:HE22	58:8:283:ILE:HA	1.60	0.67
48:s:8:ASN:OD1	56:n:42:GLU:CD	2.36	0.67
55:v:124:VAL:HG11	55:v:195:VAL:HG21	1.75	0.67
26:V:75:VAL:HA	26:V:135:MET:O	1.95	0.67
31:A:2492:C:H42	31:A:2546:G:H22	1.41	0.67
50:u:106:GLU:CA	53:w:138:TRP:CZ2	2.77	0.67
54:d:51:LYS:HD2	54:d:196:TYR:CZ	2.29	0.67
50:u:103:PHE:CZ	53:w:138:TRP:CB	2.66	0.67
31:A:2464:G:H1	31:A:2467:A:H62	1.40	0.67
28:X:121:GLY:HA3	28:X:138:TYR:O	1.94	0.67
18:N:65:TRP:HB2	18:N:105:GLU:HB2	1.77	0.66
31:A:1060:A:H2	31:A:1150:G:H1	1.43	0.66
32:0:101:TYR:CD1	48:s:7:LYS:C	2.73	0.66
10:D:98:GLY:H	10:D:286:PRO:HB3	1.59	0.66
31:A:1926:A:H1'	52:a:1444:U:O4'	1.96	0.66
38:h:67:ARG:NH1	58:8:68:ARG:N	2.16	0.66
38:h:67:ARG:NE	58:8:69:ASN:H	1.92	0.66
50:u:101:ASN:O	50:u:105:ARG:HB2	1.96	0.66
31:A:2134:G:H22	31:A:2192:U:H3	1.42	0.66
18:N:30:GLY:HA2	18:N:107:SER:HB3	1.77	0.66
21:Q:148:ILE:HG12	21:Q:168:ILE:HG12	1.77	0.66
31:A:897:A:N1	43:m:119:CYS:HB3	2.11	0.66
31:A:2764:U:C4	31:A:2774:U:O4	2.49	0.66
48:s:10:PHE:CD1	52:a:1266:A:H4'	2.30	0.66
21:Q:160:ARG:CZ	52:a:317:G:C8	2.79	0.66
43:m:109:VAL:O	43:m:118:ARG:NH1	2.23	0.66
55:v:29:ILE:HG23	55:v:33:LEU:HD23	1.78	0.66
10:D:275:VAL:HG21	21:Q:122:ILE:HG21	1.78	0.66
18:N:35:GLN:HE21	18:N:100:GLY:HA2	1.60	0.66
27:W:53:G:H8	27:W:70:G:H21	1.44	0.66
31:A:1385:G:H4'	31:A:1818:U:H3	1.61	0.66
47:r:53:ARG:HG3	53:w:149:PRO:CD	2.25	0.66
55:v:20:GLY:HA2	55:v:100:LYS:HE2	1.78	0.66
10:D:125:GLN:O	10:D:138:GLN:HB3	1.96	0.65
12:F:91:CYS:O	12:F:139:GLY:HA2	1.96	0.65
31:A:726:G:N7	44:o:57:LEU:HD11	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:897:A:H2'	43:m:122:GLY:O	1.94	0.65
33:b:145:LEU:O	33:b:149:GLN:HB2	1.96	0.65
57:x:90:ILE:CG2	57:x:91:PHE:N	2.52	0.65
5:5:14:CYS:HA	5:5:26:ILE:O	1.97	0.65
9:C:163:LYS:NZ	36:f:162:ALA:HB2	2.12	0.65
31:A:2764:U:O4	31:A:2774:U:O4	2.14	0.65
53:w:136:ASP:HB3	53:w:139:GLU:CD	2.20	0.65
31:A:1196:A:N6	31:A:1201:A:H61	1.93	0.65
31:A:1928:C:N4	52:a:1358:C:O2'	2.30	0.65
21:Q:216:LYS:HG3	21:Q:218:ARG:H	1.61	0.65
47:r:53:ARG:HG3	53:w:149:PRO:HG2	1.79	0.65
31:A:1235:A:H62	31:A:1256:G:N2	1.93	0.65
32:0:101:TYR:CG	48:s:7:LYS:O	2.49	0.65
43:m:65:GLN:HE22	57:x:86:PRO:CD	2.09	0.65
16:L:2:ILE:HB	16:L:33:ALA:HB3	1.78	0.64
32:0:96:LYS:NZ	52:a:1259:A:O3'	2.04	0.64
47:r:51:VAL:HG22	53:w:147:ASN:HA	1.80	0.64
52:a:956:C:N3	52:a:972:G:N2	2.45	0.64
15:K:56:LYS:O	15:K:60:GLU:HB2	1.97	0.64
55:v:124:VAL:CG1	55:v:195:VAL:HG22	2.28	0.64
13:G:91:ARG:HA	13:G:109:ARG:HH22	1.62	0.64
9:C:37:LYS:HE3	9:C:50:ARG:HE	1.61	0.64
48:s:19:ILE:HG23	48:s:23:ASN:HD22	1.62	0.64
54:d:19:PRO:CD	54:d:186:LEU:HD13	2.27	0.64
12:F:89:VAL:HA	12:F:206:ASP:O	1.97	0.64
23:S:198:PHE:HA	23:S:208:ARG:O	1.97	0.64
41:k:90:ARG:HG2	41:k:115:LEU:HD23	1.80	0.64
55:v:42:VAL:HG13	55:v:79:VAL:HG21	1.78	0.64
12:F:167:PHE:CE2	43:m:101:ARG:CZ	2.81	0.64
19:O:108:ILE:O	19:O:122:TYR:HB3	1.98	0.64
52:a:1356:C:H2'	52:a:1357:A:H8	1.63	0.64
47:r:51:VAL:CG2	53:w:147:ASN:OD1	2.42	0.64
54:d:162:LYS:HB2	54:d:183:TRP:CE2	2.23	0.64
22:R:97:LEU:O	22:R:101:ALA:HB2	1.99	0.63
35:e:246:GLY:HA3	54:d:195:GLU:CG	2.26	0.63
40:j:101:ILE:HG13	40:j:167:ILE:HG23	1.79	0.63
50:u:109:ARG:HG2	50:u:111:GLY:H	1.62	0.63
33:b:201:ASP:HB2	58:8:66:ARG:CG	2.28	0.63
34:c:180:ARG:NH2	52:a:1055:G:O2'	2.31	0.63
38:h:20:ARG:NH1	38:h:70:LYS:O	2.31	0.63
3:3:146:ARG:HH22	25:U:140:VAL:HG21	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:g:138:LYS:O	37:g:142:HIS:HB2	1.99	0.63
38:h:67:ARG:HB3	58:8:67:CYS:HA	1.81	0.63
55:v:124:VAL:HG13	55:v:195:VAL:HG22	1.81	0.63
31:A:1505:C:N3	31:A:1515:G:N2	2.43	0.63
38:h:51:HIS:O	38:h:57:TYR:HA	1.99	0.63
42:l:114:ARG:NH1	52:a:449:C:OP1	2.32	0.63
50:u:106:GLU:HB2	53:w:138:TRP:CH2	2.30	0.63
33:b:114:ARG:HE	33:b:152:LEU:HD11	1.64	0.63
41:k:93:VAL:HB	41:k:119:VAL:HG12	1.80	0.63
54:d:89:MET:HE1	54:d:178:ILE:CG1	2.28	0.63
54:d:199:ARG:O	54:d:200:GLN:HB2	1.99	0.63
55:v:19:GLU:HG2	55:v:22:ARG:HG3	1.80	0.63
35:e:246:GLY:HA2	54:d:191:LEU:HD22	1.79	0.62
49:t:156:ARG:HH22	52:a:168:C:H1'	1.64	0.62
50:u:99:LEU:HB2	53:w:171:GLN:HE22	1.63	0.62
23:S:211:GLY:H	31:A:1245:U:H4'	1.64	0.62
9:C:29:ILE:HG22	9:C:57:LEU:HD22	1.81	0.62
17:M:203:GLU:HB3	31:A:649:A:H5''	1.82	0.62
46:q:76:VAL:O	46:q:96:LYS:HA	1.99	0.62
9:C:146:ARG:NH2	31:A:1811:A:OP2	2.33	0.62
21:Q:123:MET:O	21:Q:127:ASN:HB2	1.99	0.62
52:a:670:A:H61	52:a:681:A:H61	1.46	0.62
52:a:840:U:H2'	52:a:841:A:H8	1.64	0.62
52:a:1013:G:O2'	52:a:1138:G:N2	2.32	0.62
31:A:540:A:H62	31:A:2055:U:H3	1.48	0.62
33:b:184:GLY:O	58:8:59:LEU:HD22	2.00	0.62
14:H:57:ILE:HB	14:H:61:GLY:H	1.65	0.62
31:A:897:A:C6	43:m:119:CYS:HA	2.34	0.62
43:m:65:GLN:HE22	57:x:86:PRO:N	1.97	0.62
47:r:37:SER:HA	47:r:40:ILE:HG12	1.81	0.62
53:w:96:LYS:HG2	53:w:119:PRO:HA	1.82	0.62
23:S:214:GLN:HE22	31:A:1189:G:H21	1.47	0.62
26:V:76:LYS:O	26:V:134:VAL:HA	1.99	0.62
41:k:135:LYS:HG2	50:u:118:ARG:HB3	1.81	0.62
9:C:139:ASN:O	9:C:186:ALA:HA	2.00	0.62
49:t:81:LYS:HE2	52:a:62:G:H8	1.64	0.62
52:a:344:A:O2'	52:a:422:A:N7	2.33	0.62
12:F:167:PHE:CD2	43:m:101:ARG:CZ	2.82	0.62
13:G:104:MET:HA	13:G:107:LEU:HB3	1.81	0.62
52:a:1438:G:H2'	52:a:1439:U:C6	2.34	0.62
55:v:25:TYR:HB2	55:v:98:THR:HB	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:183:LEU:HD21	55:v:193:ILE:HG22	1.81	0.62
49:t:139:ILE:HG12	49:t:160:LEU:HD22	1.81	0.61
52:a:1135:G:HO2'	56:n:99:SER:HG	1.41	0.61
18:N:14:ARG:NH1	31:A:984:G:N7	2.48	0.61
22:R:6:ARG:NH2	31:A:29:A:OP2	2.33	0.61
38:h:4:ASP:OD2	38:h:81:ARG:NH1	2.34	0.61
43:m:56:ASN:HB2	43:m:59:ARG:HB2	1.82	0.61
47:r:28:ILE:HG21	47:r:62:ILE:HG22	1.82	0.61
52:a:401:G:OP2	54:d:8:ARG:NH1	2.32	0.61
53:w:103:PHE:HB2	53:w:166:ILE:HG21	1.81	0.61
52:a:1020:C:H2'	52:a:1021:G:H8	1.65	0.61
4:4:110:ILE:H	4:4:143:TYR:HE1	1.46	0.61
12:F:167:PHE:HE2	43:m:101:ARG:NH1	1.97	0.61
37:g:30:ILE:HG23	37:g:39:ALA:HB1	1.83	0.61
50:u:103:PHE:CG	53:w:138:TRP:CG	2.85	0.61
13:G:198:LYS:HG3	13:G:200:LYS:HB3	1.82	0.61
48:s:32:VAL:HA	48:s:50:ALA:HB3	1.83	0.61
54:d:179:ILE:HG23	54:d:183:TRP:CB	2.29	0.61
31:A:890:G:O2'	31:A:891:G:H5'	2.00	0.61
54:d:21:LEU:HG	54:d:57:HIS:HA	1.83	0.61
55:v:123:LYS:HG3	55:v:168:VAL:O	2.00	0.61
55:v:180:ILE:HA	55:v:195:VAL:HG13	1.83	0.61
31:A:726:G:N1	44:o:53:LEU:HD21	2.16	0.61
33:b:52:ARG:NE	58:8:74:GLY:H	1.97	0.61
43:m:134:GLN:HG2	43:m:135:ARG:HB2	1.83	0.61
50:u:103:PHE:HE1	53:w:167:ILE:HD12	1.63	0.61
56:n:17:GLU:HG3	56:n:59:LEU:HD22	1.83	0.61
12:F:155:ARG:O	12:F:159:LEU:HB2	2.01	0.61
31:A:1238:G:H1	31:A:1252:C:H42	1.47	0.61
8:B:58:A:H5'	12:F:77:ASN:HD22	1.65	0.61
11:E:97:ARG:NH1	31:A:38:C:O2	2.33	0.61
15:K:84:MET:HG2	15:K:96:TRP:HE1	1.66	0.61
31:A:897:A:C2	43:m:123:ILE:CD1	2.83	0.61
31:A:1196:A:H61	31:A:1201:A:N6	1.97	0.61
52:a:780:G:H1	52:a:803:U:H3	1.48	0.61
28:X:123:VAL:HG12	28:X:137:VAL:HG22	1.83	0.61
46:q:75:ASN:ND2	52:a:247:G:OP1	2.33	0.61
50:u:100:LEU:CD2	53:w:164:THR:CG2	2.76	0.61
31:A:2492:C:H42	31:A:2546:G:N2	1.99	0.60
34:c:20:SER:OG	34:c:22:TRP:NE1	2.32	0.60
35:e:235:ARG:HB3	35:e:270:LEU:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:Q:160:ARG:NH2	52:a:317:G:H1'	2.16	0.60
31:A:1121:G:H21	31:A:1126:A:N6	1.92	0.60
47:r:42:GLU:O	47:r:79:ASN:ND2	2.34	0.60
54:d:137:MET:HG2	54:d:172:LYS:CG	2.18	0.60
55:v:33:LEU:HD13	55:v:88:ILE:HG21	1.82	0.60
54:d:162:LYS:HB3	54:d:183:TRP:HH2	1.62	0.60
26:V:152:LEU:HD12	26:V:154:ASP:H	1.67	0.60
50:u:106:GLU:CB	53:w:138:TRP:CH2	2.85	0.60
52:a:465:G:N1	52:a:481:A:OP2	2.33	0.60
31:A:721:U:H3	31:A:732:A:N6	1.99	0.60
33:b:6:TRP:HB3	33:b:220:LYS:HZ1	1.66	0.60
55:v:42:VAL:HG11	55:v:68:VAL:HG11	1.83	0.60
22:R:110:MET:HE2	23:S:234:THR:H	1.67	0.60
35:e:276:LEU:HD11	35:e:280:ARG:HH11	1.67	0.60
40:j:103:LEU:O	40:j:164:GLN:HA	2.01	0.60
9:C:137:ILE:HG21	9:C:186:ALA:HB1	1.84	0.60
15:K:123:ILE:HG12	15:K:246:ILE:HG23	1.84	0.60
31:A:903:G:O2'	31:A:904:U:H5'	2.02	0.60
34:c:67:LYS:HG2	34:c:72:ILE:HG12	1.82	0.60
50:u:98:ARG:HB2	53:w:168:ASN:CB	2.31	0.60
52:a:1209:A:N6	52:a:1222:G:O2'	2.35	0.60
9:C:131:MET:HE1	9:C:137:ILE:HD11	1.84	0.60
12:F:92:GLY:HA3	31:A:2323:C:H42	1.67	0.60
31:A:904:U:O5'	31:A:904:U:H6	1.83	0.60
50:u:107:VAL:N	53:w:138:TRP:CZ3	2.70	0.60
58:8:304:LEU:HD13	58:8:306:PRO:HD3	1.82	0.60
28:X:142:ILE:HG22	28:X:143:GLN:HG3	1.84	0.60
31:A:899:A:H2'	31:A:900:G:C8	2.37	0.60
52:a:306:C:H2'	52:a:307:A:H8	1.66	0.60
31:A:1133:U:H2'	31:A:1134:G:H8	1.67	0.59
42:l:68:PRO:O	42:l:99:ARG:NH2	2.35	0.59
43:m:56:ASN:O	43:m:60:VAL:N	2.35	0.59
47:r:51:VAL:CG1	53:w:146:GLU:O	2.47	0.59
3:3:127:ARG:NH2	31:A:478:A:OP1	2.35	0.59
19:O:17:ILE:HD12	31:A:2707:A:H4'	1.84	0.59
21:Q:151:ILE:HB	21:Q:165:TYR:HB2	1.84	0.59
35:e:263:GLU:OE1	54:d:191:LEU:HD12	2.02	0.59
58:8:268:VAL:HG21	58:8:305:GLN:HB3	1.84	0.59
12:F:167:PHE:CD2	43:m:101:ARG:NH1	2.71	0.59
10:D:200:SER:HA	10:D:259:THR:O	2.02	0.59
31:A:890:G:C2'	31:A:891:G:H5'	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l:5:LYS:O	42:l:9:ARG:NH1	2.35	0.59
52:a:141:U:H2'	52:a:142:G:H8	1.67	0.59
53:w:136:ASP:CB	53:w:139:GLU:HG2	2.20	0.59
19:O:60:LYS:O	19:O:64:LEU:HB2	2.03	0.59
43:m:135:ARG:NH2	52:a:898:A:N7	2.39	0.59
11:E:86:ARG:NH2	31:A:670:A:N3	2.45	0.59
39:i:166:LYS:NZ	52:a:1126:G:OP2	2.32	0.59
52:a:437:C:OP1	54:d:114:ARG:NH1	2.35	0.59
10:D:227:LYS:HB3	31:A:2596:C:H4'	1.84	0.59
22:R:92:LEU:O	23:S:133:GLN:NE2	2.36	0.59
31:A:897:A:H2'	43:m:122:GLY:C	2.26	0.59
54:d:89:MET:CE	54:d:178:ILE:HG12	2.33	0.59
54:d:188:ILE:HG22	54:d:189:ASN:N	2.18	0.59
35:e:239:ARG:HD3	35:e:240:PRO:HD2	1.83	0.59
53:w:114:LEU:HD22	53:w:141:LEU:HG	1.83	0.59
31:A:313:A:N1	31:A:323:G:O6	2.36	0.59
31:A:1926:A:O2'	52:a:1443:G:H2'	2.02	0.59
33:b:79:LYS:HE2	58:8:317:HIS:O	2.03	0.59
34:c:25:GLN:O	34:c:29:TYR:N	2.35	0.59
40:j:155:ARG:NH2	52:a:924:A:N1	2.51	0.59
42:l:17:ASN:ND2	52:a:504:C:OP2	2.36	0.59
29:Y:87:ARG:NH1	31:A:2095:U:OP1	2.36	0.59
35:e:225:HIS:HE1	35:e:290:ARG:H	1.50	0.59
42:l:71:GLY:O	42:l:99:ARG:NH1	2.36	0.59
46:q:62:GLN:HA	46:q:112:VAL:O	2.03	0.59
52:a:1203:G:H2'	52:a:1227:A:H61	1.68	0.59
9:C:133:LEU:CD2	36:f:159:LYS:CE	2.65	0.58
12:F:116:GLN:HE21	12:F:148:LEU:HD21	1.68	0.58
31:A:525:A:N3	31:A:591:C:O2'	2.35	0.58
31:A:984:G:H2'	31:A:985:A:H2'	1.85	0.58
33:b:202:ILE:HD11	38:h:67:ARG:HH21	1.67	0.58
43:m:121:ARG:NH2	52:a:1256:U:O3'	2.36	0.58
24:T:47:ARG:HA	24:T:50:ILE:HG22	1.86	0.58
38:h:81:ARG:NH2	38:h:83:SER:O	2.31	0.58
40:j:102:LYS:O	40:j:191:VAL:HA	2.03	0.58
46:q:66:ILE:HD12	46:q:75:ASN:HB3	1.86	0.58
49:t:99:GLU:OE1	49:t:145:LYS:NZ	2.35	0.58
50:u:98:ARG:HB2	53:w:168:ASN:OD1	2.04	0.58
55:v:155:ARG:HG2	55:v:162:SER:HA	1.84	0.58
9:C:142:ILE:HA	9:C:180:ILE:HD11	1.85	0.58
22:R:16:LYS:NZ	31:A:1248:G:N7	2.48	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:33:ARG:O	31:A:1273:G:N2	2.36	0.58
31:A:17:C:O2'	31:A:564:U:OP1	2.21	0.58
31:A:1789:U:OP2	31:A:1794:A:N6	2.36	0.58
37:g:28:ASN:OD1	37:g:36:LYS:NZ	2.36	0.58
43:m:58:LYS:NZ	52:a:1215:C:O2	2.37	0.58
54:d:19:PRO:CD	54:d:186:LEU:CD1	2.81	0.58
57:x:90:ILE:CG2	57:x:91:PHE:H	1.91	0.58
3:3:140:ASN:ND2	31:A:125:A:OP2	2.36	0.58
18:N:39:PRO:HB3	18:N:99:PRO:HD3	1.85	0.58
33:b:20:PHE:HZ	58:8:291:GLN:HE22	1.52	0.58
35:e:246:GLY:CA	54:d:191:LEU:HD22	2.32	0.58
50:u:99:LEU:N	53:w:171:GLN:OE1	2.24	0.58
53:w:158:ILE:HG22	53:w:162:GLN:HE21	1.67	0.58
55:v:83:LEU:HD23	55:v:95:VAL:HG21	1.85	0.58
3:3:125:LYS:HE2	31:A:164:A:H5''	1.86	0.58
31:A:2456:A:N6	31:A:2602:U:OP1	2.37	0.58
32:0:96:LYS:HG3	52:a:1260:G:OP2	2.03	0.58
32:0:101:TYR:CB	48:s:7:LYS:O	2.52	0.58
33:b:77:LYS:O	58:8:319:ARG:NH1	2.37	0.58
35:e:246:GLY:C	54:d:195:GLU:OE1	2.42	0.58
55:v:123:LYS:HE2	55:v:167:PHE:HD2	1.55	0.58
55:v:125:TYR:HD2	55:v:167:PHE:CE2	2.21	0.58
11:E:126:ARG:HH21	31:A:1278:U:H5''	1.68	0.58
17:M:138:ARG:NH2	31:A:235:G:O2'	2.37	0.58
31:A:897:A:C8	43:m:122:GLY:HA3	2.39	0.58
52:a:127:A:N1	52:a:191:G:O6	2.36	0.58
4:4:150:LEU:HD22	4:4:153:LEU:HG	1.86	0.58
12:F:68:LEU:O	12:F:72:GLU:HB2	2.03	0.58
14:H:43:LYS:HG2	14:H:44:LYS:HG2	1.85	0.58
16:L:23:ARG:NH1	31:A:2579:U:O2'	2.37	0.58
31:A:1296:A:OP2	31:A:1682:C:N4	2.37	0.58
39:i:176:ARG:NH1	52:a:1321:U:OP2	2.35	0.58
10:D:240:THR:HG23	31:A:2046:G:H21	1.69	0.57
31:A:1291:C:H5''	31:A:1292:G:H5'	1.86	0.57
39:i:106:GLN:NE2	52:a:1238:C:O2	2.35	0.57
40:j:98:LYS:N	40:j:170:LEU:O	2.37	0.57
52:a:455:C:H3'	52:a:456:U:H2'	1.85	0.57
56:n:17:GLU:O	56:n:21:HIS:HB2	2.04	0.57
31:A:2707:A:H62	31:A:2737:G:H21	1.51	0.57
32:0:100:LYS:HD3	52:a:1260:G:H5''	1.85	0.57
53:w:119:PRO:HG2	53:w:121:HIS:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:34:ILE:HG12	31:A:2303:A:H61	1.68	0.57
21:Q:160:ARG:HH12	52:a:317:G:C1'	1.96	0.57
25:U:162:VAL:HG12	25:U:176:ILE:HG22	1.86	0.57
31:A:1393:U:O2'	31:A:2230:A:N3	2.37	0.57
39:i:173:ARG:NH2	52:a:1067:U:OP1	2.37	0.57
50:u:103:PHE:CE2	53:w:138:TRP:HB3	2.32	0.57
54:d:165:THR:O	54:d:173:GLY:HA2	2.04	0.57
58:8:316:SER:HB3	58:8:325:SER:HB2	1.86	0.57
26:V:85:LYS:HD3	26:V:104:LEU:HD13	1.87	0.57
43:m:61:GLU:HB3	57:x:85:PRO:HB2	1.85	0.57
49:t:89:ARG:NH2	52:a:293:C:O2	2.36	0.57
52:a:542:U:N3	52:a:594:C:O2	2.38	0.57
4:4:114:ARG:HE	4:4:132:LEU:HD23	1.69	0.57
36:f:121:ASP:HA	36:f:124:LEU:HB2	1.86	0.57
29:Y:102:ASN:HB3	31:A:2247:C:H1'	1.85	0.57
30:Z:110:LYS:NZ	31:A:75:C:OP1	2.38	0.57
50:u:106:GLU:C	53:w:138:TRP:HH2	2.10	0.57
52:a:605:U:H2'	52:a:606:A:H8	1.69	0.57
12:F:107:ILE:O	12:F:111:ALA:CB	2.53	0.57
47:r:50:ARG:HH22	50:u:138:LYS:HD3	1.69	0.57
50:u:119:ARG:NH1	50:u:120:ARG:O	2.37	0.57
52:a:600:U:O4	52:a:700:G:O2'	2.21	0.57
54:d:190:GLU:O	54:d:194:VAL:HG23	2.04	0.57
14:H:55:GLU:OE1	14:H:83:LYS:NZ	2.37	0.57
26:V:107:LYS:HB2	26:V:125:ILE:O	2.05	0.57
40:j:142:TYR:O	40:j:157:HIS:HA	2.05	0.57
52:a:400:U:OP2	54:d:13:ARG:NH1	2.38	0.57
3:3:127:ARG:NH1	3:3:134:ILE:O	2.37	0.57
6:6:106:MET:O	6:6:110:LYS:HB2	2.04	0.57
9:C:206:SER:HA	9:C:209:TRP:HD1	1.69	0.57
21:Q:143:ILE:HD11	21:Q:206:ILE:HD13	1.87	0.57
27:W:52:G:N2	27:W:71:C:O2'	2.37	0.57
31:A:318:A:N3	31:A:338:G:O2'	2.36	0.57
31:A:1130:C:H2'	31:A:1131:A:H8	1.68	0.57
31:A:2705:G:OP1	31:A:2731:C:N4	2.38	0.57
32:0:100:LYS:HD3	52:a:1260:G:H5'	1.85	0.57
52:a:895:A:H2'	52:a:896:G:H8	1.69	0.57
53:w:142:LYS:O	53:w:146:GLU:HG3	2.05	0.57
6:6:123:ARG:NH2	31:A:1405:A:OP2	2.37	0.57
22:R:11:ARG:O	22:R:15:LYS:HB2	2.05	0.57
31:A:1103:C:C4	31:A:1104:C:N4	2.73	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:u:104:ARG:C	53:w:138:TRP:CH2	2.83	0.57
11:E:99:THR:OG1	31:A:454:G:N3	2.38	0.56
20:P:152:VAL:HA	20:P:155:LEU:HB3	1.85	0.56
21:Q:124:GLY:O	21:Q:128:LYS:HB2	2.05	0.56
23:S:197:VAL:HG23	23:S:210:ILE:HG13	1.85	0.56
38:h:67:ARG:HD3	58:8:67:CYS:C	2.30	0.56
11:E:204:LYS:HA	11:E:225:THR:HB	1.87	0.56
20:P:64:VAL:HG11	20:P:142:ASP:HB3	1.87	0.56
31:A:1111:G:N2	31:A:1114:A:OP2	2.38	0.56
33:b:25:ARG:NH1	52:a:798:U:OP1	2.38	0.56
34:c:48:GLN:O	34:c:52:LYS:HB2	2.05	0.56
41:k:131:ARG:HH21	50:u:120:ARG:HH11	1.53	0.56
43:m:80:LEU:HD23	43:m:83:ASN:HD22	1.70	0.56
51:y:131:ARG:NH1	51:y:147:GLU:OE1	2.39	0.56
54:d:50:GLU:CD	54:d:188:ILE:HG23	2.30	0.56
11:E:253:GLN:O	11:E:257:GLN:HB2	2.05	0.56
38:h:83:SER:HB2	38:h:89:ILE:HG22	1.87	0.56
42:l:54:ARG:HA	42:l:64:THR:HA	1.85	0.56
52:a:989:G:H2'	52:a:990:G:H8	1.70	0.56
52:a:1187:A:H61	52:a:1244:C:H2'	1.71	0.56
52:a:1427:U:H2'	52:a:1428:A:H8	1.71	0.56
53:w:105:TRP:HD1	53:w:170:TRP:HD1	1.52	0.56
55:v:121:PRO:HB3	55:v:197:LYS:HD2	1.87	0.56
55:v:124:VAL:HG12	55:v:195:VAL:CG2	2.33	0.56
58:8:262:SER:OG	58:8:281:GLY:O	2.22	0.56
11:E:222:ASN:ND2	31:A:329:C:O2'	2.36	0.56
19:O:27:ARG:NH1	31:A:2707:A:OP2	2.38	0.56
31:A:1020:C:H2'	31:A:1021:A:H8	1.70	0.56
31:A:1573:C:H2'	31:A:1574:G:H8	1.71	0.56
33:b:122:ARG:NH2	33:b:125:GLN:OE1	2.39	0.56
34:c:39:ILE:HD12	34:c:99:VAL:HG13	1.88	0.56
36:f:200:ARG:NH1	52:a:622:G:OP1	2.37	0.56
50:u:103:PHE:HD1	53:w:138:TRP:HD1	1.20	0.56
10:D:235:ILE:O	10:D:248:LYS:NZ	2.37	0.56
12:F:89:VAL:HG22	12:F:207:VAL:HG22	1.88	0.56
21:Q:226:LEU:HD11	52:a:1380:C:O3'	2.05	0.56
31:A:898:G:H1	43:m:121:ARG:CB	2.16	0.56
34:c:134:GLN:HE21	34:c:139:VAL:HG11	1.71	0.56
38:h:50:LYS:HA	38:h:58:PHE:O	2.05	0.56
48:s:40:ILE:HG21	48:s:67:VAL:HA	1.86	0.56
58:8:366:MET:N	58:8:366:MET:SD	2.78	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2599:G:OP2	31:A:2600:G:N2	2.38	0.56
48:s:18:LYS:HE3	48:s:31:ILE:HB	1.88	0.56
52:a:877:G:O2'	52:a:1482:C:OP1	2.24	0.56
52:a:1237:A:H5''	52:a:1238:C:H5	1.70	0.56
54:d:114:ARG:HB3	54:d:122:ILE:HD11	1.87	0.56
58:8:320:GLU:OE1	58:8:323:ARG:NH2	2.35	0.56
10:D:275:VAL:HG11	21:Q:126:LEU:HD11	1.86	0.56
31:A:2707:A:N6	31:A:2737:G:H21	2.03	0.56
43:m:113:ARG:HH21	48:s:65:ARG:HG3	1.71	0.56
52:a:490:A:OP1	54:d:10:LYS:NZ	2.37	0.56
16:L:97:ARG:HH12	52:a:309:A:H5''	1.70	0.56
22:R:49:ASP:OD1	22:R:52:ARG:NH1	2.38	0.56
33:b:202:ILE:HG12	58:8:66:ARG:HG2	1.88	0.56
34:c:105:CYS:SG	34:c:106:VAL:N	2.79	0.56
35:e:154:GLU:OE2	35:e:209:ARG:NH2	2.39	0.56
54:d:162:LYS:CG	54:d:183:TRP:CZ2	2.88	0.56
40:j:112:GLU:O	40:j:116:LYS:HB2	2.06	0.56
31:A:309:A:N1	31:A:331:A:O2'	2.37	0.56
33:b:178:ARG:NH1	52:a:1025:C:OP1	2.39	0.56
11:E:79:LYS:NZ	31:A:609:G:OP1	2.39	0.55
23:S:204:LYS:HG2	31:A:1001:A:H5'	1.88	0.55
33:b:76:THR:H	33:b:168:VAL:HG21	1.71	0.55
35:e:177:ILE:HG12	35:e:191:VAL:HG12	1.87	0.55
35:e:233:ALA:HB2	52:a:813:A:H5'	1.87	0.55
45:p:54:LEU:O	45:p:58:GLU:HB2	2.06	0.55
51:y:80:GLN:HB2	51:y:115:ARG:HA	1.87	0.55
52:a:1412:U:H2'	52:a:1413:G:H8	1.71	0.55
53:w:114:LEU:HD21	53:w:145:LEU:HD21	1.88	0.55
54:d:180:ASP:O	54:d:183:TRP:HB2	2.05	0.55
12:F:208:CYS:SG	31:A:2320:G:N2	2.80	0.55
22:R:5:LYS:NZ	31:A:1219:U:O2	2.37	0.55
25:U:109:LEU:HB2	25:U:146:MET:HE1	1.88	0.55
31:A:897:A:C2'	43:m:122:GLY:C	2.79	0.55
47:r:51:VAL:CA	53:w:147:ASN:HA	2.32	0.55
52:a:243:C:H2'	52:a:244:A:H8	1.72	0.55
1:1:34:LEU:HD23	24:T:67:LEU:HD21	1.88	0.55
33:b:7:ASN:HB2	58:8:345:VAL:HG13	1.86	0.55
38:h:68:ASN:CG	58:8:70:ALA:HB2	2.31	0.55
52:a:1362:A:N1	52:a:1436:G:O6	2.39	0.55
53:w:105:TRP:CD1	53:w:170:TRP:HD1	2.24	0.55
11:E:105:ARG:NH2	31:A:685:G:OP1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:51:ALA:HA	19:O:123:ILE:HD11	1.89	0.55
35:e:246:GLY:C	54:d:195:GLU:HG2	2.31	0.55
38:h:67:ARG:CG	58:8:67:CYS:HA	2.36	0.55
52:a:1486:U:H2'	52:a:1487:C:C6	2.42	0.55
53:w:113:ALA:HA	53:w:128:PRO:O	2.06	0.55
10:D:210:GLY:HA2	10:D:251:PRO:HB3	1.88	0.55
23:S:128:VAL:HG22	23:S:133:GLN:HG2	1.89	0.55
31:A:1096:G:N2	31:A:1123:A:O2'	2.39	0.55
33:b:6:TRP:H	58:8:348:LYS:HG2	1.70	0.55
44:o:51:ARG:NH2	52:a:676:A:N7	2.53	0.55
49:t:154:ALA:HA	49:t:157:LYS:HB2	1.88	0.55
52:a:347:G:H1	52:a:358:U:H3	1.55	0.55
54:d:137:MET:SD	54:d:172:LYS:NZ	2.80	0.55
6:6:123:ARG:HH22	31:A:1404:C:H3'	1.72	0.55
16:L:61:VAL:O	16:L:84:ALA:HA	2.06	0.55
23:S:146:ARG:NH1	31:A:1189:G:OP1	2.39	0.55
31:A:423:G:OP2	31:A:2423:A:O2'	2.24	0.55
31:A:1041:G:H1	31:A:1176:C:H42	1.55	0.55
33:b:99:LYS:NZ	52:a:1048:G:OP1	2.40	0.55
52:a:1363:U:H2'	52:a:1364:G:H8	1.70	0.55
52:a:1393:U:H3	52:a:1407:G:H1	1.53	0.55
54:d:2:SER:OG	54:d:3:ARG:N	2.40	0.55
58:8:291:GLN:CD	58:8:327:SER:HB2	2.31	0.55
11:E:168:ALA:HB1	11:E:245:LEU:HD11	1.89	0.55
26:V:76:LYS:HB2	26:V:137:ILE:HD11	1.89	0.55
28:X:123:VAL:HA	28:X:136:SER:O	2.06	0.55
31:A:641:C:O2	31:A:651:U:O2'	2.25	0.55
31:A:1343:A:N1	31:A:1354:C:O2'	2.38	0.55
38:h:67:ARG:CZ	58:8:68:ARG:N	2.68	0.55
52:a:962:G:N7	52:a:966:G:N1	2.55	0.55
53:w:130:TYR:HD2	53:w:140:GLU:OE2	1.88	0.55
19:O:37:GLN:HE22	31:A:1298:A:H2	1.55	0.55
22:R:3:ARG:N	31:A:1269:G:N7	2.55	0.55
22:R:25:ARG:HH22	31:A:2035:A:H5'	1.71	0.55
31:A:542:C:OP1	31:A:571:G:N1	2.39	0.55
31:A:1801:A:N6	31:A:1838:G:O2'	2.36	0.55
11:E:119:LYS:NZ	31:A:2461:A:OP2	2.40	0.55
20:P:100:THR:O	20:P:104:ALA:HB2	2.06	0.55
29:Y:107:ARG:HG2	29:Y:116:PHE:HB3	1.89	0.55
31:A:1934:C:OP1	52:a:1466:G:N9	2.34	0.55
34:c:143:LYS:O	34:c:147:LYS:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:p:6:LEU:HA	45:p:18:ARG:O	2.06	0.55
48:s:36:ARG:HD3	48:s:72:GLY:HA3	1.88	0.55
51:y:169:ARG:NH1	52:a:1447:U:OP2	2.39	0.55
52:a:376:U:OP2	54:d:3:ARG:NE	2.38	0.55
55:v:125:TYR:HD2	55:v:167:PHE:CZ	2.25	0.55
3:3:127:ARG:HE	3:3:132:ARG:HG3	1.72	0.55
16:L:6:THR:OG1	16:L:21:CYS:SG	2.65	0.55
31:A:896:G:C6	48:s:76:PRO:HG3	2.41	0.55
31:A:1155:A:N7	31:A:2505:A:O2'	2.39	0.55
31:A:2300:U:O2	31:A:2342:G:O6	2.24	0.55
33:b:20:PHE:CE1	58:8:329:LYS:HG2	2.42	0.55
54:d:139:ARG:HB3	54:d:142:GLN:HG2	1.88	0.55
54:d:180:ASP:HB3	54:d:183:TRP:CD1	2.42	0.55
55:v:31:ARG:HB2	55:v:61:ARG:HG2	1.89	0.55
55:v:183:LEU:O	55:v:186:SER:HB2	2.06	0.55
31:A:709:C:O2'	31:A:745:A:N6	2.38	0.54
31:A:902:G:H2'	31:A:903:G:H5'	1.88	0.54
33:b:40:LYS:HD3	58:8:290:SER:HA	1.89	0.54
43:m:107:ASN:HA	43:m:110:ALA:HB3	1.88	0.54
16:L:34:ARG:NH1	31:A:2690:G:OP1	2.41	0.54
23:S:214:GLN:HE21	31:A:1021:A:H1'	1.72	0.54
31:A:1793:A:H1'	31:A:2624:G:H21	1.72	0.54
31:A:2612:G:N2	31:A:2615:A:OP2	2.36	0.54
46:q:81:LEU:HD13	46:q:90:ARG:HD2	1.88	0.54
54:d:19:PRO:HG2	54:d:186:LEU:HD13	1.83	0.54
58:8:365:ALA:C	58:8:366:MET:O	2.50	0.54
16:L:31:ARG:HH11	31:A:2009:U:H1'	1.70	0.54
21:Q:174:ASN:HA	21:Q:179:THR:HA	1.89	0.54
26:V:105:ASN:OD1	26:V:107:LYS:NZ	2.39	0.54
31:A:2464:G:N2	31:A:2467:A:N7	2.53	0.54
33:b:165:VAL:HB	33:b:187:THR:HG22	1.89	0.54
55:v:124:VAL:HB	55:v:168:VAL:HG12	1.87	0.54
5:5:6:SER:HB3	31:A:2483:C:H5''	1.89	0.54
9:C:256:ARG:HE	9:C:260:LYS:HD3	1.72	0.54
23:S:139:GLY:H	23:S:221:ILE:HB	1.72	0.54
28:X:70:ARG:NH1	31:A:2274:A:O2'	2.41	0.54
35:e:175:ARG:HA	35:e:192:GLY:O	2.07	0.54
44:o:69:LYS:NZ	52:a:702:C:OP1	2.40	0.54
52:a:833:U:H4'	52:a:834:G:H5''	1.89	0.54
52:a:960:U:C4	52:a:961:U:O4	2.60	0.54
38:h:109:SER:OG	52:a:590:A:N3	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:127:GLY:O	55:v:194:ARG:N	2.36	0.54
7:7:74:ARG:NH1	31:A:1177:U:O4	2.40	0.54
33:b:79:LYS:HZ2	58:8:316:SER:C	2.15	0.54
41:k:33:GLN:HB3	41:k:40:ILE:HB	1.88	0.54
43:m:99:ILE:HA	43:m:102:LYS:HG2	1.88	0.54
51:y:101:SER:O	51:y:165:GLN:NE2	2.41	0.54
52:a:1479:G:H2'	52:a:1480:A:C8	2.42	0.54
58:8:280:ILE:HG23	58:8:283:ILE:HG12	1.90	0.54
18:N:124:LYS:NZ	31:A:2500:C:N3	2.48	0.54
20:P:61:ARG:NH2	20:P:89:ASP:OD1	2.41	0.54
33:b:201:ASP:CG	58:8:66:ARG:CD	2.78	0.54
35:e:227:ASN:ND2	35:e:285:ALA:O	2.40	0.54
38:h:12:CYS:O	38:h:16:ALA:HB2	2.08	0.54
55:v:64:ARG:HH11	55:v:91:ARG:HH22	1.54	0.54
56:n:34:VAL:HA	56:n:41:TRP:CH2	2.43	0.54
15:K:219:ASN:O	15:K:222:LYS:NZ	2.41	0.54
36:f:115:ARG:HE	36:f:117:ASP:HB2	1.72	0.54
43:m:106:PHE:HA	43:m:109:VAL:HB	1.90	0.54
54:d:135:THR:HA	54:d:174:LEU:HG	1.90	0.54
16:L:24:ILE:HG22	16:L:39:ILE:HG22	1.90	0.54
33:b:187:THR:N	58:8:66:ARG:HH22	2.04	0.54
52:a:327:A:N3	52:a:339:U:O2'	2.35	0.54
32:O:100:LYS:CB	52:a:1260:G:H5'	2.37	0.54
35:e:304:GLU:OE2	38:h:118:ARG:NE	2.30	0.54
16:L:24:ILE:HG21	16:L:33:ALA:HB2	1.89	0.53
20:P:75:VAL:HA	20:P:83:TYR:O	2.08	0.53
34:c:42:CYS:O	34:c:46:TYR:HB2	2.09	0.53
52:a:932:A:OP1	56:n:3:ARG:NH2	2.41	0.53
53:w:111:GLY:HA3	53:w:129:TYR:CE1	2.43	0.53
11:E:207:PHE:HB2	11:E:246:VAL:HG22	1.91	0.53
15:K:58:THR:O	15:K:62:ARG:HB2	2.07	0.53
19:O:19:ARG:NH1	31:A:1689:C:O2'	2.41	0.53
24:T:57:SER:HA	24:T:99:ILE:HA	1.90	0.53
26:V:114:LYS:HD3	26:V:118:GLU:HB2	1.89	0.53
31:A:596:A:N1	31:A:820:G:O2'	2.40	0.53
31:A:897:A:C6	43:m:119:CYS:SG	2.98	0.53
33:b:107:ASN:ND2	52:a:1022:U:O2	2.40	0.53
35:e:153:GLU:OE1	35:e:183:LYS:NZ	2.41	0.53
50:u:96:GLU:HB3	53:w:172:GLN:OE1	2.07	0.53
52:a:347:G:O6	52:a:358:U:O4	2.26	0.53
53:w:123:THR:HG22	53:w:125:PRO:HD3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:77:ASN:ND2	31:A:1040:U:OP1	2.41	0.53
31:A:579:U:O2'	31:A:1011:A:N1	2.40	0.53
33:b:20:PHE:HB2	58:8:329:LYS:HE3	1.91	0.53
10:D:142:GLU:OE1	10:D:166:ARG:NH2	2.38	0.53
31:A:1379:C:N4	31:A:1393:U:OP2	2.41	0.53
31:A:2300:U:O2	31:A:2342:G:C6	2.61	0.53
33:b:90:ARG:HH12	58:8:359:ARG:HA	1.73	0.53
34:c:8:LEU:HD13	34:c:195:TYR:HD1	1.73	0.53
34:c:171:LYS:HE3	34:c:175:ARG:HH22	1.74	0.53
46:q:75:ASN:HA	46:q:97:TYR:O	2.08	0.53
8:B:10:G:O5'	20:P:61:ARG:NH1	2.41	0.53
12:F:87:ILE:HA	12:F:208:CYS:O	2.08	0.53
18:N:46:GLN:NE2	31:A:2502:G:OP1	2.41	0.53
31:A:259:C:H42	31:A:268:G:H1	1.56	0.53
33:b:5:TYR:CZ	58:8:344:LEU:HD11	2.43	0.53
33:b:7:ASN:HD22	58:8:345:VAL:CA	2.21	0.53
38:h:68:ASN:ND2	58:8:70:ALA:HB2	2.23	0.53
47:r:57:LYS:HZ1	52:a:611:A:H5''	1.73	0.53
48:s:18:LYS:NZ	48:s:31:ILE:O	2.38	0.53
50:u:106:GLU:CA	53:w:138:TRP:HH2	2.08	0.53
51:y:115:ARG:NH1	51:y:133:GLU:OE1	2.41	0.53
52:a:35:C:H2'	52:a:36:G:H8	1.73	0.53
14:H:47:LYS:NZ	31:A:412:G:OP2	2.37	0.53
19:O:73:ARG:HH21	31:A:1475:U:H4'	1.73	0.53
26:V:89:ILE:HG22	26:V:101:ILE:HG22	1.91	0.53
31:A:309:A:N3	31:A:328:C:O2'	2.40	0.53
33:b:91:ALA:HB2	33:b:222:VAL:HG13	1.89	0.53
35:e:173:ARG:NH2	52:a:1030:G:OP2	2.42	0.53
38:h:67:ARG:HG3	38:h:68:ASN:N	2.23	0.53
42:l:101:THR:OG1	42:l:102:LEU:N	2.42	0.53
43:m:135:ARG:NH1	52:a:898:A:OP2	2.39	0.53
50:u:127:GLU:O	50:u:131:ARG:CB	2.56	0.53
55:v:28:ASN:HA	55:v:64:ARG:HB3	1.90	0.53
55:v:121:PRO:O	55:v:176:VAL:HG11	2.08	0.53
3:3:133:LYS:HE3	31:A:471:U:H5''	1.91	0.53
9:C:152:ARG:HG2	31:A:1828:U:H2'	1.91	0.53
10:D:93:MET:HE1	10:D:169:GLN:HB2	1.91	0.53
38:h:67:ARG:HH12	58:8:65:GLU:C	2.16	0.53
43:m:57:HIS:N	52:a:1277:A:OP1	2.31	0.53
52:a:1234:A:H2'	52:a:1235:A:H4'	1.90	0.53
2:2:24:ASN:HB2	2:2:27:SER:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:181:SER:OG	9:C:184:CYS:SG	2.67	0.53
12:F:87:ILE:HG22	12:F:209:ILE:HA	1.90	0.53
19:O:44:ILE:HG22	19:O:123:ILE:HB	1.91	0.53
21:Q:122:ILE:HA	21:Q:125:ILE:HG22	1.91	0.53
22:R:10:ALA:O	22:R:14:ARG:HB2	2.09	0.53
31:A:897:A:N3	43:m:123:ILE:CG1	2.71	0.53
31:A:1533:A:N3	31:A:1611:G:O2'	2.42	0.53
37:g:15:ASP:H	37:g:20:ASN:H	1.57	0.53
40:j:100:ARG:HH12	52:a:1074:U:H4'	1.74	0.53
50:u:115:GLU:OE2	50:u:130:LYS:NZ	2.35	0.53
55:v:23:ARG:HB2	55:v:98:THR:HG23	1.90	0.53
1:1:16:ARG:NH2	31:A:2633:C:OP1	2.42	0.53
23:S:148:LYS:HB2	31:A:1189:G:H5'	1.89	0.53
24:T:90:ASN:ND2	31:A:506:G:O2'	2.42	0.53
31:A:724:G:H21	31:A:729:A:H62	1.56	0.53
31:A:763:A:OP2	31:A:1791:C:N4	2.42	0.53
32:0:87:LEU:CB	43:m:105:ARG:HH21	1.79	0.53
33:b:60:LEU:HD22	58:8:65:GLU:CD	2.34	0.53
35:e:236:VAL:HG11	35:e:282:THR:HG22	1.91	0.53
52:a:567:U:H3	54:d:124:ASP:HB2	1.74	0.53
9:C:103:PRO:HA	9:C:191:VAL:HA	1.90	0.53
11:E:69:PHE:O	11:E:256:ASN:ND2	2.39	0.53
16:L:104:ARG:NH1	16:L:121:LEU:O	2.42	0.53
29:Y:115:ARG:HH12	29:Y:145:LEU:HD21	1.73	0.53
35:e:222:THR:HB	35:e:264:ASN:HB2	1.90	0.53
36:f:129:LYS:NZ	36:f:191:ALA:O	2.41	0.53
48:s:55:ARG:NH1	48:s:79:ASN:OD1	2.42	0.53
52:a:493:C:OP2	54:d:55:ARG:NH1	2.37	0.53
53:w:119:PRO:HD3	53:w:150:TRP:HB3	1.90	0.53
13:G:63:LEU:HB2	13:G:76:TYR:HE1	1.73	0.52
31:A:1836:C:O2'	31:A:1985:A:OP2	2.27	0.52
32:0:94:VAL:HG22	48:s:67:VAL:HG12	1.91	0.52
43:m:65:GLN:NE2	57:x:86:PRO:N	2.56	0.52
50:u:103:PHE:CA	53:w:138:TRP:CD1	2.90	0.52
52:a:685:U:H2'	52:a:686:G:H8	1.74	0.52
55:v:180:ILE:HD11	55:v:197:LYS:HB3	1.90	0.52
28:X:97:ARG:HH22	31:A:2279:U:H5''	1.72	0.52
31:A:88:A:H3'	31:A:89:A:H2'	1.91	0.52
31:A:845:C:H2'	31:A:846:A:H8	1.74	0.52
31:A:1117:G:N2	31:A:1118:U:O4	2.42	0.52
41:k:96:LYS:HG3	41:k:123:THR:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:a:928:C:H42	56:n:57:ALA:HB1	1.74	0.52
56:n:40:LYS:C	56:n:41:TRP:CG	2.87	0.52
9:C:141:GLU:HB2	9:C:184:CYS:HB3	1.92	0.52
31:A:726:G:C8	44:o:57:LEU:HD21	2.45	0.52
31:A:1615:G:H2'	31:A:1616:A:H8	1.73	0.52
33:b:13:MET:HE1	33:b:51:ALA:HB2	1.90	0.52
34:c:86:GLU:HB3	34:c:90:GLN:HB2	1.91	0.52
38:h:67:ARG:HG3	38:h:68:ASN:H	1.73	0.52
52:a:1444:U:H2'	52:a:1445:C:C6	2.45	0.52
6:6:140:LYS:HE2	31:A:1461:G:H5'	1.90	0.52
10:D:99:MET:HG2	10:D:113:THR:HG22	1.92	0.52
21:Q:170:ILE:HG23	21:Q:219:LEU:HB2	1.92	0.52
25:U:144:LYS:NZ	25:U:162:VAL:O	2.43	0.52
31:A:656:A:H61	31:A:2366:G:H21	1.55	0.52
33:b:94:HIS:HB2	33:b:155:ILE:HG22	1.91	0.52
33:b:211:ILE:HG13	58:8:317:HIS:NE2	2.23	0.52
41:k:134:LYS:HD2	52:a:728:G:H5''	1.92	0.52
52:a:7:G:O2'	52:a:269:A:O4'	2.27	0.52
52:a:772:U:H2'	52:a:773:A:H8	1.74	0.52
52:a:1437:A:H2'	52:a:1438:G:C8	2.44	0.52
2:2:35:THR:O	31:A:2303:A:N6	2.41	0.52
10:D:204:ILE:HG23	10:D:284:GLY:HA2	1.91	0.52
11:E:120:LYS:HA	31:A:2073:A:H4'	1.92	0.52
15:K:99:THR:HA	22:R:99:GLN:HE22	1.73	0.52
24:T:57:SER:OG	24:T:60:GLU:OE1	2.25	0.52
31:A:890:G:H2'	31:A:891:G:H8	1.75	0.52
31:A:2133:A:N6	31:A:2181:U:O2'	2.40	0.52
31:A:2761:U:OP2	31:A:2773:C:N4	2.38	0.52
34:c:81:PRO:HG3	34:c:116:ARG:HG2	1.92	0.52
41:k:48:GLY:O	52:a:631:G:N2	2.43	0.52
44:o:21:SER:HB2	44:o:24:PHE:HD2	1.75	0.52
45:p:28:ARG:NH1	52:a:361:C:O3'	2.43	0.52
52:a:876:G:O2'	52:a:1452:A:N7	2.43	0.52
2:2:15:CYS:O	2:2:31:SER:HA	2.10	0.52
13:G:100:ARG:HG2	13:G:104:MET:HE2	1.90	0.52
15:K:58:THR:O	15:K:62:ARG:CB	2.58	0.52
18:N:71:ASP:OD2	31:A:916:G:N2	2.42	0.52
31:A:182:A:N6	31:A:2447:A:O2'	2.43	0.52
31:A:902:G:C2'	31:A:903:G:H5'	2.40	0.52
32:0:71:GLU:HG3	32:0:72:VAL:HG13	1.92	0.52
37:g:58:PRO:HA	37:g:61:VAL:HG12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:p:28:ARG:NH2	52:a:361:C:O2'	2.36	0.52
50:u:97:GLU:HB2	53:w:172:GLN:HG2	1.90	0.52
52:a:1253:G:OP2	57:x:55:GLY:N	2.43	0.52
56:n:37:LEU:HB2	56:n:41:TRP:HZ2	1.68	0.52
16:L:22:ILE:O	16:L:40:VAL:HB	2.09	0.52
21:Q:144:ARG:HH12	27:W:53:G:H22	1.57	0.52
24:T:79:LEU:HD22	24:T:134:ILE:HD12	1.92	0.52
31:A:901:C:C2'	31:A:902:G:H5''	2.39	0.52
31:A:1886:A:H2'	31:A:1887:G:H8	1.75	0.52
35:e:181:GLY:HA2	35:e:186:GLN:O	2.10	0.52
50:u:111:GLY:HA2	50:u:114:GLN:HG2	1.91	0.52
52:a:1274:U:OP1	57:x:65:LYS:NZ	2.42	0.52
1:l:47:PHE:HZ	19:O:45:LYS:HE2	1.75	0.52
6:6:115:ARG:HH12	31:A:1490:G:H5''	1.74	0.52
9:C:178:ARG:NH1	31:A:1810:C:OP2	2.43	0.52
25:U:112:TYR:HB2	30:Z:84:LYS:HE2	1.91	0.52
31:A:1876:A:H62	31:A:1889:G:H21	1.57	0.52
44:o:30:THR:HG21	44:o:82:LEU:HD13	1.91	0.52
45:p:27:ARG:NH2	52:a:280:A:OP1	2.43	0.52
58:8:363:ALA:O	58:8:364:GLU:HB3	2.09	0.52
8:B:38:C:O2	20:P:149:HIS:NE2	2.42	0.52
15:K:172:LEU:HB2	15:K:174:ARG:HH11	1.75	0.52
20:P:72:ARG:NH1	20:P:142:ASP:OD2	2.41	0.52
31:A:208:A:O2'	31:A:432:G:N3	2.42	0.52
31:A:2495:A:O2'	31:A:2553:G:N2	2.42	0.52
33:b:201:ASP:CG	58:8:66:ARG:HH11	2.18	0.52
45:p:54:LEU:O	45:p:58:GLU:CB	2.57	0.52
55:v:23:ARG:HD2	55:v:98:THR:O	2.10	0.52
58:8:285:GLY:HA2	58:8:324:VAL:O	2.09	0.52
24:T:99:ILE:HD11	24:T:137:ARG:HD3	1.92	0.52
26:V:76:LYS:HE2	26:V:137:ILE:HD11	1.93	0.52
30:Z:135:LYS:O	30:Z:139:ALA:HB2	2.10	0.52
32:0:101:TYR:CE1	48:s:8:ASN:HB2	2.44	0.52
33:b:103:GLY:N	33:b:179:GLU:OE2	2.42	0.52
47:r:81:GLU:OE1	50:u:104:ARG:NH2	2.39	0.52
50:u:107:VAL:CG2	53:w:138:TRP:CZ3	2.67	0.52
52:a:622:G:H2'	52:a:623:A:H8	1.74	0.52
52:a:1136:A:O2'	56:n:97:ARG:NH2	2.31	0.52
55:v:21:ALA:HB3	55:v:73:VAL:HG22	1.92	0.52
7:7:48:SER:OG	7:7:49:SER:N	2.43	0.51
22:R:40:ILE:HG23	23:S:198:PHE:HE2	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:167:ARG:NH1	25:U:171:THR:OG1	2.42	0.51
27:W:61:G:N2	27:W:64:A:OP2	2.44	0.51
31:A:232:G:OP2	31:A:234:C:N4	2.43	0.51
31:A:1462:G:H1	31:A:1584:C:N4	2.05	0.51
31:A:1926:A:O2'	52:a:1443:G:C2'	2.58	0.51
31:A:2107:G:H1	31:A:2210:C:N4	2.04	0.51
35:e:154:GLU:HG3	35:e:180:VAL:HG12	1.91	0.51
49:t:151:ASN:HA	49:t:155:ARG:HH11	1.76	0.51
52:a:808:U:OP2	52:a:818:G:N1	2.43	0.51
54:d:21:LEU:HD23	54:d:104:ILE:HB	1.92	0.51
55:v:88:ILE:HD12	55:v:93:ILE:HD12	1.91	0.51
9:C:64:ARG:NH2	9:C:145:GLY:O	2.43	0.51
11:E:78:GLU:O	17:M:88:GLN:NE2	2.43	0.51
12:F:180:ASN:HB3	31:A:2332:G:H4'	1.92	0.51
19:O:34:LEU:HD23	19:O:54:MET:HE3	1.91	0.51
45:p:32:ASP:OD1	45:p:33:LEU:N	2.43	0.51
55:v:104:GLY:O	55:v:106:ASP:N	2.44	0.51
10:D:199:ILE:O	10:D:260:LYS:HA	2.11	0.51
20:P:87:ILE:HG22	20:P:94:THR:HG22	1.91	0.51
24:T:121:ARG:O	31:A:1650:A:N6	2.44	0.51
26:V:109:LYS:HD3	26:V:125:ILE:HD12	1.91	0.51
27:W:30:A:O2'	27:W:38:G:O2'	2.28	0.51
31:A:1949:G:N2	31:A:1976:C:O2'	2.43	0.51
32:O:96:LYS:HG2	52:a:1259:A:OP1	2.09	0.51
33:b:78:ASN:HA	33:b:81:ALA:HB2	1.91	0.51
33:b:223:PHE:HZ	58:8:359:ARG:HB3	1.76	0.51
47:r:51:VAL:HA	53:w:147:ASN:CA	2.32	0.51
52:a:280:A:H2'	52:a:281:G:H8	1.76	0.51
52:a:1253:G:N2	52:a:1279:G:O2'	2.40	0.51
21:Q:138:ARG:HH12	21:Q:201:PRO:HA	1.75	0.51
31:A:545:U:H2'	31:A:546:G:H8	1.76	0.51
31:A:1391:C:O2'	31:A:1821:G:O2'	2.28	0.51
33:b:79:LYS:CD	58:8:317:HIS:HB2	2.38	0.51
37:g:133:ASP:OD1	37:g:136:ARG:NH2	2.44	0.51
43:m:117:ILE:HG23	43:m:127:LEU:HD13	1.91	0.51
52:a:1166:C:OP1	56:n:9:ARG:NH1	2.43	0.51
52:a:1371:G:H1	52:a:1427:U:H3	1.59	0.51
8:B:81:U:O2'	31:A:927:A:N3	2.42	0.51
19:O:43:ARG:HA	19:O:123:ILE:O	2.10	0.51
19:O:77:LEU:HD11	19:O:83:LYS:HD2	1.91	0.51
20:P:128:ALA:HB2	20:P:159:ALA:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:704:A:O2'	31:A:1374:A:N3	2.41	0.51
31:A:2492:C:N4	31:A:2546:G:H22	2.06	0.51
35:e:218:THR:HG23	35:e:224:PRO:HG3	1.92	0.51
43:m:65:GLN:NE2	57:x:86:PRO:O	2.38	0.51
44:o:21:SER:N	52:a:698:C:HO2'	2.07	0.51
45:p:21:ALA:N	45:p:32:ASP:OD2	2.41	0.51
55:v:67:PHE:CZ	55:v:102:LEU:HD12	2.46	0.51
2:2:45:ARG:NH2	31:A:2361:U:OP1	2.44	0.51
26:V:167:ILE:HG22	26:V:169:ASP:H	1.75	0.51
31:A:817:C:O2	31:A:2461:A:O2'	2.28	0.51
31:A:992:U:O2'	31:A:2290:A:N3	2.37	0.51
50:u:127:GLU:O	50:u:131:ARG:HB3	2.11	0.51
52:a:1399:G:H21	52:a:1402:A:H2	1.59	0.51
58:8:342:PRO:O	58:8:346:PHE:N	2.40	0.51
31:A:290:A:H2'	31:A:291:G:H8	1.76	0.51
33:b:6:TRP:CG	58:8:348:LYS:HZ3	2.29	0.51
33:b:201:ASP:OD2	58:8:66:ARG:CD	2.58	0.51
9:C:56:ARG:HG3	9:C:81:PRO:HB2	1.92	0.51
26:V:138:LEU:HG	26:V:140:GLU:H	1.76	0.51
31:A:1933:A:C2	52:a:1445:C:O4'	2.63	0.51
33:b:209:ASP:OD1	58:8:316:SER:N	2.44	0.51
46:q:96:LYS:NZ	52:a:249:G:OP2	2.33	0.51
52:a:1484:C:H2'	52:a:1485:C:C6	2.46	0.51
53:w:109:ASN:HD22	53:w:132:TRP:NE1	2.09	0.51
8:B:9:U:OP1	20:P:53:ARG:NH2	2.39	0.51
12:F:165:ARG:CZ	43:m:97:VAL:HG22	2.40	0.51
12:F:167:PHE:HE2	43:m:101:ARG:CZ	2.23	0.51
31:A:897:A:N1	43:m:119:CYS:CB	2.73	0.51
31:A:1332:G:OP2	31:A:1332:G:N2	2.44	0.51
38:h:31:ILE:HD11	38:h:130:LEU:HD21	1.92	0.51
47:r:53:ARG:HG3	53:w:149:PRO:CG	2.39	0.51
48:s:50:ALA:HB1	48:s:57:HIS:HB3	1.92	0.51
52:a:419:A:OP2	52:a:433:G:N2	2.43	0.51
58:8:257:GLN:NE2	58:8:283:ILE:HA	2.25	0.51
1:1:45:SER:HA	19:O:108:ILE:HG23	1.93	0.51
10:D:235:ILE:HD12	10:D:250:MET:HE1	1.93	0.51
12:F:70:LYS:HD2	12:F:75:TYR:HB2	1.91	0.51
12:F:116:GLN:OE1	32:0:42:HIS:ND1	2.43	0.51
31:A:1457:G:O2'	31:A:1496:A:N1	2.43	0.51
38:h:67:ARG:HD3	58:8:67:CYS:O	2.11	0.51
50:u:106:GLU:CD	53:w:136:ASP:CG	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:y:84:LEU:HD11	51:y:153:LEU:HD11	1.93	0.51
58:8:317:HIS:HB3	58:8:324:VAL:HG12	1.93	0.51
13:G:119:VAL:HG12	13:G:176:ARG:HD2	1.93	0.50
15:K:169:THR:HG23	15:K:170:GLN:HG2	1.93	0.50
31:A:1874:U:OP1	31:A:2427:G:O2'	2.28	0.50
33:b:21:GLY:O	33:b:207:ASN:ND2	2.44	0.50
41:k:21:SER:OG	41:k:22:ALA:N	2.43	0.50
55:v:16:SER:HB2	55:v:101:PRO:HD2	1.93	0.50
19:O:101:ASN:O	27:W:43:G:N2	2.43	0.50
31:A:1112:A:O2'	31:A:1133:U:O2'	2.22	0.50
39:i:132:VAL:HG11	39:i:146:ILE:HG12	1.94	0.50
6:6:127:LYS:NZ	31:A:1402:G:OP2	2.45	0.50
25:U:127:ASN:ND2	25:U:131:GLU:OE1	2.43	0.50
26:V:52:GLU:HG3	26:V:53:ARG:HG3	1.92	0.50
31:A:804:A:OP2	31:A:2085:A:O2'	2.29	0.50
53:w:148:LYS:C	53:w:150:TRP:H	2.18	0.50
54:d:174:LEU:N	54:d:174:LEU:CD1	2.73	0.50
15:K:56:LYS:O	24:T:147:LYS:NZ	2.45	0.50
22:R:52:ARG:O	22:R:56:ASP:HB2	2.11	0.50
26:V:67:ARG:HH12	26:V:92:ILE:HD11	1.77	0.50
31:A:2557:C:O2'	31:A:2758:A:N3	2.41	0.50
35:e:179:VAL:HG22	35:e:189:VAL:HG12	1.93	0.50
55:v:184:ASN:HD21	55:v:194:ARG:NH2	2.09	0.50
31:A:892:C:H6	31:A:892:C:O5'	1.95	0.50
38:h:19:ASN:ND2	52:a:775:U:O2'	2.45	0.50
38:h:67:ARG:CB	58:8:67:CYS:HA	2.41	0.50
40:j:143:CYS:SG	52:a:1316:G:O2'	2.67	0.50
53:w:119:PRO:HG3	53:w:150:TRP:CD1	2.46	0.50
56:n:41:TRP:N	56:n:41:TRP:CD1	2.77	0.50
30:Z:65:LEU:HB3	30:Z:68:LEU:HD13	1.93	0.50
33:b:31:MET:HE2	33:b:197:PRO:HD3	1.93	0.50
50:u:100:LEU:HD11	53:w:168:ASN:CG	2.35	0.50
52:a:185:G:C6	55:v:25:TYR:CD2	3.00	0.50
52:a:1176:C:H2'	52:a:1177:A:H8	1.76	0.50
9:C:140:ILE:HD11	9:C:150:LEU:HD12	1.93	0.50
13:G:55:ALA:HB3	13:G:66:LYS:HB2	1.93	0.50
18:N:115:ARG:O	18:N:119:ALA:HB3	2.12	0.50
27:W:19:A:N3	31:A:2020:C:O2'	2.45	0.50
52:a:227:U:H2'	52:a:228:G:H8	1.76	0.50
52:a:438:C:H2'	52:a:439:G:H8	1.77	0.50
6:6:113:ARG:NH1	31:A:1548:A:OP1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:250:GLY:O	11:E:254:TYR:CB	2.60	0.50
17:M:143:LEU:O	17:M:147:ALA:N	2.44	0.50
19:O:106:ARG:HE	19:O:124:GLU:HG3	1.76	0.50
20:P:103:LYS:HE3	20:P:122:LYS:HB3	1.93	0.50
21:Q:147:ASP:OD1	21:Q:211:HIS:ND1	2.40	0.50
30:Z:129:GLY:H	30:Z:132:LEU:HD12	1.76	0.50
33:b:90:ARG:NH2	58:8:359:ARG:HB2	2.26	0.50
52:a:258:U:H2'	52:a:259:A:H8	1.75	0.50
52:a:613:G:H1'	52:a:681:A:H5'	1.94	0.50
4:4:118:GLN:NE2	31:A:2436:U:O4	2.45	0.50
9:C:51:GLY:HA3	31:A:702:C:H5''	1.94	0.50
19:O:43:ARG:NE	19:O:124:GLU:OE1	2.44	0.50
22:R:11:ARG:NH2	31:A:524:A:O2'	2.45	0.50
24:T:111:LEU:HB2	24:T:127:ARG:HB3	1.93	0.50
26:V:75:VAL:HB	26:V:134:VAL:HB	1.93	0.50
31:A:1454:G:H2'	31:A:1455:A:H8	1.76	0.50
52:a:676:A:H2'	52:a:677:A:C8	2.47	0.50
9:C:194:VAL:HG13	31:A:1830:U:H3	1.77	0.49
10:D:237:ALA:HB3	10:D:241:PRO:HG3	1.93	0.49
17:M:220:SER:OG	31:A:649:A:OP1	2.28	0.49
38:h:67:ARG:CD	58:8:69:ASN:N	2.75	0.49
40:j:178:ASP:O	40:j:182:GLN:HB2	2.12	0.49
44:o:21:SER:N	52:a:699:U:O4'	2.45	0.49
52:a:1437:A:H2'	52:a:1438:G:H8	1.76	0.49
54:d:187:LYS:C	54:d:188:ILE:HG13	2.36	0.49
55:v:52:GLU:HB3	55:v:67:PHE:HB2	1.93	0.49
9:C:27:ASN:ND2	31:A:1445:G:OP2	2.45	0.49
33:b:201:ASP:HB2	58:8:66:ARG:CB	2.42	0.49
35:e:142:LYS:HG2	35:e:146:GLU:HG3	1.93	0.49
45:p:31:ARG:HH11	52:a:555:A:H1'	1.77	0.49
52:a:893:G:N1	52:a:1286:G:OP2	2.40	0.49
31:A:376:U:O2'	31:A:378:A:N1	2.38	0.49
31:A:894:G:C5	31:A:895:C:N4	2.80	0.49
41:k:83:VAL:HG21	41:k:88:MET:HE2	1.93	0.49
50:u:106:GLU:N	53:w:138:TRP:HZ2	1.88	0.49
52:a:551:C:H2'	52:a:552:G:H8	1.77	0.49
55:v:42:VAL:HB	55:v:48:ILE:HD11	1.94	0.49
3:3:142:SER:O	31:A:1636:U:O2'	2.28	0.49
7:7:60:MET:SD	31:A:977:G:O2'	2.66	0.49
10:D:200:SER:HB2	10:D:291:ARG:HB2	1.94	0.49
12:F:150:TYR:O	12:F:154:ASP:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:M:135:PRO:HD2	17:M:138:ARG:HD2	1.95	0.49
27:W:54:A:OP2	27:W:70:G:N2	2.35	0.49
31:A:1052:G:H5''	31:A:1053:A:H5''	1.93	0.49
34:c:60:ILE:HG12	34:c:78:MET:HE2	1.94	0.49
35:e:147:LYS:O	35:e:149:ARG:N	2.45	0.49
38:h:67:ARG:CD	58:8:69:ASN:H	2.25	0.49
52:a:142:G:H1	52:a:147:C:N4	2.10	0.49
52:a:989:G:H2'	52:a:990:G:C8	2.48	0.49
3:3:96:THR:O	31:A:697:U:O2'	2.30	0.49
11:E:60:PHE:O	11:E:196:ARG:NH1	2.45	0.49
11:E:249:GLU:HA	11:E:252:ILE:HG22	1.95	0.49
20:P:70:ARG:HH12	31:A:2395:A:H5''	1.78	0.49
30:Z:89:MET:HE2	30:Z:149:PRO:HG2	1.95	0.49
52:a:139:G:H1	52:a:150:C:H42	1.60	0.49
52:a:1335:G:H2'	52:a:1336:G:H8	1.78	0.49
55:v:126:ILE:N	55:v:166:GLY:O	2.39	0.49
4:4:149:ALA:HB2	17:M:127:ARG:HG3	1.94	0.49
5:5:20:ARG:NH1	31:A:2758:A:OP1	2.46	0.49
15:K:155:VAL:HB	15:K:223:VAL:HG22	1.94	0.49
15:K:194:ARG:NH1	31:A:2657:G:OP2	2.41	0.49
19:O:101:ASN:OD1	27:W:44:U:O2'	2.30	0.49
23:S:124:PHE:HE1	23:S:135:ILE:HG23	1.77	0.49
29:Y:87:ARG:HD2	29:Y:97:ARG:HD3	1.93	0.49
31:A:864:U:H2'	31:A:865:A:H8	1.77	0.49
35:e:246:GLY:C	54:d:195:GLU:CG	2.86	0.49
52:a:1340:U:H2'	52:a:1341:G:C8	2.47	0.49
53:w:136:ASP:O	53:w:140:GLU:CG	2.61	0.49
53:w:139:GLU:O	53:w:143:VAL:HG23	2.12	0.49
58:8:63:ALA:HA	58:8:66:ARG:HB2	1.94	0.49
15:K:85:PHE:HB3	15:K:96:TRP:HZ2	1.78	0.49
31:A:2422:G:O2'	31:A:2428:A:N6	2.44	0.49
52:a:429:G:O2'	52:a:431:C:N4	2.45	0.49
55:v:33:LEU:HA	55:v:37:GLU:OE2	2.12	0.49
11:E:222:ASN:O	31:A:332:G:O2'	2.28	0.49
11:E:250:GLY:O	11:E:254:TYR:HB2	2.13	0.49
18:N:101:ARG:NH1	31:A:916:G:O2'	2.39	0.49
31:A:1933:A:H2	52:a:1445:C:O4'	1.96	0.49
38:h:67:ARG:NH1	58:8:68:ARG:HG2	2.27	0.49
52:a:57:U:H2'	52:a:58:G:C8	2.47	0.49
53:w:114:LEU:HD11	53:w:159:LEU:HD13	1.94	0.49
25:U:106:ARG:NH2	25:U:143:ASP:OD1	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:883:C:H2'	31:A:884:G:H8	1.77	0.49
31:A:894:G:C6	31:A:895:C:N4	2.81	0.49
31:A:2108:G:H1	31:A:2209:U:H3	1.59	0.49
31:A:2308:U:O2'	31:A:2391:C:O2	2.30	0.49
38:h:117:ASP:O	38:h:121:ARG:HB2	2.12	0.49
41:k:66:ARG:NH2	52:a:639:G:O6	2.43	0.49
52:a:616:C:H2'	52:a:617:A:H8	1.78	0.49
52:a:616:C:H2'	52:a:617:A:C8	2.47	0.49
9:C:133:LEU:CD1	36:f:159:LYS:HE2	2.43	0.49
12:F:118:PRO:HB2	12:F:140:ILE:HG22	1.94	0.49
22:R:17:ILE:HG22	22:R:35:ILE:HG22	1.94	0.49
22:R:114:GLU:HG3	23:S:172:ILE:HD13	1.94	0.49
24:T:79:LEU:O	24:T:83:ALA:HB2	2.13	0.49
31:A:699:U:H2'	31:A:700:A:H8	1.78	0.49
31:A:1157:A:O2'	31:A:2532:C:O2	2.31	0.49
49:t:79:ALA:HB1	49:t:81:LYS:HD2	1.95	0.49
52:a:374:C:H5''	54:d:126:PRO:HD2	1.95	0.49
52:a:1439:U:H2'	52:a:1440:G:C8	2.48	0.49
58:8:315:LEU:O	58:8:317:HIS:N	2.45	0.49
10:D:117:PHE:O	10:D:274:ARG:NH2	2.46	0.48
19:O:26:GLN:NE2	31:A:1296:A:O4'	2.46	0.48
31:A:693:G:O6	31:A:805:A:N6	2.46	0.48
50:u:99:LEU:HB2	53:w:171:GLN:NE2	2.28	0.48
52:a:978:U:H3	52:a:981:G:H22	1.61	0.48
52:a:1218:G:HO2'	52:a:1261:G:HO2'	1.55	0.48
56:n:34:VAL:HA	56:n:41:TRP:HH2	1.78	0.48
20:P:125:GLU:OE2	20:P:162:HIS:NE2	2.42	0.48
31:A:1935:G:H2'	31:A:1936:G:C8	2.48	0.48
35:e:224:PRO:HD2	35:e:289:MET:HE2	1.93	0.48
46:q:81:LEU:HD22	46:q:90:ARG:HG2	1.95	0.48
49:t:152:THR:H	49:t:155:ARG:HD2	1.78	0.48
11:E:150:ILE:HG23	31:A:671:C:H5''	1.95	0.48
15:K:176:HIS:NE2	15:K:179:ARG:O	2.45	0.48
22:R:78:TYR:CZ	22:R:82:ILE:HD11	2.49	0.48
52:a:68:C:H2'	52:a:69:G:H8	1.77	0.48
52:a:206:C:H2'	52:a:207:G:H8	1.78	0.48
52:a:228:G:H1	52:a:240:U:H3	1.61	0.48
54:d:58:TYR:OH	54:d:88:GLU:OE2	2.27	0.48
55:v:29:ILE:O	55:v:64:ARG:HG2	2.13	0.48
9:C:174:SER:OG	31:A:1809:G:O6	2.30	0.48
10:D:219:ARG:HH12	31:A:2006:G:H21	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:208:PHE:HB3	11:E:229:LEU:HB2	1.96	0.48
31:A:133:A:O2'	31:A:134:A:N7	2.45	0.48
31:A:596:A:H62	31:A:1272:A:H2	1.61	0.48
31:A:1103:C:N4	31:A:1104:C:N4	2.61	0.48
33:b:163:ASP:O	33:b:186:PRO:HG2	2.14	0.48
52:a:240:U:H2'	52:a:241:A:C8	2.48	0.48
2:2:18:CYS:O	2:2:49:ARG:NH2	2.47	0.48
9:C:46:THR:OG1	31:A:1815:U:O2	2.31	0.48
18:N:51:ARG:HG3	18:N:64:ILE:HD11	1.94	0.48
18:N:128:ARG:NH1	31:A:1057:A:OP1	2.40	0.48
21:Q:215:ARG:HD3	31:A:1763:G:H5''	1.95	0.48
23:S:165:GLY:HA2	23:S:170:THR:HA	1.96	0.48
26:V:74:THR:OG1	26:V:137:ILE:O	2.31	0.48
31:A:895:C:H3'	31:A:895:C:H6	1.79	0.48
31:A:1401:G:H21	31:A:1604:A:H2	1.61	0.48
31:A:2118:U:N3	31:A:2199:G:N1	2.51	0.48
39:i:78:ARG:HD3	39:i:141:GLY:HA2	1.96	0.48
52:a:68:C:H2'	52:a:69:G:C8	2.48	0.48
58:8:288:HIS:O	58:8:292:ILE:HG13	2.12	0.48
1:1:21:LYS:HG2	24:T:48:ARG:HB3	1.96	0.48
18:N:115:ARG:O	18:N:119:ALA:CB	2.62	0.48
22:R:52:ARG:HG2	22:R:55:ARG:HE	1.79	0.48
31:A:1757:G:H2'	31:A:1758:G:C8	2.48	0.48
33:b:6:TRP:N	58:8:348:LYS:HG2	2.29	0.48
33:b:20:PHE:CD1	58:8:329:LYS:HG2	2.47	0.48
35:e:246:GLY:N	54:d:191:LEU:HD22	2.28	0.48
38:h:67:ARG:HG3	58:8:70:ALA:HB3	1.94	0.48
39:i:79:LYS:HB2	39:i:176:ARG:HD3	1.95	0.48
49:t:81:LYS:HE2	52:a:62:G:C8	2.44	0.48
50:u:106:GLU:HB2	53:w:138:TRP:CE2	2.43	0.48
52:a:467:C:N4	52:a:477:G:O2'	2.34	0.48
21:Q:138:ARG:NH1	21:Q:200:SER:O	2.47	0.48
24:T:50:ILE:HD13	24:T:76:ILE:HD12	1.94	0.48
52:a:142:G:H1	52:a:147:C:H42	1.60	0.48
52:a:1181:G:O2'	52:a:1314:A:OP1	2.30	0.48
52:a:1256:U:H2'	52:a:1257:G:H8	1.78	0.48
52:a:1487:C:H2'	52:a:1488:C:C6	2.49	0.48
1:1:13:LYS:HD3	31:A:1284:U:H5''	1.95	0.48
11:E:81:ARG:O	11:E:85:HIS:CB	2.61	0.48
11:E:125:ARG:HE	31:A:685:G:H1'	1.78	0.48
15:K:84:MET:HE2	22:R:104:ASN:HD21	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:233:ALA:O	35:e:272:SER:OG	2.29	0.48
55:v:120:SER:O	55:v:122:TYR:N	2.46	0.48
15:K:161:VAL:HG21	15:K:200:ILE:HD11	1.95	0.48
31:A:1962:G:N3	52:a:1367:A:H2	2.12	0.48
33:b:60:LEU:CD1	58:8:65:GLU:HB3	2.39	0.48
35:e:254:ARG:HE	54:d:47:ARG:NH1	2.12	0.48
8:B:45:G:H3'	12:F:145:ARG:HH12	1.79	0.48
9:C:71:TYR:HA	9:C:113:VAL:HB	1.95	0.48
31:A:615:G:H21	31:A:669:C:H5'	1.79	0.48
31:A:932:A:H2'	31:A:933:G:H8	1.79	0.48
31:A:976:C:H2'	31:A:977:G:H8	1.78	0.48
31:A:2114:G:H1	31:A:2203:U:H3	1.61	0.48
34:c:24:SER:OG	34:c:25:GLN:N	2.45	0.48
42:l:42:PRO:HB3	42:l:89:ASP:HB3	1.96	0.48
43:m:58:LYS:HE3	57:x:85:PRO:HD3	1.95	0.48
52:a:13:U:O2'	52:a:863:A:OP2	2.29	0.48
52:a:895:A:H2'	52:a:896:G:C8	2.48	0.48
57:x:70:SER:O	57:x:75:ARG:NH1	2.45	0.48
9:C:254:ARG:NH2	31:A:1854:C:O3'	2.47	0.47
17:M:190:SER:OG	31:A:635:C:OP2	2.27	0.47
21:Q:116:ARG:HH22	27:W:35:U:H5''	1.79	0.47
23:S:145:GLN:HE21	31:A:1189:G:H1'	1.78	0.47
31:A:2692:A:H61	31:A:2750:G:H1	1.61	0.47
47:r:52:ASN:CA	53:w:149:PRO:HG3	2.44	0.47
52:a:941:U:O2	52:a:992:C:N4	2.47	0.47
54:d:13:ARG:NH1	54:d:31:ASP:OD2	2.47	0.47
11:E:89:ILE:O	11:E:93:GLN:HB2	2.14	0.47
15:K:123:ILE:HD11	15:K:126:ARG:HD2	1.97	0.47
15:K:131:ILE:HG23	15:K:153:VAL:HG21	1.96	0.47
21:Q:124:GLY:O	21:Q:128:LYS:CB	2.62	0.47
29:Y:87:ARG:HB3	29:Y:97:ARG:HE	1.79	0.47
31:A:827:C:OP1	31:A:1206:C:O2'	2.29	0.47
31:A:903:G:C2'	31:A:904:U:H5'	2.44	0.47
31:A:2118:U:O2	31:A:2199:G:N2	2.37	0.47
52:a:306:C:H2'	52:a:307:A:C8	2.47	0.47
52:a:1035:U:H3	52:a:1048:G:H22	1.61	0.47
22:R:90:LEU:HD23	22:R:93:ASN:HD21	1.79	0.47
31:A:182:A:H2	31:A:2451:A:H62	1.61	0.47
31:A:898:G:H3'	31:A:899:A:H5'	1.96	0.47
31:A:1934:C:OP1	52:a:1466:G:N7	2.41	0.47
46:q:95:LYS:NZ	52:a:208:C:OP2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:r:52:ASN:C	53:w:149:PRO:HG3	2.40	0.47
52:a:1009:U:OP1	56:n:84:ARG:NH1	2.47	0.47
55:v:45:HIS:CD2	55:v:79:VAL:HG23	2.50	0.47
10:D:204:ILE:HG21	10:D:285:LYS:HG2	1.96	0.47
11:E:242:ALA:HB3	17:M:81:ARG:HD3	1.97	0.47
15:K:57:CYS:O	15:K:61:TRP:HB2	2.14	0.47
17:M:111:GLY:HA2	31:A:1211:G:H5''	1.96	0.47
29:Y:120:ARG:NH1	31:A:1385:G:OP2	2.48	0.47
31:A:1513:C:H2'	31:A:1514:A:H8	1.79	0.47
31:A:2563:U:H5''	31:A:2564:U:H5'	1.96	0.47
52:a:127:A:H2	52:a:191:G:H1	1.60	0.47
54:d:19:PRO:HG3	54:d:186:LEU:HD12	1.91	0.47
55:v:125:TYR:CD2	55:v:167:PHE:CZ	3.02	0.47
10:D:239:THR:OG1	31:A:2589:A:N7	2.35	0.47
20:P:160:ARG:NH1	31:A:2393:A:O2'	2.31	0.47
31:A:737:G:O5'	31:A:1453:G:O2'	2.31	0.47
31:A:898:G:C2	43:m:121:ARG:HB3	2.49	0.47
31:A:1466:G:O6	31:A:1485:U:O2	2.33	0.47
41:k:39:THR:O	41:k:55:SER:OG	2.29	0.47
45:p:36:VAL:HG13	45:p:49:ASN:HB3	1.96	0.47
49:t:117:LYS:HD2	49:t:131:LEU:HD11	1.97	0.47
52:a:676:A:H2'	52:a:677:A:H8	1.79	0.47
55:v:24:LEU:HD11	55:v:68:VAL:HB	1.97	0.47
56:n:40:LYS:HD3	56:n:40:LYS:HA	1.59	0.47
58:8:63:ALA:O	58:8:66:ARG:O	2.33	0.47
10:D:239:THR:N	31:A:2589:A:OP2	2.45	0.47
15:K:175:ARG:HH21	15:K:184:LYS:HD3	1.80	0.47
17:M:131:GLY:O	31:A:842:G:N2	2.47	0.47
26:V:77:VAL:HG11	26:V:82:GLU:HG2	1.96	0.47
31:A:8:G:O2'	31:A:2646:U:O4	2.28	0.47
31:A:2013:A:O3'	31:A:2740:G:N2	2.47	0.47
37:g:99:LEU:HD23	37:g:102:ARG:HE	1.79	0.47
40:j:130:MET:HB2	40:j:168:ASP:HB2	1.96	0.47
54:d:188:ILE:HG22	54:d:189:ASN:H	1.79	0.47
58:8:61:GLU:O	58:8:65:GLU:HG3	2.15	0.47
21:Q:226:LEU:HD11	52:a:1380:C:H4'	1.96	0.47
25:U:106:ARG:NH1	31:A:128:U:OP2	2.48	0.47
29:Y:118:LYS:NZ	31:A:2234:G:OP1	2.38	0.47
30:Z:107:ARG:HA	30:Z:110:LYS:HB3	1.97	0.47
31:A:599:C:H2'	31:A:600:A:H8	1.79	0.47
31:A:726:G:C5	44:o:57:LEU:HD11	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1859:G:H2'	31:A:1860:G:H8	1.80	0.47
31:A:2345:A:H2'	31:A:2346:A:C8	2.50	0.47
31:A:2594:A:H5''	31:A:2595:G:H5'	1.97	0.47
32:O:100:LYS:CD	52:a:1260:G:C5'	2.91	0.47
34:c:183:ARG:HG2	52:a:1055:G:H5''	1.96	0.47
35:e:142:LYS:HG3	35:e:145:LYS:HB3	1.97	0.47
35:e:222:THR:OG1	35:e:223:PHE:N	2.47	0.47
40:j:104:ARG:NH1	52:a:1227:A:OP2	2.48	0.47
41:k:91:ALA:N	41:k:115:LEU:O	2.46	0.47
43:m:121:ARG:HH22	52:a:1257:G:H5'	1.79	0.47
52:a:685:U:H2'	52:a:686:G:C8	2.50	0.47
12:F:107:ILE:O	12:F:111:ALA:HB3	2.14	0.47
29:Y:74:ILE:HG22	29:Y:81:LYS:HG2	1.97	0.47
36:f:110:THR:HA	36:f:203:SER:HA	1.95	0.47
40:j:159:GLU:HB3	56:n:98:SER:HB3	1.97	0.47
47:r:54:LEU:HB3	47:r:58:GLN:HB2	1.97	0.47
52:a:280:A:O2'	52:a:555:A:N1	2.48	0.47
53:w:136:ASP:O	53:w:140:GLU:HG3	2.15	0.47
22:R:97:LEU:HA	22:R:100:ILE:HG12	1.96	0.47
31:A:1407:C:H2'	31:A:1408:A:H8	1.80	0.47
34:c:165:ALA:HB1	52:a:1006:G:H5''	1.97	0.47
44:o:24:PHE:O	44:o:28:CYS:CB	2.62	0.47
47:r:71:ILE:HD11	52:a:683:U:H1'	1.97	0.47
52:a:883:C:O2'	52:a:1292:C:OP2	2.26	0.47
9:C:208:ARG:HD3	9:C:214:PRO:HD3	1.97	0.47
10:D:125:GLN:O	10:D:138:GLN:CB	2.63	0.47
23:S:194:LYS:HG2	23:S:213:ARG:HD3	1.97	0.47
30:Z:135:LYS:O	30:Z:139:ALA:CB	2.63	0.47
31:A:1235:A:N6	31:A:1256:G:H21	2.01	0.47
31:A:1487:C:H42	31:A:1557:G:N2	2.13	0.47
31:A:2490:U:OP1	31:A:2546:G:N2	2.44	0.47
33:b:5:TYR:CE1	58:8:344:LEU:HD21	2.49	0.47
36:f:114:LEU:HB2	36:f:172:ILE:HB	1.96	0.47
41:k:24:LYS:HA	41:k:86:GLN:HE22	1.80	0.47
42:l:44:LYS:HD2	52:a:1441:A:H5'	1.97	0.47
58:8:257:GLN:NE2	58:8:282:GLY:O	2.48	0.47
3:3:146:ARG:HH12	25:U:140:VAL:HG11	1.80	0.46
9:C:104:ARG:HB3	9:C:190:GLN:HG3	1.95	0.46
28:X:152:ALA:O	28:X:156:GLU:HB2	2.16	0.46
29:Y:108:VAL:HG21	29:Y:129:ILE:HD13	1.97	0.46
31:A:744:G:N2	31:A:745:A:N7	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:42:ILE:HD11	58:8:291:GLN:NE2	2.30	0.46
33:b:223:PHE:HE2	58:8:359:ARG:HD2	1.80	0.46
51:y:137:PHE:HA	51:y:143:VAL:HG12	1.97	0.46
31:A:727:A:H2	44:o:41:GLU:OE2	1.88	0.46
43:m:136:THR:OG1	43:m:140:CYS:SG	2.73	0.46
16:L:38:VAL:HG12	16:L:61:VAL:HG22	1.97	0.46
20:P:138:LYS:HA	20:P:165:VAL:HB	1.98	0.46
31:A:1725:A:H2'	31:A:1726:A:H8	1.80	0.46
33:b:201:ASP:OD2	58:8:66:ARG:HD2	2.15	0.46
52:a:716:A:O2'	52:a:1472:G:N2	2.49	0.46
52:a:1129:G:O2'	52:a:1130:G:N7	2.40	0.46
55:v:35:ASN:HD21	55:v:105:MET:HE3	1.79	0.46
5:5:16:LEU:HD21	31:A:1060:A:H4'	1.97	0.46
9:C:34:ARG:NH2	9:C:40:ASN:O	2.49	0.46
13:G:128:GLN:HA	13:G:170:LYS:HA	1.98	0.46
21:Q:217:ALA:HB2	27:W:52:G:C8	2.50	0.46
24:T:138:ASP:OD1	24:T:139:ILE:N	2.49	0.46
32:O:100:LYS:CD	52:a:1260:G:H5'	2.45	0.46
35:e:246:GLY:CA	54:d:195:GLU:CG	2.94	0.46
42:l:4:ILE:HG12	46:q:89:ARG:HD2	1.98	0.46
52:a:162:C:H2'	52:a:163:G:C8	2.50	0.46
52:a:670:A:N6	52:a:681:A:H61	2.11	0.46
52:a:1304:G:H2'	52:a:1305:G:C8	2.50	0.46
54:d:155:SER:O	54:d:157:ARG:N	2.46	0.46
56:n:40:LYS:C	56:n:41:TRP:CD1	2.94	0.46
10:D:223:THR:HG21	31:A:1712:A:H1'	1.97	0.46
15:K:84:MET:HE3	15:K:84:MET:HB2	1.71	0.46
17:M:215:ARG:HG3	17:M:216:ALA:H	1.81	0.46
22:R:10:ALA:O	22:R:14:ARG:CB	2.63	0.46
31:A:890:G:H2'	31:A:891:G:H5'	1.98	0.46
31:A:1844:U:O4	31:A:1914:A:N6	2.48	0.46
31:A:1871:U:H2'	31:A:1872:G:H8	1.81	0.46
33:b:19:HIS:HE1	58:8:332:GLU:CD	2.24	0.46
50:u:100:LEU:CD1	53:w:168:ASN:ND2	2.55	0.46
52:a:527:C:H2'	52:a:528:U:C6	2.50	0.46
53:w:97:PRO:HB2	53:w:117:THR:HB	1.97	0.46
6:6:123:ARG:NH1	31:A:1404:C:OP2	2.49	0.46
22:R:82:ILE:HA	22:R:85:LEU:HB3	1.97	0.46
31:A:652:C:N4	31:A:657:U:O4	2.49	0.46
40:j:119:MET:SD	40:j:123:ARG:NE	2.89	0.46
40:j:150:VAL:HG21	52:a:912:G:H21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:m:33:LYS:HA	43:m:39:HIS:HB3	1.96	0.46
52:a:133:A:H2'	52:a:134:C:C6	2.50	0.46
54:d:41:ARG:NH2	54:d:49:GLU:OE1	2.49	0.46
9:C:269:ARG:HH22	31:A:1808:C:H5	1.63	0.46
19:O:61:MET:HE1	19:O:76:ALA:HA	1.97	0.46
26:V:67:ARG:HD3	26:V:97:SER:HA	1.98	0.46
31:A:1640:C:O2'	31:A:1646:A:N1	2.38	0.46
31:A:2116:C:N3	31:A:2201:G:O6	2.49	0.46
33:b:202:ILE:HD11	38:h:67:ARG:NH2	2.31	0.46
35:e:181:GLY:HA3	35:e:187:VAL:HG12	1.97	0.46
43:m:127:LEU:N	52:a:1256:U:OP1	2.44	0.46
52:a:449:C:O2	52:a:497:C:O2'	2.33	0.46
52:a:876:G:N2	52:a:1481:U:OP1	2.35	0.46
52:a:1374:C:H2'	52:a:1375:A:C8	2.51	0.46
17:M:115:ARG:NH1	31:A:578:U:OP1	2.49	0.46
31:A:471:U:H2'	31:A:472:A:H8	1.81	0.46
31:A:726:G:N7	44:o:57:LEU:CD1	2.78	0.46
33:b:20:PHE:CG	58:8:329:LYS:HE3	2.51	0.46
38:h:15:ASN:ND2	52:a:774:C:O2	2.49	0.46
38:h:67:ARG:NH1	58:8:65:GLU:C	2.74	0.46
49:t:145:LYS:HD3	49:t:150:ARG:HD2	1.97	0.46
52:a:869:U:H2'	52:a:870:U:C6	2.51	0.46
55:v:42:VAL:HA	55:v:45:HIS:CD2	2.44	0.46
58:8:343:LYS:HA	58:8:346:PHE:CE2	2.50	0.46
18:N:39:PRO:HD3	18:N:99:PRO:HG3	1.98	0.46
22:R:52:ARG:HD2	22:R:55:ARG:HH11	1.81	0.46
43:m:115:LYS:H	43:m:118:ARG:HH21	1.63	0.46
52:a:1271:G:O2'	52:a:1310:C:O2'	2.30	0.46
53:w:111:GLY:HA3	53:w:129:TYR:CZ	2.51	0.46
31:A:1994:G:O2'	31:A:1996:U:OP2	2.32	0.46
31:A:2270:G:H5''	31:A:2271:C:H5	1.80	0.46
33:b:196:ASN:HB3	33:b:199:LEU:HG	1.97	0.46
35:e:181:GLY:CA	35:e:186:GLN:O	2.63	0.46
37:g:150:ALA:HA	41:k:70:PHE:HB3	1.98	0.46
38:h:44:PHE:HB3	38:h:77:PHE:HE1	1.81	0.46
41:k:121:ASP:H	47:r:81:GLU:HB2	1.80	0.46
41:k:128:ASN:ND2	52:a:666:A:H5'	2.31	0.46
52:a:255:C:H2'	52:a:256:A:H8	1.81	0.46
52:a:670:A:H61	52:a:681:A:N6	2.11	0.46
52:a:772:U:H2'	52:a:773:A:C8	2.51	0.46
9:C:37:LYS:HD3	9:C:56:ARG:HH22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:81:PHE:O	22:R:85:LEU:CB	2.60	0.45
31:A:902:G:O2'	31:A:903:G:H5'	2.16	0.45
31:A:1037:A:N3	31:A:1180:C:O2'	2.48	0.45
35:e:199:SER:O	35:e:203:LYS:HB2	2.16	0.45
38:h:64:ARG:HH12	38:h:75:ASN:HB2	1.81	0.45
39:i:82:ILE:HD11	39:i:135:HIS:CE1	2.52	0.45
41:k:62:ARG:HA	41:k:66:ARG:HD3	1.98	0.45
41:k:121:ASP:HB3	47:r:81:GLU:HG3	1.98	0.45
52:a:423:A:H2	52:a:428:U:H3	1.60	0.45
52:a:1081:C:N3	52:a:1087:G:O6	2.48	0.45
52:a:1166:C:H2'	52:a:1167:U:C6	2.51	0.45
52:a:1361:U:H2'	52:a:1362:A:H8	1.81	0.45
53:w:98:ARG:HA	53:w:99:LEU:HG	1.98	0.45
58:8:318:ASP:OD2	58:8:323:ARG:NH2	2.45	0.45
18:N:56:ARG:NE	31:A:2486:A:O2'	2.49	0.45
22:R:33:ARG:NH2	31:A:588:A:O2'	2.49	0.45
28:X:76:ARG:HD2	31:A:2373:C:H4'	1.98	0.45
31:A:1599:C:O2	31:A:1600:A:O2'	2.31	0.45
31:A:2085:A:H2'	31:A:2086:G:H8	1.80	0.45
31:A:2417:G:H1	31:A:2433:C:H42	1.63	0.45
33:b:60:LEU:HD22	58:8:65:GLU:HG2	1.97	0.45
39:i:162:ARG:HD2	39:i:166:LYS:HD3	1.98	0.45
42:l:5:LYS:H	42:l:8:ILE:HG12	1.82	0.45
44:o:59:LYS:NZ	52:a:604:G:O3'	2.49	0.45
45:p:59:LYS:HA	45:p:59:LYS:HD2	1.69	0.45
47:r:52:ASN:HA	53:w:149:PRO:HG3	1.97	0.45
47:r:57:LYS:NZ	52:a:611:A:H5''	2.32	0.45
52:a:376:U:OP1	52:a:377:G:O2'	2.23	0.45
52:a:786:C:H2'	52:a:787:G:C8	2.51	0.45
52:a:1340:U:H2'	52:a:1341:G:H8	1.81	0.45
52:a:1375:A:H2	52:a:1423:G:H22	1.63	0.45
55:v:17:ASP:HA	55:v:100:LYS:HB3	1.98	0.45
55:v:21:ALA:HB3	55:v:73:VAL:HG13	1.98	0.45
9:C:256:ARG:NH1	31:A:1809:G:OP1	2.50	0.45
10:D:115:ILE:O	10:D:275:VAL:HA	2.16	0.45
11:E:82:ALA:HB2	17:M:88:GLN:HG3	1.99	0.45
11:E:148:TRP:CD1	11:E:150:ILE:HG12	2.51	0.45
19:O:77:LEU:HA	19:O:86:VAL:HG21	1.98	0.45
25:U:116:GLN:HB2	25:U:137:THR:O	2.16	0.45
31:A:426:C:O2	31:A:1874:U:O2'	2.32	0.45
31:A:2009:U:H3'	31:A:2010:C:H2'	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:77:ARG:HG3	39:i:82:ILE:HG22	1.97	0.45
41:k:55:SER:OG	41:k:56:ALA:N	2.50	0.45
52:a:272:G:H2'	52:a:273:G:H8	1.81	0.45
52:a:507:A:H4'	52:a:508:A:H3'	1.97	0.45
52:a:1166:C:H2'	52:a:1167:U:H6	1.81	0.45
54:d:43:GLN:HB3	54:d:47:ARG:HH22	1.81	0.45
54:d:142:GLN:NE2	54:d:145:ILE:O	2.49	0.45
58:8:356:PHE:O	58:8:359:ARG:HG2	2.16	0.45
9:C:37:LYS:NZ	31:A:1825:A:OP2	2.47	0.45
9:C:133:LEU:HG	36:f:159:LYS:NZ	2.31	0.45
13:G:163:VAL:HG12	13:G:173:VAL:HA	1.98	0.45
18:N:38:GLU:HB3	18:N:127:ILE:HB	1.97	0.45
28:X:88:LYS:HB2	28:X:91:ALA:HB2	1.98	0.45
33:b:79:LYS:NZ	58:8:316:SER:C	2.75	0.45
33:b:141:VAL:O	33:b:145:LEU:CB	2.65	0.45
34:c:27:LYS:NZ	34:c:31:GLU:OE2	2.49	0.45
37:g:120:LEU:O	37:g:124:LEU:HB2	2.15	0.45
41:k:116:LEU:HD21	41:k:119:VAL:HG13	1.98	0.45
52:a:112:G:H2'	52:a:113:A:C8	2.52	0.45
52:a:705:U:OP1	52:a:770:G:O2'	2.33	0.45
8:B:41:U:H1'	8:B:46:A:H61	1.80	0.45
10:D:222:MET:HB3	31:A:2007:U:H5'	1.99	0.45
11:E:202:ALA:HA	11:E:225:THR:HG21	1.98	0.45
23:S:146:ARG:O	23:S:217:THR:OG1	2.30	0.45
24:T:113:LYS:HE2	31:A:1344:G:H5''	1.97	0.45
26:V:110:HIS:HB3	31:A:495:A:H5'	1.99	0.45
26:V:136:LEU:HD13	26:V:168:VAL:HG11	1.99	0.45
31:A:1732:G:N2	31:A:1991:A:O2'	2.50	0.45
31:A:1844:U:H5''	31:A:1845:G:H5'	1.98	0.45
31:A:1873:G:H4'	31:A:2428:A:H4'	1.98	0.45
33:b:79:LYS:HZ3	58:8:318:ASP:N	2.14	0.45
33:b:177:LEU:HD21	33:b:199:LEU:HB3	1.98	0.45
41:k:128:ASN:HD22	52:a:665:C:H4'	1.81	0.45
52:a:23:G:H2'	52:a:24:C:C6	2.51	0.45
52:a:97:G:H2'	52:a:98:U:C6	2.51	0.45
52:a:232:U:N3	52:a:235:U:OP2	2.41	0.45
52:a:265:U:OP1	52:a:558:U:O2'	2.29	0.45
52:a:585:U:H2'	52:a:586:G:C8	2.51	0.45
54:d:12:ILE:HG23	54:d:17:ALA:HA	1.97	0.45
54:d:184:VAL:HG23	54:d:184:VAL:O	2.15	0.45
55:v:25:TYR:O	55:v:95:VAL:HA	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:123:LYS:CE	55:v:167:PHE:CG	2.96	0.45
55:v:127:GLY:O	55:v:193:ILE:CA	2.63	0.45
4:4:119:HIS:CE1	4:4:120:LEU:HD13	2.52	0.45
11:E:162:SER:O	11:E:166:ALA:HB2	2.17	0.45
20:P:100:THR:O	20:P:104:ALA:CB	2.64	0.45
21:Q:218:ARG:HG2	31:A:2736:G:H4'	1.99	0.45
24:T:111:LEU:O	24:T:126:LYS:HA	2.17	0.45
31:A:144:A:N3	31:A:2223:A:O2'	2.48	0.45
31:A:313:A:N1	31:A:323:G:C6	2.85	0.45
31:A:726:G:C8	44:o:57:LEU:HD11	2.50	0.45
31:A:1077:C:H2'	31:A:1078:A:H8	1.82	0.45
31:A:1423:U:O2'	31:A:1555:G:O2'	2.33	0.45
31:A:1433:U:H2'	31:A:1434:G:C8	2.52	0.45
46:q:118:ARG:HD2	52:a:235:U:H4'	1.99	0.45
52:a:925:G:N2	52:a:1311:C:OP2	2.46	0.45
58:8:264:VAL:HG22	58:8:281:GLY:H	1.81	0.45
9:C:65:ARG:HH12	9:C:124:ASN:HA	1.81	0.45
18:N:28:CYS:HB2	18:N:67:ARG:HH12	1.81	0.45
31:A:1672:U:O2'	31:A:1770:C:O2	2.31	0.45
31:A:2051:G:H2'	31:A:2052:G:C8	2.51	0.45
32:0:97:PHE:CE2	48:s:9:PRO:HD3	2.52	0.45
39:i:81:ALA:HB2	39:i:137:GLY:HA3	1.98	0.45
51:y:126:GLY:O	52:a:478:G:O2'	2.34	0.45
10:D:145:ARG:HE	10:D:147:ARG:HD2	1.82	0.45
11:E:81:ARG:O	11:E:85:HIS:HB2	2.17	0.45
16:L:15:GLY:HA3	16:L:50:THR:HG21	1.99	0.45
31:A:170:U:H2'	31:A:171:G:H8	1.82	0.45
31:A:1238:G:H1	31:A:1252:C:N4	2.15	0.45
33:b:215:ARG:O	33:b:219:THR:CB	2.64	0.45
52:a:22:G:H2'	52:a:23:G:C8	2.52	0.45
52:a:198:G:H2'	52:a:199:A:C8	2.51	0.45
52:a:621:G:H2'	52:a:622:G:C8	2.52	0.45
52:a:785:G:O6	52:a:798:U:O4	2.35	0.45
52:a:899:U:H3	52:a:1179:G:H1	1.65	0.45
52:a:1253:G:H22	52:a:1279:G:HO2'	1.61	0.45
55:v:126:ILE:HB	55:v:166:GLY:O	2.17	0.45
56:n:9:ARG:HH11	56:n:13:ARG:HH11	1.64	0.45
5:5:7:VAL:HG12	5:5:36:GLN:HE22	1.82	0.45
13:G:165:VAL:HG22	13:G:171:VAL:HG22	1.99	0.45
19:O:106:ARG:HB3	19:O:124:GLU:HB2	1.97	0.45
28:X:122:LEU:O	28:X:137:VAL:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:241:A:H2'	31:A:242:A:H8	1.81	0.45
31:A:605:C:H2'	31:A:606:A:H8	1.82	0.45
31:A:892:C:C2'	31:A:893:C:H5'	2.47	0.45
31:A:1604:A:H2'	31:A:1605:A:C8	2.52	0.45
39:i:90:GLY:H	39:i:128:TYR:HA	1.81	0.45
52:a:182:G:H2'	52:a:183:A:H8	1.82	0.45
52:a:566:C:H5'	52:a:567:U:H5''	1.98	0.45
52:a:607:C:H2'	52:a:608:G:C8	2.52	0.45
53:w:114:LEU:HD13	53:w:141:LEU:HD11	1.98	0.45
56:n:31:ILE:HG12	56:n:44:HIS:HD2	1.82	0.45
56:n:40:LYS:O	56:n:41:TRP:CG	2.70	0.45
58:8:329:LYS:HE2	58:8:332:GLU:OE2	2.16	0.45
1:1:18:ASN:ND2	31:A:14:A:O3'	2.48	0.45
2:2:10:LYS:HZ3	31:A:2302:C:H5	1.63	0.45
9:C:57:LEU:O	9:C:59:ARG:NH2	2.47	0.45
12:F:178:HIS:HB2	12:F:181:TYR:HA	1.98	0.45
21:Q:149:VAL:HG12	21:Q:208:VAL:HA	1.98	0.45
31:A:1336:C:O2'	31:A:1413:A:N3	2.48	0.45
42:l:47:SER:N	52:a:477:G:O6	2.42	0.45
52:a:541:U:H2'	52:a:542:U:C6	2.51	0.45
55:v:76:ALA:HA	55:v:79:VAL:HG12	1.97	0.45
55:v:130:ALA:HB2	55:v:191:GLN:HB2	1.99	0.45
25:U:121:THR:HG23	25:U:124:ALA:H	1.82	0.44
26:V:157:LYS:NZ	31:A:306:G:O3'	2.50	0.44
29:Y:100:PHE:CE2	31:A:2247:C:H5''	2.52	0.44
31:A:199:G:N2	31:A:201:A:N3	2.64	0.44
31:A:885:G:H1	31:A:911:U:H3	1.63	0.44
31:A:1384:C:O2'	31:A:1819:A:N3	2.46	0.44
32:0:94:VAL:CG2	48:s:67:VAL:HG12	2.46	0.44
32:0:100:LYS:CD	52:a:1260:G:H5''	2.47	0.44
40:j:133:VAL:HG13	40:j:166:LEU:HB3	1.98	0.44
41:k:114:ILE:O	41:k:116:LEU:N	2.50	0.44
52:a:662:G:H2'	52:a:663:A:C8	2.52	0.44
52:a:872:A:O2'	52:a:1348:C:OP2	2.32	0.44
52:a:1300:C:P	57:x:56:ARG:HH22	2.40	0.44
55:v:127:GLY:O	55:v:128:ASN:HB3	2.17	0.44
58:8:317:HIS:CA	58:8:324:VAL:HA	2.33	0.44
58:8:329:LYS:HB3	58:8:332:GLU:OE2	2.17	0.44
4:4:107:LYS:HB2	31:A:663:A:H5'	1.99	0.44
11:E:59:ASN:HB3	11:E:178:PHE:HE1	1.82	0.44
31:A:892:C:O5'	31:A:892:C:C6	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1529:A:H2'	31:A:1530:G:C8	2.52	0.44
31:A:1739:G:H2'	31:A:1740:G:H8	1.82	0.44
34:c:141:PHE:O	34:c:145:MET:HB3	2.17	0.44
50:u:106:GLU:HB3	53:w:139:GLU:CD	2.37	0.44
52:a:1123:G:H2'	52:a:1124:A:H8	1.83	0.44
19:O:38:LEU:HD22	19:O:58:VAL:HG21	1.97	0.44
29:Y:77:PHE:HA	29:Y:141:ALA:HB2	1.99	0.44
31:A:55:G:H1	31:A:112:C:N4	2.11	0.44
33:b:30:ARG:HD3	33:b:30:ARG:H	1.82	0.44
33:b:40:LYS:HD2	58:8:330:LYS:HE2	1.99	0.44
33:b:141:VAL:O	33:b:145:LEU:HB3	2.17	0.44
52:a:649:U:O2	52:a:651:G:N1	2.51	0.44
8:B:8:G:O6	8:B:115:C:N4	2.50	0.44
18:N:33:ALA:O	18:N:131:PHE:HA	2.17	0.44
26:V:90:SER:HB2	26:V:102:LYS:HD3	1.99	0.44
30:Z:120:ARG:NE	30:Z:123:GLU:OE1	2.50	0.44
31:A:1354:C:H2'	31:A:1355:G:H8	1.82	0.44
31:A:1454:G:H2'	31:A:1455:A:C8	2.52	0.44
31:A:1605:A:H2'	31:A:1606:A:C8	2.52	0.44
33:b:60:LEU:HD22	58:8:65:GLU:CG	2.47	0.44
33:b:135:LYS:O	33:b:139:ALA:HB2	2.17	0.44
50:u:96:GLU:HB3	53:w:172:GLN:NE2	2.31	0.44
56:n:3:ARG:HH21	56:n:6:LEU:HD11	1.81	0.44
58:8:69:ASN:HB3	58:8:73:GLU:HG2	1.99	0.44
18:N:36:ALA:HA	18:N:129:THR:HG22	2.00	0.44
20:P:128:ALA:HB1	20:P:162:HIS:HB2	1.99	0.44
31:A:1408:A:H5'	31:A:1488:A:H1'	1.99	0.44
31:A:2627:C:H4'	31:A:2628:C:H5'	2.00	0.44
33:b:136:ARG:NH1	52:a:1106:C:O3'	2.51	0.44
35:e:197:VAL:HG23	35:e:198:VAL:HG23	1.99	0.44
40:j:143:CYS:HG	52:a:1316:G:HO2'	1.63	0.44
51:y:134:VAL:O	51:y:145:ARG:HA	2.17	0.44
52:a:137:C:H2'	52:a:138:A:H8	1.83	0.44
52:a:1456:A:H2'	52:a:1457:G:C8	2.53	0.44
55:v:34:ASN:OD1	55:v:35:ASN:N	2.50	0.44
55:v:183:LEU:HD21	55:v:193:ILE:CG2	2.48	0.44
56:n:20:TYR:HE2	56:n:51:PRO:HB3	1.81	0.44
8:B:92:U:OP1	18:N:17:MET:N	2.50	0.44
17:M:203:GLU:HG2	31:A:649:A:H8	1.83	0.44
20:P:126:MET:HA	20:P:129:LYS:HG2	2.00	0.44
26:V:149:HIS:HB2	31:A:307:C:H5''	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1385:G:N2	31:A:1388:A:OP2	2.45	0.44
31:A:1665:U:O4	31:A:1666:A:N6	2.51	0.44
35:e:165:VAL:HG23	52:a:871:G:H1'	2.00	0.44
38:h:67:ARG:NH2	58:8:66:ARG:HA	2.32	0.44
49:t:85:GLN:O	49:t:89:ARG:HG2	2.18	0.44
52:a:585:U:H2'	52:a:586:G:H8	1.83	0.44
54:d:88:GLU:HA	54:d:93:ASN:HD22	1.82	0.44
3:3:102:ARG:NH2	3:3:138:LYS:O	2.44	0.44
9:C:116:THR:OG1	9:C:117:GLU:OE1	2.31	0.44
11:E:106:ALA:HB2	31:A:812:G:H8	1.83	0.44
15:K:115:TYR:HB2	15:K:153:VAL:HG12	1.99	0.44
24:T:58:TYR:O	24:T:62:LEU:HB2	2.17	0.44
31:A:1487:C:H42	31:A:1557:G:H22	1.66	0.44
31:A:2296:G:HO2'	31:A:2344:A:HO2'	1.65	0.44
37:g:98:ALA:O	37:g:102:ARG:HB2	2.18	0.44
52:a:1361:U:H2'	52:a:1362:A:C8	2.51	0.44
52:a:1363:U:H2'	52:a:1364:G:C8	2.51	0.44
54:d:191:LEU:O	54:d:195:GLU:HG3	2.18	0.44
56:n:37:LEU:O	56:n:41:TRP:CH2	2.70	0.44
58:8:354:GLN:HA	58:8:357:ARG:NH1	2.33	0.44
15:K:83:TRP:CG	15:K:84:MET:H	2.36	0.44
27:W:12:C:O2'	27:W:87:A:O2'	2.31	0.44
31:A:545:U:H2'	31:A:546:G:C8	2.53	0.44
31:A:2599:G:C2	31:A:2600:G:H1'	2.53	0.44
33:b:92:ARG:HE	33:b:229:ARG:HD2	1.82	0.44
33:b:201:ASP:HB2	58:8:66:ARG:HB3	1.99	0.44
33:b:211:ILE:CG1	58:8:317:HIS:CE1	2.98	0.44
41:k:83:VAL:HG22	41:k:86:GLN:HB2	1.98	0.44
52:a:14:U:H1'	52:a:863:A:H5''	2.00	0.44
52:a:283:C:H2'	52:a:284:A:C8	2.53	0.44
52:a:684:C:H2'	52:a:685:U:H6	1.82	0.44
52:a:1071:U:H2'	52:a:1072:A:H8	1.83	0.44
54:d:21:LEU:HB2	54:d:104:ILE:HD12	2.00	0.44
55:v:52:GLU:OE1	55:v:103:GLU:HA	2.18	0.44
31:A:631:G:OP2	31:A:632:G:N2	2.51	0.44
32:0:94:VAL:CG2	48:s:67:VAL:CG1	2.95	0.44
34:c:15:THR:HG22	34:c:192:LYS:HD3	1.99	0.44
38:h:67:ARG:NH1	58:8:65:GLU:O	2.46	0.44
52:a:239:U:H2'	52:a:240:U:C6	2.53	0.44
58:8:364:GLU:OE1	58:8:364:GLU:HA	2.18	0.44
22:R:3:ARG:NH2	31:A:1220:U:O2	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:157:VAL:HG21	25:U:178:LEU:HD13	1.99	0.43
31:A:570:C:H2'	31:A:571:G:C8	2.53	0.43
31:A:818:U:O2'	31:A:2074:A:N1	2.51	0.43
31:A:1407:C:H2'	31:A:1408:A:C8	2.53	0.43
33:b:19:HIS:CE1	58:8:332:GLU:HB3	2.53	0.43
34:c:92:VAL:HA	34:c:95:LEU:HD13	2.00	0.43
36:f:158:ARG:HB2	36:f:168:TYR:HE2	1.82	0.43
52:a:155:A:H2'	52:a:156:A:C8	2.53	0.43
52:a:292:A:H2'	52:a:293:C:H6	1.84	0.43
52:a:387:G:H2'	52:a:388:G:H8	1.83	0.43
52:a:1274:U:H2'	52:a:1275:G:H8	1.82	0.43
52:a:1400:C:H3'	52:a:1401:A:C8	2.53	0.43
54:d:196:TYR:CD1	54:d:196:TYR:C	2.96	0.43
9:C:255:SER:HG	31:A:1807:C:HO2'	1.65	0.43
13:G:129:LEU:HG	13:G:202:VAL:HG22	2.00	0.43
15:K:116:VAL:HG22	15:K:154:ILE:HB	2.00	0.43
27:W:13:G:N2	27:W:40:U:O2'	2.43	0.43
31:A:1968:G:H5'	31:A:2567:G:H21	1.82	0.43
33:b:7:ASN:ND2	58:8:348:LYS:HB3	2.32	0.43
33:b:40:LYS:HB2	58:8:330:LYS:HZ3	1.82	0.43
38:h:66:ARG:HD3	38:h:74:LEU:HD13	2.00	0.43
39:i:180:ARG:HH21	52:a:1135:G:H4'	1.83	0.43
45:p:6:LEU:HD22	45:p:17:TYR:HB3	2.00	0.43
50:u:100:LEU:HG	53:w:164:THR:HG23	2.00	0.43
52:a:466:C:H2'	52:a:478:G:C8	2.52	0.43
52:a:1366:G:O2'	52:a:1432:A:N6	2.51	0.43
53:w:112:LEU:HD12	53:w:137:ALA:HB1	1.98	0.43
58:8:367:ALA:HB3	58:8:368:ARG:HG2	2.00	0.43
17:M:161:ASN:HD21	31:A:639:A:H62	1.65	0.43
19:O:38:LEU:HD11	19:O:123:ILE:HG21	1.99	0.43
19:O:80:ILE:HD12	19:O:86:VAL:HG22	2.00	0.43
26:V:120:GLY:O	31:A:495:A:O2'	2.24	0.43
34:c:42:CYS:O	34:c:46:TYR:CB	2.66	0.43
51:y:151:GLU:H	51:y:151:GLU:HG3	1.60	0.43
52:a:185:G:H22	55:v:98:THR:HA	1.82	0.43
52:a:398:C:O2'	52:a:489:G:OP1	2.35	0.43
52:a:716:A:N3	52:a:1461:U:O2'	2.47	0.43
53:w:144:LEU:O	53:w:148:LYS:HG2	2.18	0.43
9:C:152:ARG:NE	31:A:1828:U:OP2	2.50	0.43
31:A:794:A:H2'	31:A:795:U:H4'	2.01	0.43
31:A:897:A:H1'	43:m:123:ILE:HG12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:1704:A:N3	31:A:1706:C:N4	2.66	0.43
31:A:2022:C:H2'	31:A:2023:G:H8	1.82	0.43
33:b:202:ILE:HG12	58:8:66:ARG:CG	2.48	0.43
33:b:223:PHE:CE1	58:8:355:THR:HB	2.54	0.43
38:h:67:ARG:HD3	58:8:69:ASN:N	2.33	0.43
43:m:47:ILE:HD11	52:a:1250:U:C4	2.53	0.43
44:o:43:HIS:CE1	44:o:46:ASP:HB2	2.53	0.43
52:a:610:U:H2'	52:a:611:A:C8	2.53	0.43
52:a:663:A:H2'	52:a:664:A:C8	2.53	0.43
54:d:187:LYS:C	54:d:188:ILE:CG1	2.92	0.43
4:4:112:ARG:NH1	31:A:2377:C:OP1	2.51	0.43
12:F:68:LEU:HA	12:F:71:GLU:HG2	2.00	0.43
23:S:145:GLN:NE2	23:S:214:GLN:OE1	2.51	0.43
31:A:146:U:O2	31:A:148:C:N4	2.45	0.43
37:g:15:ASP:N	37:g:20:ASN:O	2.52	0.43
38:h:67:ARG:NH2	58:8:65:GLU:O	2.43	0.43
43:m:53:GLU:HB2	43:m:96:GLU:HG2	2.00	0.43
51:y:107:HIS:HA	51:y:140:ARG:CZ	2.49	0.43
56:n:43:ILE:O	56:n:46:LYS:CA	2.66	0.43
8:B:92:U:H5'	18:N:17:MET:HB2	2.00	0.43
21:Q:217:ALA:HB2	27:W:52:G:H8	1.83	0.43
31:A:1874:U:O3'	31:A:2426:G:N2	2.50	0.43
31:A:2601:U:H5'	31:A:2602:U:H5'	2.01	0.43
32:0:96:LYS:HZ1	52:a:1259:A:C2'	2.23	0.43
37:g:14:SER:O	37:g:24:ASN:ND2	2.52	0.43
38:h:96:ILE:HA	38:h:97:PRO:HD3	1.72	0.43
50:u:106:GLU:OE2	53:w:136:ASP:OD2	2.36	0.43
52:a:165:A:H2'	52:a:177:A:H61	1.84	0.43
52:a:732:G:H2'	52:a:733:G:H8	1.83	0.43
58:8:369:ALA:O	58:8:371:MET:HG2	2.18	0.43
30:Z:107:ARG:O	30:Z:111:ARG:HB2	2.19	0.43
31:A:330:U:O2'	31:A:349:A:N3	2.52	0.43
31:A:426:C:H2'	31:A:427:A:C8	2.54	0.43
31:A:591:C:H2'	31:A:592:G:C8	2.54	0.43
33:b:52:ARG:CD	58:8:73:GLU:HG3	2.45	0.43
38:h:67:ARG:CD	58:8:67:CYS:C	2.91	0.43
38:h:109:SER:HA	38:h:114:ILE:HG22	2.00	0.43
48:s:23:ASN:ND2	48:s:43:THR:O	2.52	0.43
49:t:136:TYR:CE2	52:a:175:G:H4'	2.53	0.43
52:a:684:C:H2'	52:a:685:U:C6	2.53	0.43
54:d:51:LYS:HE3	54:d:51:LYS:HB3	1.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:167:PHE:HE2	43:m:101:ARG:NH2	2.07	0.43
15:K:214:GLY:HA2	15:K:217:LEU:HG	2.01	0.43
18:N:53:ALA:O	18:N:57:ASN:HB2	2.19	0.43
20:P:73:LEU:HD23	20:P:139:VAL:HG21	2.00	0.43
20:P:123:ILE:HD12	20:P:123:ILE:HA	1.87	0.43
33:b:21:GLY:HA2	33:b:207:ASN:HB2	2.01	0.43
34:c:147:LYS:O	34:c:151:LEU:CB	2.66	0.43
52:a:1212:C:N4	52:a:1220:G:O6	2.52	0.43
54:d:70:ARG:O	54:d:74:LYS:HB2	2.19	0.43
2:2:46:LEU:HB2	2:2:57:LYS:HD2	2.00	0.43
9:C:131:MET:HE3	9:C:131:MET:HB2	1.86	0.43
9:C:218:GLY:HA2	9:C:221:MET:HE3	2.01	0.43
18:N:12:GLN:HA	31:A:919:A:H62	1.84	0.43
23:S:188:GLU:OE2	23:S:218:ARG:NH1	2.52	0.43
29:Y:107:ARG:HA	29:Y:117:VAL:O	2.19	0.43
31:A:715:G:O2'	31:A:737:G:N2	2.43	0.43
31:A:1986:G:H2'	31:A:1987:G:C8	2.54	0.43
31:A:2464:G:C8	31:A:2518:C:H5''	2.54	0.43
36:f:110:THR:O	36:f:175:LEU:HA	2.19	0.43
48:s:10:PHE:CE1	52:a:1266:A:H4'	2.53	0.43
52:a:20:C:H2'	52:a:21:U:C6	2.54	0.43
52:a:574:U:H2'	52:a:575:G:C8	2.54	0.43
56:n:22:LEU:O	56:n:26:SER:OG	2.35	0.43
15:K:147:VAL:HG23	15:K:149:MET:HG2	2.00	0.43
16:L:11:ALA:O	16:L:99:PHE:N	2.46	0.43
20:P:73:LEU:HB3	20:P:86:VAL:HG22	2.01	0.43
31:A:468:U:O2	31:A:471:U:O2'	2.35	0.43
31:A:470:G:O2'	31:A:481:G:O6	2.36	0.43
31:A:958:C:OP1	31:A:1195:U:O2'	2.33	0.43
31:A:2204:A:H3'	31:A:2205:G:H8	1.84	0.43
31:A:2316:G:H2'	31:A:2317:G:C8	2.54	0.43
52:a:35:C:H2'	52:a:36:G:C8	2.52	0.43
52:a:227:U:H2'	52:a:228:G:C8	2.53	0.43
55:v:80:ILE:HD13	55:v:97:ILE:HG22	2.01	0.43
55:v:172:SER:HB3	55:v:175:GLU:OE1	2.19	0.43
58:8:72:MET:HB3	58:8:72:MET:HE3	1.71	0.43
8:B:91:G:N2	18:N:38:GLU:OE2	2.46	0.42
10:D:135:ASN:HD22	10:D:175:SER:HA	1.83	0.42
31:A:383:A:H61	31:A:413:A:H3'	1.84	0.42
31:A:592:G:H2'	31:A:593:G:H8	1.84	0.42
31:A:1125:U:H3'	31:A:1126:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:2539:U:C2	31:A:2783:A:N7	2.87	0.42
40:j:119:MET:HE2	40:j:167:ILE:HD11	2.00	0.42
40:j:129:ILE:HA	40:j:170:LEU:HD13	2.01	0.42
40:j:150:VAL:HG13	52:a:921:C:O2'	2.19	0.42
48:s:13:ASN:HB3	56:n:46:LYS:HZ3	1.84	0.42
51:y:130:ARG:HG2	51:y:153:LEU:HG	2.00	0.42
52:a:372:C:O3'	54:d:67:LYS:NZ	2.48	0.42
55:v:156:THR:O	55:v:160:SER:HA	2.18	0.42
55:v:172:SER:HB3	55:v:175:GLU:CD	2.44	0.42
4:4:140:ARG:HA	4:4:143:TYR:HB3	2.02	0.42
11:E:251:THR:O	11:E:255:LEU:CB	2.62	0.42
13:G:43:ILE:HG12	31:A:2769:G:H4'	2.01	0.42
13:G:166:GLU:OE2	13:G:170:LYS:NZ	2.52	0.42
30:Z:72:THR:OG1	30:Z:75:GLN:OE1	2.37	0.42
52:a:131:G:H2'	52:a:132:A:C8	2.53	0.42
52:a:1384:G:H2'	52:a:1385:U:H6	1.83	0.42
53:w:111:GLY:HA2	53:w:130:TYR:O	2.19	0.42
54:d:80:GLY:HA3	54:d:190:GLU:HB3	2.01	0.42
7:7:88:GLU:HG3	7:7:89:TRP:CD1	2.54	0.42
28:X:122:LEU:HG	28:X:140:ARG:HG3	2.02	0.42
30:Z:88:PHE:HA	30:Z:91:ARG:HE	1.85	0.42
31:A:226:A:H61	31:A:240:A:H5''	1.84	0.42
31:A:1926:A:O2'	52:a:1443:G:O2'	2.28	0.42
33:b:209:ASP:HA	58:8:316:SER:HA	2.01	0.42
39:i:124:TYR:HA	39:i:127:ASN:HD22	1.84	0.42
53:w:119:PRO:HG3	53:w:150:TRP:CG	2.53	0.42
11:E:158:ARG:NH1	31:A:630:C:OP2	2.51	0.42
21:Q:160:ARG:NH2	52:a:317:G:O4'	2.50	0.42
31:A:74:G:H22	31:A:109:A:H2	1.67	0.42
31:A:92:U:H2'	31:A:93:A:C8	2.54	0.42
35:e:218:THR:OG1	35:e:219:LYS:N	2.52	0.42
38:h:67:ARG:NH1	58:8:67:CYS:H	2.17	0.42
38:h:81:ARG:HD2	38:h:131:CYS:HB3	2.02	0.42
43:m:44:ILE:HB	43:m:47:ILE:HD12	2.02	0.42
47:r:70:ARG:HB3	47:r:77:PHE:HE1	1.84	0.42
49:t:117:LYS:NZ	49:t:127:PRO:O	2.52	0.42
52:a:18:U:H2'	52:a:19:C:C6	2.55	0.42
52:a:1244:C:H1'	52:a:1250:U:H5	1.84	0.42
52:a:1275:G:H5''	57:x:73:ASN:ND2	2.33	0.42
55:v:127:GLY:O	55:v:193:ILE:HG23	2.18	0.42
7:7:80:PRO:HA	7:7:81:PRO:HD3	1.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:116:ASP:OD2	31:A:1685:G:O2'	2.34	0.42
20:P:125:GLU:HG3	20:P:129:LYS:HE3	2.01	0.42
24:T:42:SER:OG	31:A:1287:G:O6	2.32	0.42
31:A:1154:A:H4'	31:A:1155:A:H5''	2.00	0.42
32:O:96:LYS:NZ	52:a:1259:A:O2'	2.49	0.42
39:i:78:ARG:H	39:i:145:ALA:HB2	1.84	0.42
52:a:1464:U:H2'	52:a:1465:G:H8	1.85	0.42
9:C:68:LYS:HB3	9:C:115:GLY:HA2	2.01	0.42
12:F:107:ILE:O	12:F:111:ALA:HB2	2.18	0.42
21:Q:127:ASN:HD21	21:Q:177:ILE:N	2.18	0.42
28:X:101:PHE:HB3	28:X:135:VAL:HG23	2.02	0.42
29:Y:95:THR:HG21	31:A:2095:U:H4'	2.01	0.42
31:A:825:C:O2'	31:A:1245:U:O2	2.29	0.42
31:A:843:C:H2'	31:A:844:G:C8	2.54	0.42
31:A:1118:U:H2'	31:A:1119:G:C8	2.54	0.42
31:A:1406:A:O2'	31:A:1417:U:O2	2.30	0.42
31:A:2316:G:H2'	31:A:2317:G:H8	1.85	0.42
32:O:97:PHE:HE2	48:s:9:PRO:HD3	1.84	0.42
17:M:134:MET:HA	17:M:135:PRO:HD3	1.82	0.42
18:N:124:LYS:NZ	31:A:2484:C:O2	2.46	0.42
31:A:2047:A:O2'	31:A:2049:G:OP2	2.31	0.42
34:c:11:ARG:NH1	34:c:186:LEU:O	2.44	0.42
34:c:187:GLN:NE2	52:a:1137:U:O2'	2.47	0.42
35:e:241:ALA:HB2	35:e:266:LEU:HD12	2.01	0.42
52:a:486:G:H2'	52:a:487:A:C8	2.55	0.42
52:a:1214:G:N2	52:a:1217:A:OP2	2.30	0.42
55:v:24:LEU:HD13	55:v:79:VAL:CG1	2.49	0.42
10:D:269:ILE:HG22	10:D:276:VAL:HG13	2.01	0.42
12:F:88:VAL:HG11	31:A:2331:G:H5'	2.01	0.42
13:G:43:ILE:HG13	31:A:2766:A:H5'	2.02	0.42
17:M:223:GLU:O	17:M:227:ALA:HB2	2.20	0.42
20:P:124:GLY:HA2	20:P:127:ILE:HG22	2.02	0.42
31:A:919:A:H2'	31:A:920:A:C8	2.54	0.42
31:A:1450:G:H2'	31:A:1451:G:C8	2.55	0.42
31:A:1468:C:O2'	31:A:1578:A:N3	2.39	0.42
42:l:52:VAL:HG12	42:l:66:TYR:HA	2.00	0.42
42:l:121:LYS:NZ	52:a:448:G:H5''	2.35	0.42
43:m:135:ARG:HD3	52:a:897:C:C5	2.54	0.42
49:t:89:ARG:HH12	52:a:300:A:H61	1.66	0.42
50:u:103:PHE:CE2	53:w:138:TRP:CB	2.98	0.42
52:a:139:G:H1	52:a:150:C:N4	2.16	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:a:182:G:H2'	52:a:183:A:C8	2.55	0.42
52:a:732:G:H2'	52:a:733:G:C8	2.55	0.42
52:a:1216:G:H2'	52:a:1217:A:C8	2.55	0.42
53:w:118:ILE:HG22	53:w:119:PRO:O	2.19	0.42
10:D:141:TYR:CD2	10:D:142:GLU:HG3	2.55	0.42
11:E:96:ARG:HD2	31:A:455:A:C6	2.55	0.42
22:R:27:ALA:O	22:R:34:THR:OG1	2.36	0.42
31:A:1287:G:O2'	31:A:2026:G:O6	2.34	0.42
31:A:2767:A:H3'	31:A:2768:A:H5''	2.02	0.42
33:b:14:MET:O	33:b:19:HIS:NE2	2.36	0.42
35:e:199:SER:O	35:e:203:LYS:CB	2.68	0.42
48:s:9:PRO:HD2	56:n:42:GLU:OE2	2.20	0.42
52:a:1044:U:P	52:a:1057:G:H1	2.42	0.42
55:v:83:LEU:HD23	55:v:95:VAL:CG2	2.48	0.42
9:C:228:HIS:CE1	9:C:237:ILE:HG13	2.55	0.42
10:D:149:LEU:HD21	10:D:157:LEU:HD12	2.02	0.42
31:A:25:G:H4'	31:A:1281:G:H4'	2.02	0.42
31:A:932:A:H2'	31:A:933:G:C8	2.55	0.42
31:A:1060:A:N1	31:A:1150:G:O6	2.53	0.42
34:c:196:CYS:SG	34:c:197:ALA:N	2.93	0.42
48:s:30:ILE:HG23	48:s:59:PRO:HB3	2.01	0.42
49:t:137:SER:O	49:t:140:ASP:HB2	2.20	0.42
52:a:490:A:O3'	54:d:14:ARG:NH1	2.53	0.42
52:a:780:G:N2	52:a:803:U:O2	2.45	0.42
8:B:78:U:O2	8:B:101:A:N7	2.53	0.41
10:D:95:THR:HG21	10:D:118:LYS:HE3	2.02	0.41
16:L:21:CYS:HA	16:L:41:ALA:HA	2.01	0.41
31:A:818:U:H2'	31:A:819:G:C8	2.55	0.41
31:A:1843:C:H42	31:A:1986:G:H1	1.68	0.41
31:A:2308:U:H2'	31:A:2309:U:C6	2.55	0.41
33:b:112:GLU:OE2	33:b:116:HIS:NE2	2.53	0.41
34:c:12:LEU:HD23	34:c:12:LEU:HA	1.88	0.41
46:q:66:ILE:HD11	46:q:77:GLU:HG3	2.02	0.41
51:y:124:SER:OG	51:y:125:LYS:N	2.52	0.41
20:P:143:ARG:HH11	31:A:2310:U:H5''	1.85	0.41
21:Q:141:PRO:HD2	21:Q:206:ILE:HD11	2.02	0.41
22:R:31:LEU:HA	22:R:31:LEU:HD12	1.84	0.41
24:T:33:THR:HG22	24:T:135:VAL:HG22	2.02	0.41
31:A:587:G:O2'	31:A:1275:A:OP1	2.38	0.41
31:A:682:C:H2'	31:A:683:C:H6	1.85	0.41
31:A:865:A:H2'	31:A:866:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:A:897:A:C6	43:m:119:CYS:CB	3.03	0.41
31:A:1063:U:H2'	31:A:1064:A:C8	2.55	0.41
38:h:67:ARG:NH1	58:8:67:CYS:N	2.67	0.41
52:a:449:C:H2'	52:a:450:A:H8	1.84	0.41
52:a:795:C:H2'	52:a:796:C:C6	2.55	0.41
58:8:271:LEU:CD1	58:8:304:LEU:HA	2.50	0.41
13:G:160:GLU:OE1	13:G:176:ARG:NH2	2.49	0.41
18:N:13:HIS:CD2	31:A:982:G:H5''	2.55	0.41
23:S:202:LYS:HG3	23:S:203:LYS:H	1.86	0.41
31:A:10:G:H2'	31:A:11:G:C8	2.55	0.41
31:A:1159:G:O6	31:A:2038:U:O2'	2.37	0.41
31:A:2283:A:N6	31:A:2290:A:OP2	2.52	0.41
33:b:40:LYS:NZ	58:8:294:HIS:CE1	2.88	0.41
34:c:61:ALA:HA	34:c:125:ASN:HD22	1.84	0.41
49:t:99:GLU:HB2	49:t:150:ARG:NH2	2.36	0.41
53:w:114:LEU:O	53:w:127:SER:HA	2.20	0.41
55:v:16:SER:HA	55:v:22:ARG:HD2	2.02	0.41
20:P:70:ARG:NH2	20:P:139:VAL:O	2.40	0.41
24:T:47:ARG:HH22	31:A:529:G:P	2.43	0.41
31:A:233:G:O2'	31:A:2449:A:OP1	2.39	0.41
31:A:867:G:N2	31:A:2286:A:O4'	2.51	0.41
32:0:93:GLN:HE21	48:s:67:VAL:HB	1.84	0.41
33:b:40:LYS:HB2	58:8:330:LYS:NZ	2.35	0.41
33:b:196:ASN:HD22	33:b:199:LEU:HG	1.85	0.41
50:u:106:GLU:OE1	53:w:136:ASP:CG	2.64	0.41
56:n:8:GLN:HA	56:n:11:LYS:HB2	2.02	0.41
58:8:280:ILE:HD13	58:8:280:ILE:HG21	1.69	0.41
12:F:126:SER:HA	12:F:132:VAL:HG12	2.02	0.41
13:G:134:TYR:HA	13:G:146:SER:O	2.21	0.41
19:O:12:LYS:HB2	31:A:1689:C:H3'	2.03	0.41
27:W:51:U:O2	31:A:2709:C:O2'	2.39	0.41
31:A:577:G:H21	31:A:581:A:H8	1.68	0.41
32:0:96:LYS:HE3	52:a:1260:G:P	2.16	0.41
33:b:40:LYS:HD3	58:8:290:SER:CA	2.50	0.41
33:b:79:LYS:CE	58:8:317:HIS:C	2.93	0.41
35:e:247:VAL:O	54:d:195:GLU:CD	2.63	0.41
37:g:50:ILE:HD12	37:g:50:ILE:HA	1.85	0.41
40:j:129:ILE:HG23	40:j:169:ILE:HA	2.02	0.41
42:l:11:THR:OG1	42:l:12:ARG:N	2.42	0.41
52:a:205:U:H2'	52:a:206:C:C6	2.55	0.41
52:a:1373:C:H2'	52:a:1374:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:d:57:HIS:CG	54:d:186:LEU:HD22	2.53	0.41
3:3:119:SER:OG	31:A:693:G:O3'	2.37	0.41
9:C:88:CYS:O	9:C:99:TYR:HA	2.21	0.41
21:Q:174:ASN:HB3	21:Q:179:THR:HG23	2.02	0.41
22:R:49:ASP:OD1	31:A:569:G:N2	2.53	0.41
25:U:105:PRO:O	31:A:131:C:N4	2.54	0.41
52:a:1440:G:O5'	52:a:1440:G:H8	2.03	0.41
56:n:25:ARG:HH11	56:n:55:ALA:HA	1.85	0.41
56:n:31:ILE:HG12	56:n:44:HIS:CD2	2.56	0.41
23:S:182:VAL:HG22	23:S:224:ILE:HG12	2.01	0.41
24:T:103:ALA:HA	24:T:134:ILE:HA	2.02	0.41
31:A:1015:C:O2'	31:A:1028:A:N3	2.43	0.41
35:e:223:PHE:HB2	35:e:240:PRO:HB3	2.02	0.41
39:i:94:PHE:HB2	39:i:130:VAL:O	2.20	0.41
43:m:70:ILE:HG23	57:x:89:PRO:O	2.19	0.41
52:a:786:C:H42	52:a:797:G:H1	1.68	0.41
7:7:69:ARG:HG3	7:7:73:LYS:NZ	2.36	0.41
9:C:255:SER:OG	31:A:1813:A:O2'	2.32	0.41
11:E:102:THR:HG21	11:E:142:GLY:HA3	2.02	0.41
11:E:133:LEU:O	31:A:1277:G:N2	2.53	0.41
12:F:175:PHE:HA	31:A:2320:G:H4'	2.02	0.41
27:W:26:G:H8	27:W:87:A:H2	1.67	0.41
27:W:59:C:H2'	27:W:60:A:H8	1.86	0.41
31:A:1762:C:H42	31:A:1766:G:H1	1.69	0.41
43:m:59:ARG:HA	43:m:62:TYR:HB2	2.03	0.41
43:m:137:LYS:HG2	43:m:140:CYS:HB2	2.03	0.41
52:a:785:G:N1	52:a:798:U:N3	2.66	0.41
52:a:1110:C:H2'	52:a:1111:G:H8	1.85	0.41
52:a:1176:C:H2'	52:a:1177:A:C8	2.55	0.41
58:8:268:VAL:HG11	58:8:305:GLN:HB3	2.03	0.41
5:5:10:ILE:HG21	31:A:2494:C:H42	1.85	0.41
7:7:54:LYS:O	7:7:58:HIS:N	2.50	0.41
8:B:32:A:H61	8:B:54:G:H21	1.69	0.41
10:D:167:HIS:CD2	10:D:289:LEU:HD22	2.56	0.41
11:E:254:TYR:OH	11:E:258:ARG:NH1	2.39	0.41
12:F:167:PHE:HD2	43:m:101:ARG:CZ	2.26	0.41
17:M:210:LEU:H	17:M:230:CYS:HB2	1.85	0.41
20:P:126:MET:O	20:P:130:SER:HB3	2.21	0.41
22:R:28:HIS:HB3	22:R:38:GLN:HG3	2.02	0.41
22:R:33:ARG:HG2	31:A:1273:G:H21	1.86	0.41
28:X:154:LYS:NZ	31:A:960:A:N1	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Y:99:GLN:HG3	31:A:2248:U:H5''	2.02	0.41
30:Z:104:ASP:O	30:Z:108:MET:HB2	2.21	0.41
31:A:895:C:C3'	31:A:895:C:C6	3.03	0.41
31:A:1487:C:N4	31:A:1557:G:H22	2.18	0.41
31:A:1488:A:H2'	31:A:1489:A:C8	2.56	0.41
31:A:1592:A:H4'	31:A:1593:U:H3'	2.02	0.41
31:A:2356:G:H2'	31:A:2357:A:H8	1.86	0.41
33:b:31:MET:HB3	33:b:35:ILE:HG13	2.02	0.41
33:b:79:LYS:NZ	58:8:317:HIS:C	2.72	0.41
34:c:77:HIS:HB3	34:c:117:ILE:HD11	2.02	0.41
38:h:9:ILE:HD12	38:h:32:THR:HG23	2.03	0.41
43:m:40:GLY:H	43:m:48:ARG:CZ	2.33	0.41
44:o:24:PHE:O	44:o:28:CYS:HB2	2.21	0.41
50:u:98:ARG:HE	53:w:168:ASN:CB	2.19	0.41
52:a:355:G:H2'	52:a:356:C:C6	2.56	0.41
52:a:660:A:H2'	52:a:661:A:C8	2.56	0.41
52:a:912:G:H2'	52:a:913:A:H8	1.86	0.41
52:a:1100:A:H2'	52:a:1101:A:C8	2.56	0.41
53:w:145:LEU:CD1	53:w:156:MET:HG3	2.51	0.41
55:v:100:LYS:HA	55:v:101:PRO:HD3	1.77	0.41
55:v:128:ASN:OD1	55:v:191:GLN:HB3	2.21	0.41
58:8:315:LEU:HD23	58:8:327:SER:H	1.85	0.41
5:5:6:SER:O	5:5:6:SER:OG	2.26	0.41
9:C:90:ILE:HD11	9:C:98:ARG:HB2	2.03	0.41
9:C:94:ASP:HA	31:A:1530:G:H21	1.86	0.41
11:E:201:PRO:O	11:E:225:THR:OG1	2.36	0.41
14:H:74:LEU:HA	14:H:78:LEU:HB2	2.01	0.41
29:Y:92:ASN:OD1	29:Y:94:LYS:NZ	2.39	0.41
31:A:530:U:H2'	31:A:531:A:H8	1.86	0.41
31:A:838:U:O2'	31:A:2082:U:N3	2.53	0.41
31:A:1330:G:H21	31:A:1647:C:H5'	1.85	0.41
31:A:1444:A:H2'	31:A:1445:G:H8	1.86	0.41
31:A:2045:A:O2'	31:A:2471:G:N2	2.51	0.41
32:0:95:GLU:HA	32:0:98:ARG:HG2	2.03	0.41
35:e:297:ARG:HH12	38:h:66:ARG:NH1	2.19	0.41
38:h:77:PHE:HE2	38:h:79:LEU:HD12	1.85	0.41
38:h:80:LYS:O	38:h:131:CYS:HB2	2.21	0.41
47:r:44:GLY:O	47:r:70:ARG:NH1	2.54	0.41
52:a:198:G:H2'	52:a:199:A:H8	1.85	0.41
8:B:10:G:OP1	20:P:57:HIS:NE2	2.52	0.40
12:F:132:VAL:HG22	12:F:138:LEU:HD21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:36:ALA:O	22:R:40:ILE:HG12	2.22	0.40
24:T:102:LYS:HG2	24:T:135:VAL:HB	2.02	0.40
31:A:645:A:O2'	31:A:2421:C:OP1	2.31	0.40
31:A:686:A:N3	31:A:2460:U:O2'	2.49	0.40
31:A:1424:A:O2'	31:A:1490:G:O2'	2.31	0.40
31:A:1703:G:O2'	31:A:2005:U:O4	2.30	0.40
52:a:970:G:H2'	52:a:971:G:C8	2.57	0.40
52:a:1265:C:N3	56:n:52:ARG:NH1	2.69	0.40
52:a:1384:G:H2'	52:a:1385:U:C6	2.56	0.40
18:N:6:ARG:HB3	31:A:880:U:H5''	2.01	0.40
21:Q:170:ILE:N	21:Q:182:ARG:O	2.42	0.40
27:W:67:U:H2'	27:W:68:A:C8	2.56	0.40
29:Y:103:LEU:HA	29:Y:122:SER:HA	2.03	0.40
31:A:568:C:H2'	31:A:569:G:C8	2.57	0.40
31:A:1050:G:H4'	31:A:1051:U:H5'	2.02	0.40
33:b:145:LEU:O	33:b:149:GLN:CB	2.68	0.40
34:c:100:GLN:O	34:c:104:ASN:ND2	2.54	0.40
35:e:254:ARG:HH22	54:d:195:GLU:HB3	1.85	0.40
36:f:147:ARG:HD2	36:f:147:ARG:HA	1.92	0.40
40:j:129:ILE:HG12	40:j:169:ILE:HG23	2.03	0.40
41:k:110:ARG:NH1	50:u:98:ARG:O	2.39	0.40
42:l:23:ALA:HB2	42:l:61:PHE:HD2	1.87	0.40
52:a:137:C:H2'	52:a:138:A:C8	2.55	0.40
52:a:175:G:H2'	52:a:176:C:C6	2.56	0.40
52:a:717:G:H4'	52:a:1462:A:H4'	2.02	0.40
8:B:24:G:H2'	8:B:25:G:C5	2.57	0.40
10:D:157:LEU:HD13	10:D:165:MET:H	1.87	0.40
11:E:90:THR:O	11:E:94:ASN:HB2	2.22	0.40
11:E:233:SER:OG	31:A:623:A:N6	2.53	0.40
16:L:102:ILE:HD12	16:L:106:LEU:HD11	2.03	0.40
17:M:98:LYS:NZ	31:A:675:U:OP1	2.44	0.40
23:S:192:ASP:HB3	23:S:216:ILE:HD13	2.04	0.40
31:A:385:U:H2'	31:A:386:A:H8	1.86	0.40
31:A:426:C:H2'	31:A:427:A:H8	1.85	0.40
31:A:892:C:HO2'	31:A:893:C:H5'	1.82	0.40
31:A:1941:A:H2'	31:A:1942:A:C8	2.56	0.40
42:l:51:LYS:HB2	42:l:51:LYS:HE2	1.90	0.40
43:m:120:TYR:HB2	43:m:127:LEU:HD21	2.04	0.40
43:m:126:LYS:HZ1	43:m:136:THR:HG22	1.84	0.40
49:t:85:GLN:O	49:t:88:THR:N	2.54	0.40
51:y:104:LYS:HE3	52:a:738:A:H1'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:a:425:C:H2'	52:a:426:A:C8	2.56	0.40
52:a:1301:G:P	57:x:56:ARG:HH21	2.44	0.40
52:a:1422:A:H2'	52:a:1423:G:C8	2.56	0.40
31:A:1227:U:H2'	31:A:1228:A:H8	1.86	0.40
31:A:2653:U:H3	31:A:2800:G:H1	1.69	0.40
52:a:3:U:H5'	52:a:4:C:OP2	2.22	0.40
52:a:461:C:H2'	52:a:462:U:C6	2.56	0.40
52:a:785:G:H2'	52:a:786:C:H6	1.86	0.40
9:C:25:ARG:NH2	31:A:1603:A:OP1	2.54	0.40
25:U:140:VAL:HA	25:U:172:LYS:HE3	2.04	0.40
31:A:2013:A:H1'	31:A:2704:U:H1'	2.04	0.40
31:A:2118:U:O4	31:A:2199:G:O6	2.40	0.40
31:A:2464:G:N7	31:A:2518:C:H2'	2.36	0.40
40:j:110:LEU:O	40:j:114:SER:HB2	2.20	0.40
48:s:16:LEU:HD23	56:n:46:LYS:HZ1	1.85	0.40
50:u:134:ARG:NH1	52:a:671:C:O5'	2.54	0.40
51:y:107:HIS:HB3	51:y:109:VAL:HG23	2.04	0.40
52:a:292:A:H2'	52:a:293:C:C6	2.57	0.40
52:a:530:U:OP2	52:a:706:G:N1	2.48	0.40
52:a:1256:U:N3	52:a:1277:A:C2	2.90	0.40
53:w:99:LEU:HD22	53:w:116:GLN:HA	2.02	0.40
53:w:145:LEU:HA	53:w:145:LEU:HD23	1.79	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	44/56 (79%)	40 (91%)	4 (9%)	0	100	100
2	2	49/65 (75%)	39 (80%)	10 (20%)	0	100	100
3	3	55/61 (90%)	49 (89%)	6 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4	67/73 (92%)	59 (88%)	8 (12%)	0	100	100
5	5	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
6	6	47/142 (33%)	46 (98%)	1 (2%)	0	100	100
7	7	44/116 (38%)	41 (93%)	3 (7%)	0	100	100
9	C	245/271 (90%)	213 (87%)	32 (13%)	0	100	100
10	D	210/221 (95%)	188 (90%)	22 (10%)	0	100	100
11	E	208/243 (86%)	180 (86%)	28 (14%)	0	100	100
12	F	173/220 (79%)	161 (93%)	12 (7%)	0	100	100
13	G	171/182 (94%)	161 (94%)	10 (6%)	0	100	100
14	H	51/155 (33%)	47 (92%)	4 (8%)	0	100	100
15	K	191/197 (97%)	178 (93%)	13 (7%)	0	100	100
16	L	119/121 (98%)	104 (87%)	15 (13%)	0	100	100
17	M	175/192 (91%)	163 (93%)	11 (6%)	1 (1%)	21	50
18	N	132/135 (98%)	111 (84%)	21 (16%)	0	100	100
19	O	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
20	P	118/123 (96%)	116 (98%)	2 (2%)	0	100	100
21	Q	116/156 (74%)	100 (86%)	16 (14%)	0	100	100
22	R	113/127 (89%)	105 (93%)	8 (7%)	0	100	100
23	S	145/201 (72%)	118 (81%)	27 (19%)	0	100	100
24	T	142/199 (71%)	125 (88%)	17 (12%)	0	100	100
25	U	90/122 (74%)	86 (96%)	4 (4%)	0	100	100
26	V	122/145 (84%)	109 (89%)	13 (11%)	0	100	100
28	X	98/137 (72%)	87 (89%)	11 (11%)	0	100	100
29	Y	72/77 (94%)	66 (92%)	6 (8%)	0	100	100
30	Z	88/109 (81%)	87 (99%)	1 (1%)	0	100	100
32	0	62/94 (66%)	54 (87%)	6 (10%)	2 (3%)	3	17
33	b	225/236 (95%)	195 (87%)	29 (13%)	1 (0%)	30	59
34	c	211/218 (97%)	181 (86%)	28 (13%)	2 (1%)	14	42
35	e	169/253 (67%)	150 (89%)	17 (10%)	2 (1%)	10	35
36	f	109/146 (75%)	85 (78%)	24 (22%)	0	100	100
37	g	147/155 (95%)	130 (88%)	16 (11%)	1 (1%)	18	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	h	132/134 (98%)	116 (88%)	16 (12%)	0	100	100
39	i	131/157 (83%)	107 (82%)	23 (18%)	1 (1%)	16	44
40	j	96/122 (79%)	83 (86%)	13 (14%)	0	100	100
41	k	116/138 (84%)	104 (90%)	12 (10%)	0	100	100
42	l	121/123 (98%)	100 (83%)	21 (17%)	0	100	100
43	m	108/126 (86%)	90 (83%)	18 (17%)	0	100	100
44	o	60/90 (67%)	59 (98%)	1 (2%)	0	100	100
45	p	78/88 (89%)	61 (78%)	17 (22%)	0	100	100
46	q	76/108 (70%)	64 (84%)	12 (16%)	0	100	100
47	r	62/101 (61%)	58 (94%)	4 (6%)	0	100	100
48	s	76/92 (83%)	61 (80%)	15 (20%)	0	100	100
49	t	103/108 (95%)	93 (90%)	10 (10%)	0	100	100
50	u	42/137 (31%)	39 (93%)	3 (7%)	0	100	100
51	y	106/236 (45%)	96 (91%)	10 (9%)	0	100	100
53	w	82/121 (68%)	79 (96%)	0	3 (4%)	2	16
54	d	197/201 (98%)	173 (88%)	22 (11%)	2 (1%)	12	40
55	v	188/198 (95%)	171 (91%)	14 (7%)	3 (2%)	7	29
56	n	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
57	x	35/47 (74%)	30 (86%)	4 (11%)	1 (3%)	3	19
58	8	150/370 (40%)	116 (77%)	18 (12%)	16 (11%)	0	2
All	All	6213/7898 (79%)	5499 (88%)	679 (11%)	35 (1%)	23	50

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	0	72	VAL
35	e	148	ILE
53	w	149	PRO
55	v	105	MET
58	8	72	MET
58	8	73	GLU
58	8	299	ASP
58	8	300	ILE
58	8	303	VAL
58	8	316	SER

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Mol	Chain	Res	Type
58	8	330	LYS
58	8	366	MET
58	8	367	ALA
58	8	370	ASP
58	8	371	MET
34	c	89	PRO
54	d	5	ARG
55	v	121	PRO
58	8	360	ILE
58	8	368	ARG
17	M	197	PRO
33	b	169	ASP
39	i	159	ALA
53	w	150	TRP
34	c	88	ARG
35	e	302	PRO
57	x	90	ILE
58	8	306	PRO
58	8	364	GLU
37	g	9	GLU
32	0	73	TRP
54	d	168	PRO
55	v	120	SER
53	w	119	PRO
58	8	307	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	39/49 (80%)	39 (100%)	0	100	100
2	2	48/59 (81%)	46 (96%)	2 (4%)	26	52
3	3	47/50 (94%)	47 (100%)	0	100	100
4	4	59/62 (95%)	58 (98%)	1 (2%)	53	67
5	5	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	6	46/124 (37%)	46 (100%)	0	100	100
7	7	40/96 (42%)	40 (100%)	0	100	100
9	C	195/216 (90%)	194 (100%)	1 (0%)	81	81
10	D	174/182 (96%)	174 (100%)	0	100	100
11	E	176/205 (86%)	174 (99%)	2 (1%)	65	74
12	F	148/183 (81%)	148 (100%)	0	100	100
13	G	147/154 (96%)	147 (100%)	0	100	100
14	H	47/134 (35%)	47 (100%)	0	100	100
15	K	167/171 (98%)	167 (100%)	0	100	100
16	L	101/101 (100%)	100 (99%)	1 (1%)	68	75
17	M	135/144 (94%)	134 (99%)	1 (1%)	76	78
18	N	107/108 (99%)	105 (98%)	2 (2%)	50	66
19	O	96/96 (100%)	96 (100%)	0	100	100
20	P	99/100 (99%)	99 (100%)	0	100	100
21	Q	104/135 (77%)	103 (99%)	1 (1%)	68	75
22	R	102/114 (90%)	102 (100%)	0	100	100
23	S	129/174 (74%)	128 (99%)	1 (1%)	73	77
24	T	126/176 (72%)	126 (100%)	0	100	100
25	U	81/103 (79%)	81 (100%)	0	100	100
26	V	112/129 (87%)	111 (99%)	1 (1%)	70	76
28	X	85/111 (77%)	85 (100%)	0	100	100
29	Y	64/67 (96%)	63 (98%)	1 (2%)	55	68
30	Z	83/97 (86%)	82 (99%)	1 (1%)	63	72
32	0	56/83 (68%)	56 (100%)	0	100	100
33	b	192/201 (96%)	191 (100%)	1 (0%)	81	81
34	c	185/188 (98%)	185 (100%)	0	100	100
35	e	132/203 (65%)	128 (97%)	4 (3%)	36	59
36	f	98/125 (78%)	97 (99%)	1 (1%)	68	75
37	g	120/126 (95%)	120 (100%)	0	100	100
38	h	117/117 (100%)	115 (98%)	2 (2%)	53	67
39	i	103/123 (84%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	j	90/110 (82%)	89 (99%)	1 (1%)	65	74
41	k	92/109 (84%)	91 (99%)	1 (1%)	65	74
42	l	106/106 (100%)	106 (100%)	0	100	100
43	m	97/109 (89%)	97 (100%)	0	100	100
44	o	58/85 (68%)	58 (100%)	0	100	100
45	p	71/79 (90%)	70 (99%)	1 (1%)	59	70
46	q	70/95 (74%)	70 (100%)	0	100	100
47	r	56/96 (58%)	56 (100%)	0	100	100
48	s	67/81 (83%)	67 (100%)	0	100	100
49	t	86/89 (97%)	86 (100%)	0	100	100
50	u	40/118 (34%)	40 (100%)	0	100	100
51	y	97/213 (46%)	95 (98%)	2 (2%)	47	64
53	w	75/109 (69%)	74 (99%)	1 (1%)	61	71
54	d	178/180 (99%)	175 (98%)	3 (2%)	53	67
55	v	160/168 (95%)	157 (98%)	3 (2%)	50	66
56	n	89/90 (99%)	89 (100%)	0	100	100
57	x	28/37 (76%)	28 (100%)	0	100	100
58	8	129/310 (42%)	123 (95%)	6 (5%)	23	50
All	All	5383/6724 (80%)	5342 (99%)	41 (1%)	70	77

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

Mol	Chain	Res	Type
2	2	13	LEU
2	2	48	LEU
4	4	153	LEU
9	C	172	LEU
11	E	245	LEU
11	E	246	VAL
16	L	120	VAL
17	M	196	LEU
18	N	94	VAL
18	N	127	ILE
21	Q	127	ASN
23	S	163	LEU
26	V	64	LEU

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Mol	Chain	Res	Type
29	Y	103	LEU
30	Z	125	GLU
33	b	201	ASP
35	e	212	ILE
35	e	266	LEU
35	e	303	MET
35	e	305	GLU
36	f	113	VAL
38	h	67	ARG
38	h	79	LEU
40	j	133	VAL
41	k	25	ILE
45	p	46	THR
51	y	114	VAL
51	y	159	LEU
53	w	167	ILE
54	d	21	LEU
54	d	160	LEU
54	d	174	LEU
55	v	24	LEU
55	v	37	GLU
55	v	175	GLU
58	8	283	ILE
58	8	303	VAL
58	8	304	LEU
58	8	305	GLN
58	8	314	ILE
58	8	368	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (100) such sidechains are listed below:

Mol	Chain	Res	Type
2	2	58	HIS
4	4	118	GLN
4	4	145	ASN
5	5	36	GLN
9	C	84	ASN
10	D	167	HIS
10	D	209	GLN
11	E	71	ASN
11	E	118	GLN
11	E	153	ASN

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Mol	Chain	Res	Type
12	F	60	ASN
12	F	77	ASN
12	F	116	GLN
12	F	168	GLN
13	G	103	GLN
13	G	151	HIS
15	K	97	ASN
15	K	139	ASN
15	K	170	GLN
15	K	202	HIS
16	L	3	GLN
16	L	73	ASN
16	L	82	ASN
17	M	88	GLN
17	M	161	ASN
18	N	13	HIS
18	N	35	GLN
18	N	57	ASN
19	O	37	GLN
20	P	81	HIS
20	P	93	HIS
21	Q	115	GLN
21	Q	127	ASN
21	Q	158	ASN
22	R	99	GLN
22	R	104	ASN
23	S	145	GLN
23	S	212	HIS
23	S	214	GLN
24	T	52	GLN
25	U	113	GLN
26	V	93	HIS
26	V	95	HIS
26	V	130	HIS
28	X	102	HIS
29	Y	93	HIS
32	0	76	ASN
34	c	18	HIS
34	c	34	GLN
34	c	100	GLN
34	c	104	ASN
34	c	125	ASN

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Mol	Chain	Res	Type
34	c	187	GLN
35	e	158	GLN
35	e	171	HIS
35	e	264	ASN
35	e	278	ASN
36	f	160	ASN
37	g	64	GLN
37	g	85	HIS
37	g	148	ASN
38	h	19	ASN
38	h	51	HIS
38	h	68	ASN
38	h	94	GLN
39	i	127	ASN
40	j	149	HIS
40	j	151	HIS
41	k	127	HIS
41	k	128	ASN
42	l	77	HIS
43	m	56	ASN
43	m	65	GLN
43	m	83	ASN
43	m	125	HIS
47	r	59	GLN
47	r	83	GLN
48	s	69	HIS
49	t	85	GLN
50	u	124	ASN
51	y	165	GLN
53	w	109	ASN
53	w	116	GLN
53	w	155	GLN
53	w	162	GLN
54	d	57	HIS
54	d	112	ASN
54	d	115	HIS
54	d	142	GLN
55	v	45	HIS
55	v	96	ASN
55	v	154	GLN
55	v	163	ASN
55	v	196	ASN

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Mol	Chain	Res	Type
56	n	15	ASN
56	n	44	HIS
58	8	58	GLN
58	8	257	GLN
58	8	269	GLN
58	8	294	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	W	101/106 (95%)	30 (29%)	4 (3%)
31	A	2808/2810 (99%)	596 (21%)	4 (0%)
52	a	1477/1491 (99%)	310 (20%)	0
8	B	116/121 (95%)	21 (18%)	1 (0%)
All	All	4502/4528 (99%)	957 (21%)	9 (0%)

All (957) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	B	4	U
8	B	10	G
8	B	14	U
8	B	15	A
8	B	16	G
8	B	25	G
8	B	31	C
8	B	36	A
8	B	42	C
8	B	53	U
8	B	54	G
8	B	58	A
8	B	61	C
8	B	67	U
8	B	74	A
8	B	89	A
8	B	92	U
8	B	101	A
8	B	111	G
8	B	117	A
8	B	119	G
27	W	16	G

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Mol	Chain	Res	Type
27	W	17	A
27	W	22	A
27	W	23	G
27	W	28	U
27	W	29	U
27	W	30	A
27	W	31	U
27	W	32	C
27	W	33	A
27	W	34	U
27	W	35	U
27	W	36	A
27	W	37	C
27	W	38	G
27	W	39	A
27	W	48	A
27	W	53	G
27	W	64	A
27	W	65	U
27	W	71	C
27	W	76	G
27	W	77	A
27	W	83	C
27	W	84	C
27	W	88	C
27	W	90	G
27	W	95	A
27	W	97	A
27	W	98	G
31	A	9	A
31	A	10	G
31	A	11	G
31	A	12	A
31	A	13	A
31	A	14	A
31	A	15	G
31	A	26	G
31	A	33	A
31	A	45	A
31	A	46	C
31	A	54	G
31	A	70	A

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Mol	Chain	Res	Type
31	A	72	A
31	A	73	U
31	A	74	G
31	A	82	G
31	A	84	G
31	A	85	U
31	A	98	G
31	A	99	A
31	A	100	G
31	A	112	C
31	A	116	A
31	A	117	A
31	A	118	U
31	A	123	C
31	A	130	U
31	A	131	C
31	A	143	G
31	A	144	A
31	A	147	C
31	A	149	A
31	A	158	C
31	A	159	A
31	A	173	C
31	A	181	A
31	A	184	A
31	A	189	A
31	A	201	A
31	A	207	A
31	A	226	A
31	A	233	G
31	A	250	A
31	A	251	G
31	A	252	C
31	A	262	G
31	A	264	A
31	A	266	A
31	A	275	U
31	A	276	G
31	A	284	A
31	A	287	A
31	A	294	U
31	A	295	C

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Mol	Chain	Res	Type
31	A	297	U
31	A	298	G
31	A	304	A
31	A	316	G
31	A	320	U
31	A	330	U
31	A	331	A
31	A	332	G
31	A	333	A
31	A	338	G
31	A	340	A
31	A	347	G
31	A	352	C
31	A	361	C
31	A	365	A
31	A	368	U
31	A	370	A
31	A	377	G
31	A	378	A
31	A	379	C
31	A	383	A
31	A	384	G
31	A	392	G
31	A	398	G
31	A	399	U
31	A	415	U
31	A	416	C
31	A	417	A
31	A	418	G
31	A	423	G
31	A	424	A
31	A	436	G
31	A	447	C
31	A	448	C
31	A	466	A
31	A	467	G
31	A	468	U
31	A	469	A
31	A	479	G
31	A	489	A
31	A	491	A
31	A	493	G

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Mol	Chain	Res	Type
31	A	504	G
31	A	507	G
31	A	512	A
31	A	515	U
31	A	516	A
31	A	519	A
31	A	524	A
31	A	529	G
31	A	541	G
31	A	542	C
31	A	543	A
31	A	544	G
31	A	545	U
31	A	554	G
31	A	555	A
31	A	557	C
31	A	558	A
31	A	559	G
31	A	560	A
31	A	573	G
31	A	583	G
31	A	585	A
31	A	608	U
31	A	609	G
31	A	610	G
31	A	611	C
31	A	613	U
31	A	614	G
31	A	623	A
31	A	624	A
31	A	630	C
31	A	632	G
31	A	633	A
31	A	638	U
31	A	639	A
31	A	643	A
31	A	646	G
31	A	649	A
31	A	657	U
31	A	665	U
31	A	667	G
31	A	680	G

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Mol	Chain	Res	Type
31	A	686	A
31	A	688	C
31	A	696	A
31	A	697	U
31	A	722	G
31	A	724	G
31	A	728	A
31	A	731	U
31	A	734	G
31	A	737	G
31	A	740	G
31	A	741	U
31	A	745	A
31	A	757	U
31	A	758	U
31	A	768	G
31	A	773	U
31	A	775	A
31	A	776	G
31	A	782	G
31	A	786	G
31	A	787	G
31	A	788	G
31	A	793	A
31	A	795	U
31	A	802	C
31	A	803	G
31	A	811	A
31	A	816	G
31	A	823	C
31	A	838	U
31	A	841	G
31	A	856	U
31	A	857	G
31	A	859	A
31	A	861	A
31	A	866	G
31	A	869	G
31	A	879	G
31	A	887	G
31	A	889	G
31	A	890	G

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Mol	Chain	Res	Type
31	A	891	G
31	A	892	C
31	A	893	C
31	A	895	C
31	A	897	A
31	A	900	G
31	A	901	C
31	A	902	G
31	A	903	G
31	A	905	A
31	A	906	C
31	A	907	C
31	A	908	A
31	A	915	G
31	A	916	G
31	A	919	A
31	A	924	U
31	A	937	U
31	A	938	G
31	A	946	A
31	A	947	A
31	A	970	G
31	A	974	G
31	A	981	G
31	A	987	A
31	A	989	G
31	A	993	C
31	A	1001	A
31	A	1002	G
31	A	1008	A
31	A	1011	A
31	A	1013	C
31	A	1017	G
31	A	1018	A
31	A	1024	A
31	A	1037	A
31	A	1040	U
31	A	1041	G
31	A	1045	G
31	A	1050	G
31	A	1051	U
31	A	1054	U

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Mol	Chain	Res	Type
31	A	1055	A
31	A	1061	G
31	A	1062	G
31	A	1065	G
31	A	1072	A
31	A	1075	G
31	A	1098	A
31	A	1099	G
31	A	1101	A
31	A	1105	A
31	A	1106	C
31	A	1112	A
31	A	1116	A
31	A	1118	U
31	A	1125	U
31	A	1139	A
31	A	1140	G
31	A	1143	C
31	A	1147	U
31	A	1148	G
31	A	1150	G
31	A	1155	A
31	A	1158	U
31	A	1160	A
31	A	1162	C
31	A	1163	G
31	A	1169	A
31	A	1170	A
31	A	1175	U
31	A	1183	A
31	A	1196	A
31	A	1197	A
31	A	1198	A
31	A	1225	G
31	A	1227	U
31	A	1240	G
31	A	1241	U
31	A	1245	U
31	A	1254	U
31	A	1258	A
31	A	1259	C
31	A	1261	A

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Mol	Chain	Res	Type
31	A	1271	G
31	A	1272	A
31	A	1274	A
31	A	1277	G
31	A	1286	A
31	A	1293	C
31	A	1294	A
31	A	1296	A
31	A	1305	A
31	A	1308	A
31	A	1310	C
31	A	1315	G
31	A	1321	A
31	A	1322	A
31	A	1333	U
31	A	1342	A
31	A	1346	U
31	A	1366	C
31	A	1371	C
31	A	1373	U
31	A	1379	C
31	A	1386	A
31	A	1399	A
31	A	1400	U
31	A	1405	A
31	A	1413	A
31	A	1416	A
31	A	1423	U
31	A	1424	A
31	A	1427	A
31	A	1431	C
31	A	1432	U
31	A	1433	U
31	A	1436	U
31	A	1437	G
31	A	1448	A
31	A	1449	C
31	A	1458	C
31	A	1461	G
31	A	1472	A
31	A	1476	G
31	A	1480	A

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Mol	Chain	Res	Type
31	A	1481	U
31	A	1484	G
31	A	1486	U
31	A	1493	C
31	A	1494	G
31	A	1497	A
31	A	1501	G
31	A	1502	A
31	A	1511	U
31	A	1512	U
31	A	1513	C
31	A	1519	A
31	A	1520	A
31	A	1521	G
31	A	1522	A
31	A	1524	G
31	A	1525	G
31	A	1528	U
31	A	1529	A
31	A	1531	A
31	A	1532	G
31	A	1544	A
31	A	1557	G
31	A	1558	U
31	A	1559	A
31	A	1568	U
31	A	1569	A
31	A	1570	C
31	A	1571	G
31	A	1592	A
31	A	1593	U
31	A	1594	A
31	A	1600	A
31	A	1603	A
31	A	1612	A
31	A	1620	U
31	A	1621	C
31	A	1622	A
31	A	1628	A
31	A	1635	C
31	A	1643	G
31	A	1644	A

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Mol	Chain	Res	Type
31	A	1662	A
31	A	1682	C
31	A	1683	G
31	A	1684	C
31	A	1708	C
31	A	1710	G
31	A	1711	C
31	A	1734	A
31	A	1750	C
31	A	1751	A
31	A	1752	C
31	A	1753	A
31	A	1755	A
31	A	1756	G
31	A	1762	C
31	A	1766	G
31	A	1774	G
31	A	1778	G
31	A	1783	A
31	A	1796	A
31	A	1801	A
31	A	1810	C
31	A	1812	A
31	A	1818	U
31	A	1819	A
31	A	1821	G
31	A	1826	U
31	A	1829	A
31	A	1839	A
31	A	1882	U
31	A	1884	A
31	A	1885	C
31	A	1915	A
31	A	1920	G
31	A	1923	C
31	A	1926	A
31	A	1927	A
31	A	1928	C
31	A	1930	A
31	A	1931	U
31	A	1943	G
31	A	1944	G

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Mol	Chain	Res	Type
31	A	1945	U
31	A	1950	A
31	A	1951	A
31	A	1957	U
31	A	1969	U
31	A	1974	A
31	A	1981	C
31	A	1984	A
31	A	1985	A
31	A	1986	G
31	A	1996	U
31	A	2005	U
31	A	2006	G
31	A	2007	U
31	A	2011	G
31	A	2034	C
31	A	2035	A
31	A	2037	G
31	A	2045	A
31	A	2046	G
31	A	2047	A
31	A	2048	U
31	A	2069	C
31	A	2070	A
31	A	2073	A
31	A	2074	A
31	A	2075	G
31	A	2076	A
31	A	2077	C
31	A	2082	U
31	A	2083	G
31	A	2091	A
31	A	2094	G
31	A	2101	G
31	A	2103	G
31	A	2106	U
31	A	2107	G
31	A	2118	U
31	A	2122	C
31	A	2123	U
31	A	2124	G
31	A	2125	C

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Mol	Chain	Res	Type
31	A	2126	G
31	A	2128	A
31	A	2129	G
31	A	2130	C
31	A	2132	U
31	A	2133	A
31	A	2134	G
31	A	2137	G
31	A	2139	A
31	A	2140	A
31	A	2142	G
31	A	2144	G
31	A	2145	A
31	A	2146	A
31	A	2147	G
31	A	2148	A
31	A	2151	G
31	A	2159	C
31	A	2160	C
31	A	2162	G
31	A	2163	G
31	A	2173	G
31	A	2174	C
31	A	2175	C
31	A	2176	A
31	A	2178	C
31	A	2179	A
31	A	2181	U
31	A	2183	A
31	A	2184	G
31	A	2185	A
31	A	2186	U
31	A	2187	A
31	A	2189	C
31	A	2191	C
31	A	2192	U
31	A	2195	G
31	A	2198	A
31	A	2199	G
31	A	2201	G
31	A	2204	A
31	A	2209	U

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Mol	Chain	Res	Type
31	A	2212	A
31	A	2220	G
31	A	2229	U
31	A	2230	A
31	A	2240	G
31	A	2242	A
31	A	2254	A
31	A	2255	G
31	A	2256	A
31	A	2266	U
31	A	2268	G
31	A	2269	G
31	A	2271	C
31	A	2272	G
31	A	2283	A
31	A	2286	A
31	A	2295	A
31	A	2297	G
31	A	2300	U
31	A	2304	A
31	A	2317	G
31	A	2322	A
31	A	2323	C
31	A	2325	G
31	A	2342	G
31	A	2343	C
31	A	2344	A
31	A	2348	G
31	A	2352	A
31	A	2353	A
31	A	2361	U
31	A	2362	G
31	A	2364	C
31	A	2367	C
31	A	2374	C
31	A	2378	C
31	A	2394	A
31	A	2396	G
31	A	2400	G
31	A	2402	C
31	A	2405	A
31	A	2406	G

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Mol	Chain	Res	Type
31	A	2408	G
31	A	2419	G
31	A	2423	A
31	A	2432	G
31	A	2436	U
31	A	2442	A
31	A	2443	A
31	A	2444	C
31	A	2445	G
31	A	2446	G
31	A	2452	A
31	A	2458	U
31	A	2464	G
31	A	2465	A
31	A	2466	U
31	A	2487	G
31	A	2493	A
31	A	2508	U
31	A	2509	U
31	A	2511	G
31	A	2515	C
31	A	2518	C
31	A	2519	G
31	A	2520	A
31	A	2521	U
31	A	2522	G
31	A	2524	C
31	A	2535	C
31	A	2537	C
31	A	2549	G
31	A	2552	U
31	A	2579	U
31	A	2583	A
31	A	2584	G
31	A	2589	A
31	A	2590	C
31	A	2591	G
31	A	2593	G
31	A	2594	A
31	A	2597	U
31	A	2598	G
31	A	2599	G

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Mol	Chain	Res	Type
31	A	2601	U
31	A	2602	U
31	A	2603	C
31	A	2619	A
31	A	2626	U
31	A	2627	C
31	A	2630	U
31	A	2632	U
31	A	2646	U
31	A	2647	A
31	A	2653	U
31	A	2671	A
31	A	2672	G
31	A	2674	A
31	A	2680	G
31	A	2690	G
31	A	2702	G
31	A	2706	U
31	A	2708	C
31	A	2719	G
31	A	2729	A
31	A	2731	C
31	A	2732	G
31	A	2736	G
31	A	2744	A
31	A	2751	A
31	A	2753	C
31	A	2762	G
31	A	2764	U
31	A	2766	A
31	A	2768	A
31	A	2770	C
31	A	2771	A
31	A	2780	G
31	A	2783	A
31	A	2784	G
31	A	2796	A
52	a	5	A
52	a	6	U
52	a	7	G
52	a	10	G
52	a	31	U

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Mol	Chain	Res	Type
52	a	32	G
52	a	33	A
52	a	40	G
52	a	45	A
52	a	48	C
52	a	49	U
52	a	50	U
52	a	52	A
52	a	55	C
52	a	62	G
52	a	72	A
52	a	75	U
52	a	82	U
52	a	83	C
52	a	85	A
52	a	90	C
52	a	92	G
52	a	100	A
52	a	104	A
52	a	105	C
52	a	106	G
52	a	114	A
52	a	115	C
52	a	121	C
52	a	127	A
52	a	130	G
52	a	143	G
52	a	147	C
52	a	148	G
52	a	150	C
52	a	152	G
52	a	166	G
52	a	167	G
52	a	174	A
52	a	180	A
52	a	191	G
52	a	202	G
52	a	216	U
52	a	218	G
52	a	221	A
52	a	222	G
52	a	230	G

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Mol	Chain	Res	Type
52	a	237	G
52	a	238	C
52	a	252	G
52	a	260	G
52	a	269	A
52	a	277	A
52	a	287	C
52	a	296	A
52	a	299	C
52	a	300	A
52	a	303	G
52	a	315	A
52	a	317	G
52	a	322	G
52	a	323	C
52	a	324	A
52	a	325	G
52	a	338	U
52	a	343	C
52	a	344	A
52	a	349	G
52	a	353	A
52	a	355	G
52	a	358	U
52	a	360	A
52	a	369	U
52	a	377	G
52	a	382	C
52	a	383	A
52	a	384	G
52	a	392	A
52	a	393	C
52	a	395	G
52	a	399	G
52	a	400	U
52	a	410	U
52	a	411	U
52	a	416	G
52	a	423	A
52	a	424	G
52	a	426	A
52	a	429	G

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Mol	Chain	Res	Type
52	a	432	G
52	a	433	G
52	a	434	U
52	a	443	A
52	a	444	A
52	a	447	A
52	a	453	G
52	a	456	U
52	a	459	C
52	a	466	C
52	a	469	G
52	a	472	G
52	a	475	G
52	a	478	G
52	a	479	U
52	a	481	A
52	a	495	A
52	a	507	A
52	a	510	G
52	a	511	A
52	a	512	U
52	a	514	G
52	a	520	A
52	a	521	A
52	a	524	C
52	a	525	G
52	a	536	G
52	a	543	A
52	a	544	A
52	a	566	C
52	a	577	A
52	a	578	C
52	a	579	A
52	a	580	G
52	a	600	U
52	a	601	G
52	a	602	G
52	a	613	G
52	a	630	G
52	a	650	A
52	a	651	G
52	a	659	A

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Mol	Chain	Res	Type
52	a	660	A
52	a	669	A
52	a	670	A
52	a	671	C
52	a	672	G
52	a	695	A
52	a	696	C
52	a	697	A
52	a	703	A
52	a	725	A
52	a	741	U
52	a	742	A
52	a	757	G
52	a	762	A
52	a	763	A
52	a	765	C
52	a	766	G
52	a	768	U
52	a	769	G
52	a	775	U
52	a	776	A
52	a	780	G
52	a	784	U
52	a	790	U
52	a	791	C
52	a	794	C
52	a	795	C
52	a	796	C
52	a	797	G
52	a	798	U
52	a	799	G
52	a	821	A
52	a	822	A
52	a	825	A
52	a	834	G
52	a	838	A
52	a	849	A
52	a	851	G
52	a	863	A
52	a	875	G
52	a	876	G
52	a	883	C

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Mol	Chain	Res	Type
52	a	884	A
52	a	909	U
52	a	915	G
52	a	918	A
52	a	920	G
52	a	924	A
52	a	925	G
52	a	926	A
52	a	938	G
52	a	941	U
52	a	942	G
52	a	945	A
52	a	946	U
52	a	948	C
52	a	953	A
52	a	954	A
52	a	958	U
52	a	961	U
52	a	963	A
52	a	964	A
52	a	969	A
52	a	973	G
52	a	974	U
52	a	975	G
52	a	978	U
52	a	980	C
52	a	981	G
52	a	982	G
52	a	985	A
52	a	986	C
52	a	992	C
52	a	994	C
52	a	995	A
52	a	1003	C
52	a	1005	U
52	a	1014	U
52	a	1027	U
52	a	1034	U
52	a	1038	G
52	a	1041	A
52	a	1043	G
52	a	1044	U

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Mol	Chain	Res	Type
52	a	1047	C
52	a	1050	A
52	a	1057	G
52	a	1066	G
52	a	1073	G
52	a	1074	U
52	a	1075	U
52	a	1079	A
52	a	1080	A
52	a	1082	G
52	a	1088	U
52	a	1089	U
52	a	1091	G
52	a	1095	C
52	a	1099	G
52	a	1100	A
52	a	1105	A
52	a	1107	U
52	a	1114	G
52	a	1115	A
52	a	1116	U
52	a	1119	G
52	a	1130	G
52	a	1131	U
52	a	1132	G
52	a	1144	A
52	a	1149	A
52	a	1150	U
52	a	1160	U
52	a	1161	A
52	a	1162	U
52	a	1163	G
52	a	1174	C
52	a	1175	A
52	a	1184	A
52	a	1186	A
52	a	1187	A
52	a	1188	U
52	a	1189	G
52	a	1195	G
52	a	1198	A
52	a	1204	U

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Mol	Chain	Res	Type
52	a	1205	C
52	a	1206	G
52	a	1208	G
52	a	1222	G
52	a	1223	A
52	a	1227	A
52	a	1229	C
52	a	1233	A
52	a	1234	A
52	a	1235	A
52	a	1243	C
52	a	1246	C
52	a	1247	A
52	a	1248	G
52	a	1250	U
52	a	1253	G
52	a	1265	C
52	a	1266	A
52	a	1267	A
52	a	1271	G
52	a	1280	A
52	a	1288	A
52	a	1294	A
52	a	1295	G
52	a	1311	C
52	a	1312	A
52	a	1317	G
52	a	1319	G
52	a	1327	C
52	a	1328	G
52	a	1346	C
52	a	1347	A
52	a	1351	C
52	a	1368	G
52	a	1371	G
52	a	1390	A
52	a	1395	A
52	a	1397	C
52	a	1400	C
52	a	1401	A
52	a	1402	A
52	a	1403	G

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Mol	Chain	Res	Type
52	a	1405	A
52	a	1418	A
52	a	1441	A
52	a	1443	G
52	a	1452	A
52	a	1454	G
52	a	1455	U
52	a	1466	G
52	a	1478	G
52	a	1479	G
52	a	1480	A

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	B	57	U
27	W	29	U
27	W	32	C
27	W	33	A
27	W	97	A
31	A	5	A
31	A	97	A
31	A	514	A
31	A	556	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

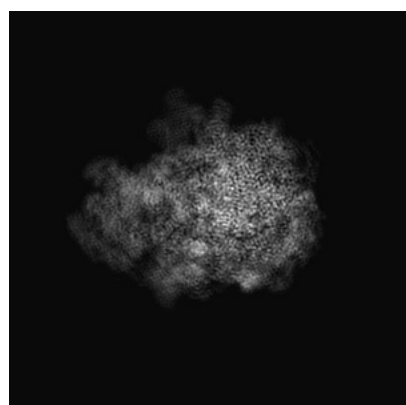
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6709. These allow visual inspection of the internal detail of the map and identification of artifacts.

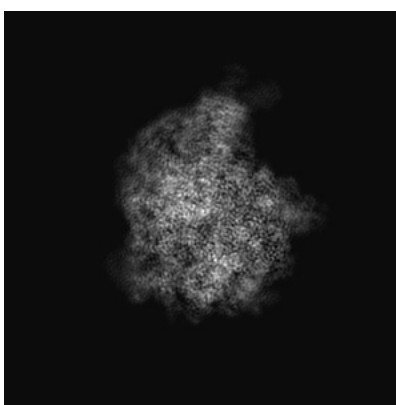
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

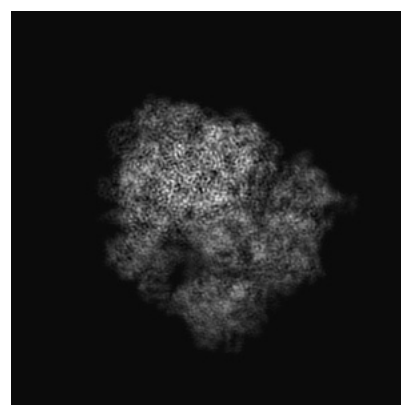
6.1.1 Primary map



X



Y

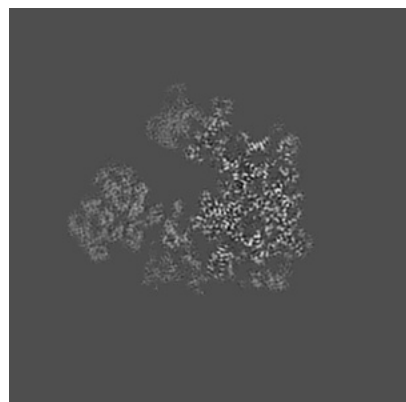


Z

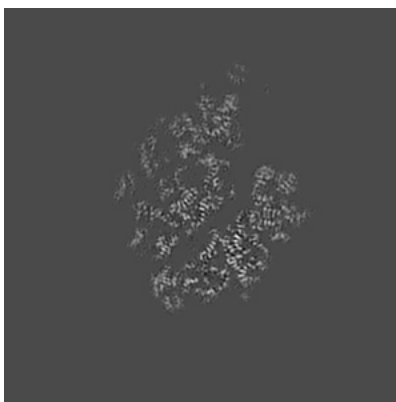
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

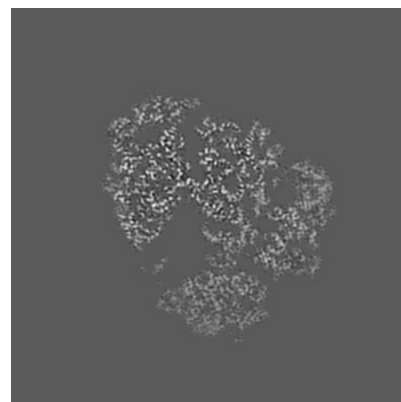
6.2.1 Primary map



X Index: 192



Y Index: 192

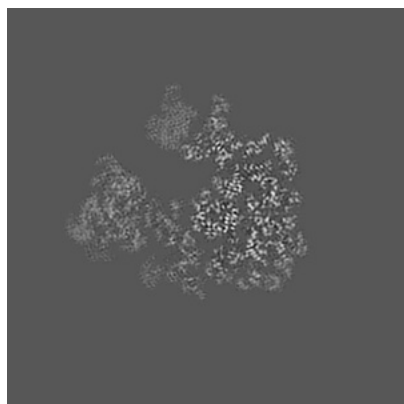


Z Index: 192

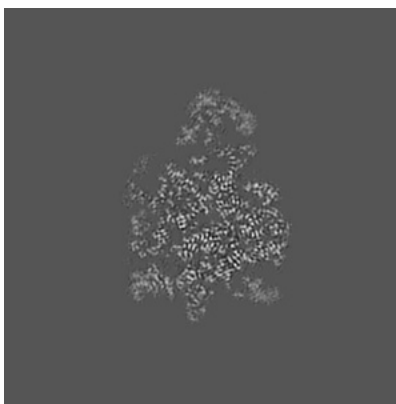
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 196



Y Index: 220

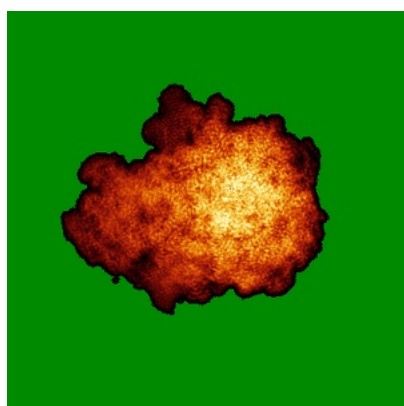


Z Index: 203

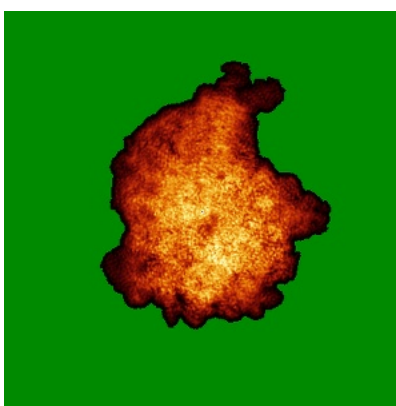
The images above show the largest variance slices of the map in three orthogonal directions.

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

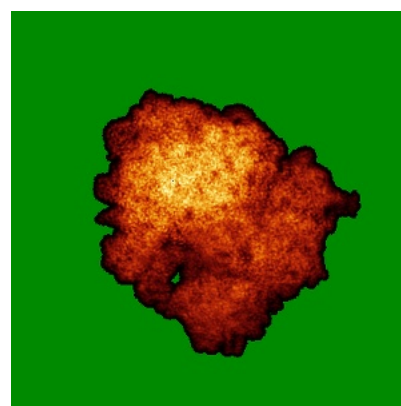
6.4.1 Primary map



X



Y

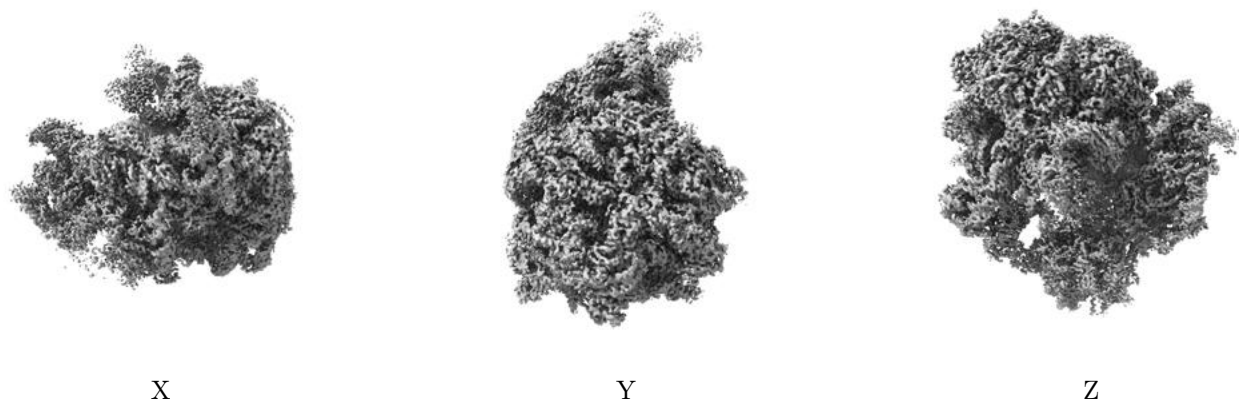


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

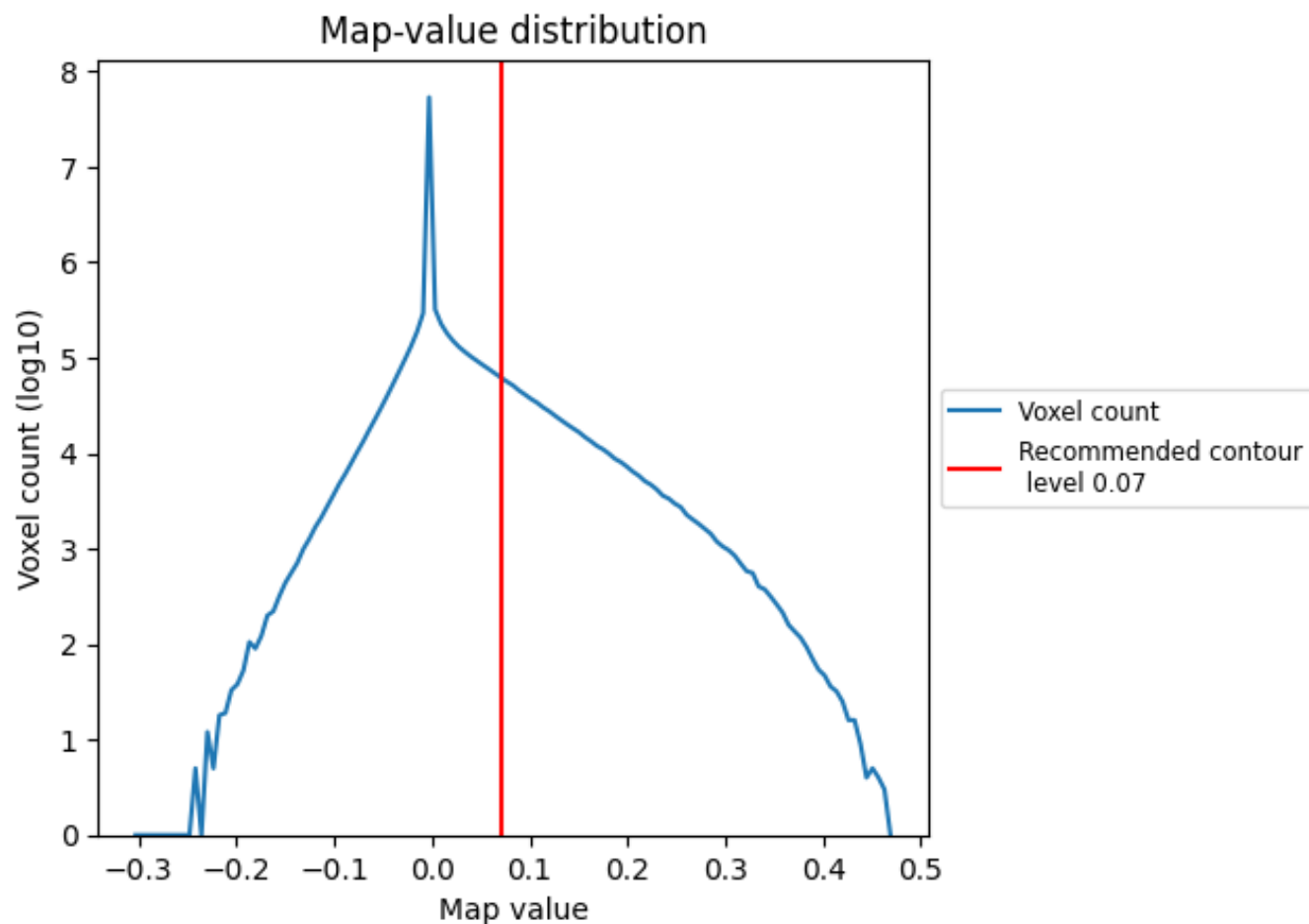
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

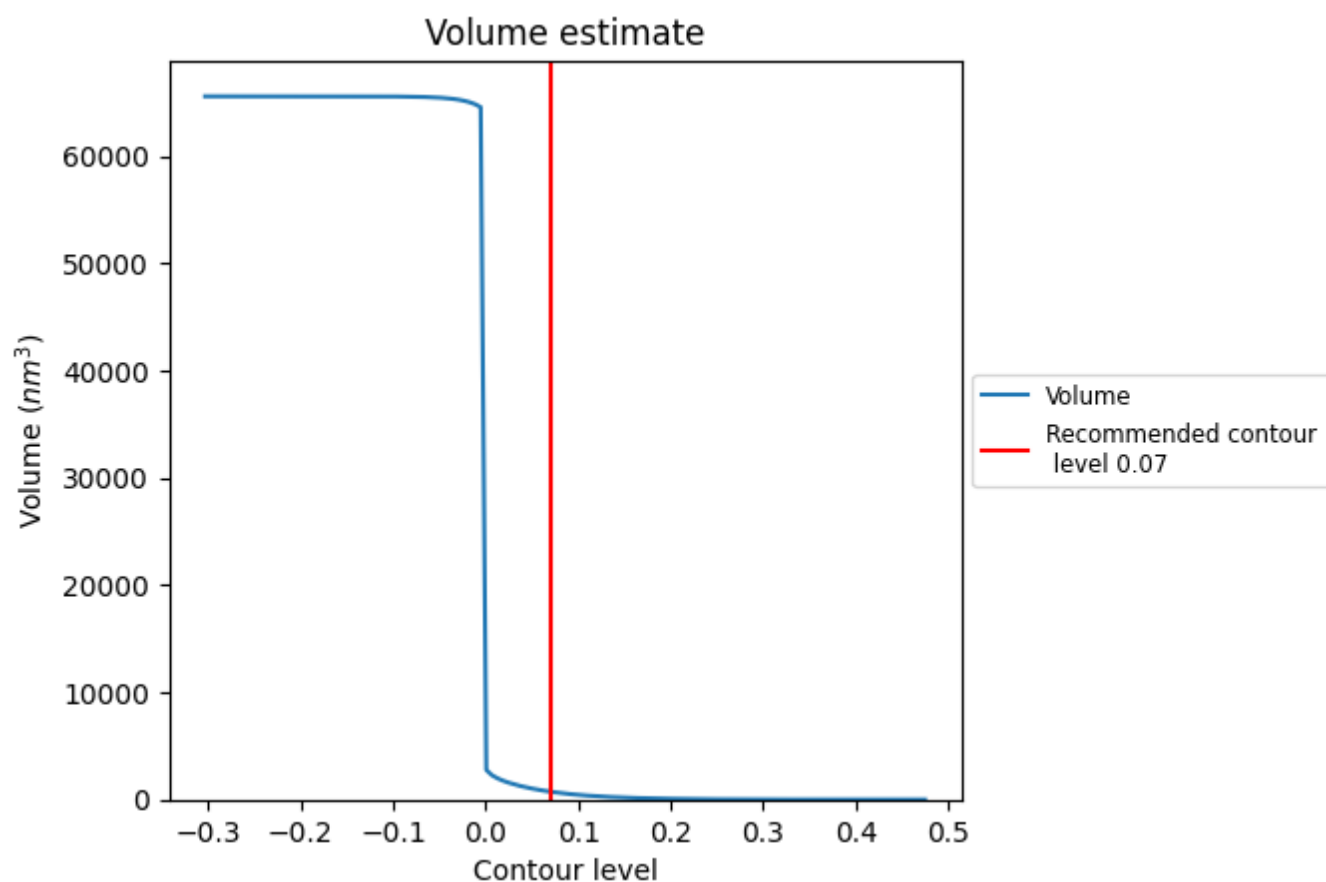
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

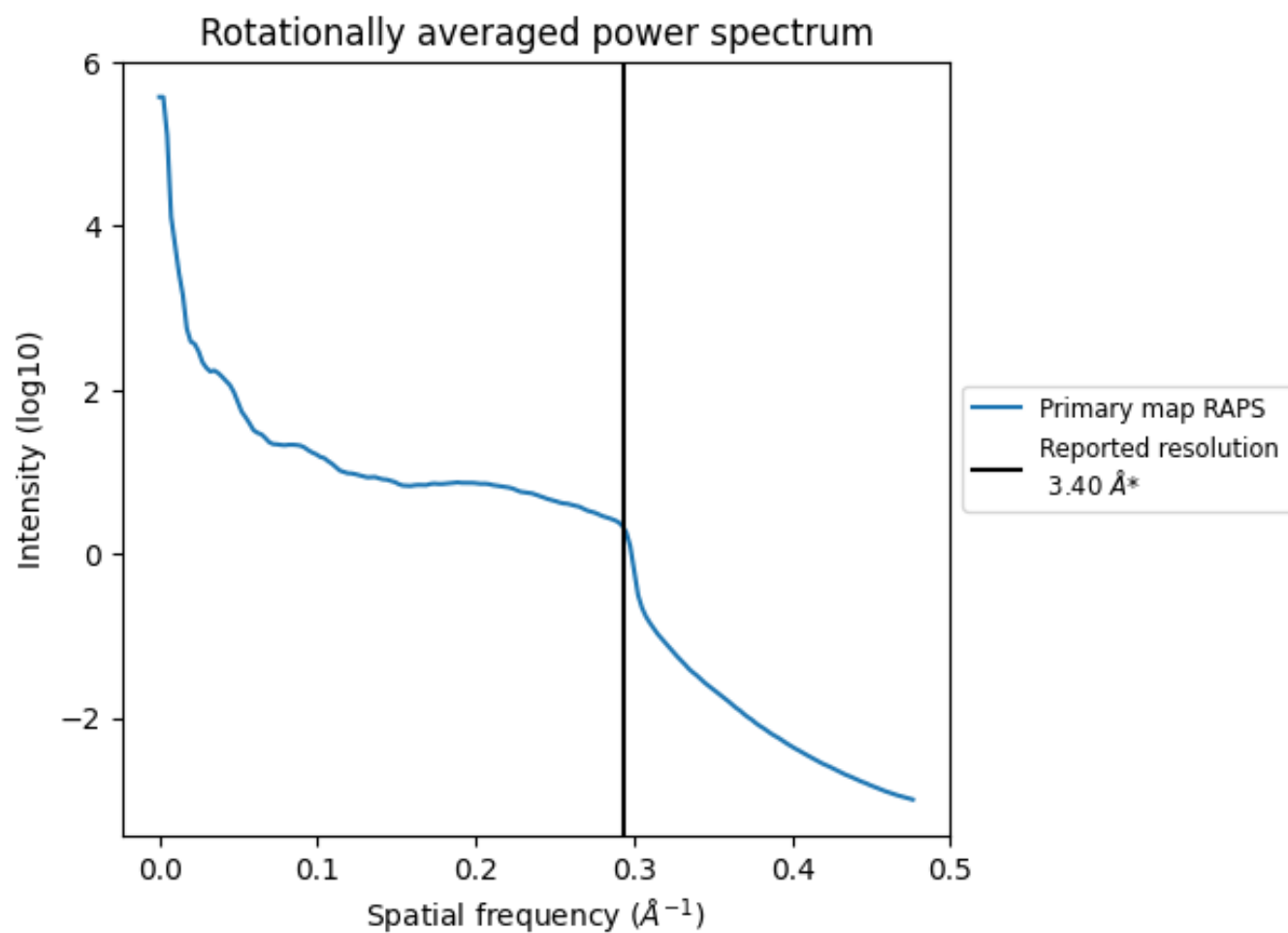
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 735 nm³; this corresponds to an approximate mass of 664 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

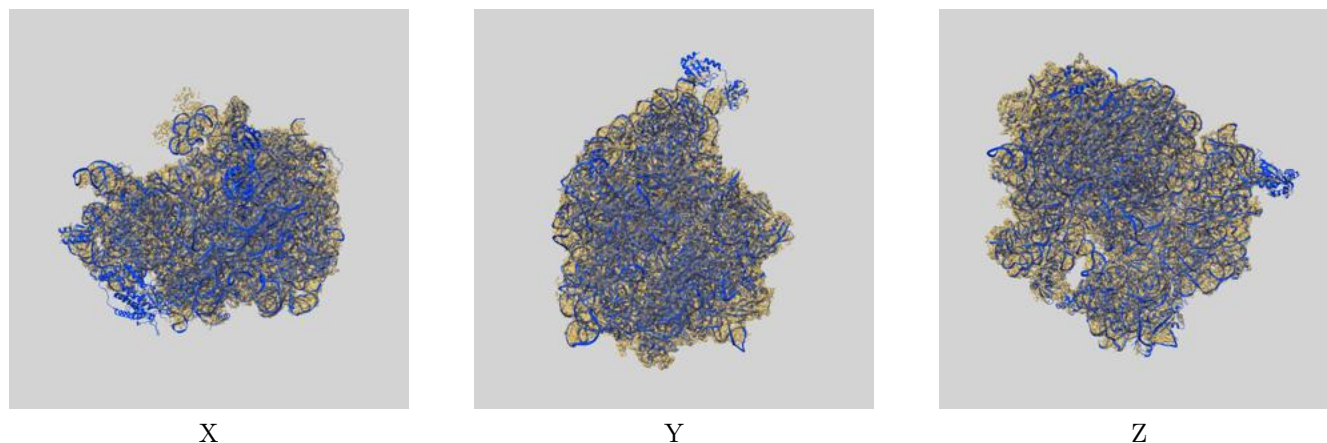
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

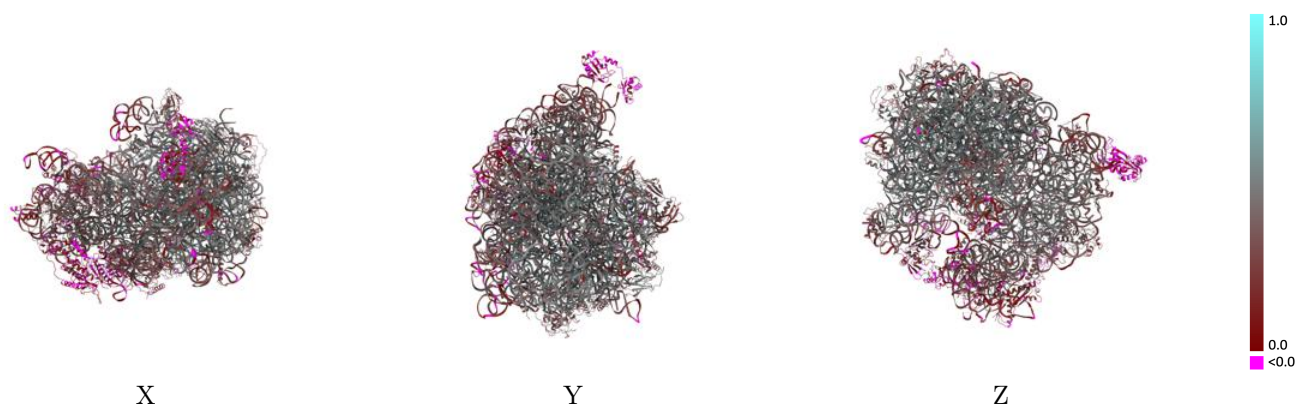
This section contains information regarding the fit between EMDB map EMD-6709 and PDB model 5X8P. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



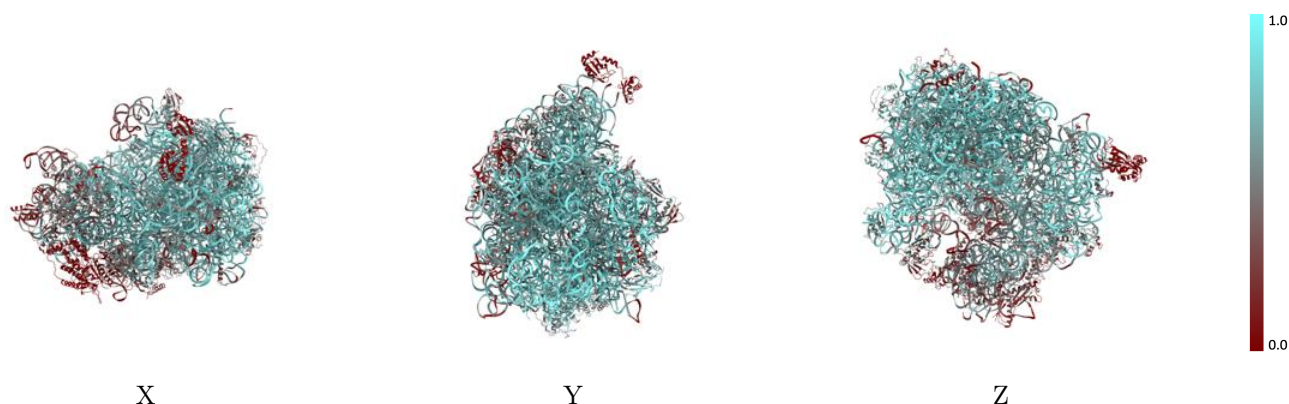
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



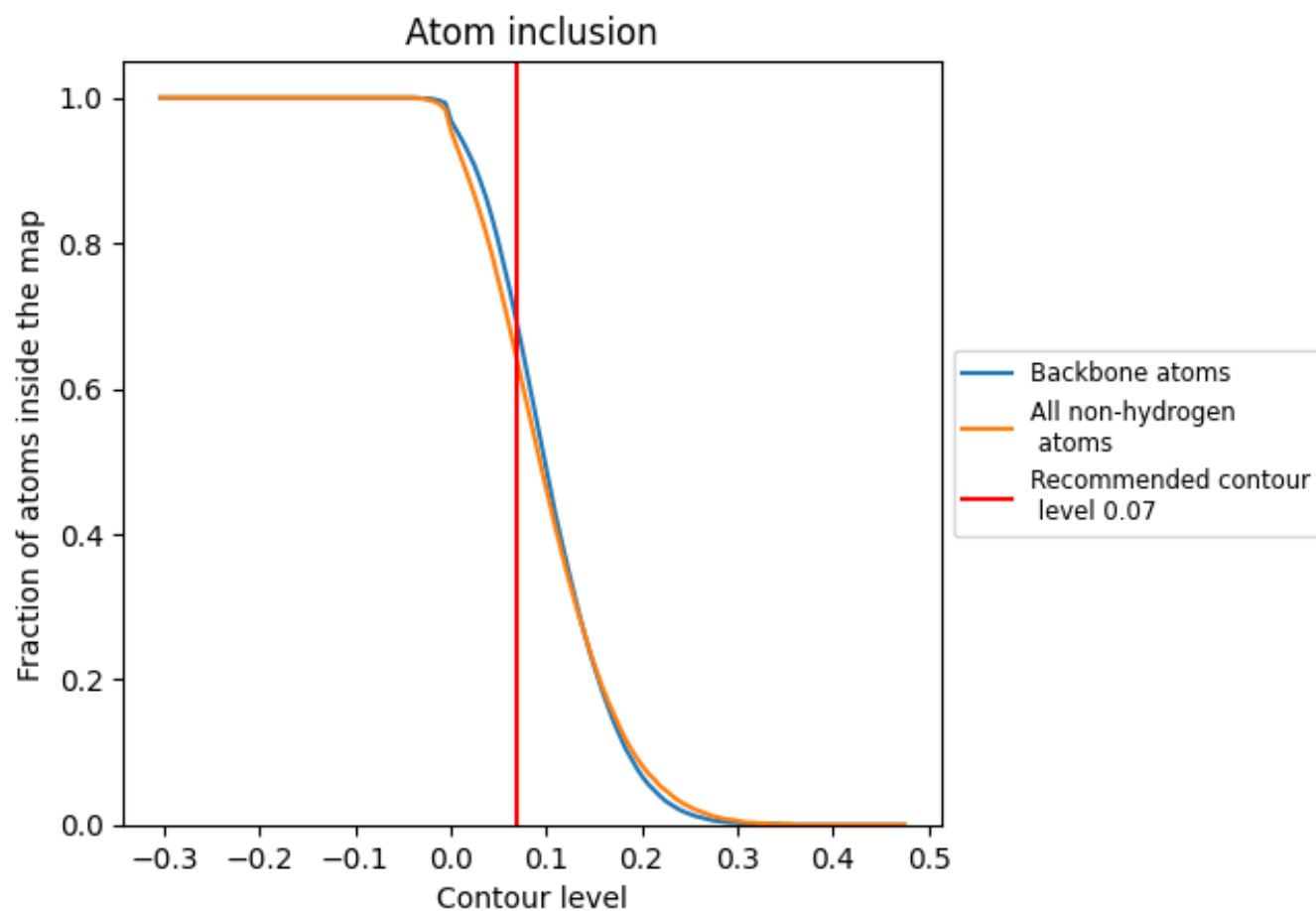
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6370	 0.3770
0	 0.1470	 0.1010
1	 0.6300	 0.4030
2	 0.5600	 0.3230
3	 0.6750	 0.4490
4	 0.6970	 0.4600
5	 0.6530	 0.3820
6	 0.4810	 0.3530
7	 0.6500	 0.4450
8	 0.0060	 0.0030
A	 0.7680	 0.4390
B	 0.7720	 0.3940
C	 0.6000	 0.4010
D	 0.6650	 0.4390
E	 0.6040	 0.3820
F	 0.3250	 0.2190
G	 0.4690	 0.3260
H	 0.2330	 0.2400
K	 0.5820	 0.4030
L	 0.5480	 0.3940
M	 0.6680	 0.4220
N	 0.6250	 0.3930
O	 0.6630	 0.4200
P	 0.5760	 0.3490
Q	 0.5940	 0.3900
R	 0.6490	 0.3930
S	 0.5480	 0.3760
T	 0.5480	 0.3770
U	 0.4930	 0.3680
V	 0.5190	 0.3490
W	 0.7950	 0.4450
X	 0.5950	 0.3980
Y	 0.6290	 0.4280
Z	 0.5090	 0.3550
a	 0.6890	 0.3720



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Chain	Atom inclusion	Q-score
b	 0.0590	 0.1410
c	 0.3420	 0.2870
d	 0.4050	 0.3200
e	 0.4770	 0.3310
f	 0.2460	 0.2140
g	 0.1640	 0.1820
h	 0.3790	 0.2850
i	 0.2490	 0.2130
j	 0.2450	 0.2480
k	 0.3140	 0.2520
l	 0.5380	 0.3930
m	 0.2450	 0.1450
n	 0.3370	 0.2590
o	 0.2600	 0.2480
p	 0.5020	 0.3410
q	 0.4420	 0.3440
r	 0.3370	 0.2620
s	 0.2290	 0.1610
t	 0.4350	 0.2550
u	 0.2040	 0.1680
v	 0.0190	 -0.0060
w	 0.0350	 0.0090
x	 0.3010	 0.2430
y	 0.3660	 0.3140