Full wwPDB EM Validation Report ⓘ

Oct 24, 2026 – 10:46 am BST

PDB ID	:	9TRT / pdb_00009trt
EMDB ID	:	EMD-56197
Title	:	Structure of the Plant mitochondrial pre-initiation complex 3, (SSU,mtIF3,mRNA,tRNA)
Authors	:	Skaltsogiannis, V.; Giege, P.; Soufari, H.
Deposited on	:	2025-12-27
Resolution	:	3.05 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:

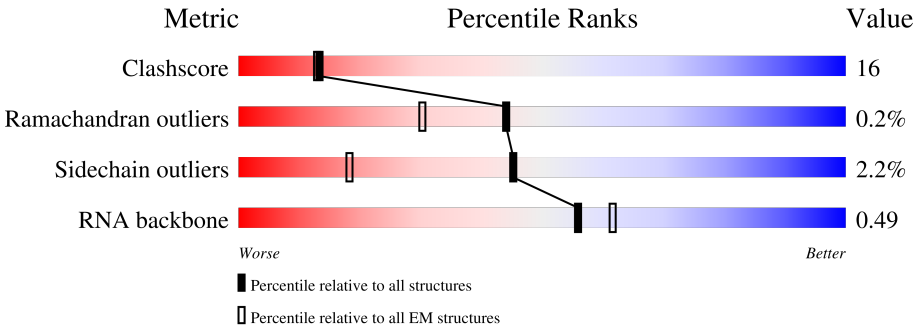
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

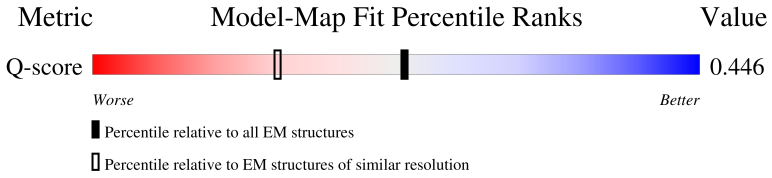
1 Overall quality at a glance

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

The reported resolution of this entry is 3.05 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	13971 (2.55 - 3.55)

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 <=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	2	1601	7% 50% 40% 9%
2	5	77	58% 6% 51% 40% .
3	6	5	60% 40% 60%

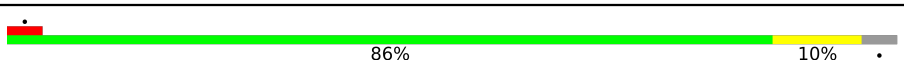
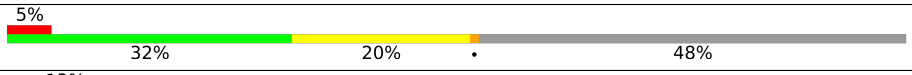
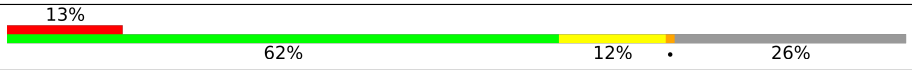
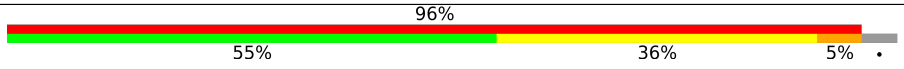
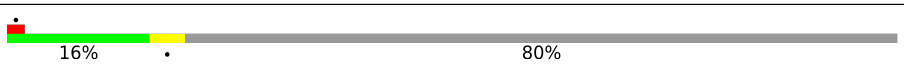
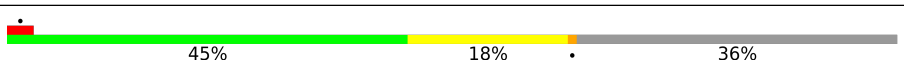
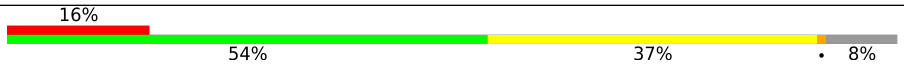
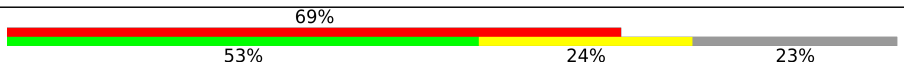
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Mol	Chain	Length	Quality of chain
4	8	520	18% 28% 9% 63%
5	A	212	60% 34%
6	B	554	13% 67% 17% 16%
7	C	362	6% 59% 31% 8%
8	D	501	15% 57% 26% 17%
9	E	138	48% 24% 27%
10	F	157	87% 82% 18%
11	G	129	73% 26%
12	H	383	12% 40% 14% 45%
13	I	228	43% 6% 50%
14	J	304	7% 24% 17% 58%
15	K	125	81% 18%
16	L	154	64% 8% 29%
17	M	155	61% 5% 35%
18	N	414	22% 5% 72%
19	O	136	60% 21% 19%
20	P	110	7% 58% 25% 17%
21	Q	237	28% 9% 62%
22	R	212	40% 62% 16% 22%
23	S	100	16% 45% 30% 25%
24	T	94	51% 47%
25	U	192	41% 35% 31% 34%
26	V	193	5% 60% 24% 15%
27	W	483	66% 13% 21%
28	X	496	32% 8% 59%

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Mol	Chain	Length	Quality of chain
29	Y	102	
30	Z	153	
31	a	424	
32	b	80	
33	c	128	
34	d	110	
35	e	383	
36	f	410	
37	g	668	
38	h	384	
39	i	725	
40	k	153	
41	l	576	

2 Entry composition

There are 42 unique types of molecules in this entry. The entry contains 92974 atoms, of which 1558 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1599	34252	15300	6247	11106	1599	0	0

- Molecule 2 is a RNA chain called initiator tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5	77	1641	733	294	537	77	0	0

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	5	107	48	19	35	5	0	0

- Molecule 4 is a protein called Translation initiation factor IF3-1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	8	190	3075	968	1558	272	270	7	0	0

- Molecule 5 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	204	1611	1032	284	285	10	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	467	3877	2520	701	643	13	0	0

- Molecule 7 is a protein called Ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	333	Total	C	N	O	S	0	0
			2806	1793	540	462	11		

- Molecule 8 is a protein called S5 DRBM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	417	Total	C	N	O	S	0	0
			3425	2146	603	664	12		

- Molecule 9 is a protein called Ribosomal protein bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	101	Total	C	N	O	S	0	0
			823	535	145	138	5		

- Molecule 10 is a protein called Small ribosomal subunit protein uS7m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	157	Total	C	N	O	S	0	0
			1254	793	244	213	4		

- Molecule 11 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	128	Total	C	N	O	S	0	0
			1037	652	193	189	3		

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	212	Total	C	N	O	S	0	0
			1671	1048	308	310	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS10 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	113	Total	C	N	O	S	0	0
			941	602	174	159	6		

- Molecule 14 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	127	Total	C	N	O	S	0	0
			988	608	195	181	4		

- Molecule 15 is a protein called Small ribosomal subunit protein uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	124	Total	C	N	O	S	0	0
			993	614	209	166	4		

- Molecule 16 is a protein called Ribosomal protein uS13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	110	Total	C	N	O	S	0	0
			873	529	185	154	5		

- Molecule 17 is a protein called Small ribosomal subunit protein uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	101	Total	C	N	O	S	0	0
			843	524	174	140	5		

- Molecule 18 is a protein called Small ribosomal subunit protein uS15c.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	116	Total	C	N	O	S	0	0
			941	593	170	171	7		

- Molecule 19 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	110	Total	C	N	O	S	0	0
			869	550	169	144	6		

- Molecule 20 is a protein called Small ribosomal subunit protein uS17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	91	Total	C	N	O	S	0	0
			717	455	135	124	3		

- Molecule 21 is a protein called Small ribosomal subunit protein bS18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	90	Total	C	N	O	S	0	0
			724	460	127	134	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	166	Total	C	N	O	S	0	0
			1299	819	236	237	7		

- Molecule 23 is a protein called Ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	75	Total	C	N	O	S	0	0
			611	386	120	103	2		

- Molecule 24 is a protein called 30S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	50	Total	C	N	O	S	0	0
			408	260	79	68	1		

- Molecule 25 is a protein called Ribosomal protein mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	127	Total	C	N	O	S	0	0
			1014	647	184	178	5		

- Molecule 26 is a protein called Ribosomal protein mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	164	Total	C	N	O	S	0	0
			1399	874	266	255	4		

- Molecule 27 is a protein called Small ribosomal subunit protein mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	380	Total	C	N	O	S	0	0
			3062	1955	535	559	13		

- Molecule 28 is a protein called RRM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	204	Total	C	N	O	S	0	0
			1613	1011	262	329	11		

- Molecule 29 is a protein called MOSC domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	98	Total	C	N	O	S	0	0
			793	495	159	137	2		

- Molecule 30 is a protein called Ribosomal Protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	80	Total	C	N	O	S	0	0
			649	422	121	104	2		

- Molecule 31 is a protein called Small ribosomal subunit protein mS35 mitochondrial conserved domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	315	Total	C	N	O	S	0	0
			2486	1546	448	482	10		

- Molecule 32 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	77	Total	C	N	O	S	0	0
			610	378	116	108	8		

- Molecule 33 is a protein called Small ribosomal subunit protein mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	26	Total	C	N	O	S	0	0
			232	145	54	32	1		

- Molecule 34 is a protein called IGR domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	78	Total	C	N	O	S	0	0
			616	403	110	102	1		

- Molecule 35 is a protein called Ribosomal protein mS45.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	246	Total	C	N	O	S	0	0
			2074	1310	374	380	10		

- Molecule 36 is a protein called Ribosomal protein mS47.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	377	Total	C	N	O	S	0	0
			2922	1843	486	573	20		

- Molecule 37 is a protein called Small ribosomal subunit protein mS81 (rPPR8).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	103	Total	C	N	O	S	0	0
			814	524	132	151	7		

- Molecule 38 is a protein called Adenylyl cyclase.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	310	Total	C	N	O	S	0	0
			2463	1557	438	455	13		

- Molecule 39 is a protein called PROP1-like PPR domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	336	Total	C	N	O	S	0	0
			2722	1716	458	533	15		

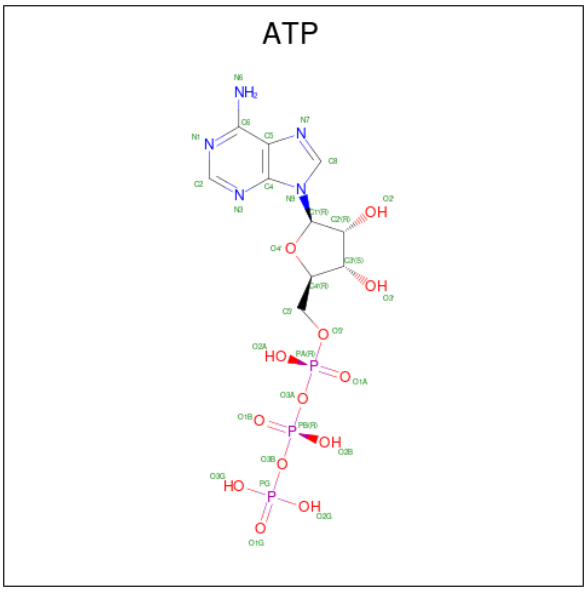
- Molecule 40 is a protein called RRM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	28	Total	C	N	O	S	0	0
			220	139	42	35	4		

- Molecule 41 is a protein called Small ribosomal subunit protein mS80 (rPPR6).

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	442	Total	C	N	O	S	0	0
			3468	2209	573	663	23		

- Molecule 42 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
42	W	1	Total	C	N	O	P	0
			31	10	5	13	3	

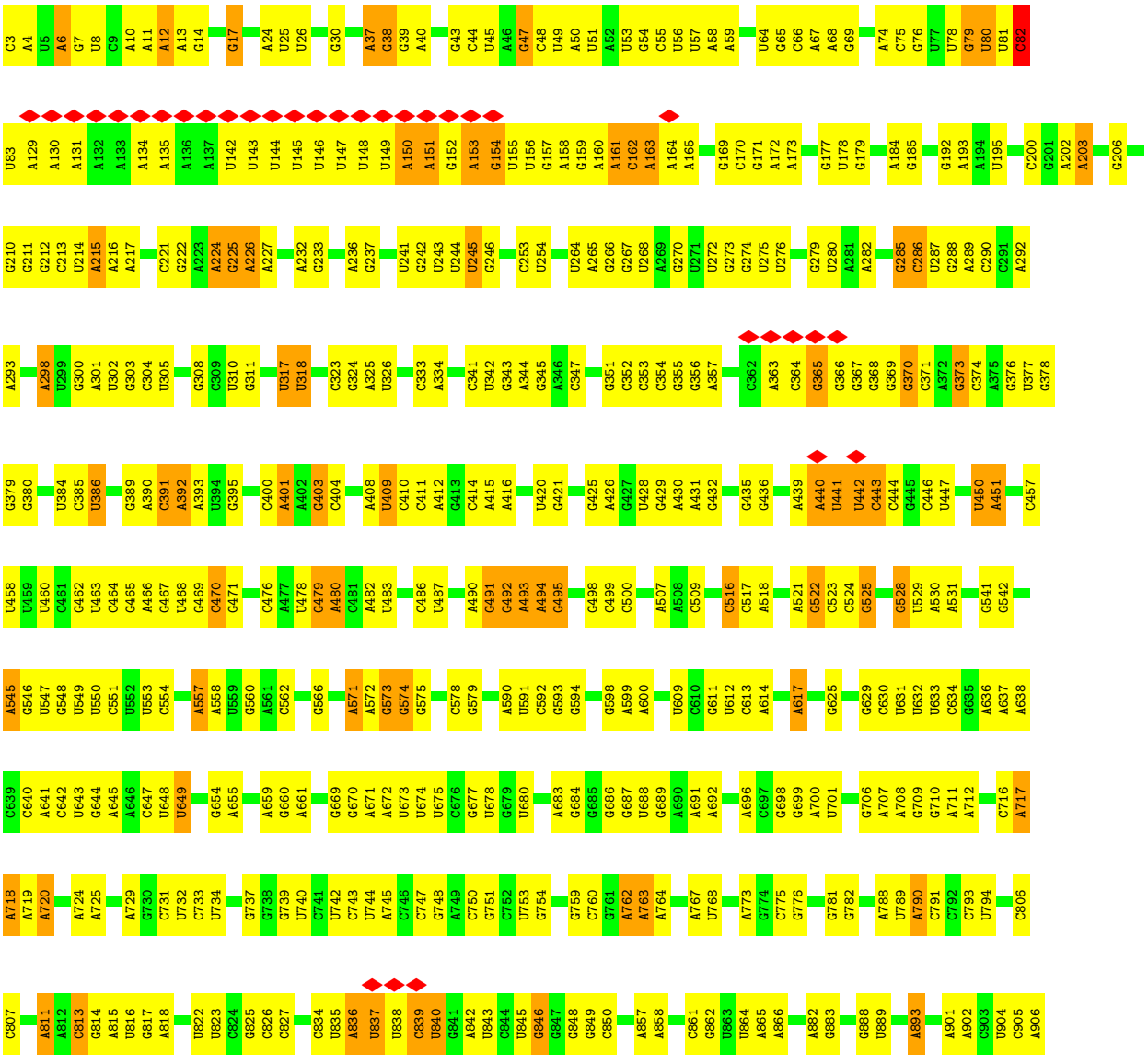
3 Residue-property plots (i)

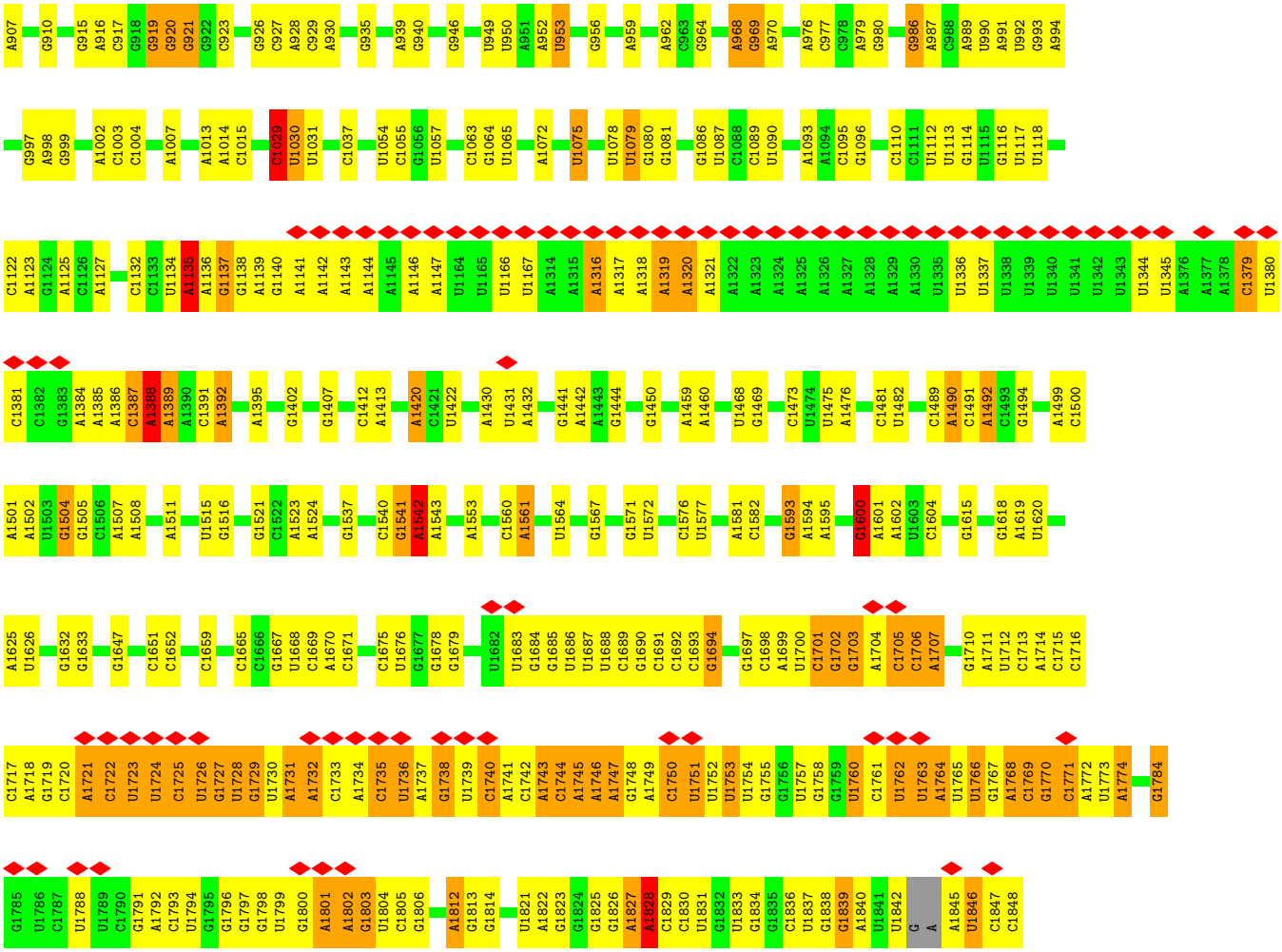
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S rRNA

Chain 2:



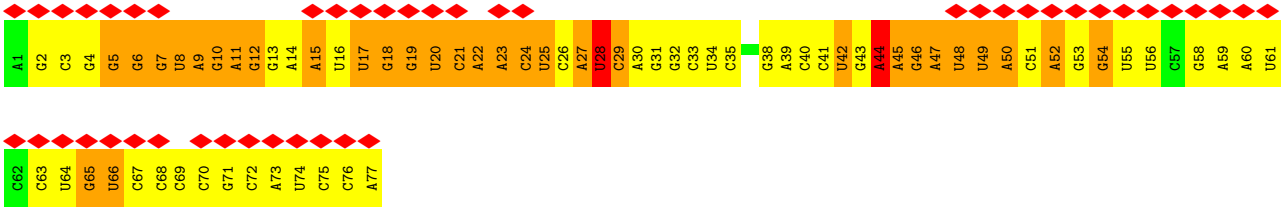




• Molecule 2: initiator tRNA

Chain 5:

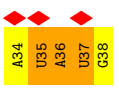




• Molecule 3: mRNA

Chain 6:

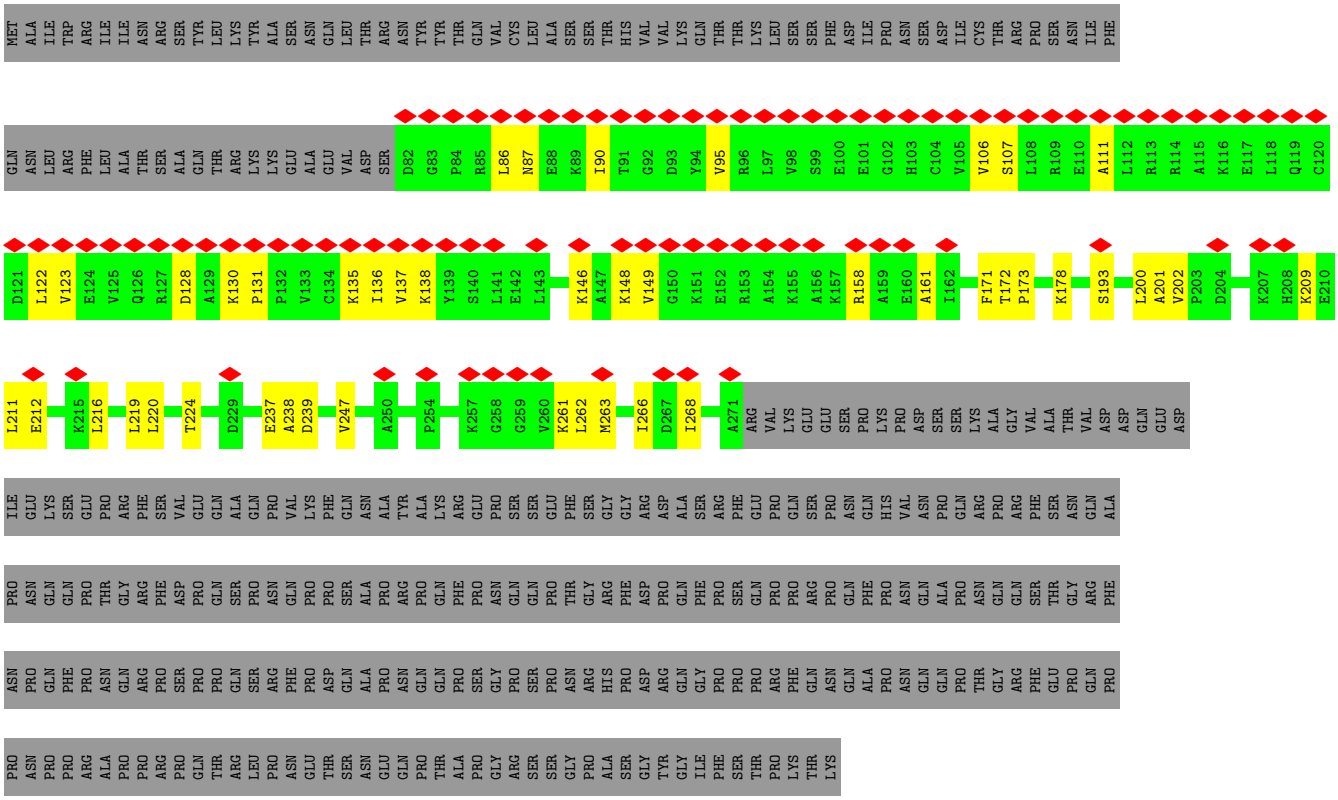




• Molecule 4: Translation initiation factor IF3-1, mitochondrial

Chain 8:

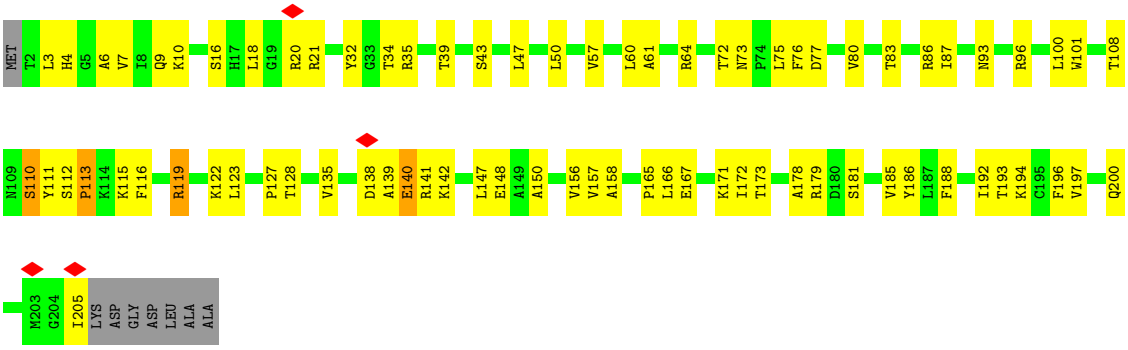




• Molecule 5: Ribosomal protein S2

Chain A:

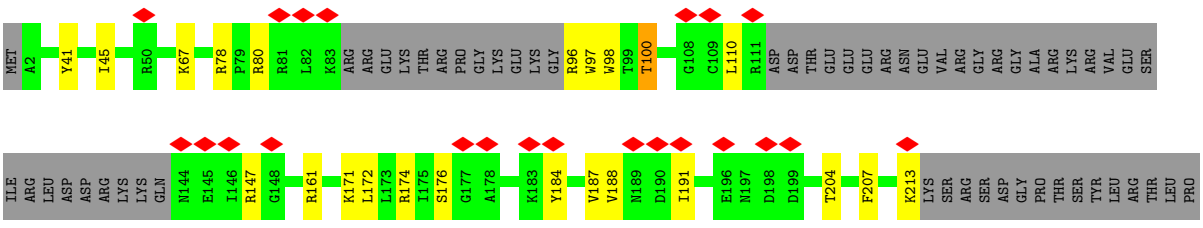


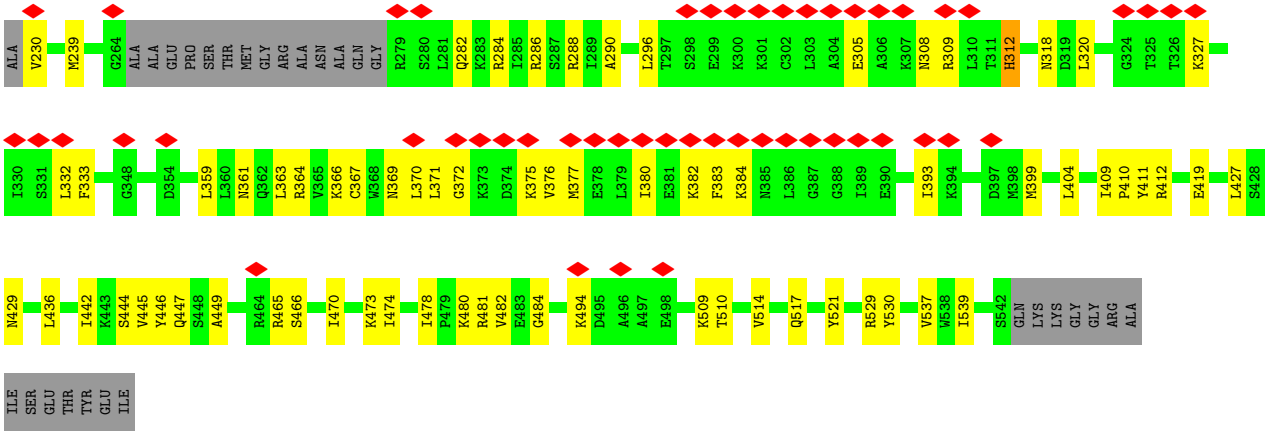


• Molecule 6: Small ribosomal subunit protein uS3m

Chain B:



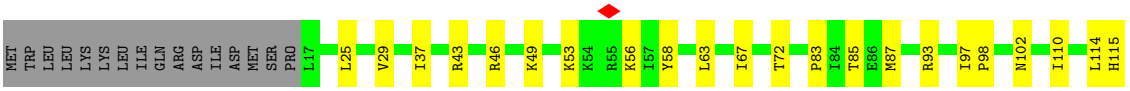


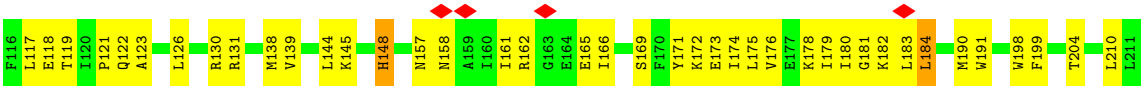


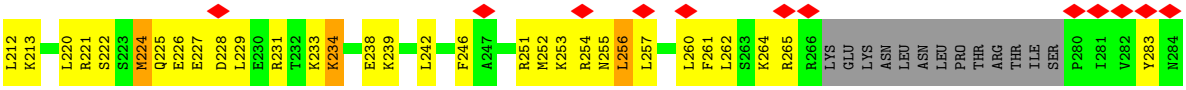
• Molecule 7: Ribosomal protein S4

Chain C:







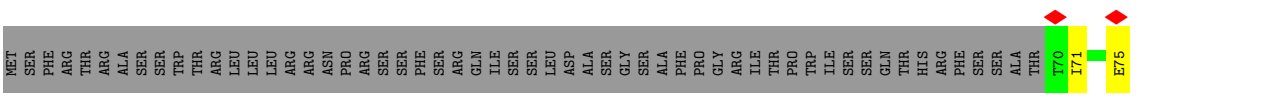


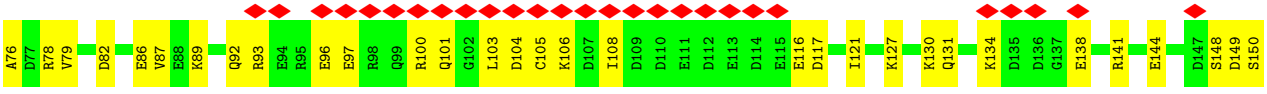


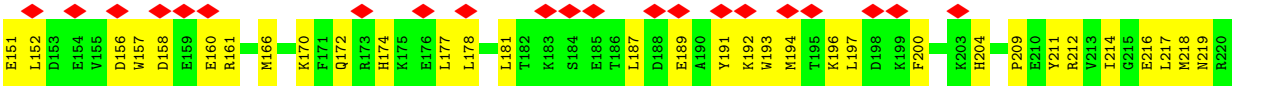
• Molecule 8: S5 DRBM domain-containing protein

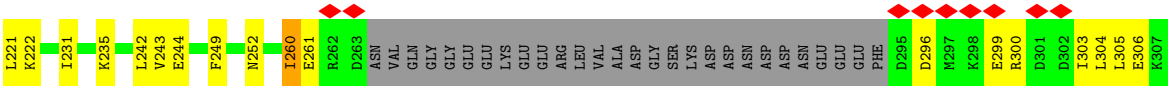
Chain D:

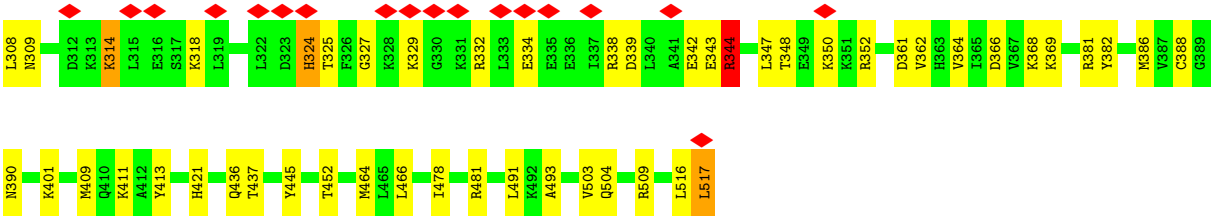






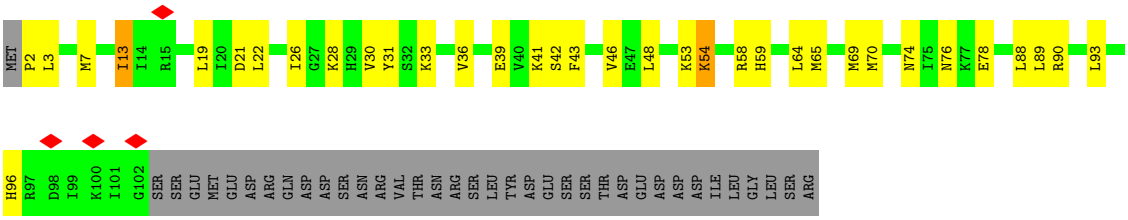




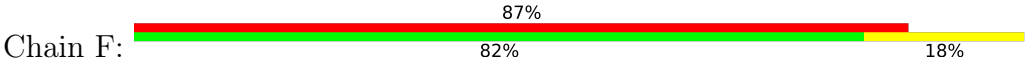


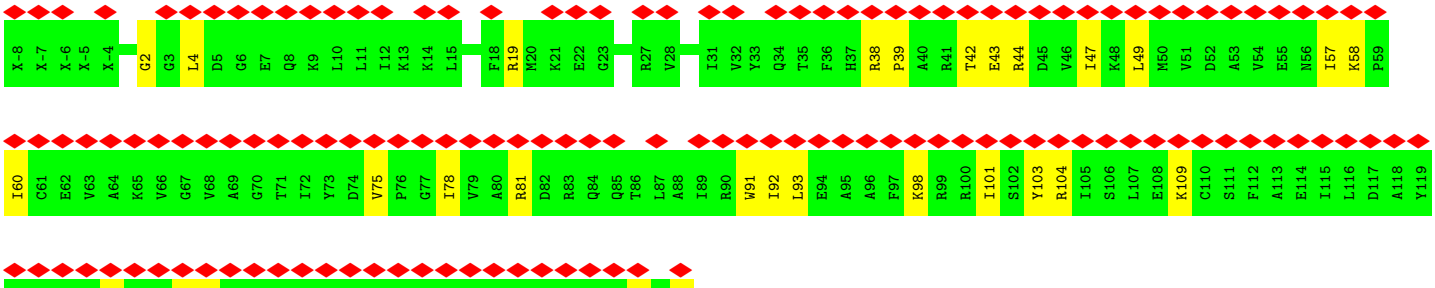
• Molecule 9: Ribosomal protein bS6m





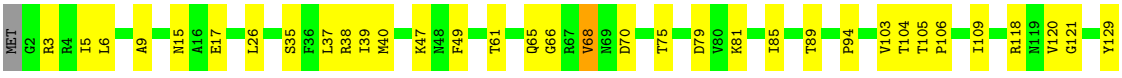
• Molecule 10: Small ribosomal subunit protein uS7m



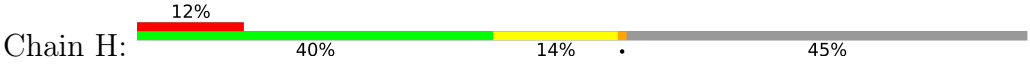


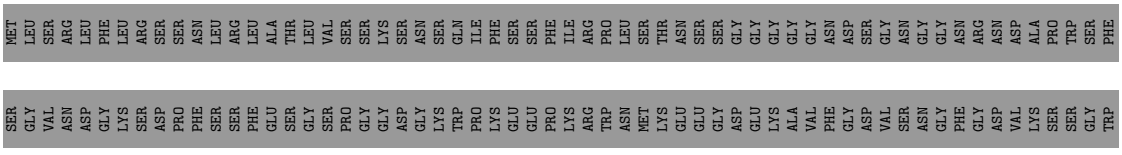
• Molecule 11: 30S ribosomal protein S8, chloroplastic

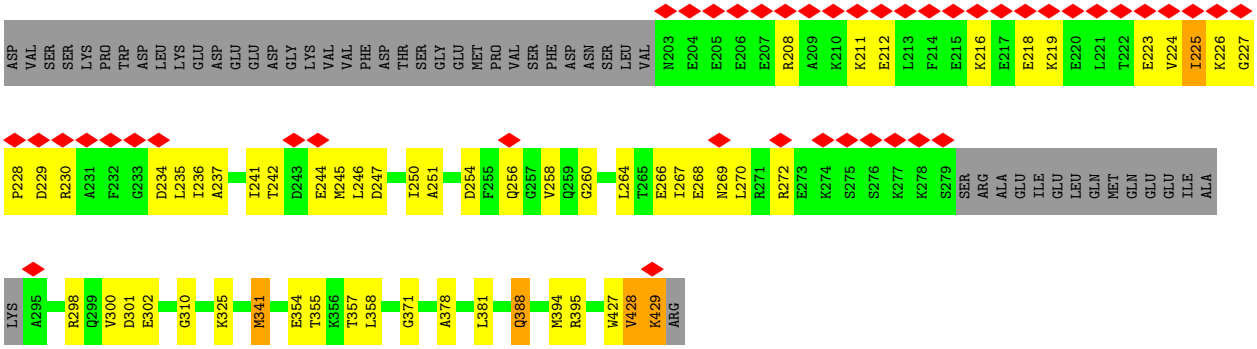




• Molecule 12: 30S ribosomal protein S9



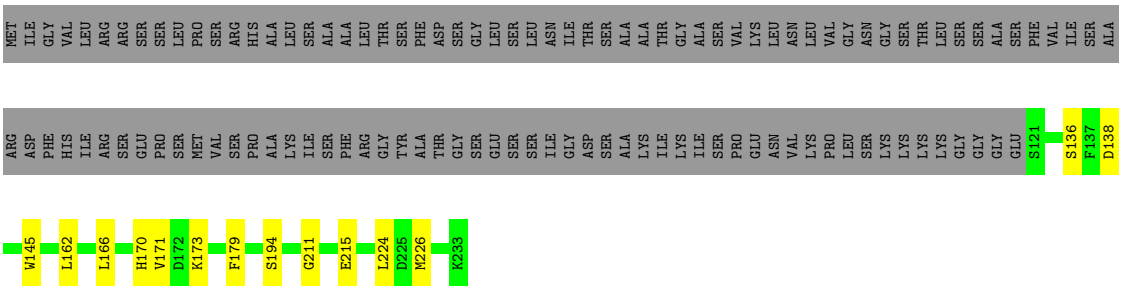




• Molecule 13: Small ribosomal subunit protein uS10 domain-containing protein

Chain I:

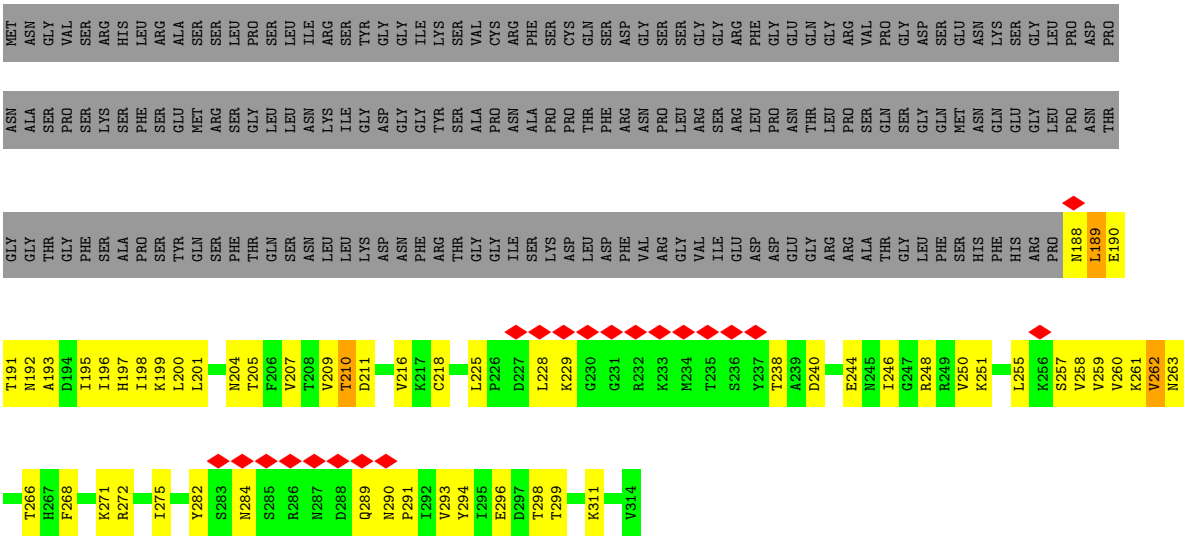




• Molecule 14: Ribosomal protein S11

Chain J:

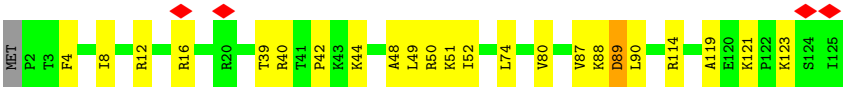




• Molecule 15: Small ribosomal subunit protein uS12m

Chain K:

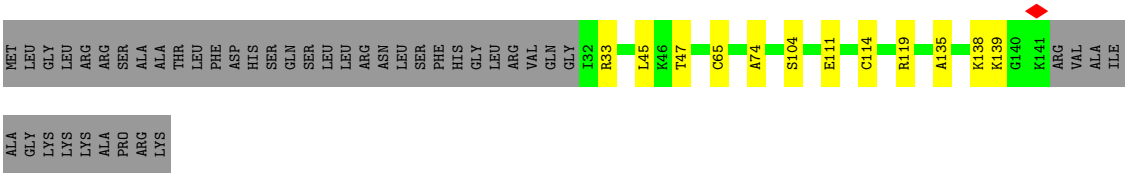




• Molecule 16: Ribosomal protein uS13m

Chain L:

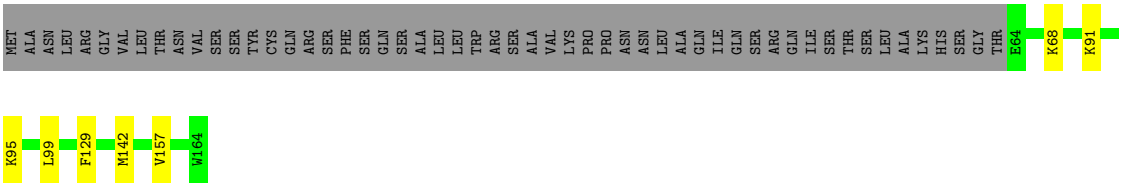




• Molecule 17: Small ribosomal subunit protein uS14m

Chain M:

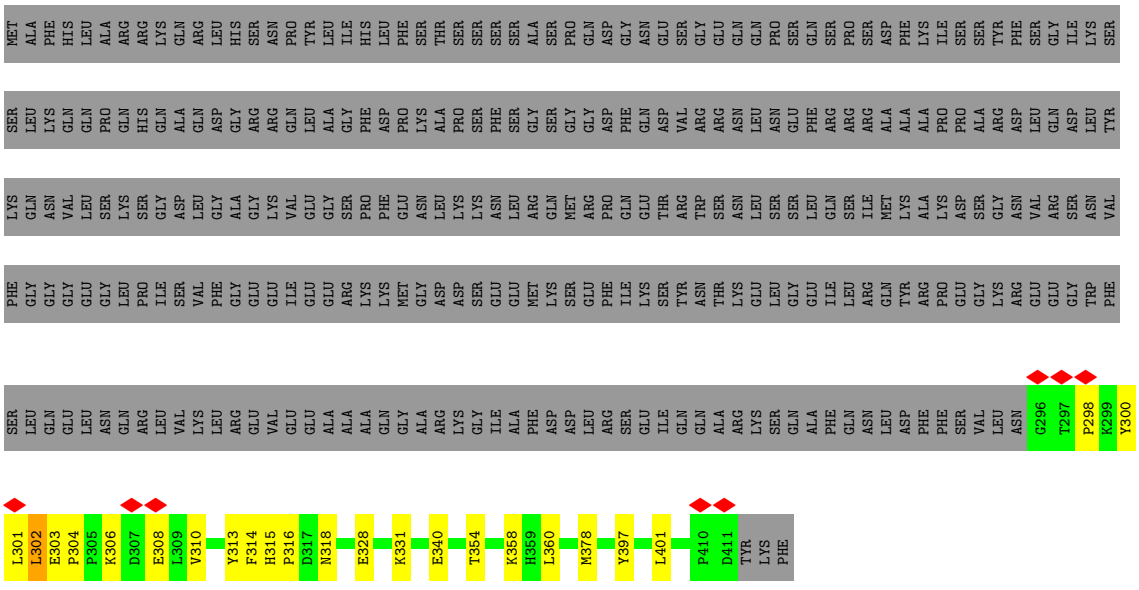




• Molecule 18: Small ribosomal subunit protein uS15c

Chain N:

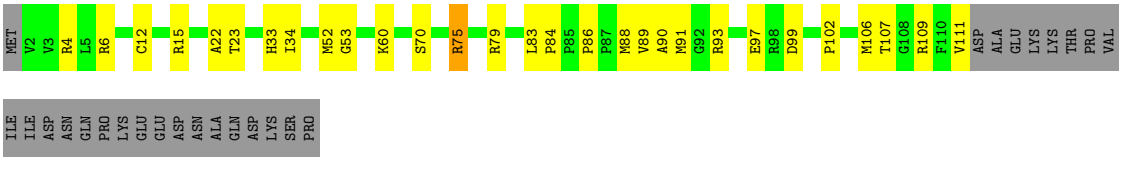




• Molecule 19: 30S ribosomal protein S16

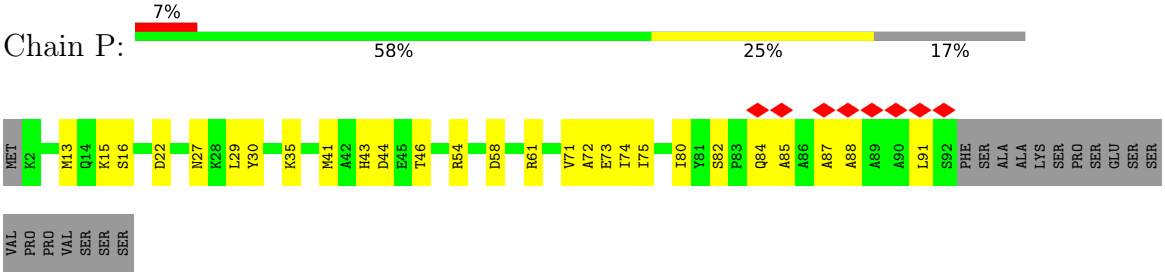
Chain O:





• Molecule 20: Small ribosomal subunit protein uS17c

Chain P:



• Molecule 21: Small ribosomal subunit protein bS18c

Chain Q:



• Molecule 22: Small ribosomal subunit protein uS19m

Chain R:



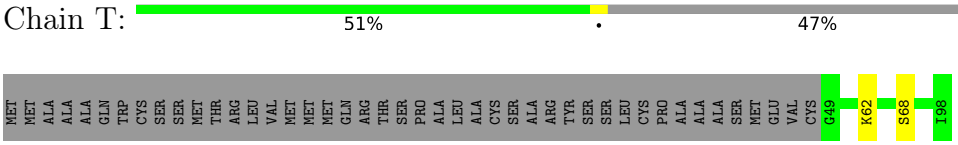
• Molecule 23: Ribosomal protein S21

Chain S:



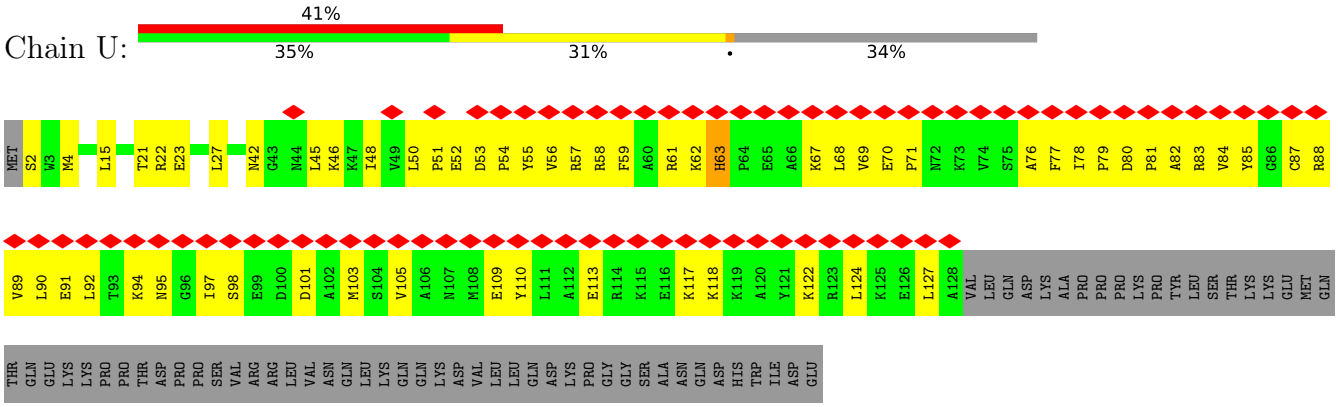
• Molecule 24: 30S ribosomal protein S31, mitochondrial

Chain T:



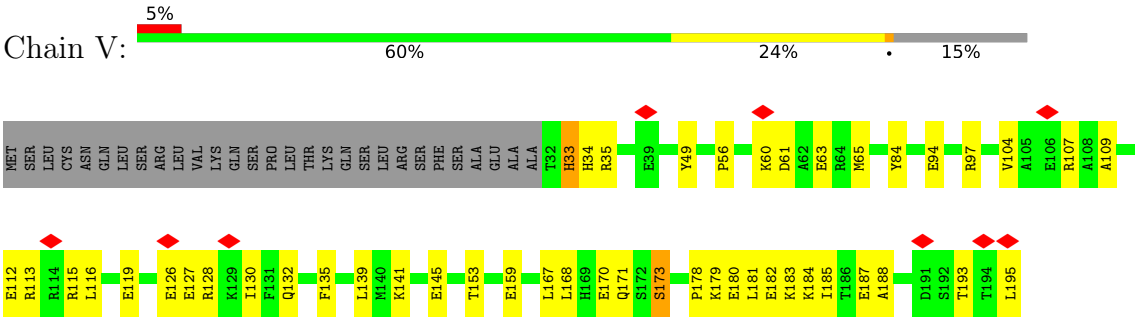
• Molecule 25: Ribosomal protein mS23

Chain U:



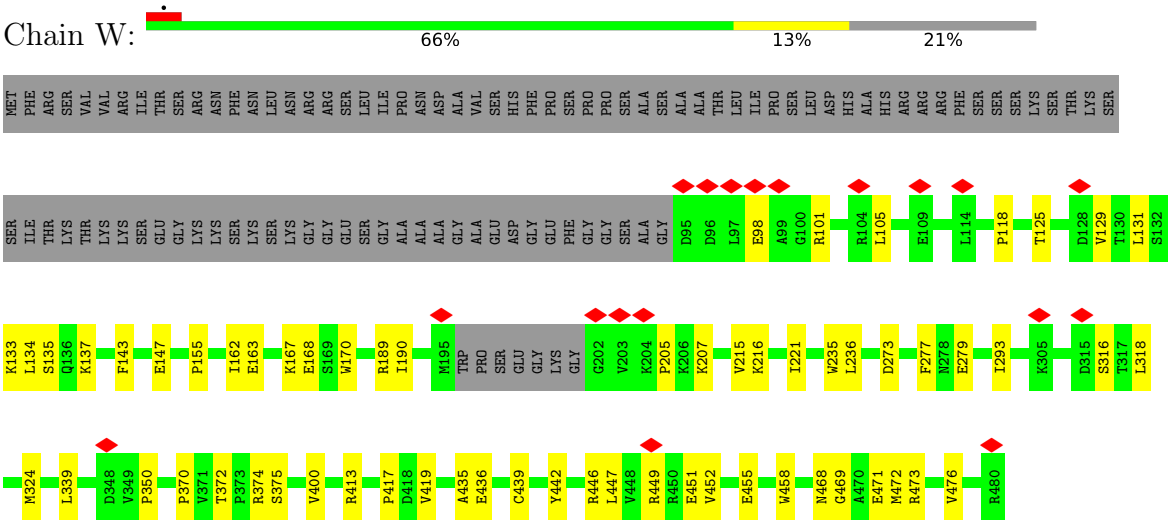
• Molecule 26: Ribosomal protein mS26

Chain V:



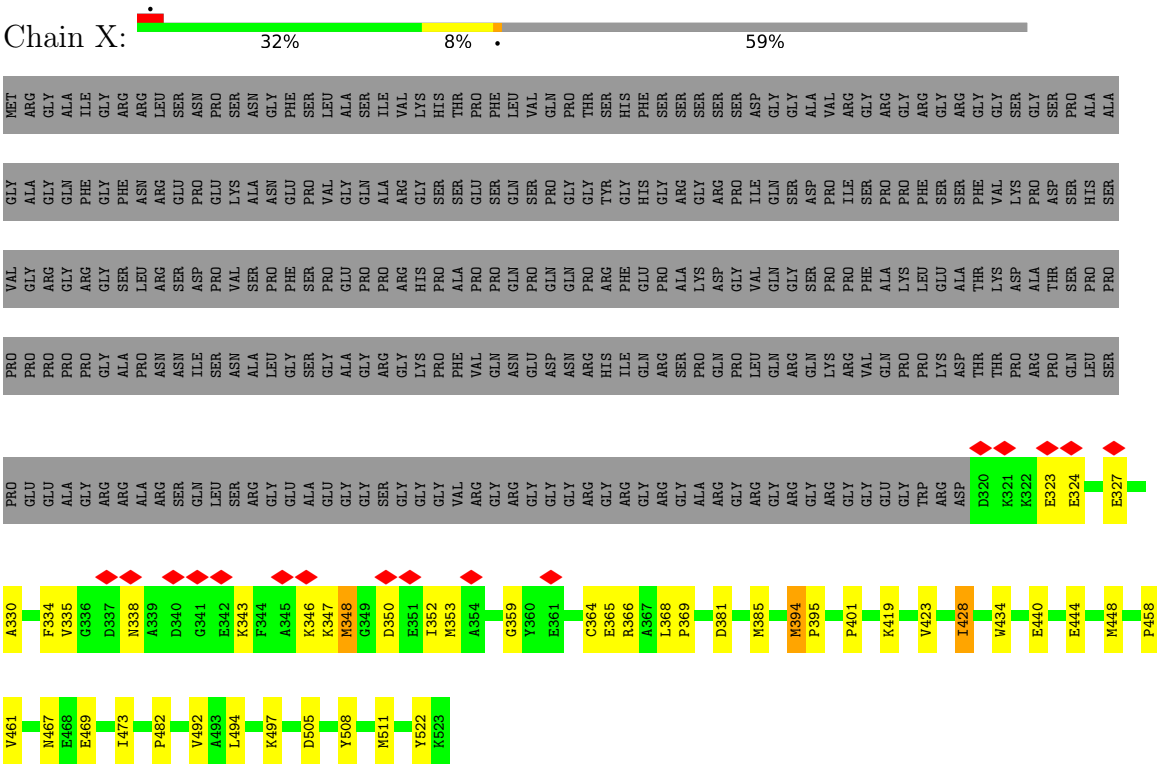
• Molecule 27: Small ribosomal subunit protein mS29

Chain W:



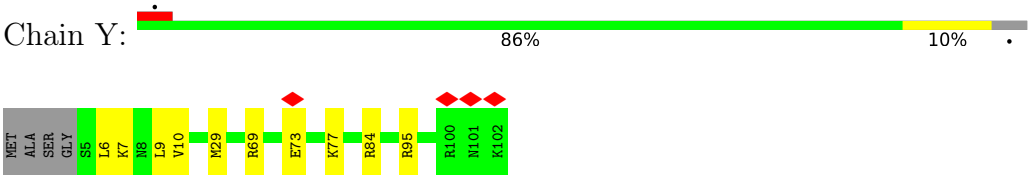
• Molecule 28: RRM domain-containing protein

Chain X:



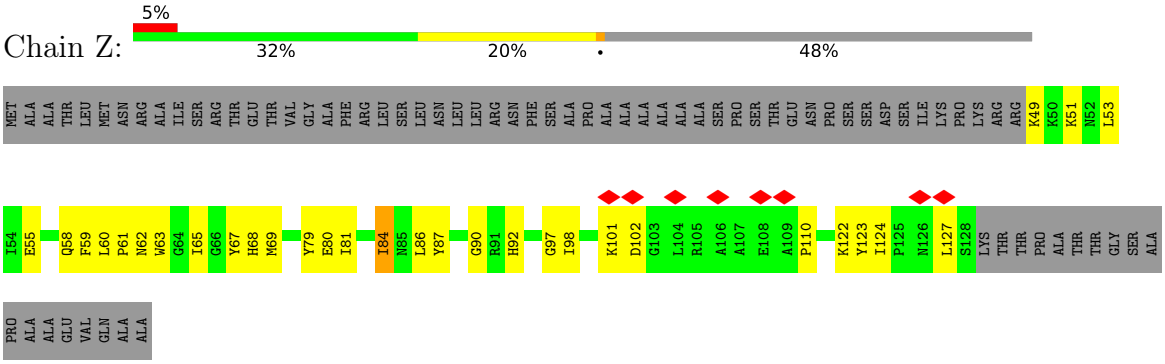
• Molecule 29: MOSC domain-containing protein

Chain Y:



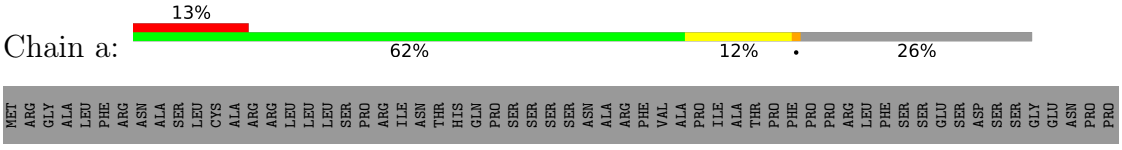
• Molecule 30: Ribosomal Protein S34, mitochondrial

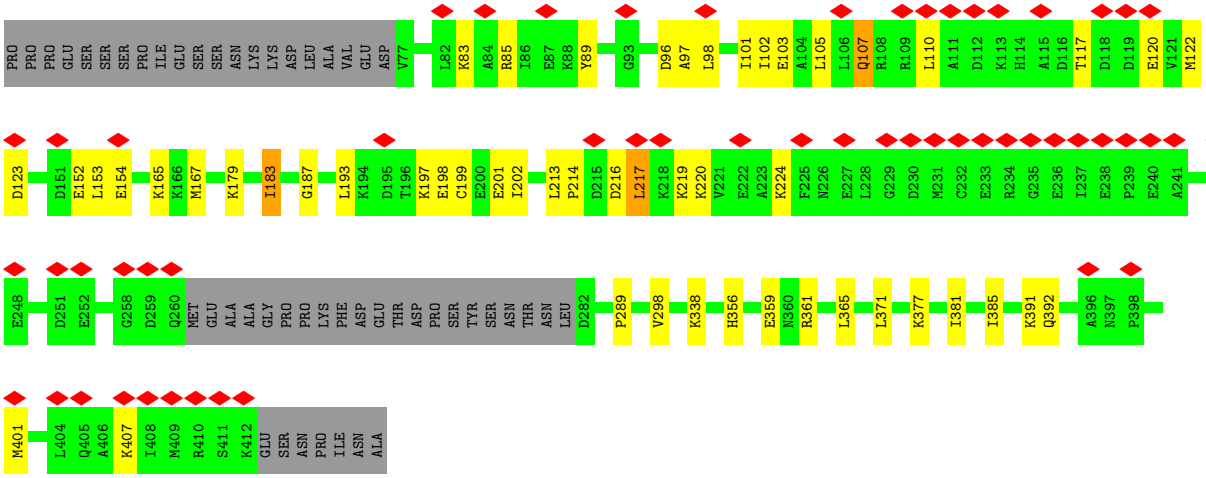
Chain Z:



• Molecule 31: Small ribosomal subunit protein mS35 mitochondrial conserved domain-containing protein

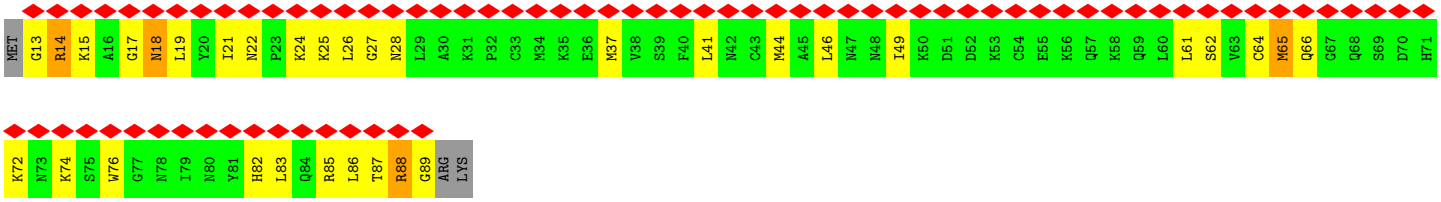
Chain a:





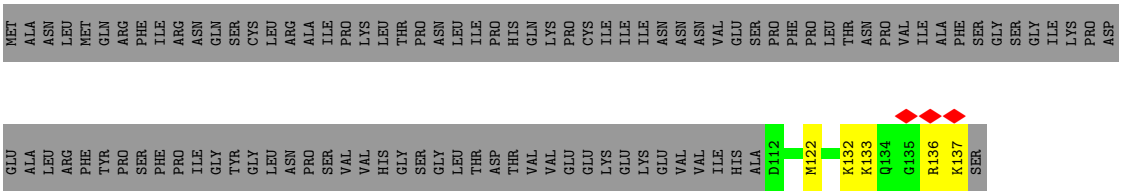
• Molecule 32: CBS domain-containing protein





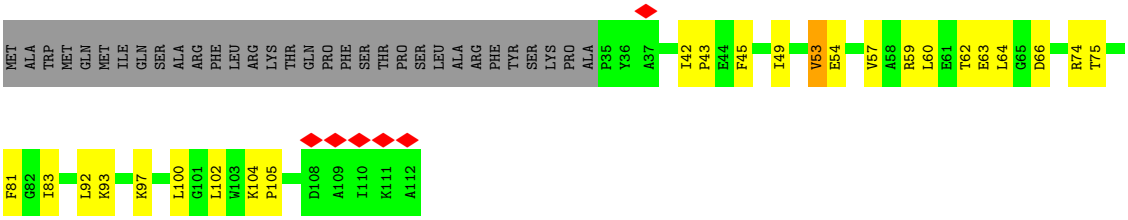
• Molecule 33: Small ribosomal subunit protein mS38





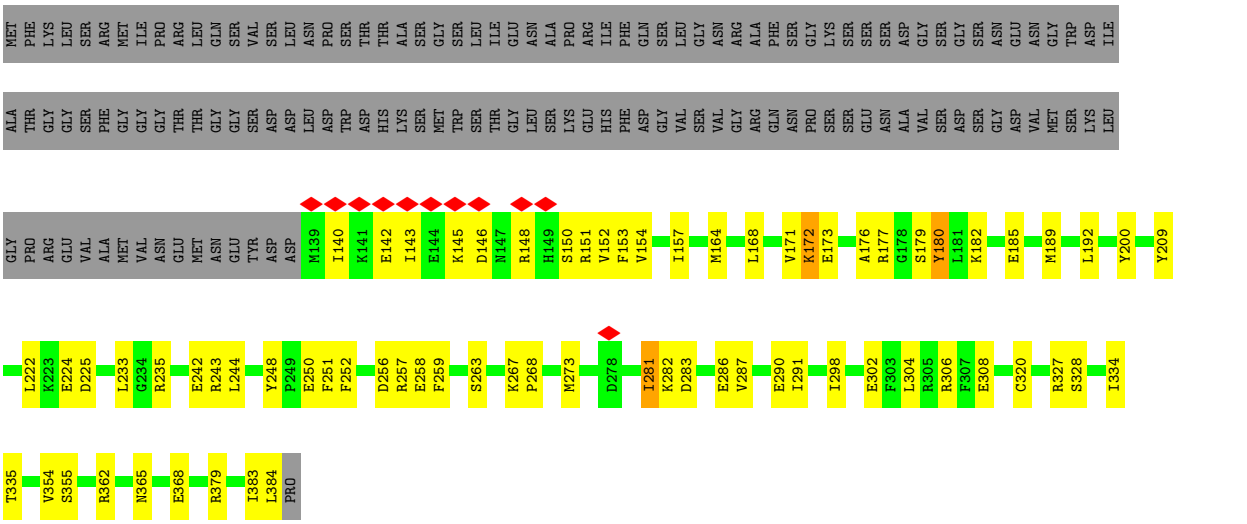
• Molecule 34: IGR domain-containing protein





• Molecule 35: Ribosomal protein mS45

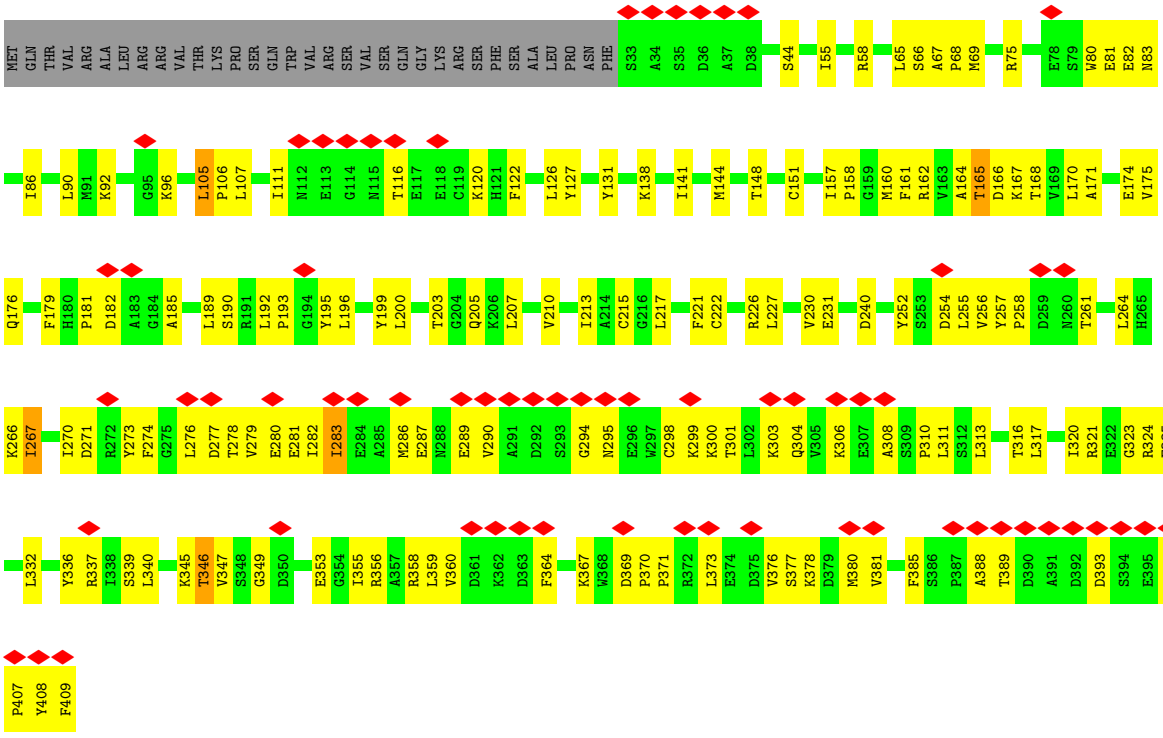




• Molecule 36: Ribosomal protein mS47

Chain f:

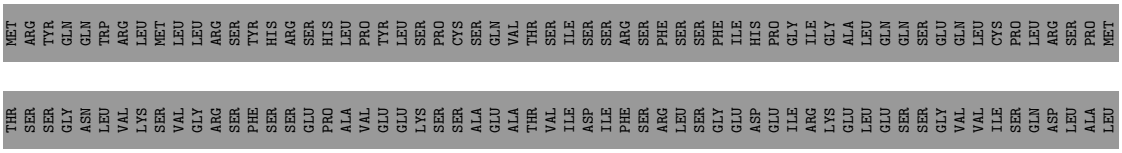


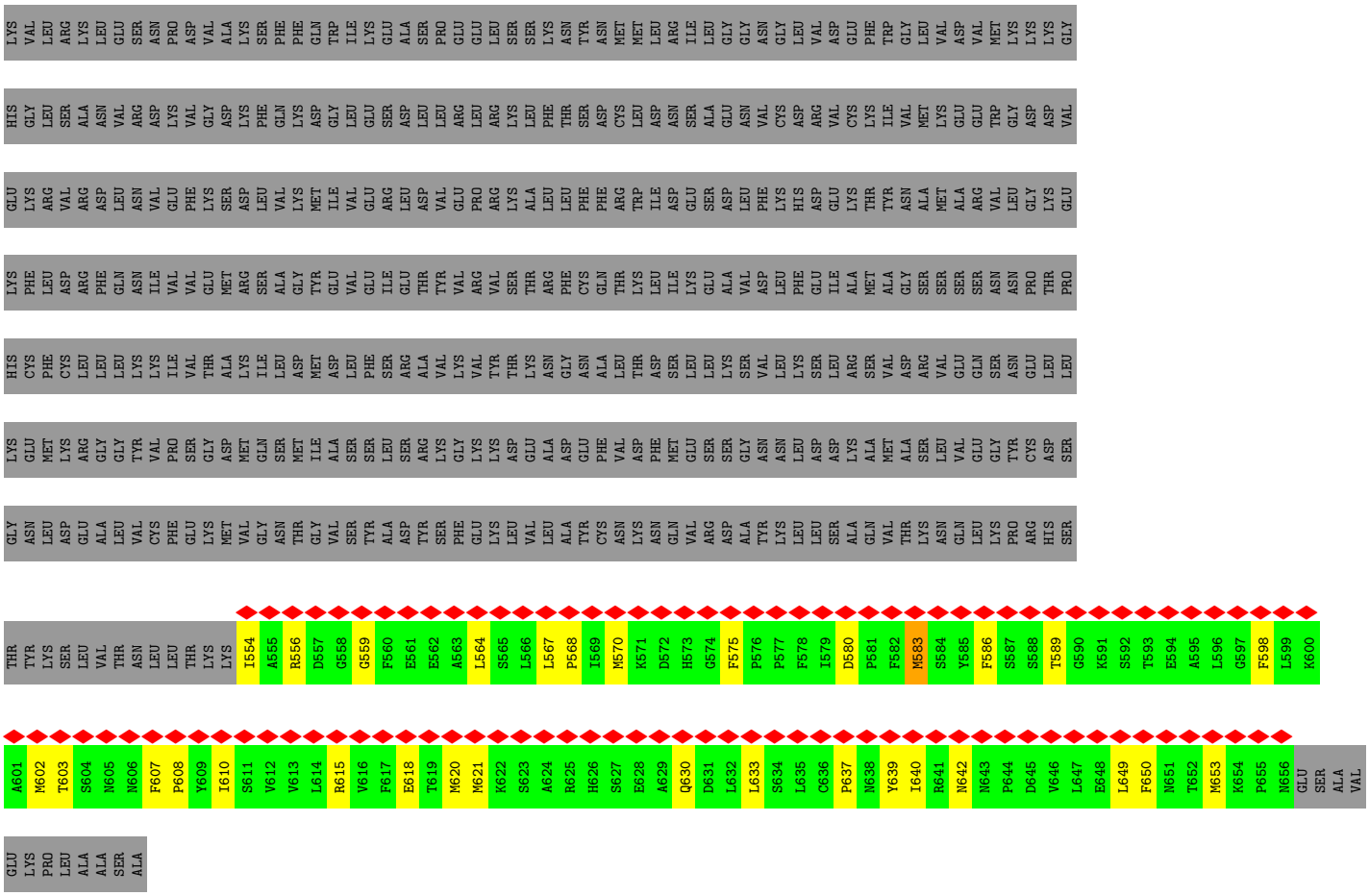


• Molecule 37: Small ribosomal subunit protein mS81 (rPPR8)

Chain g:



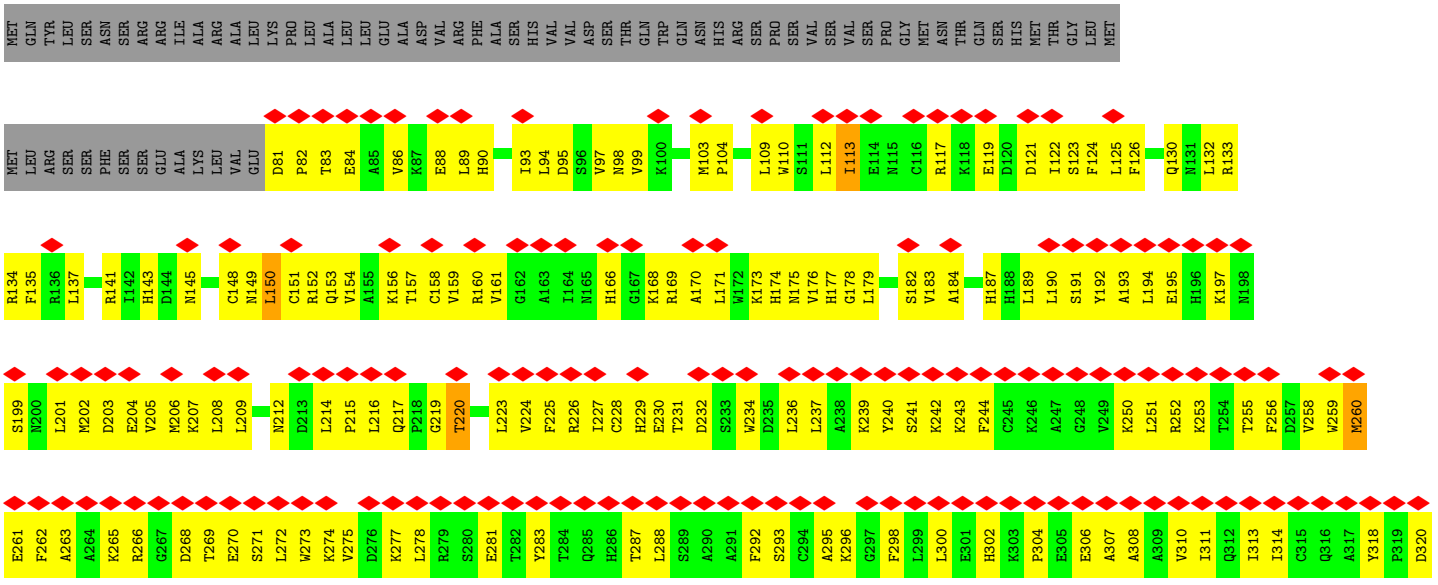


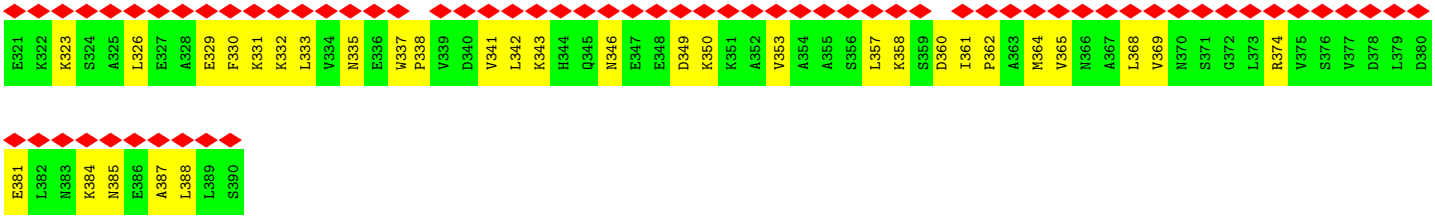


• Molecule 38: Adenylyl cyclase

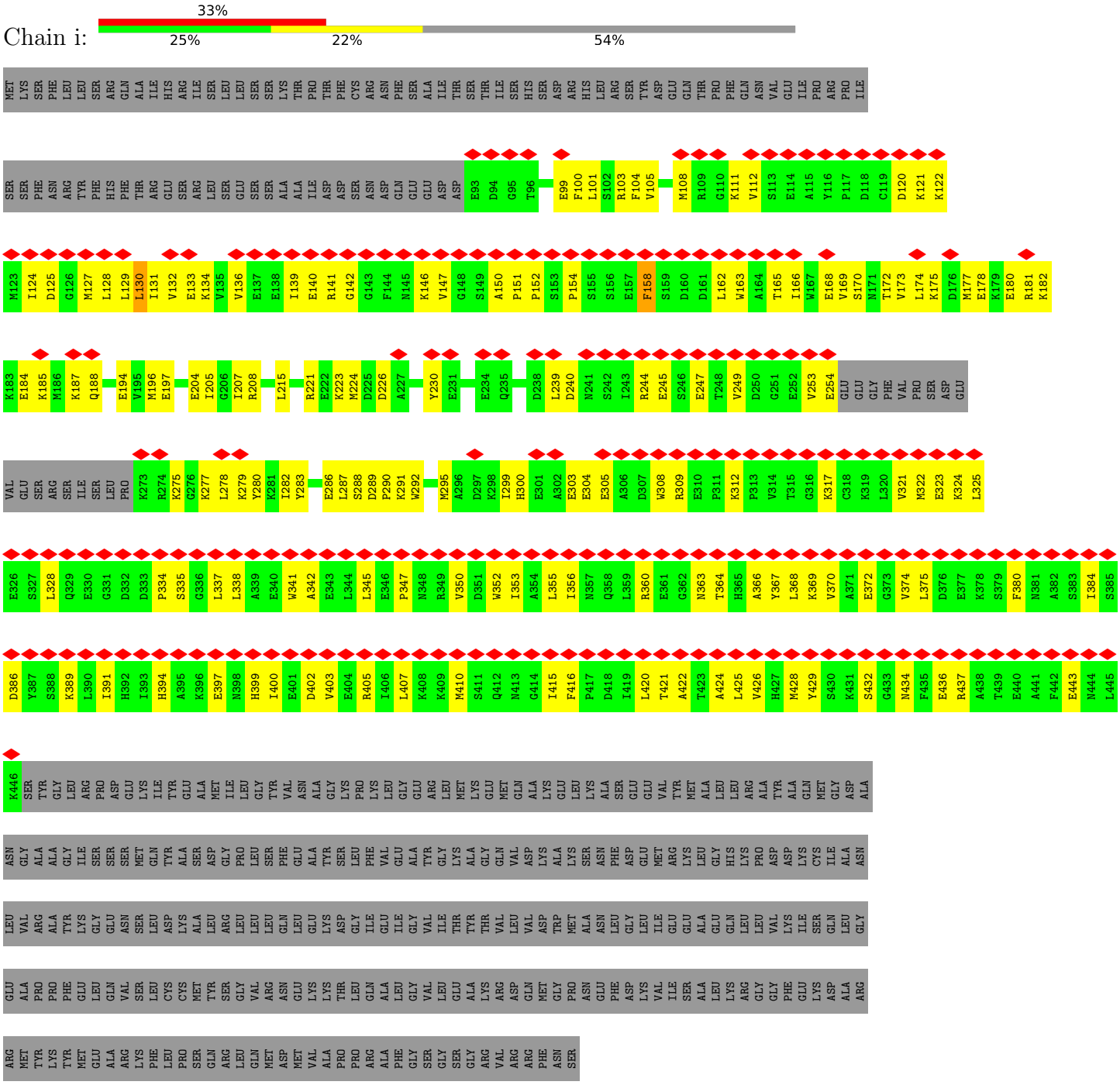
Chain h:







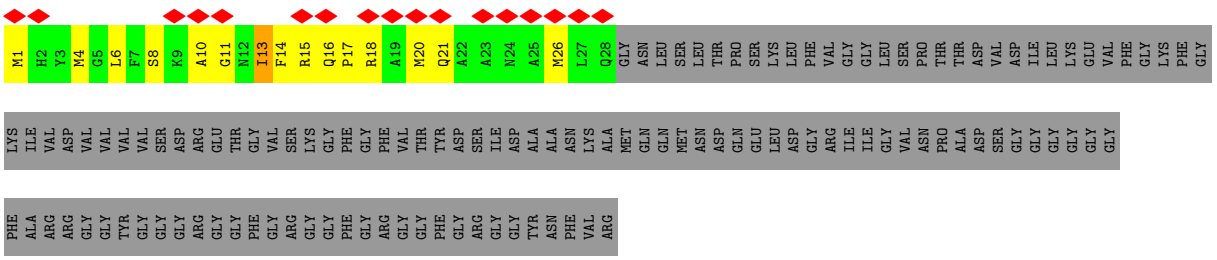
• Molecule 39: PROP1-like PPR domain-containing protein



• Molecule 40: RRM domain-containing protein

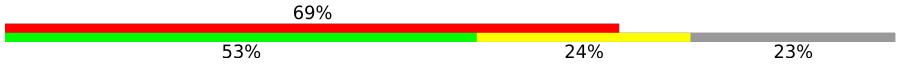
Chain k:

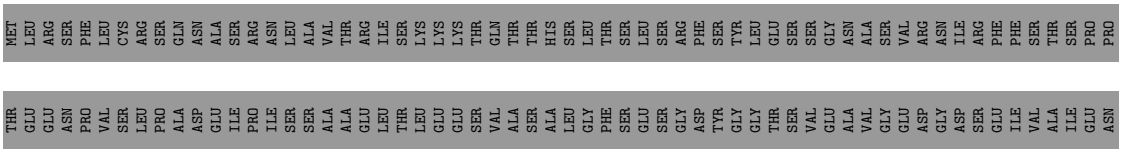


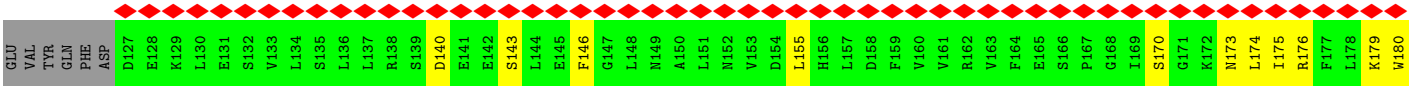


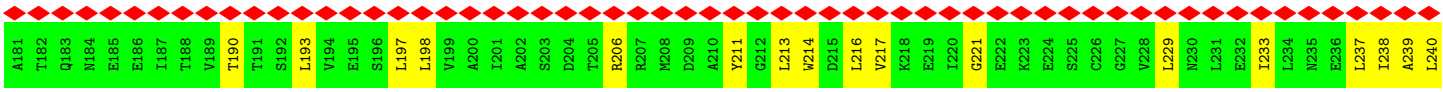
• Molecule 41: Small ribosomal subunit protein mS80 (rPPR6)

Chain l:

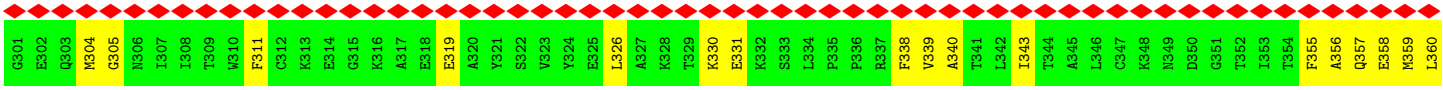


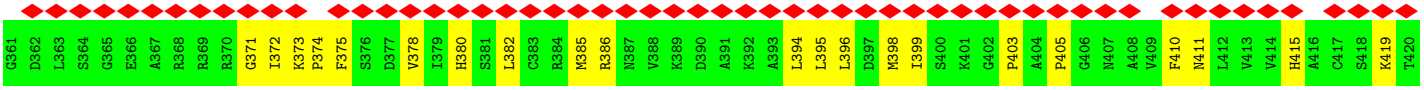


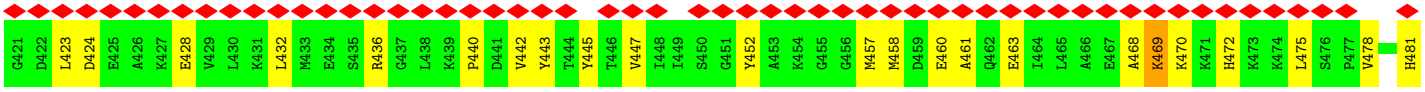


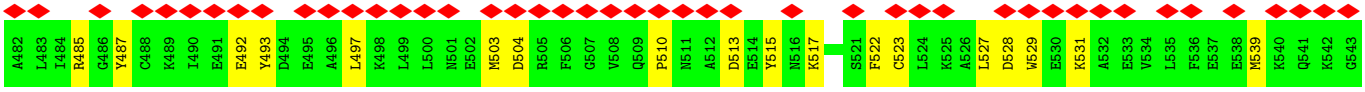


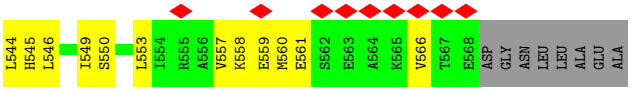












4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18894	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.654	Depositor
Minimum map value	-0.281	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.24	Depositor
Map size (Å)	676.2, 676.2, 676.2	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.966, 0.966, 0.966	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MG, UR3, 4OC, ATP, MA6, G7M

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	2	0.55	0/38185	0.78	19/59524 (0.0%)
2	5	0.56	0/1834	0.88	2/2854 (0.1%)
3	6	0.85	0/119	1.00	0/183
4	8	0.23	0/1539	0.45	0/2055
5	A	0.29	0/1647	0.43	1/2227 (0.0%)
6	B	0.34	0/3969	0.49	0/5320
7	C	0.13	0/2859	0.30	0/3828
8	D	0.23	0/3474	0.36	0/4647
9	E	0.12	0/838	0.27	0/1121
10	F	0.21	0/1225	0.44	0/1641
11	G	0.12	0/1054	0.22	0/1418
12	H	0.34	0/1696	0.47	0/2273
13	I	0.41	0/964	0.43	0/1293
14	J	0.13	0/1000	0.32	0/1340
15	K	0.22	0/1010	0.44	0/1345
16	L	0.31	0/883	0.43	0/1176
17	M	0.41	0/856	0.38	0/1134
18	N	0.13	0/958	0.33	2/1280 (0.2%)
19	O	0.14	0/890	0.29	0/1196
20	P	0.12	0/730	0.25	0/984
21	Q	0.12	0/733	0.28	0/978
22	R	0.28	0/1323	0.43	0/1772
23	S	0.35	0/614	0.47	0/809
24	T	0.40	0/416	0.40	0/547
25	U	0.11	0/1036	0.29	0/1395
26	V	0.22	0/1423	0.34	0/1895
27	W	0.34	0/3139	0.44	0/4250
28	X	0.34	0/1644	0.49	0/2216
29	Y	0.36	0/807	0.46	0/1077
30	Z	0.11	0/669	0.32	0/900
31	a	0.34	0/2523	0.50	0/3386
32	b	0.64	0/618	0.93	0/822

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	c	0.40	0/233	0.55	0/296
34	d	0.13	0/628	0.30	0/840
35	e	0.19	0/2118	0.34	0/2828
36	f	0.11	0/2981	0.31	0/4033
37	g	0.17	0/835	0.43	0/1129
38	h	0.09	0/2511	0.28	0/3391
39	i	0.13	0/2772	0.34	0/3725
40	k	0.11	0/224	0.33	0/297
41	l	0.20	0/3523	0.43	0/4739
All	All	0.41	0/96500	0.61	24/138164 (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
5	A	0	1
8	D	0	1
15	K	0	2
32	b	0	3
All	All	0	7

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2	1387	C	N1-C2-O2	9.32	124.49	118.90
1	2	1387	C	C2-N1-C1'	7.83	127.41	118.80
2	5	44	A	C3'-C2'-C1'	-7.60	95.98	101.30
1	2	1387	C	N3-C2-O2	-7.20	116.86	121.90
1	2	1542	A	N7-C8-N9	6.85	117.23	113.80
1	2	1542	A	C5-N7-C8	-6.68	100.56	103.90
2	5	28	U	P-O3'-C3'	6.59	127.61	119.70
1	2	1600	G	C3'-C2'-C1'	6.29	105.70	101.30
1	2	1135	A	O4'-C1'-N9	5.93	112.95	108.20
1	2	1029	C	C2-N1-C1'	5.86	125.24	118.80
1	2	1388	A	O4'-C1'-N9	5.77	112.81	108.20
1	2	1387	C	C6-N1-C1'	-5.58	114.10	120.80
1	2	1593	G	O4'-C1'-N9	5.55	112.64	108.20
1	2	1542	A	C4-C5-N7	5.52	113.46	110.70
1	2	1620	U	O4'-C1'-N1	5.52	112.36	108.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	110	SER	N-CA-C	-5.50	101.43	109.63
1	2	1075	U	O5'-C5'-C4'	5.42	113.74	109.40
1	2	1542	A	C6-C5-N7	-5.41	128.51	132.30
1	2	1132	C	C2-N1-C1'	5.28	124.61	118.80
1	2	82	C	C2-N3-C4	-5.22	117.29	119.90
1	2	986	G	C4-N9-C1'	5.18	133.23	126.50
1	2	1541	G	O5'-C5'-C4'	5.12	113.49	109.40
18	N	302	LEU	CA-C-N	-5.03	113.60	123.56
18	N	302	LEU	C-N-CA	-5.03	113.60	123.56

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A	119	ARG	Sidechain
8	D	344	ARG	Sidechain
15	K	12	ARG	Sidechain
15	K	16	ARG	Sidechain
32	b	14	ARG	Sidechain
32	b	85	ARG	Sidechain
32	b	88	ARG	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	34252	0	17267	646	0
2	5	1641	0	831	132	0
3	6	107	0	54	10	0
4	8	1517	1558	1609	35	0
5	A	1611	0	1633	91	0
6	B	3877	0	4008	74	0
7	C	2806	0	2971	160	0
8	D	3425	0	3453	170	0
9	E	823	0	879	32	0
10	F	1254	0	1268	22	0
11	G	1037	0	1058	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	H	1671	0	1713	85	0
13	I	941	0	970	8	0
14	J	988	0	1022	71	0
15	K	993	0	1052	23	0
16	L	873	0	904	6	0
17	M	843	0	884	3	0
18	N	941	0	978	22	0
19	O	869	0	898	29	0
20	P	717	0	755	20	0
21	Q	724	0	744	31	0
22	R	1299	0	1307	19	0
23	S	611	0	687	40	0
24	T	408	0	444	1	0
25	U	1014	0	1061	91	0
26	V	1399	0	1427	45	0
27	W	3062	0	3030	39	0
28	X	1613	0	1559	37	0
29	Y	793	0	834	7	0
30	Z	649	0	662	46	0
31	a	2486	0	2376	48	0
32	b	610	0	626	39	0
33	c	232	0	278	5	0
34	d	616	0	674	25	0
35	e	2074	0	2074	86	0
36	f	2922	0	2870	192	0
37	g	814	0	801	19	0
38	h	2463	0	2488	259	0
39	i	2722	0	2680	207	0
40	k	220	0	223	36	0
41	l	3468	0	3524	98	0
42	W	31	0	12	0	0
All	All	91416	1558	74588	2684	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 16.

All (2684) 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)
7:C:175:LEU:HD11	7:C:198:TRP:HB3	1.26	1.16
8:D:181:LEU:HD23	8:D:193:TRP:HB2	1.28	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:182:LYS:HA	7:C:182:LYS:HE2	1.31	1.12
38:h:193:ALA:HB2	38:h:201:LEU:HD23	1.30	1.10
39:i:403:VAL:HG11	39:i:428:MET:HE1	1.25	1.10
1:2:1667:G:H5'	33:c:122:MET:HE3	1.24	1.09
36:f:369:ASP:HB3	36:f:370:PRO:HD3	1.33	1.09
30:Z:69:MET:HA	30:Z:69:MET:HE3	1.35	1.07
36:f:213:ILE:HD11	36:f:221:PHE:HB2	1.31	1.07
1:2:202:A:H2'	1:2:203:A:H5"	1.34	1.06
7:C:289:LEU:HD21	35:e:151:ARG:HE	1.20	1.06
8:D:170:LYS:HE3	8:D:204:HIS:HB3	1.37	1.06
1:2:163:A:H4'	1:2:164:A:H5'	1.36	1.05
1:2:162:C:H3'	1:2:163:A:H5"	1.30	1.04
5:A:43:SER:HB3	40:k:4:MET:HE1	1.35	1.04
7:C:254:ARG:HH22	39:i:226:ASP:HA	1.26	1.00
14:J:284:ASN:HB3	32:b:46:LEU:CD2	1.91	1.00
7:C:257:LEU:HD21	8:D:194:MET:HE1	1.40	1.00
7:C:93:ARG:HD3	7:C:98:PRO:HG2	1.39	0.99
39:i:363:ASN:HB3	39:i:366:ALA:HB3	1.42	0.99
25:U:52:GLU:HG3	25:U:90:LEU:HD22	1.43	0.99
14:J:272:ARG:HD3	23:S:40:LEU:HD23	1.44	0.98
1:2:1726:U:H3	1:2:1744:C:N4	1.58	0.98
18:N:298:PRO:HD2	18:N:301:LEU:HD22	1.44	0.98
2:5:21:C:H3'	2:5:22:A:H4'	1.44	0.97
14:J:189:LEU:HD12	21:Q:246:GLU:HG3	1.46	0.97
1:2:1750:C:H3'	1:2:1751:U:H5"	1.44	0.96
4:8:123:VAL:H	4:8:136:ILE:HD11	1.28	0.96
38:h:206:MET:HA	38:h:209:LEU:HD23	1.47	0.95
8:D:138:GLU:HB2	8:D:141:ARG:HB2	1.47	0.95
23:S:64:ILE:HG23	23:S:68:GLU:HG3	1.48	0.94
5:A:3:LEU:HB2	36:f:255:LEU:HD12	1.48	0.94
2:5:12:G:H3'	2:5:13:G:H8	1.32	0.94
11:G:17:GLU:HG3	11:G:68:VAL:HG22	1.49	0.94
39:i:402:ASP:HA	39:i:405:ARG:HE	1.31	0.93
5:A:20:ARG:HH21	5:A:21:ARG:HG2	1.34	0.93
28:X:348:MET:HE1	28:X:353:MET:HB3	1.49	0.93
38:h:110:TRP:HA	38:h:113:ILE:HD12	1.50	0.93
1:2:919:G:H1	3:6:36:A:H5'	1.32	0.93
7:C:183:LEU:HB3	8:D:71:ILE:HD12	1.51	0.92
35:e:267:LYS:HD2	35:e:268:PRO:HD2	1.51	0.92
14:J:259:VAL:HG13	14:J:294:TYR:HB2	1.52	0.92
1:2:1137:G:H3'	1:2:1138:G:H21	1.36	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:337:ARG:HH12	36:f:389:THR:HG23	1.35	0.91
38:h:234:TRP:HH2	38:h:263:ALA:HA	1.36	0.91
14:J:284:ASN:HB3	32:b:46:LEU:HD21	1.53	0.90
7:C:178:LYS:NZ	35:e:251:PHE:HB3	1.85	0.90
35:e:140:ILE:HA	35:e:143:ILE:HD13	1.53	0.90
1:2:1540:C:HO2'	1:2:1542:A:H8	0.96	0.90
2:5:25:U:H2'	2:5:26:C:H6	1.35	0.90
12:H:241:ILE:HD13	39:i:295:MET:HE1	1.52	0.89
4:8:200:LEU:HD22	4:8:202:VAL:HG13	1.55	0.88
38:h:122:ILE:HD12	38:h:126:PHE:HE2	1.37	0.88
36:f:192:LEU:HD22	36:f:196:LEU:HD23	1.54	0.88
1:2:669:G:H2'	1:2:670:G:C8	2.08	0.88
1:2:1726:U:H3	1:2:1744:C:H42	0.89	0.88
5:A:108:THR:HG23	5:A:148:GLU:HG2	1.56	0.88
7:C:257:LEU:HD21	8:D:194:MET:CE	2.04	0.88
1:2:1801:A:H5'	15:K:44:LYS:HE2	1.55	0.87
7:C:265:ARG:HB2	39:i:244:ARG:HH22	1.38	0.87
1:2:1734:A:H2'	1:2:1735:C:H4'	1.54	0.86
2:5:12:G:H3'	2:5:13:G:C8	2.11	0.86
7:C:178:LYS:HZ1	35:e:251:PHE:HB3	1.40	0.86
2:5:25:U:H2'	2:5:26:C:C6	2.10	0.86
2:5:70:C:H2'	2:5:71:G:C8	2.09	0.86
14:J:290:ASN:HD21	23:S:36:LEU:HB2	1.40	0.86
7:C:182:LYS:HG3	7:C:220:LEU:HD22	1.56	0.86
15:K:114:ARG:HB2	15:K:119:ALA:HB3	1.55	0.86
38:h:133:ARG:HD3	38:h:178:GLY:HA3	1.57	0.86
5:A:9:GLN:HA	5:A:9:GLN:HE21	1.40	0.85
1:2:1763:U:H4'	1:2:1764:A:H5'	1.58	0.85
7:C:257:LEU:CD2	8:D:194:MET:HE1	2.06	0.85
5:A:35:ARG:HB3	25:U:48:ILE:HG22	1.57	0.85
7:C:204:THR:HA	8:D:116:GLU:HG2	1.58	0.85
38:h:206:MET:HG2	38:h:209:LEU:HD21	1.58	0.85
26:V:33:HIS:HB2	26:V:35:ARG:HE	1.39	0.85
25:U:92:LEU:HB3	25:U:97:ILE:HG21	1.58	0.84
1:2:202:A:C2'	1:2:203:A:H5"	2.06	0.84
12:H:227:GLY:O	12:H:230:ARG:HG2	1.78	0.84
40:k:18:ARG:HA	40:k:21:GLN:HE21	1.42	0.84
12:H:241:ILE:HG12	12:H:246:LEU:HD13	1.58	0.84
8:D:166:MET:HA	8:D:166:MET:HE3	1.57	0.84
38:h:361:ILE:HG22	38:h:362:PRO:HD3	1.59	0.83
39:i:162:LEU:O	39:i:166:ILE:HD12	1.79	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:225:ILE:HG22	12:H:226:LYS:H	1.41	0.83
37:g:586:PHE:HB3	37:g:620:MET:HE1	1.61	0.83
15:K:44:LYS:HD2	15:K:44:LYS:H	1.41	0.83
38:h:81:ASP:HB2	38:h:82:PRO:HD3	1.59	0.83
2:5:52:A:H2'	2:5:53:G:C8	2.13	0.83
19:O:86:PRO:HG2	19:O:89:VAL:HG13	1.60	0.83
14:J:284:ASN:CB	32:b:46:LEU:HD21	2.08	0.83
38:h:260:MET:HG2	38:h:293:SER:HB2	1.58	0.83
7:C:58:TYR:HB3	8:D:409:MET:HE1	1.61	0.82
20:P:88:ALA:HA	20:P:91:LEU:HD12	1.60	0.82
5:A:16:SER:HB2	5:A:178:ALA:HB1	1.61	0.82
1:2:200:C:H5	1:2:246:G:H1	1.26	0.82
5:A:43:SER:H	40:k:4:MET:HE2	1.44	0.82
8:D:93:ARG:NH1	8:D:93:ARG:HA	1.94	0.82
36:f:170:LEU:HD12	36:f:207:LEU:HD12	1.61	0.81
9:E:46:VAL:HG12	26:V:195:LEU:HD23	1.61	0.81
39:i:158:PHE:HB3	39:i:162:LEU:HD23	1.63	0.81
1:2:612:U:H2'	1:2:613:C:C6	2.16	0.81
14:J:262:VAL:HG11	14:J:271:LYS:HB3	1.61	0.81
7:C:260:LEU:HD23	8:D:181:LEU:HD12	1.63	0.81
36:f:282:ILE:HG23	36:f:286:MET:HE1	1.61	0.81
1:2:162:C:H3'	1:2:163:A:C5'	2.11	0.81
1:2:3:C:O2'	1:2:4:A:H2'	1.81	0.80
5:A:9:GLN:HE22	25:U:77:PHE:HE2	1.28	0.80
1:2:24:A:N3	1:2:1072:A:O2'	2.13	0.80
30:Z:53:LEU:HD13	30:Z:69:MET:HG3	1.61	0.80
36:f:55:ILE:HD12	36:f:92:LYS:HB2	1.63	0.80
12:H:241:ILE:CD1	39:i:295:MET:HE1	2.10	0.80
25:U:88:ARG:O	25:U:92:LEU:HD13	1.82	0.80
39:i:104:PHE:HZ	39:i:166:ILE:HG23	1.45	0.80
30:Z:59:PHE:O	30:Z:60:LEU:HD23	1.82	0.80
12:H:241:ILE:CG1	12:H:246:LEU:HD13	2.12	0.80
35:e:151:ARG:HG2	35:e:151:ARG:HH11	1.47	0.79
1:2:491:G:H2'	1:2:492:G:C8	2.17	0.79
1:2:670:G:H2'	1:2:671:A:H8	1.45	0.79
38:h:156:LYS:HA	38:h:159:VAL:HG12	1.62	0.79
1:2:573:G:O2'	1:2:817:G:H5'	1.82	0.79
30:Z:62:ASN:H	38:h:145:ASN:HD21	1.31	0.79
39:i:108:MET:HA	39:i:108:MET:HE3	1.62	0.78
12:H:223:GLU:HA	25:U:117:LYS:HE3	1.63	0.78
19:O:91:MET:HE3	34:d:100:LEU:HD13	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:97:GLU:HA	8:D:100:ARG:HH21	1.49	0.78
5:A:57:VAL:HG11	5:A:192:ILE:HG23	1.64	0.78
22:R:149:LYS:HG3	22:R:153:ALA:HB2	1.66	0.78
30:Z:69:MET:HA	30:Z:69:MET:CE	2.14	0.78
7:C:190:MET:O	7:C:190:MET:HE3	1.84	0.77
14:J:299:THR:O	21:Q:227:MET:HG2	1.84	0.77
39:i:342:ALA:HA	39:i:347:PRO:HD3	1.65	0.77
7:C:180:ILE:HG22	7:C:191:TRP:CZ2	2.19	0.77
14:J:189:LEU:CD1	21:Q:246:GLU:HG3	2.15	0.77
11:G:37:LEU:HD23	11:G:40:MET:HE3	1.66	0.77
23:S:93:ILE:HG12	32:b:86:LEU:HD11	1.66	0.77
1:2:709:G:H2'	1:2:710:G:C8	2.20	0.77
7:C:256:LEU:HD12	7:C:286:SER:CB	2.14	0.77
1:2:1746:A:H2'	1:2:1747:A:C8	2.20	0.77
7:C:256:LEU:HD12	7:C:286:SER:OG	1.85	0.77
32:b:86:LEU:C	32:b:88:ARG:H	1.91	0.77
36:f:189:LEU:HA	36:f:192:LEU:HD11	1.66	0.77
36:f:337:ARG:NH1	36:f:389:THR:HG23	2.00	0.77
38:h:86:VAL:HG21	38:h:121:ASP:HB2	1.66	0.77
38:h:214:LEU:HD12	38:h:215:PRO:HD2	1.67	0.77
37:g:642:ASN:HB3	41:l:372:ILE:HG21	1.67	0.76
39:i:308:TRP:HB3	40:k:6:LEU:HD11	1.67	0.76
7:C:325:THR:HG21	7:C:327:LYS:NZ	2.01	0.76
36:f:192:LEU:HD23	36:f:215:CYS:HB3	1.67	0.76
8:D:517:LEU:HD11	35:e:273:MET:HE1	1.68	0.76
8:D:177:LEU:HD23	8:D:197:LEU:HD12	1.68	0.76
19:O:86:PRO:HG2	19:O:89:VAL:CG1	2.16	0.76
4:8:211:LEU:HD13	4:8:212:GLU:N	2.00	0.76
31:a:117:THR:HA	31:a:120:GLU:HG2	1.68	0.76
1:2:816:U:H4'	1:2:817:G:OP2	1.85	0.76
7:C:312:ILE:HD12	7:C:312:ILE:O	1.86	0.76
8:D:300:ARG:O	8:D:304:LEU:HG	1.86	0.75
1:2:1524:A:H2	1:2:1537:G:H21	1.32	0.75
8:D:181:LEU:CD2	8:D:193:TRP:HB2	2.12	0.75
1:2:1727:G:O2'	1:2:1728:U:H5'	1.86	0.75
38:h:296:LYS:HE3	38:h:333:LEU:HG	1.68	0.75
38:h:206:MET:HA	38:h:209:LEU:CD2	2.17	0.75
38:h:204:GLU:O	38:h:208:LEU:HG	1.85	0.75
1:2:79:G:H22	1:2:161:A:H2	1.35	0.75
1:2:148:U:H2'	1:2:149:U:C6	2.21	0.75
12:H:236:ILE:HG23	12:H:241:ILE:CG2	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:346:THR:HG22	36:f:347:VAL:HG23	1.69	0.74
1:2:292:A:O2'	1:2:293:A:H5'	1.87	0.74
38:h:295:ALA:HB1	38:h:307:ALA:HB1	1.70	0.74
1:2:1618:G:H2'	1:2:1619:A:C8	2.23	0.74
2:5:24:C:H2'	2:5:25:U:C6	2.22	0.74
5:A:20:ARG:HH11	40:k:20:MET:HG2	1.53	0.74
41:l:190:THR:H	41:l:193:LEU:HD12	1.52	0.74
36:f:213:ILE:CD1	36:f:221:PHE:HB2	2.12	0.74
39:i:400:ILE:HD11	39:i:432:SER:HB2	1.70	0.74
25:U:92:LEU:HB3	25:U:97:ILE:CG2	2.17	0.74
35:e:365:ASN:HB2	35:e:368:GLU:HG2	1.69	0.74
40:k:17:PRO:O	40:k:21:GLN:HG2	1.87	0.74
1:2:493:A:H4'	1:2:494:A:OP1	1.86	0.74
2:5:70:C:H2'	2:5:71:G:H8	1.53	0.74
38:h:201:LEU:O	38:h:205:VAL:HG12	1.86	0.74
1:2:492:G:O2'	1:2:494:A:H1'	1.88	0.74
1:2:1703:G:H2'	1:2:1704:A:O4'	1.88	0.74
38:h:97:VAL:HG13	38:h:135:PHE:CD2	2.22	0.74
39:i:139:ILE:HD12	39:i:140:GLU:N	2.03	0.74
39:i:245:GLU:O	39:i:249:VAL:HG23	1.87	0.74
8:D:187:LEU:HD13	39:i:244:ARG:HH21	1.52	0.73
30:Z:69:MET:HE1	30:Z:123:TYR:HB3	1.67	0.73
38:h:228:CYS:HA	38:h:231:THR:OG1	1.88	0.73
1:2:1746:A:H2'	1:2:1747:A:H8	1.52	0.73
2:5:52:A:H2'	2:5:53:G:H8	1.53	0.73
31:a:216:ASP:HA	31:a:219:LYS:HE3	1.70	0.73
36:f:273:TYR:HB3	36:f:286:MET:HE2	1.69	0.73
1:2:919:G:N1	3:6:36:A:H5'	2.01	0.73
11:G:17:GLU:HG3	11:G:68:VAL:CG2	2.18	0.73
1:2:442:U:O2'	1:2:443:C:H5"	1.89	0.73
8:D:334:GLU:O	8:D:338:ARG:HG3	1.88	0.73
2:5:8:U:H1'	2:5:22:A:C2	2.23	0.73
2:5:59:A:H1'	2:5:61:U:OP2	1.88	0.73
23:S:89:LYS:HE3	32:b:19:LEU:HG	1.71	0.73
39:i:104:PHE:CZ	39:i:166:ILE:HG23	2.23	0.73
1:2:613:C:H2'	1:2:614:A:C8	2.24	0.73
36:f:58:ARG:HH12	36:f:66:SER:HB3	1.54	0.73
1:2:1669:C:H1'	4:8:178:LYS:NZ	2.04	0.73
1:2:1701:C:H2'	1:2:1702:G:C8	2.23	0.73
36:f:203:THR:HG22	36:f:304:GLN:HB2	1.70	0.73
36:f:280:GLU:HG2	36:f:281:GLU:OE1	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:287:GLU:O	36:f:290:VAL:HG12	1.88	0.73
38:h:251:LEU:HB3	38:h:256:PHE:CE1	2.24	0.73
1:2:710:G:H2'	1:2:711:A:C8	2.24	0.73
1:2:172:A:H5'	1:2:173:A:H5"	1.70	0.72
2:5:11:A:N3	2:5:12:G:H1'	2.04	0.72
5:A:188:PHE:O	5:A:192:ILE:HG12	1.88	0.72
37:g:607:PHE:HD1	37:g:608:PRO:HD2	1.54	0.72
41:l:458:MET:HA	41:l:458:MET:HE3	1.71	0.72
12:H:241:ILE:HD13	39:i:295:MET:CE	2.19	0.72
12:H:219:LYS:HD2	25:U:127:LEU:HD11	1.70	0.72
20:P:82:SER:OG	20:P:85:ALA:HB3	1.89	0.72
12:H:224:VAL:HG12	12:H:225:ILE:H	1.53	0.72
36:f:270:ILE:H	36:f:270:ILE:HD12	1.54	0.72
36:f:377:SER:H	36:f:380:MET:HE2	1.53	0.72
38:h:90:HIS:HD2	38:h:94:LEU:HD13	1.55	0.72
2:5:14:A:H3'	2:5:15:A:H8	1.54	0.72
8:D:174:HIS:HB2	8:D:200:PHE:HE2	1.53	0.72
37:g:630:GLN:HG2	37:g:650:PHE:HE2	1.55	0.72
40:k:10:ALA:HB3	40:k:13:ILE:HD11	1.72	0.72
36:f:111:ILE:CD1	36:f:116:THR:HG22	2.20	0.71
1:2:164:A:H2'	1:2:165:A:C8	2.25	0.71
1:2:164:A:H2'	1:2:165:A:H8	1.55	0.71
1:2:1667:G:C5'	33:c:122:MET:HE3	2.14	0.71
2:5:65:G:H2'	2:5:66:U:O4'	1.90	0.71
5:A:43:SER:H	40:k:4:MET:CE	2.03	0.71
39:i:325:LEU:HA	39:i:328:LEU:HG	1.72	0.71
21:Q:196:ARG:HB2	21:Q:206:GLN:HG2	1.70	0.71
25:U:52:GLU:O	25:U:56:VAL:HG22	1.90	0.71
30:Z:98:ILE:HD11	30:Z:110:PRO:HG3	1.72	0.71
38:h:271:SER:O	38:h:275:VAL:HG12	1.90	0.71
7:C:204:THR:HA	8:D:116:GLU:CG	2.21	0.71
12:H:236:ILE:HG12	12:H:241:ILE:HG21	1.71	0.71
14:J:228:LEU:HD22	14:J:238:THR:HG23	1.73	0.71
39:i:173:VAL:O	39:i:177:MET:HG2	1.90	0.71
39:i:407:LEU:HA	39:i:410:MET:SD	2.31	0.71
1:2:457:C:O2'	1:2:458:U:H5'	1.90	0.71
2:5:55:U:H3	2:5:59:A:H62	1.38	0.71
8:D:191:TYR:O	8:D:194:MET:HB2	1.91	0.71
5:A:158:ALA:HB3	5:A:172:ILE:HD12	1.73	0.71
7:C:360:GLN:OE1	35:e:263:SER:HA	1.90	0.71
14:J:260:VAL:HG11	14:J:275:ILE:HG12	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:22:ASN:HB2	32:b:25:LYS:HG3	1.71	0.71
36:f:409:PHE:HD1	39:i:187:LYS:HE2	1.55	0.71
8:D:218:MET:HE1	35:e:168:LEU:HD23	1.73	0.71
1:2:571:A:H8	1:2:571:A:H5'	1.56	0.70
31:a:122:MET:HE2	31:a:122:MET:HA	1.72	0.70
39:i:125:ASP:O	39:i:128:LEU:HG	1.91	0.70
39:i:289:ASP:HB3	39:i:292:TRP:CD1	2.26	0.70
1:2:462:G:H2'	1:2:463:U:H5'	1.73	0.70
6:B:480:LYS:HA	6:B:480:LYS:HE3	1.73	0.70
14:J:189:LEU:HD12	21:Q:246:GLU:CG	2.20	0.70
18:N:303:GLU:HB2	26:V:173:SER:OG	1.91	0.70
1:2:323:C:H2'	1:2:324:G:H5'	1.73	0.70
38:h:119:GLU:O	38:h:122:ILE:HG12	1.91	0.70
39:i:103:ARG:HD2	39:i:173:VAL:HG13	1.73	0.70
9:E:19:LEU:HD23	9:E:65:MET:HE2	1.72	0.70
25:U:15:LEU:HB3	25:U:21:THR:HG22	1.74	0.70
38:h:190:LEU:HD23	38:h:223:LEU:HB3	1.73	0.70
2:5:24:C:H2'	2:5:25:U:H6	1.57	0.70
4:8:135:LYS:C	4:8:136:ILE:HD12	2.17	0.70
8:D:216:GLU:OE1	39:i:215:LEU:HD21	1.91	0.70
1:2:612:U:H2'	1:2:613:C:H6	1.53	0.70
1:2:1686:U:H2'	1:2:1687:U:C6	2.26	0.70
30:Z:53:LEU:CD1	30:Z:69:MET:HG3	2.21	0.70
35:e:302:GLU:O	35:e:306:ARG:HG3	1.91	0.70
2:5:21:C:H3'	2:5:22:A:C4'	2.18	0.70
38:h:361:ILE:CG2	38:h:362:PRO:HD3	2.22	0.70
7:C:180:ILE:HG22	7:C:191:TRP:CE2	2.27	0.70
12:H:244:GLU:HB2	12:H:245:MET:CE	2.22	0.70
25:U:68:LEU:O	25:U:71:PRO:HD2	1.92	0.70
2:5:3:C:H2'	2:5:4:G:C8	2.26	0.70
11:G:85:ILE:O	11:G:89:THR:HG23	1.90	0.70
19:O:107:THR:OG1	19:O:109:ARG:HG2	1.91	0.70
25:U:91:GLU:HA	25:U:94:LYS:HG2	1.72	0.70
41:l:339:VAL:HG13	41:l:359:MET:HE2	1.74	0.70
1:2:1750:C:H3'	1:2:1751:U:C5'	2.21	0.69
1:2:1833:U:H2'	1:2:1834:G:C8	2.27	0.69
38:h:159:VAL:HG22	38:h:192:TYR:HD2	1.56	0.69
1:2:1702:G:H2'	1:2:1703:G:C8	2.27	0.69
2:5:8:U:H1'	2:5:22:A:H2	1.57	0.69
8:D:517:LEU:HD11	35:e:273:MET:CE	2.23	0.69
36:f:369:ASP:HB3	36:f:370:PRO:CD	2.17	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:368:G:O2'	1:2:369:G:H5'	1.92	0.69
8:D:93:ARG:HA	8:D:93:ARG:CZ	2.22	0.69
29:Y:9:LEU:HB3	31:a:385:ILE:HD11	1.72	0.69
36:f:261:THR:O	36:f:261:THR:HG22	1.93	0.69
39:i:436:GLU:OE2	39:i:437:ARG:HG3	1.92	0.69
8:D:350:LYS:O	8:D:350:LYS:HD2	1.92	0.69
20:P:80:ILE:HD12	20:P:80:ILE:O	1.92	0.69
39:i:178:GLU:O	39:i:181:ARG:HG3	1.90	0.69
23:S:95:ILE:HG22	40:k:26:MET:HE1	1.74	0.69
28:X:394:MET:HE3	28:X:395:PRO:HD2	1.73	0.69
38:h:306:GLU:O	38:h:310:VAL:HG23	1.91	0.69
1:2:25:U:H2'	1:2:26:U:C6	2.28	0.69
1:2:837:U:O2'	25:U:61:ARG:HG2	1.92	0.69
14:J:246:ILE:O	14:J:250:VAL:HG23	1.91	0.69
20:P:54:ARG:HG2	20:P:75:ILE:HB	1.74	0.69
1:2:65:G:H1	1:2:374:C:H5	1.39	0.69
1:2:1769:C:H4'	1:2:1770:G:OP1	1.90	0.69
6:B:309:ARG:HA	6:B:312:HIS:HB2	1.75	0.69
14:J:290:ASN:ND2	23:S:36:LEU:HB2	2.08	0.69
38:h:89:LEU:O	38:h:93:ILE:HG13	1.92	0.69
38:h:258:VAL:O	38:h:261:GLU:HG2	1.92	0.69
38:h:310:VAL:O	38:h:313:ILE:HG22	1.93	0.69
39:i:368:LEU:HD22	39:i:394:HIS:CE1	2.28	0.69
41:l:398:MET:HE1	41:l:405:PRO:HB3	1.74	0.69
1:2:323:C:C2'	1:2:324:G:H5'	2.23	0.69
1:2:647:C:O2'	1:2:648:U:H5'	1.91	0.69
1:2:861:C:H2'	1:2:862:G:O4'	1.92	0.69
1:2:1065:U:OP1	8:D:411:LYS:HE3	1.93	0.69
2:5:75:C:H2'	2:5:76:C:C6	2.28	0.69
10:F:19:ARG:HG2	10:F:93:LEU:HD13	1.73	0.69
39:i:334:PRO:HD2	39:i:369:LYS:HE3	1.75	0.69
39:i:370:VAL:O	39:i:374:VAL:HG23	1.92	0.69
1:2:155:U:O2	30:Z:122:LYS:HG3	1.93	0.69
1:2:1693:C:O2'	1:2:1694:G:H5'	1.91	0.69
2:5:51:C:H2'	2:5:52:A:C8	2.28	0.69
7:C:312:ILE:HD11	35:e:252:PHE:HD1	1.56	0.69
1:2:670:G:H2'	1:2:671:A:C8	2.26	0.69
5:A:18:LEU:O	5:A:179:ARG:HD3	1.93	0.69
12:H:267:ILE:HG22	12:H:268:GLU:OE2	1.93	0.69
38:h:341:VAL:HG23	38:h:342:LEU:CD1	2.23	0.69
1:2:161:A:H2'	1:2:162:C:H4'	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1800:G:H5”	15:K:44:LYS:NZ	2.08	0.68
8:D:366:ASP:OD1	8:D:368:LYS:HG3	1.92	0.68
7:C:251:ARG:HH22	7:C:252:MET:HB2	1.58	0.68
12:H:244:GLU:HB2	12:H:245:MET:HE1	1.74	0.68
15:K:39:THR:HG22	15:K:51:LYS:HD3	1.74	0.68
41:l:298:LEU:HD21	41:l:326:LEU:HD23	1.75	0.68
1:2:403:G:OP1	34:d:93:LYS:HD2	1.93	0.68
2:5:53:G:O2’	2:5:54:G:H5’	1.92	0.68
18:N:354:THR:O	18:N:358:LYS:HG3	1.92	0.68
36:f:92:LYS:NZ	36:f:231:GLU:HG2	2.08	0.68
36:f:389:THR:HG21	36:f:397:GLU:HG3	1.76	0.68
38:h:171:LEU:CD2	38:h:208:LEU:HB2	2.24	0.68
38:h:202:MET:HE2	38:h:227:ILE:CG2	2.23	0.68
40:k:18:ARG:HA	40:k:21:GLN:NE2	2.08	0.68
1:2:37:A:O2’	1:2:38:G:H5’	1.93	0.68
1:2:1075:U:H5”	1:2:1078:U:H5	1.58	0.68
36:f:120:LYS:HE2	36:f:340:LEU:HD11	1.76	0.68
36:f:310:PRO:HB3	36:f:373:LEU:HA	1.76	0.68
38:h:117:ARG:CZ	38:h:117:ARG:HA	2.24	0.68
2:5:51:C:H2’	2:5:52:A:H8	1.59	0.68
12:H:225:ILE:HA	12:H:228:PRO:HB3	1.76	0.68
38:h:97:VAL:HG13	38:h:135:PHE:HD2	1.59	0.68
38:h:103:MET:SD	38:h:104:PRO:HD2	2.32	0.68
18:N:300:TYR:HD1	26:V:170:GLU:OE1	1.77	0.68
30:Z:69:MET:HE1	30:Z:123:TYR:CB	2.24	0.68
7:C:130:ARG:HD2	7:C:138:MET:CE	2.24	0.68
12:H:230:ARG:CZ	25:U:79:PRO:HD2	2.24	0.68
38:h:241:SER:HA	38:h:244:PHE:CE2	2.28	0.68
5:A:181:SER:O	5:A:185:VAL:HG12	1.94	0.68
36:f:189:LEU:HA	36:f:192:LEU:CD1	2.22	0.68
39:i:194:GLU:HB3	39:i:223:LYS:NZ	2.09	0.68
1:2:50:A:H2’	1:2:51:U:C6	2.29	0.68
7:C:325:THR:HG21	7:C:327:LYS:HZ3	1.57	0.68
25:U:91:GLU:O	25:U:94:LYS:HG3	1.94	0.68
38:h:341:VAL:HG23	38:h:342:LEU:HD12	1.76	0.68
39:i:130:LEU:HD21	39:i:158:PHE:CE1	2.28	0.68
34:d:49:ILE:H	34:d:49:ILE:HD12	1.58	0.68
39:i:277:LYS:HB3	39:i:279:LYS:NZ	2.08	0.68
41:l:298:LEU:HD22	41:l:304:MET:HE1	1.76	0.68
1:2:842:A:O2’	1:2:843:U:H5’	1.94	0.67
36:f:165:THR:O	36:f:168:THR:HG22	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:302:HIS:NE2	38:h:360:ASP:HB2	2.09	0.67
1:2:1710:G:O2'	1:2:1711:A:H5'	1.94	0.67
2:5:66:U:H2'	2:5:67:C:C6	2.29	0.67
7:C:289:LEU:HD21	35:e:151:ARG:NE	2.03	0.67
30:Z:58:GLN:HG2	38:h:176:VAL:HG12	1.75	0.67
30:Z:68:HIS:HA	30:Z:79:TYR:O	1.94	0.67
31:a:407:LYS:HE2	41:l:527:LEU:HD12	1.76	0.67
36:f:127:TYR:OH	36:f:182:ASP:HB2	1.93	0.67
38:h:227:ILE:O	38:h:230:GLU:HG2	1.93	0.67
39:i:108:MET:HE3	39:i:108:MET:CA	2.24	0.67
41:l:174:LEU:HB3	41:l:197:LEU:HD11	1.76	0.67
1:2:545:A:H4'	1:2:546:G:O5'	1.93	0.67
5:A:9:GLN:NE2	25:U:77:PHE:HE2	1.92	0.67
1:2:1768:A:H2'	1:2:1769:C:H5'	1.76	0.67
2:5:64:U:C2'	2:5:65:G:H5'	2.24	0.67
8:D:138:GLU:HG3	8:D:141:ARG:HD2	1.77	0.67
36:f:55:ILE:CD1	36:f:92:LYS:HB2	2.24	0.67
36:f:190:SER:OG	36:f:324:ARG:HG2	1.93	0.67
40:k:17:PRO:HG2	40:k:20:MET:SD	2.34	0.67
1:2:968:A:H4'	1:2:969:G:H5"	1.76	0.67
9:E:41:LYS:NZ	26:V:193:THR:HG21	2.09	0.67
25:U:122:LYS:HA	25:U:122:LYS:HE2	1.76	0.67
36:f:192:LEU:HB3	36:f:193:PRO:HD2	1.76	0.67
41:l:382:LEU:HA	41:l:385:MET:HE3	1.77	0.67
18:N:315:HIS:CG	18:N:316:PRO:HD2	2.30	0.67
21:Q:186:PHE:O	21:Q:194:VAL:HG22	1.94	0.67
35:e:243:ARG:HB3	35:e:243:ARG:NH1	2.09	0.67
39:i:424:ALA:O	39:i:428:MET:HG2	1.95	0.67
1:2:835:U:H2'	1:2:836:A:O4'	1.94	0.67
1:2:1667:G:H5'	33:c:122:MET:CE	2.15	0.67
8:D:97:GLU:HA	8:D:100:ARG:NH2	2.09	0.67
8:D:131:GLN:HA	8:D:134:LYS:NZ	2.09	0.67
38:h:343:LYS:NZ	38:h:387:ALA:HB1	2.09	0.67
39:i:154:PRO:HB3	39:i:163:TRP:CG	2.30	0.67
30:Z:86:LEU:HD21	30:Z:90:GLY:HA2	1.75	0.67
1:2:64:U:H2'	1:2:65:G:C8	2.30	0.67
2:5:53:G:H2'	2:5:54:G:H8	1.60	0.67
3:6:36:A:OP1	3:6:36:A:H4'	1.95	0.67
12:H:230:ARG:NH2	25:U:79:PRO:HD2	2.10	0.67
19:O:83:LEU:HG	19:O:84:PRO:HD2	1.77	0.67
38:h:126:PHE:HB3	38:h:177:HIS:CE1	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:V:167:LEU:O	26:V:171:GLN:HG3	1.94	0.67
37:g:618:GLU:HB3	37:g:649:LEU:HD21	1.77	0.67
1:2:150:A:H2'	1:2:151:A:C4	2.31	0.66
1:2:573:G:H4'	1:2:574:G:OP1	1.94	0.66
1:2:1726:U:H4'	1:2:1727:G:OP1	1.94	0.66
37:g:583:MET:HE1	37:g:615:ARG:HG3	1.77	0.66
5:A:116:PHE:HB2	5:A:123:LEU:HD22	1.76	0.66
28:X:343:LYS:HA	28:X:346:LYS:HE3	1.77	0.66
38:h:90:HIS:NE2	38:h:94:LEU:HD22	2.10	0.66
1:2:26:U:H3	1:2:910:G:H1	1.43	0.66
1:2:939:A:H2'	1:2:940:G:C8	2.31	0.66
1:2:1750:C:C3'	1:2:1751:U:H5"	2.20	0.66
8:D:504:GLN:HG3	8:D:509:ARG:O	1.95	0.66
36:f:274:PHE:HA	36:f:282:ILE:HD12	1.77	0.66
1:2:1560:C:C4	10:F:104:ARG:NH1	2.63	0.66
1:2:1749:A:H2'	1:2:1750:C:C6	2.31	0.66
23:S:77:LEU:O	23:S:81:ILE:HG23	1.96	0.66
35:e:180:TYR:HA	35:e:256:ASP:OD2	1.96	0.66
41:l:340:ALA:HA	41:l:343:ILE:HD12	1.77	0.66
1:2:1745:A:OP1	38:h:149:ASN:HB3	1.96	0.66
41:l:198:LEU:HD12	41:l:213:LEU:HD21	1.76	0.66
1:2:48:C:H2'	1:2:49:U:C6	2.31	0.66
1:2:1481:C:H2'	1:2:1482:U:C6	2.30	0.66
7:C:182:LYS:HE2	7:C:182:LYS:CA	2.13	0.66
12:H:242:THR:HB	12:H:244:GLU:OE1	1.96	0.66
1:2:390:A:H2'	1:2:391:C:O4'	1.96	0.66
1:2:654:G:H2'	1:2:655:A:H8	1.60	0.66
7:C:180:ILE:HG13	7:C:181:GLY:N	2.10	0.66
35:e:383:ILE:O	35:e:384:LEU:HG	1.94	0.66
36:f:273:TYR:O	36:f:276:LEU:HD23	1.96	0.66
38:h:251:LEU:HG	38:h:255:THR:CG2	2.25	0.66
41:l:175:ILE:HG23	41:l:216:LEU:HD11	1.77	0.66
2:5:53:G:C2'	2:5:54:G:H5'	2.26	0.66
39:i:407:LEU:HD12	39:i:410:MET:SD	2.36	0.66
14:J:200:LEU:C	14:J:201:LEU:HD23	2.21	0.66
36:f:126:LEU:HD21	36:f:151:CYS:SG	2.36	0.66
38:h:342:LEU:O	38:h:350:LYS:HE2	1.96	0.66
39:i:291:LYS:O	39:i:295:MET:HG3	1.95	0.66
5:A:141:ARG:NH2	5:A:165:PRO:HD3	2.10	0.65
8:D:296:ASP:O	8:D:299:GLU:HG3	1.96	0.65
8:D:369:LYS:HG3	8:D:382:TYR:CZ	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:235:LEU:HD12	39:i:299:ILE:HG12	1.78	0.65
23:S:29:VAL:HG11	23:S:43:LEU:HB2	1.76	0.65
38:h:204:GLU:OE1	38:h:208:LEU:HD21	1.95	0.65
1:2:1770:G:H3'	1:2:1771:C:H4'	1.77	0.65
8:D:216:GLU:OE2	8:D:217:LEU:HD23	1.96	0.65
1:2:1600:G:H2'	1:2:1601:A:C8	2.31	0.65
38:h:98:ASN:OD1	38:h:99:VAL:HG23	1.96	0.65
38:h:122:ILE:HD12	38:h:126:PHE:CE2	2.26	0.65
1:2:822:U:O2'	1:2:823:U:H5'	1.96	0.65
2:5:9:A:H1'	2:5:47:A:O4'	1.97	0.65
10:F:42:THR:HG21	27:W:98:GLU:HG3	1.77	0.65
14:J:261:LYS:HE2	14:J:296:GLU:OE1	1.96	0.65
36:f:185:ALA:O	36:f:189:LEU:HG	1.97	0.65
36:f:273:TYR:OH	36:f:289:GLU:HB2	1.96	0.65
38:h:217:GLN:HB2	38:h:220:THR:HG23	1.77	0.65
39:i:277:LYS:HB3	39:i:279:LYS:HZ3	1.61	0.65
2:5:20:U:H5"	2:5:21:C:OP1	1.96	0.65
9:E:74:ASN:O	9:E:78:GLU:HG3	1.97	0.65
35:e:168:LEU:O	35:e:172:LYS:HG2	1.94	0.65
38:h:311:ILE:CD1	38:h:368:LEU:HD21	2.26	0.65
1:2:244:U:H3'	1:2:245:U:H5"	1.78	0.65
4:8:172:THR:HG23	4:8:173:PRO:HD2	1.78	0.65
5:A:6:ALA:O	5:A:9:GLN:HB3	1.97	0.65
8:D:130:LYS:HG2	8:D:134:LYS:NZ	2.11	0.65
9:E:28:LYS:O	9:E:28:LYS:HD2	1.96	0.65
12:H:234:ASP:OD2	12:H:237:ALA:HB3	1.96	0.65
35:e:283:ASP:HB3	35:e:286:GLU:HB2	1.78	0.65
6:B:239:MET:HG3	28:X:448:MET:HE1	1.79	0.65
33:c:133:LYS:O	33:c:137:LYS:HE3	1.97	0.65
36:f:389:THR:HG22	36:f:397:GLU:HB2	1.78	0.65
38:h:311:ILE:HD11	38:h:368:LEU:HD21	1.79	0.65
39:i:375:LEU:HD23	39:i:375:LEU:H	1.61	0.65
41:l:251:PHE:HB2	41:l:276:LEU:HD21	1.78	0.65
41:l:255:SER:HB2	41:l:256:LYS:HE2	1.79	0.65
1:2:490:A:O2'	1:2:491:G:H5'	1.97	0.65
2:5:50:A:H2'	2:5:51:C:C6	2.32	0.65
7:C:46:ARG:CZ	8:D:148:SER:HB3	2.27	0.65
36:f:175:VAL:HG12	36:f:308:ALA:HB1	1.79	0.65
39:i:425:LEU:HA	39:i:428:MET:SD	2.37	0.65
1:2:129:A:O2'	1:2:130:A:H5'	1.97	0.65
1:2:232:A:N7	30:Z:101:LYS:HE2	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:72:THR:HG22	5:A:101:TRP:CZ3	2.32	0.65
18:N:298:PRO:CD	18:N:301:LEU:HD22	2.24	0.65
25:U:23:GLU:HG3	25:U:27:LEU:HD23	1.79	0.65
38:h:197:LYS:HE2	38:h:230:GLU:HG3	1.77	0.65
38:h:330:PHE:HA	38:h:333:LEU:HD13	1.79	0.65
39:i:289:ASP:HB3	39:i:292:TRP:HD1	1.59	0.65
1:2:226:A:H1'	1:2:241:U:O2'	1.97	0.64
1:2:431:A:OP1	8:D:134:LYS:HD3	1.97	0.64
1:2:1797:G:H2'	1:2:1798:G:H8	1.62	0.64
26:V:127:GLU:O	26:V:130:ILE:HG13	1.97	0.64
6:B:176:SER:HG	6:B:230:VAL:N	1.95	0.64
1:2:161:A:H3'	1:2:162:C:H5"	1.80	0.64
4:8:211:LEU:HD12	4:8:216:LEU:HD21	1.80	0.64
5:A:47:LEU:HD11	12:H:250:ILE:HG22	1.79	0.64
37:g:556:ARG:HH21	37:g:589:THR:HG21	1.62	0.64
1:2:409:U:H2'	1:2:410:C:C6	2.31	0.64
1:2:638:A:N3	11:G:104:THR:HG22	2.13	0.64
1:2:660:G:H22	1:2:737:G:H1	1.45	0.64
1:2:1732:A:OP1	38:h:250:LYS:HE3	1.97	0.64
4:8:90:ILE:HG13	4:8:122:LEU:HD13	1.80	0.64
38:h:84:GLU:O	38:h:88:GLU:HG2	1.97	0.64
39:i:335:SER:HA	39:i:338:LEU:CD2	2.28	0.64
2:5:2:G:O2'	2:5:3:C:H5'	1.98	0.64
8:D:105:CYS:HB3	8:D:108:ILE:HB	1.79	0.64
8:D:219:ASN:HA	8:D:222:LYS:HE3	1.78	0.64
25:U:110:TYR:O	25:U:113:GLU:HG3	1.97	0.64
39:i:165:THR:O	39:i:169:VAL:HG23	1.97	0.64
39:i:422:ALA:O	39:i:426:VAL:HG23	1.97	0.64
9:E:46:VAL:HG12	26:V:195:LEU:CD2	2.27	0.64
1:2:285:G:H1'	1:2:287:U:OP2	1.96	0.64
1:2:457:C:H2'	1:2:458:U:O2	1.97	0.64
25:U:122:LYS:HE2	25:U:122:LYS:CA	2.28	0.64
38:h:169:ARG:HH11	38:h:169:ARG:HG3	1.62	0.64
1:2:654:G:H2'	1:2:655:A:C8	2.32	0.64
5:A:86:ARG:HH11	5:A:86:ARG:HA	1.62	0.64
7:C:227:GLU:HG3	7:C:228:ASP:N	2.13	0.64
7:C:256:LEU:HD12	7:C:286:SER:HB2	1.79	0.64
14:J:248:ARG:HG2	14:J:248:ARG:HH11	1.62	0.64
31:a:199:CYS:HA	31:a:202:ILE:HG22	1.80	0.64
38:h:234:TRP:CH2	38:h:263:ALA:HA	2.28	0.64
38:h:261:GLU:O	38:h:265:LYS:HG2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:127:MET:HE3	39:i:127:MET:N	2.13	0.64
1:2:154:G:H1'	38:h:174:HIS:HB2	1.80	0.64
1:2:724:A:H2'	1:2:725:A:C8	2.33	0.64
7:C:323:TYR:HB2	35:e:242:GLU:OE1	1.98	0.64
32:b:44:MET:HB2	32:b:49:ILE:HA	1.79	0.64
36:f:408:TYR:O	39:i:187:LYS:HG3	1.98	0.64
38:h:365:VAL:O	38:h:369:VAL:HG12	1.98	0.64
1:2:1697:G:H2'	1:2:1698:C:C6	2.33	0.63
1:2:1801:A:C5'	15:K:44:LYS:HE2	2.26	0.63
2:5:67:C:H2'	2:5:68:C:C6	2.33	0.63
39:i:133:GLU:HA	39:i:136:VAL:HG12	1.79	0.63
39:i:364:THR:O	39:i:367:TYR:HB3	1.97	0.63
1:2:48:C:H2'	1:2:49:U:H6	1.63	0.63
1:2:1711:A:H2'	1:2:1712:U:C6	2.33	0.63
8:D:93:ARG:HH12	8:D:96:GLU:HB2	1.64	0.63
18:N:298:PRO:HG2	18:N:301:LEU:HD13	1.79	0.63
38:h:190:LEU:HD21	38:h:224:VAL:HG23	1.80	0.63
38:h:191:SER:O	38:h:195:GLU:HG2	1.98	0.63
1:2:43:G:H2'	1:2:44:C:C6	2.34	0.63
1:2:376:G:O2'	1:2:377:U:H5'	1.97	0.63
1:2:1744:C:H2'	1:2:1746:A:N7	2.13	0.63
5:A:10:LYS:HD2	12:H:246:LEU:HD23	1.79	0.63
14:J:293:VAL:HG11	21:Q:247:TYR:CD2	2.33	0.63
20:P:87:ALA:O	20:P:91:LEU:HG	1.98	0.63
36:f:267:ILE:HA	36:f:270:ILE:HD13	1.80	0.63
39:i:335:SER:HA	39:i:338:LEU:HD21	1.78	0.63
4:8:106:VAL:HG12	4:8:107:SER:H	1.63	0.63
26:V:135:PHE:CE2	26:V:139:LEU:HD11	2.32	0.63
35:e:150:SER:O	35:e:154:VAL:HG23	1.98	0.63
38:h:89:LEU:HB2	38:h:112:LEU:HD23	1.79	0.63
1:2:644:G:O2'	1:2:645:A:H5'	1.99	0.63
1:2:648:U:H1'	1:2:649:U:O2	1.98	0.63
5:A:186:TYR:CD2	12:H:264:LEU:HD13	2.33	0.63
34:d:104:LYS:HG3	34:d:105:PRO:HD2	1.81	0.63
1:2:1763:U:C4'	1:2:1764:A:H5'	2.26	0.63
25:U:109:GLU:O	25:U:113:GLU:HG2	1.98	0.63
1:2:78:U:HO2'	1:2:79:G:H8	1.46	0.63
1:2:1560:C:N4	10:F:104:ARG:HH12	1.97	0.63
2:5:71:G:H2'	2:5:72:C:C6	2.33	0.63
8:D:71:ILE:HG23	8:D:75:GLU:OE1	1.98	0.63
8:D:209:PRO:HG2	39:i:197:GLU:OE2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:J:199:LYS:HE2	14:J:201:LEU:HD21	1.81	0.63
26:V:128:ARG:O	26:V:132:GLN:HG2	1.97	0.63
2:5:19:G:H2'	2:5:19:G:OP2	1.99	0.63
36:f:175:VAL:CG1	36:f:308:ALA:HB1	2.29	0.62
36:f:258:PRO:HD3	39:i:280:TYR:CZ	2.34	0.62
38:h:202:MET:HE2	38:h:227:ILE:HG22	1.81	0.62
38:h:269:THR:HG22	38:h:300:LEU:HD23	1.80	0.62
2:5:74:U:H3'	2:5:75:C:C6	2.34	0.62
7:C:312:ILE:HD11	35:e:252:PHE:CD1	2.34	0.62
39:i:249:VAL:O	39:i:253:VAL:HG23	1.99	0.62
6:B:370:LEU:HD11	31:a:98:LEU:HD21	1.80	0.62
30:Z:62:ASN:O	30:Z:65:ILE:HG22	1.99	0.62
36:f:273:TYR:HB3	36:f:286:MET:CE	2.28	0.62
36:f:310:PRO:HB3	36:f:373:LEU:HD13	1.82	0.62
40:k:16:GLN:OE1	40:k:21:GLN:HB3	2.00	0.62
2:5:11:A:H2'	2:5:12:G:O4'	1.99	0.62
5:A:72:THR:OG1	5:A:138:ASP:HA	1.99	0.62
6:B:161:ARG:HH21	6:B:429:ASN:HB3	1.64	0.62
38:h:156:LYS:HA	38:h:159:VAL:CG1	2.30	0.62
1:2:1079:U:H2'	1:2:1080:G:C8	2.35	0.62
8:D:327:GLY:HA3	8:D:329:LYS:HZ1	1.64	0.62
9:E:13:ILE:O	9:E:13:ILE:HG12	1.99	0.62
14:J:250:VAL:HG12	14:J:255:LEU:HB2	1.81	0.62
1:2:342:U:H2'	1:2:343:G:O4'	1.98	0.62
1:2:1730:U:H2'	1:2:1731:A:H8	1.65	0.62
7:C:233:LYS:HB2	7:C:301:HIS:HB2	1.82	0.62
30:Z:80:GLU:HB3	30:Z:98:ILE:HB	1.81	0.62
1:2:1740:C:H3'	1:2:1741:A:H2	1.64	0.62
6:B:380:ILE:HB	6:B:384:LYS:NZ	2.14	0.62
7:C:43:ARG:HG3	8:D:144:GLU:OE1	1.99	0.62
12:H:236:ILE:HG23	12:H:241:ILE:HG22	1.80	0.62
22:R:140:PRO:HB2	22:R:164:THR:HG21	1.80	0.62
39:i:142:GLY:CA	39:i:146:LYS:HD2	2.30	0.62
1:2:7:G:O2'	1:2:8:U:H5'	1.98	0.62
6:B:442:ILE:HD12	6:B:447:GLN:HE21	1.64	0.62
38:h:89:LEU:CB	38:h:112:LEU:HD23	2.29	0.62
5:A:34:THR:HG22	25:U:45:LEU:HD23	1.80	0.62
14:J:191:THR:HG22	21:Q:246:GLU:OE2	2.00	0.62
1:2:68:A:H4'	1:2:69:G:O5'	1.99	0.62
1:2:836:A:H3'	1:2:837:U:C6	2.34	0.62
7:C:289:LEU:HD13	35:e:150:SER:CB	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:225:ILE:HG22	12:H:226:LYS:N	2.13	0.62
14:J:195:ILE:CG2	14:J:261:LYS:HD2	2.30	0.62
39:i:278:LEU:O	39:i:279:LYS:HD3	2.00	0.62
41:l:300:GLU:O	41:l:304:MET:HG2	1.99	0.62
7:C:204:THR:CA	8:D:116:GLU:HG2	2.30	0.61
8:D:189:GLU:HG2	8:D:193:TRP:HE1	1.64	0.61
12:H:245:MET:HG2	39:i:291:LYS:NZ	2.14	0.61
39:i:142:GLY:HA3	39:i:146:LYS:HD2	1.82	0.61
5:A:166:LEU:O	5:A:166:LEU:HD22	2.00	0.61
8:D:170:LYS:HE3	8:D:204:HIS:CB	2.21	0.61
25:U:85:TYR:HA	25:U:88:ARG:NE	2.14	0.61
30:Z:62:ASN:H	38:h:145:ASN:ND2	1.99	0.61
36:f:199:TYR:HB2	36:f:270:ILE:CG2	2.31	0.61
38:h:153:GLN:OE1	38:h:156:LYS:HD3	2.01	0.61
1:2:221:C:O2'	1:2:222:G:H5'	2.01	0.61
1:2:742:U:O2'	1:2:743:C:H5'	2.00	0.61
1:2:1726:U:H2'	1:2:1727:G:C8	2.35	0.61
7:C:252:MET:HE1	7:C:290:TYR:CA	2.31	0.61
39:i:150:ALA:O	39:i:152:PRO:HD3	1.99	0.61
1:2:162:C:C3'	1:2:163:A:H5"	2.18	0.61
1:2:680:U:O2	14:J:216:VAL:HG12	2.01	0.61
1:2:1752:U:H2'	1:2:1753:U:H6	1.65	0.61
2:5:71:G:H2'	2:5:72:C:H6	1.65	0.61
5:A:9:GLN:HA	5:A:9:GLN:NE2	2.12	0.61
5:A:47:LEU:CD1	12:H:250:ILE:HG22	2.31	0.61
5:A:156:VAL:H	5:A:173:THR:HG22	1.65	0.61
7:C:182:LYS:HA	7:C:182:LYS:CE	2.17	0.61
8:D:216:GLU:OE1	39:i:215:LEU:CD2	2.48	0.61
14:J:195:ILE:HG21	14:J:261:LYS:HD2	1.82	0.61
25:U:118:LYS:O	25:U:122:LYS:HG2	2.00	0.61
31:a:214:PRO:HG2	31:a:217:LEU:HB2	1.82	0.61
36:f:58:ARG:NH1	36:f:66:SER:HB3	2.15	0.61
36:f:131:TYR:OH	36:f:407:PRO:HG3	2.01	0.61
38:h:203:ASP:O	38:h:207:LYS:HG2	2.01	0.61
19:O:52:MET:HE2	35:e:334:ILE:HG21	1.81	0.61
31:a:401:MET:H	31:a:401:MET:HE3	1.65	0.61
35:e:298:ILE:O	35:e:302:GLU:HG2	2.00	0.61
36:f:92:LYS:HZ1	36:f:231:GLU:HG2	1.65	0.61
8:D:130:LYS:HG2	8:D:134:LYS:HZ1	1.63	0.61
8:D:452:THR:HG22	8:D:452:THR:O	2.00	0.61
39:i:103:ARG:HD3	39:i:173:VAL:HG22	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:129:LEU:HD23	39:i:133:GLU:HG2	1.83	0.61
1:2:1760:U:O2'	1:2:1761:C:H5'	2.00	0.61
2:5:44:A:H4'	2:5:44:A:OP1	1.99	0.61
38:h:137:LEU:HD21	38:h:143:HIS:CD2	2.36	0.61
1:2:439:A:H2'	1:2:441:U:H1'	1.83	0.61
1:2:1730:U:H2'	1:2:1731:A:C8	2.35	0.61
2:5:49:U:H4'	2:5:51:C:OP1	2.01	0.61
7:C:344:ARG:HH11	7:C:344:ARG:HG2	1.66	0.61
36:f:264:LEU:CD1	39:i:278:LEU:HD23	2.31	0.61
38:h:193:ALA:HB2	38:h:201:LEU:CD2	2.20	0.61
38:h:295:ALA:HA	38:h:298:PHE:CD2	2.36	0.61
39:i:112:VAL:HG12	39:i:124:ILE:HG12	1.83	0.61
1:2:613:C:H2'	1:2:614:A:H8	1.62	0.61
2:5:55:U:O4	2:5:59:A:N7	2.34	0.61
7:C:102:ASN:OD1	7:C:145:LYS:HE3	2.00	0.61
7:C:257:LEU:HD11	8:D:194:MET:HE2	1.83	0.61
35:e:153:PHE:O	35:e:157:ILE:HG13	2.01	0.61
35:e:192:LEU:HD13	35:e:200:TYR:CE2	2.36	0.61
36:f:376:VAL:HA	36:f:380:MET:CE	2.29	0.61
38:h:90:HIS:CD2	38:h:94:LEU:HD13	2.36	0.61
1:2:711:A:H2'	1:2:712:A:C8	2.36	0.61
1:2:919:G:H22	3:6:36:A:C5'	2.14	0.61
26:V:180:GLU:O	26:V:184:LYS:HG2	2.00	0.61
38:h:298:PHE:HB2	38:h:307:ALA:HB2	1.83	0.61
38:h:335:ASN:OD1	38:h:381:GLU:HG2	1.99	0.61
2:5:19:G:H4'	2:5:20:U:OP1	2.01	0.60
2:5:22:A:H3'	2:5:47:A:N7	2.15	0.60
3:6:35:U:H3'	3:6:36:A:H5"	1.82	0.60
18:N:303:GLU:HB3	18:N:304:PRO:HD2	1.83	0.60
1:2:923:C:C5'	32:b:14:ARG:HH21	2.14	0.60
1:2:1800:G:H3'	15:K:44:LYS:NZ	2.16	0.60
7:C:265:ARG:HB2	39:i:244:ARG:NH2	2.12	0.60
20:P:13:MET:HB2	20:P:16:SER:HB2	1.83	0.60
39:i:321:VAL:HA	39:i:324:LYS:HG2	1.83	0.60
39:i:125:ASP:HA	39:i:128:LEU:CD2	2.32	0.60
39:i:317:LYS:O	39:i:321:VAL:HG23	2.01	0.60
25:U:52:GLU:HG3	25:U:90:LEU:CD2	2.25	0.60
38:h:270:GLU:HG2	38:h:271:SER:N	2.15	0.60
41:l:373:LYS:HG2	41:l:374:PRO:HD3	1.83	0.60
1:2:286:C:O2'	1:2:287:U:H5'	2.02	0.60
2:5:23:A:H5"	2:5:24:C:H5	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:P:43:HIS:O	20:P:71:VAL:HG12	2.02	0.60
1:2:578:C:H2'	1:2:579:G:O4'	2.00	0.60
1:2:915:G:N2	1:2:916:A:H1'	2.16	0.60
2:5:38:G:H1'	3:6:37:U:H3	1.66	0.60
2:5:48:U:H4'	2:5:49:U:O5'	2.01	0.60
10:F:78:ILE:HD11	32:b:37:MET:HB3	1.82	0.60
11:G:17:GLU:OE1	11:G:66:GLY:HA2	2.02	0.60
14:J:191:THR:HG22	21:Q:246:GLU:CD	2.27	0.60
33:c:132:LYS:HG3	33:c:136:ARG:HH21	1.67	0.60
38:h:259:TRP:CD1	38:h:275:VAL:HG21	2.36	0.60
39:i:185:LYS:NZ	39:i:185:LYS:HB3	2.17	0.60
39:i:363:ASN:ND2	39:i:366:ALA:HB2	2.17	0.60
2:5:67:C:H2'	2:5:68:C:H6	1.66	0.60
41:l:279:ARG:HD3	41:l:281:PHE:CE2	2.36	0.60
32:b:88:ARG:O	32:b:89:GLY:C	2.44	0.60
38:h:346:ASN:O	38:h:350:LYS:HG3	2.02	0.60
5:A:61:ALA:HB2	5:A:196:PHE:CE2	2.36	0.60
1:2:573:G:HO2'	1:2:817:G:H5'	1.66	0.59
1:2:632:U:O2'	1:2:633:U:H5'	2.01	0.59
1:2:659:A:H5"	21:Q:204:LYS:HD2	1.84	0.59
1:2:1836:C:O2'	1:2:1837:U:H5'	2.02	0.59
8:D:300:ARG:O	8:D:303:ILE:HG22	2.02	0.59
35:e:304:LEU:O	35:e:308:GLU:HG2	2.01	0.59
36:f:166:ASP:OD1	36:f:167:LYS:HG2	2.02	0.59
38:h:251:LEU:HG	38:h:255:THR:HG21	1.84	0.59
39:i:170:SER:O	39:i:174:LEU:HD23	2.02	0.59
1:2:435:G:O2'	1:2:436:G:H5'	2.02	0.59
1:2:636:A:O2'	1:2:637:A:H5'	2.02	0.59
1:2:826:C:O2'	1:2:827:C:H5'	2.01	0.59
1:2:919:G:H22	3:6:36:A:H5"	1.67	0.59
2:5:23:A:H3'	2:5:24:C:C6	2.37	0.59
14:J:197:HIS:C	14:J:198:ILE:HD12	2.27	0.59
39:i:384:ILE:HG23	39:i:415:ILE:HG12	1.84	0.59
41:l:415:HIS:HA	41:l:447:VAL:HG11	1.84	0.59
1:2:1792:A:H2'	1:2:1793:C:O4'	2.03	0.59
6:B:110:LEU:HD12	31:a:83:LYS:HG2	1.83	0.59
7:C:161:ILE:O	7:C:165:GLU:HG2	2.02	0.59
26:V:145:GLU:HA	26:V:145:GLU:OE2	2.01	0.59
36:f:127:TYR:CB	36:f:398:LEU:HD21	2.33	0.59
38:h:241:SER:HA	38:h:244:PHE:HE2	1.67	0.59
1:2:849:G:O2'	1:2:850:C:H5'	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1688:U:H2'	1:2:1689:C:H6	1.68	0.59
5:A:64:ARG:NH2	5:A:205:ILE:HD11	2.17	0.59
25:U:77:PHE:CE1	40:k:13:ILE:HG12	2.36	0.59
28:X:482:PRO:HD3	28:X:522:TYR:CE2	2.37	0.59
1:2:64:U:H2'	1:2:65:G:H8	1.65	0.59
1:2:177:G:H1'	1:2:373:G:H5'	1.84	0.59
1:2:1685:G:H3'	1:2:1686:U:C6	2.36	0.59
12:H:219:LYS:HD2	25:U:127:LEU:CD1	2.33	0.59
32:b:41:LEU:HA	32:b:44:MET:HE3	1.85	0.59
38:h:169:ARG:HH22	38:h:176:VAL:H	1.49	0.59
7:C:320:GLU:HG3	35:e:222:LEU:HD12	1.85	0.59
8:D:231:ILE:CG2	8:D:235:LYS:HE2	2.33	0.59
11:G:105:THR:HG22	11:G:121:GLY:O	2.02	0.59
36:f:337:ARG:HD2	36:f:388:ALA:H	1.65	0.59
38:h:229:HIS:CD2	38:h:262:PHE:HB2	2.37	0.59
1:2:464:C:O2'	1:2:465:G:H5'	2.03	0.59
1:2:834:C:H2'	1:2:835:U:O4'	2.02	0.59
1:2:1711:A:H2'	1:2:1712:U:H6	1.67	0.59
2:5:50:A:OP1	2:5:50:A:H3'	2.01	0.59
8:D:170:LYS:CE	8:D:204:HIS:HB3	2.22	0.59
8:D:181:LEU:O	8:D:181:LEU:HD13	2.03	0.59
14:J:272:ARG:CD	23:S:40:LEU:HD23	2.26	0.59
32:b:86:LEU:C	32:b:88:ARG:N	2.58	0.59
36:f:328:LEU:HD13	36:f:332:LEU:HG	1.84	0.59
38:h:95:ASP:O	38:h:99:VAL:HG23	2.03	0.59
1:2:287:U:O2'	1:2:288:G:H5"	2.03	0.59
5:A:72:THR:HB	5:A:142:LYS:HD3	1.84	0.59
7:C:37:ILE:N	7:C:37:ILE:HD12	2.18	0.59
7:C:67:ILE:HG22	7:C:350:LEU:HD12	1.85	0.59
7:C:287:LEU:HD22	8:D:178:LEU:HD23	1.85	0.59
30:Z:51:LYS:HB3	30:Z:55:GLU:OE2	2.03	0.59
30:Z:124:ILE:HG22	30:Z:127:LEU:H	1.67	0.59
1:2:882:A:H4'	1:2:883:G:OP1	2.03	0.59
2:5:63:C:H2'	2:5:64:U:C6	2.38	0.59
7:C:251:ARG:HH12	7:C:252:MET:HA	1.67	0.59
11:G:35:SER:O	11:G:39:ILE:HD12	2.02	0.59
16:L:65:CYS:HB3	27:W:370:PRO:HD3	1.85	0.59
20:P:13:MET:HE1	20:P:41:MET:SD	2.42	0.59
27:W:101:ARG:HD3	27:W:446:ARG:HB2	1.85	0.59
36:f:377:SER:H	36:f:380:MET:CE	2.16	0.59
1:2:47:G:O2'	1:2:48:C:H5'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:479:G:OP1	34:d:75:THR:HB	2.02	0.58
1:2:835:U:H2'	1:2:836:A:C4'	2.33	0.58
1:2:949:U:O2	1:2:953:U:H5	1.86	0.58
1:2:1687:U:H2'	1:2:1688:U:C6	2.38	0.58
1:2:1687:U:H2'	1:2:1688:U:H6	1.67	0.58
8:D:130:LYS:C	8:D:134:LYS:HZ2	2.10	0.58
12:H:208:ARG:HA	12:H:211:LYS:HD2	1.83	0.58
30:Z:51:LYS:HD3	30:Z:55:GLU:OE2	2.03	0.58
34:d:63:GLU:N	34:d:63:GLU:OE2	2.36	0.58
35:e:173:GLU:HG2	35:e:176:ALA:HB2	1.83	0.58
38:h:150:LEU:O	38:h:154:VAL:HG12	2.02	0.58
39:i:103:ARG:CD	39:i:173:VAL:HG13	2.32	0.58
1:2:279:G:O2'	1:2:280:U:H5'	2.04	0.58
1:2:989:A:H2'	1:2:990:U:C6	2.38	0.58
1:2:1767:G:C3'	1:2:1768:A:H5"	2.33	0.58
7:C:25:LEU:HD12	7:C:29:VAL:HG21	1.84	0.58
18:N:331:LYS:HB2	18:N:331:LYS:NZ	2.19	0.58
28:X:401:PRO:HG3	31:a:361:ARG:HG2	1.85	0.58
38:h:126:PHE:CZ	38:h:166:HIS:HB3	2.38	0.58
1:2:991:A:H2'	1:2:992:U:C6	2.38	0.58
2:5:14:A:H1'	2:5:23:A:C2	2.38	0.58
3:6:36:A:H2'	3:6:36:A:N3	2.18	0.58
8:D:421:HIS:NE2	25:U:2:SER:HB2	2.19	0.58
32:b:22:ASN:HB3	32:b:24:LYS:HG2	1.85	0.58
36:f:316:THR:O	36:f:320:ILE:HG12	2.03	0.58
36:f:356:ARG:HA	36:f:360:VAL:CG2	2.32	0.58
38:h:197:LYS:HE2	38:h:230:GLU:CG	2.34	0.58
1:2:1748:G:H2'	1:2:1749:A:C8	2.38	0.58
23:S:89:LYS:HB3	32:b:19:LEU:HD21	1.85	0.58
38:h:158:CYS:O	38:h:161:VAL:HG12	2.03	0.58
1:2:389:G:O2'	1:2:390:A:H5'	2.02	0.58
1:2:706:G:P	9:E:58:ARG:HH12	2.26	0.58
1:2:1384:A:H2'	1:2:1385:A:H8	1.68	0.58
7:C:46:ARG:NH2	8:D:148:SER:HB3	2.19	0.58
11:G:81:LYS:O	11:G:85:ILE:HG13	2.03	0.58
38:h:298:PHE:HD2	38:h:307:ALA:HA	1.68	0.58
1:2:129:A:H2'	1:2:130:A:H8	1.68	0.58
1:2:310:U:O2'	1:2:311:G:H5'	2.03	0.58
1:2:979:A:H2'	1:2:980:G:H8	1.66	0.58
1:2:1701:C:H4'	1:2:1702:G:OP1	2.03	0.58
5:A:34:THR:CG2	25:U:45:LEU:HD23	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:56:VAL:HG12	25:U:82:ALA:O	2.03	0.58
38:h:296:LYS:HD2	38:h:337:TRP:CE2	2.38	0.58
1:2:521:A:H61	15:K:89:ASP:HB2	1.68	0.58
1:2:1804:U:O2'	1:2:1805:C:H5'	2.04	0.58
8:D:166:MET:HA	8:D:166:MET:CE	2.25	0.58
10:F:43:GLU:O	10:F:44:ARG:HG2	2.04	0.58
14:J:262:VAL:HG11	14:J:271:LYS:CB	2.32	0.58
25:U:54:PRO:O	25:U:58:ARG:HG3	2.04	0.58
25:U:87:CYS:O	25:U:91:GLU:HG2	2.04	0.58
30:Z:86:LEU:HD23	30:Z:87:TYR:N	2.19	0.58
41:l:515:TYR:HB2	41:l:539:MET:HE2	1.84	0.58
1:2:1316:A:H2'	1:2:1317:A:C8	2.38	0.58
1:2:1687:U:O2'	1:2:1688:U:H5'	2.04	0.58
1:2:1688:U:H2'	1:2:1689:C:C6	2.39	0.58
2:5:12:G:H5"	2:5:13:G:OP2	2.03	0.58
5:A:20:ARG:HD2	40:k:20:MET:HE3	1.85	0.58
31:a:219:LYS:HD2	31:a:220:LYS:N	2.18	0.58
38:h:173:LYS:CD	38:h:212:ASN:HA	2.34	0.58
1:2:369:G:H2'	1:2:370:G:C8	2.38	0.58
4:8:95:VAL:HG21	4:8:111:ALA:HB2	1.85	0.58
7:C:37:ILE:HD12	7:C:37:ILE:H	1.67	0.58
12:H:355:THR:HG22	12:H:357:THR:HG23	1.86	0.58
22:R:64:THR:HG22	22:R:71:SER:HA	1.86	0.58
25:U:68:LEU:C	25:U:71:PRO:HD2	2.28	0.58
34:d:59:ARG:HH11	34:d:59:ARG:HG3	1.68	0.58
41:l:170:SER:HB2	41:l:206:ARG:NH1	2.19	0.58
41:l:503:MET:HG3	41:l:510:PRO:HG3	1.85	0.58
1:2:491:G:H4'	1:2:492:G:OP1	2.03	0.58
1:2:1767:G:H3'	1:2:1768:A:H5"	1.86	0.58
38:h:156:LYS:CA	38:h:159:VAL:HG12	2.33	0.58
39:i:112:VAL:HG11	39:i:124:ILE:HG23	1.85	0.58
2:5:17:U:H3'	2:5:18:G:H5"	1.86	0.57
14:J:199:LYS:CE	14:J:201:LEU:HD21	2.34	0.57
28:X:323:GLU:HG2	28:X:324:GLU:N	2.19	0.57
36:f:306:LYS:HA	36:f:306:LYS:HE2	1.85	0.57
39:i:139:ILE:HD12	39:i:140:GLU:H	1.66	0.57
1:2:708:A:H2'	1:2:709:G:C8	2.39	0.57
18:N:308:GLU:OE1	18:N:308:GLU:N	2.31	0.57
35:e:327:ARG:HG3	35:e:328:SER:O	2.03	0.57
38:h:292:PHE:O	38:h:296:LYS:HG2	2.04	0.57
5:A:156:VAL:H	5:A:173:THR:CG2	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:210:LEU:HD12	8:D:87:VAL:HG22	1.84	0.57
38:h:244:PHE:CE1	38:h:251:LEU:HD22	2.39	0.57
38:h:258:VAL:HA	38:h:261:GLU:CD	2.29	0.57
41:l:357:GLN:HA	41:l:360:LEU:HD23	1.85	0.57
1:2:225:G:H4'	1:2:226:A:OP1	2.04	0.57
6:B:98:TRP:HB2	28:X:330:ALA:HB1	1.85	0.57
39:i:108:MET:HE3	39:i:111:LYS:HB2	1.86	0.57
1:2:1689:C:O2'	1:2:1690:G:H5'	2.04	0.57
1:2:1729:G:O2'	1:2:1730:U:H5'	2.05	0.57
2:5:15:A:O2'	2:5:16:U:H5'	2.03	0.57
5:A:86:ARG:HH11	5:A:86:ARG:CA	2.17	0.57
6:B:377:MET:N	6:B:377:MET:HE3	2.20	0.57
7:C:118:GLU:HA	7:C:118:GLU:OE2	2.04	0.57
1:2:450:U:H4'	1:2:451:A:O5'	2.03	0.57
1:2:524:C:OP2	15:K:88:LYS:HE2	2.04	0.57
1:2:1392:A:C2	41:l:545:HIS:HB3	2.38	0.57
2:5:17:U:H3'	2:5:18:G:C5'	2.34	0.57
7:C:178:LYS:HZ3	35:e:251:PHE:HB3	1.66	0.57
36:f:127:TYR:HE2	36:f:336:TYR:HA	1.69	0.57
1:2:1740:C:H3'	1:2:1741:A:C2	2.40	0.57
1:2:1757:U:H2'	1:2:1758:G:H8	1.70	0.57
13:I:215:GLU:HG3	31:a:298:VAL:HG22	1.85	0.57
36:f:310:PRO:HB3	36:f:373:LEU:HD22	1.85	0.57
38:h:173:LYS:HG3	38:h:212:ASN:HB3	1.86	0.57
41:l:411:ASN:HB3	41:l:443:TYR:CE2	2.38	0.57
1:2:1757:U:H2'	1:2:1758:G:C8	2.38	0.57
5:A:3:LEU:CB	36:f:255:LEU:HD12	2.30	0.57
8:D:350:LYS:HD2	8:D:350:LYS:C	2.30	0.57
35:e:140:ILE:O	35:e:143:ILE:HB	2.04	0.57
36:f:199:TYR:HB2	36:f:270:ILE:HG21	1.87	0.57
39:i:112:VAL:CG1	39:i:124:ILE:HG23	2.35	0.57
39:i:425:LEU:HA	39:i:428:MET:CG	2.35	0.57
1:2:400:C:H2'	1:2:401:A:O4'	2.04	0.57
2:5:24:C:O2'	2:5:25:U:H5'	2.05	0.57
5:A:128:THR:HG21	8:D:305:LEU:HD13	1.86	0.57
36:f:274:PHE:HA	36:f:282:ILE:CD1	2.35	0.57
39:i:341:TRP:CZ2	39:i:355:LEU:HD13	2.39	0.57
1:2:273:G:O2'	1:2:274:G:H5'	2.04	0.57
1:2:836:A:H5"	1:2:837:U:C4	2.40	0.57
1:2:956:G:N2	13:I:171:VAL:HG11	2.20	0.57
6:B:174:ARG:HD2	28:X:365:GLU:HG2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:251:ARG:NH2	7:C:252:MET:HB2	2.18	0.57
8:D:101:GLN:O	8:D:103:LEU:HD23	2.05	0.57
38:h:171:LEU:HD23	38:h:208:LEU:HB2	1.86	0.57
38:h:202:MET:CE	38:h:227:ILE:HG22	2.35	0.57
38:h:225:PHE:HA	38:h:228:CYS:SG	2.45	0.57
41:l:176:ARG:HA	41:l:179:LYS:HD2	1.87	0.57
1:2:43:G:H2'	1:2:44:C:H6	1.70	0.56
1:2:80:U:H2'	1:2:81:U:C6	2.39	0.56
1:2:482:A:H4'	1:2:483:U:O5'	2.04	0.56
1:2:649:U:O2	1:2:649:U:H2'	2.02	0.56
1:2:669:G:H2'	1:2:670:G:H8	1.64	0.56
1:2:747:C:O2'	1:2:748:G:H5'	2.05	0.56
7:C:58:TYR:HB3	8:D:409:MET:CE	2.35	0.56
7:C:158:ASN:O	7:C:162:ARG:HG2	2.05	0.56
7:C:239:LYS:HD2	8:D:211:TYR:CE2	2.40	0.56
19:O:23:THR:HG22	19:O:33:HIS:CB	2.34	0.56
34:d:49:ILE:HB	34:d:53:VAL:HG11	1.87	0.56
1:2:50:A:H2'	1:2:51:U:H6	1.69	0.56
2:5:23:A:H2'	2:5:23:A:N3	2.21	0.56
6:B:305:GLU:HA	6:B:308:ASN:OD1	2.05	0.56
6:B:404:LEU:HD11	28:X:368:LEU:HD23	1.86	0.56
11:G:38:ARG:HB3	11:G:38:ARG:CZ	2.35	0.56
36:f:328:LEU:CD1	36:f:332:LEU:HG	2.35	0.56
38:h:88:GLU:OE1	38:h:88:GLU:HA	2.05	0.56
38:h:263:ALA:HB3	38:h:272:LEU:HD13	1.87	0.56
39:i:299:ILE:O	39:i:303:GLU:HG3	2.05	0.56
39:i:308:TRP:CB	40:k:6:LEU:HD11	2.34	0.56
1:2:611:G:O2'	1:2:612:U:H5'	2.05	0.56
1:2:1678:G:H2'	1:2:1679:G:O4'	2.04	0.56
1:2:1800:G:H3'	15:K:44:LYS:HZ3	1.70	0.56
5:A:32:TYR:CE2	40:k:4:MET:HB3	2.40	0.56
25:U:85:TYR:HA	25:U:88:ARG:HE	1.69	0.56
35:e:290:GLU:HA	35:e:290:GLU:OE2	2.04	0.56
38:h:194:LEU:HD23	38:h:227:ILE:HG12	1.86	0.56
39:i:363:ASN:HB3	39:i:366:ALA:CB	2.25	0.56
1:2:888:G:H2'	1:2:889:U:C6	2.40	0.56
22:R:154:LEU:HD11	22:R:169:TYR:CG	2.41	0.56
30:Z:80:GLU:O	30:Z:97:GLY:HA2	2.05	0.56
31:a:214:PRO:HB2	31:a:216:ASP:OD1	2.06	0.56
38:h:251:LEU:CD1	38:h:255:THR:HG21	2.35	0.56
41:l:170:SER:HB2	41:l:206:ARG:HH12	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1700:U:H2'	1:2:1701:C:H6	1.70	0.56
2:5:54:G:O2'	2:5:55:U:H5'	2.06	0.56
8:D:189:GLU:HA	8:D:192:LYS:HD2	1.87	0.56
8:D:339:ASP:O	8:D:342:GLU:HG3	2.06	0.56
17:M:129:PHE:HE2	17:M:142:MET:HE2	1.70	0.56
19:O:23:THR:HG22	19:O:33:HIS:HA	1.88	0.56
27:W:372:THR:HG22	27:W:374:ARG:H	1.69	0.56
38:h:133:ARG:HD3	38:h:178:GLY:CA	2.34	0.56
41:l:522:PHE:HD1	41:l:528:ASP:HB3	1.71	0.56
2:5:12:G:H2'	2:5:12:G:N3	2.19	0.56
2:5:73:A:N3	2:5:73:A:H2'	2.20	0.56
14:J:296:GLU:HB2	23:S:28:ARG:HB3	1.88	0.56
34:d:49:ILE:HD12	34:d:49:ILE:N	2.20	0.56
36:f:107:LEU:HD11	36:f:122:PHE:CD2	2.40	0.56
36:f:369:ASP:O	36:f:371:PRO:HD3	2.06	0.56
38:h:173:LYS:HG3	38:h:212:ASN:CB	2.35	0.56
38:h:197:LYS:CD	38:h:230:GLU:HG3	2.35	0.56
1:2:905:C:O2'	1:2:906:A:H5'	2.05	0.56
1:2:923:C:H5"	32:b:14:ARG:HH21	1.70	0.56
1:2:1567:G:N2	1:2:1593:G:H1'	2.20	0.56
1:2:1725:C:H5"	1:2:1726:U:OP2	2.06	0.56
27:W:435:ALA:HB1	27:W:472:MET:HE1	1.86	0.56
30:Z:61:PRO:HD3	38:h:173:LYS:O	2.05	0.56
1:2:541:G:O2'	1:2:542:G:H5'	2.05	0.56
2:5:4:G:H2'	2:5:5:G:O4'	2.06	0.56
5:A:35:ARG:HD3	40:k:14:PHE:CD2	2.40	0.56
19:O:90:ALA:HB2	26:V:49:TYR:CE1	2.41	0.56
38:h:357:LEU:O	38:h:361:ILE:HG22	2.05	0.56
6:B:282:GLN:O	6:B:286:ARG:HG3	2.06	0.56
14:J:257:SER:HA	14:J:291:PRO:O	2.06	0.56
38:h:311:ILE:O	38:h:314:ILE:HG22	2.06	0.56
1:2:529:U:C6	1:2:529:U:H5'	2.41	0.56
19:O:79:ARG:HG3	35:e:355:SER:OG	2.06	0.56
25:U:70:GLU:HG2	40:k:15:ARG:HD3	1.88	0.56
1:2:494:A:H5"	1:2:495:G:OP2	2.06	0.55
1:2:1144:A:H61	1:2:1379:C:N4	2.03	0.55
1:2:1669:C:H1'	4:8:178:LYS:HZ3	1.71	0.55
7:C:139:VAL:HG11	7:C:144:LEU:HD22	1.89	0.55
38:h:209:LEU:HD11	38:h:216:LEU:HD21	1.87	0.55
39:i:185:LYS:O	39:i:188:GLN:HG3	2.07	0.55
1:2:718:A:H2	1:2:729:A:H61	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1693:C:C2’	1:2:1694:G:H5’	2.36	0.55
1:2:1793:C:O2’	1:2:1794:U:H5’	2.06	0.55
2:5:28:U:H2’	2:5:29:C:C6	2.41	0.55
2:5:39:A:H2’	2:5:40:C:O4’	2.06	0.55
12:H:250:ILE:O	12:H:251:ALA:HB3	2.06	0.55
21:Q:165:GLU:O	21:Q:165:GLU:CD	2.50	0.55
31:a:391:LYS:HE2	41:l:559:GLU:OE1	2.06	0.55
36:f:323:GLY:HA2	36:f:326:GLN:OE1	2.06	0.55
11:G:47:LYS:HE2	11:G:65:GLN:NE2	2.21	0.55
14:J:289:GLN:HG3	21:Q:252:ASP:OD2	2.05	0.55
19:O:60:LYS:HG2	26:V:84:TYR:CD1	2.41	0.55
19:O:91:MET:HE3	34:d:100:LEU:CD1	2.34	0.55
25:U:95:ASN:OD1	39:i:389:LYS:HE2	2.07	0.55
40:k:13:ILE:H	40:k:13:ILE:HD12	1.72	0.55
2:5:3:C:H2’	2:5:4:G:H8	1.70	0.55
8:D:131:GLN:HA	8:D:134:LYS:HZ2	1.69	0.55
8:D:329:LYS:HG3	8:D:332:ARG:NH2	2.22	0.55
35:e:306:ARG:NH1	35:e:306:ARG:HB3	2.21	0.55
38:h:253:LYS:HE3	38:h:283:TYR:CD2	2.42	0.55
1:2:10:A:N6	35:e:379:ARG:HG2	2.22	0.55
1:2:462:G:C2’	1:2:463:U:H5’	2.36	0.55
23:S:78:GLU:O	23:S:81:ILE:HG13	2.07	0.55
39:i:244:ARG:HA	39:i:247:GLU:OE1	2.06	0.55
1:2:44:C:O2’	1:2:45:U:H5’	2.06	0.55
1:2:939:A:H2’	1:2:940:G:H8	1.70	0.55
1:2:1685:G:H3’	1:2:1686:U:H6	1.70	0.55
8:D:104:ASP:OD2	8:D:106:LYS:HG3	2.07	0.55
36:f:203:THR:CG2	36:f:304:GLN:HB2	2.35	0.55
1:2:81:U:H2’	1:2:82:C:C6	2.42	0.55
21:Q:193:LEU:HD21	21:Q:213:ILE:HG21	1.89	0.55
36:f:300:LYS:O	36:f:304:GLN:HG3	2.07	0.55
36:f:353:GLU:O	36:f:356:ARG:HG3	2.06	0.55
1:2:143:U:H2’	1:2:144:U:C6	2.42	0.55
5:A:128:THR:HG21	8:D:305:LEU:CD1	2.37	0.55
14:J:293:VAL:O	23:S:31:VAL:HG12	2.07	0.55
27:W:451:GLU:HG2	27:W:452:VAL:HG13	1.89	0.55
38:h:148:CYS:O	38:h:152:ARG:HG3	2.06	0.55
39:i:335:SER:O	39:i:338:LEU:HG	2.07	0.55
1:2:1718:A:O2’	1:2:1719:G:H5’	2.07	0.55
1:2:1752:U:H2’	1:2:1753:U:C6	2.41	0.55
6:B:514:VAL:HB	6:B:517:GLN:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:289:LEU:HD13	35:e:150:SER:HB3	1.88	0.55
12:H:225:ILE:HA	12:H:228:PRO:CB	2.36	0.55
12:H:325:LYS:O	12:H:325:LYS:HD3	2.07	0.55
35:e:233:LEU:HD11	35:e:235:ARG:NH1	2.22	0.55
39:i:133:GLU:HA	39:i:136:VAL:CG1	2.37	0.55
1:2:170:C:O2'	1:2:171:G:H5'	2.07	0.55
1:2:1316:A:H2'	1:2:1317:A:H8	1.72	0.55
1:2:1392:A:H2	41:l:545:HIS:HB3	1.72	0.55
8:D:92:GLN:HG3	8:D:93:ARG:HH11	1.72	0.55
1:2:1705:C:H4'	1:2:1706:C:OP2	2.05	0.54
26:V:180:GLU:OE1	26:V:180:GLU:N	2.40	0.54
35:e:140:ILE:HA	35:e:143:ILE:CD1	2.34	0.54
36:f:336:TYR:HB2	36:f:398:LEU:HD22	1.88	0.54
39:i:194:GLU:HB3	39:i:223:LYS:HZ2	1.70	0.54
39:i:334:PRO:CD	39:i:369:LYS:HE3	2.36	0.54
1:2:959:A:C2	2:5:35:C:H5'	2.42	0.54
1:2:1473:C:P	29:Y:95:ARG:HH12	2.31	0.54
1:2:1732:A:H2'	1:2:1733:C:O4'	2.07	0.54
6:B:290:ALA:HB3	6:B:318:ASN:ND2	2.21	0.54
7:C:233:LYS:HD2	7:C:238:GLU:OE1	2.06	0.54
23:S:90:LEU:HD11	32:b:21:ILE:HD11	1.89	0.54
26:V:94:GLU:O	26:V:97:ARG:HG3	2.07	0.54
39:i:407:LEU:O	39:i:410:MET:HG2	2.06	0.54
41:l:557:VAL:HA	41:l:560:MET:HE2	1.88	0.54
1:2:4:A:H1'	1:2:6:A:C2	2.42	0.54
1:2:192:G:H2'	1:2:193:A:C8	2.41	0.54
1:2:292:A:C2'	1:2:293:A:H5'	2.38	0.54
1:2:979:A:H2'	1:2:980:G:C8	2.42	0.54
1:2:1670:A:H2'	1:2:1671:C:H6	1.71	0.54
9:E:31:TYR:CE2	26:V:178:PRO:HA	2.42	0.54
9:E:42:SER:O	26:V:193:THR:HG22	2.07	0.54
26:V:128:ARG:HE	26:V:132:GLN:HE21	1.56	0.54
35:e:142:GLU:HA	35:e:145:LYS:HD2	1.89	0.54
36:f:196:LEU:O	36:f:200:LEU:HG	2.07	0.54
36:f:356:ARG:HA	36:f:360:VAL:HG23	1.88	0.54
36:f:358:ARG:HB3	36:f:358:ARG:CZ	2.38	0.54
39:i:309:ARG:HB3	39:i:350:VAL:HG21	1.88	0.54
1:2:130:A:O2'	1:2:131:A:H5'	2.07	0.54
1:2:499:C:H1'	1:2:547:U:O2'	2.08	0.54
1:2:642:C:O2'	1:2:643:U:H5'	2.08	0.54
25:U:59:PHE:HA	25:U:62:LYS:CD	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:469:GLY:O	27:W:473:ARG:HG2	2.07	0.54
36:f:267:ILE:HA	36:f:270:ILE:CD1	2.37	0.54
38:h:153:GLN:O	38:h:156:LYS:HG2	2.07	0.54
1:2:1670:A:H2'	1:2:1671:C:C6	2.42	0.54
2:5:64:U:H2'	2:5:65:G:H5'	1.89	0.54
5:A:20:ARG:NH1	40:k:20:MET:HG2	2.22	0.54
36:f:157:ILE:HA	36:f:162:ARG:HD2	1.89	0.54
39:i:184:GLU:O	39:i:187:LYS:HB2	2.08	0.54
1:2:150:A:H2'	1:2:151:A:N3	2.23	0.54
1:2:753:U:H2'	1:2:754:G:O4'	2.07	0.54
7:C:174:ILE:HA	7:C:178:LYS:HD3	1.89	0.54
8:D:121:ILE:O	8:D:121:ILE:HG12	2.07	0.54
10:F:91:TRP:CG	10:F:128:LYS:HD2	2.43	0.54
26:V:109:ALA:O	26:V:113:ARG:HG3	2.08	0.54
38:h:206:MET:HG2	38:h:209:LEU:CD2	2.35	0.54
1:2:129:A:H2'	1:2:130:A:C8	2.42	0.54
1:2:718:A:H2'	1:2:718:A:N3	2.22	0.54
11:G:94:PRO:HG2	11:G:129:TYR:CZ	2.43	0.54
25:U:23:GLU:HG3	25:U:27:LEU:CD2	2.37	0.54
35:e:164:MET:O	35:e:168:LEU:HG	2.08	0.54
36:f:258:PRO:HD3	39:i:280:TYR:CE1	2.42	0.54
38:h:145:ASN:HB3	38:h:178:GLY:O	2.07	0.54
1:2:677:G:O2'	1:2:678:U:H5'	2.08	0.54
1:2:1723:U:H2'	1:2:1724:U:C1'	2.38	0.54
18:N:331:LYS:HB2	18:N:331:LYS:HZ3	1.72	0.54
36:f:120:LYS:CE	36:f:340:LEU:HD11	2.36	0.54
36:f:165:THR:HA	36:f:222:CYS:O	2.07	0.54
38:h:89:LEU:HD13	38:h:112:LEU:N	2.23	0.54
41:l:395:LEU:HD11	41:l:410:PHE:CZ	2.43	0.54
1:2:356:G:H2'	1:2:357:A:C8	2.41	0.54
1:2:553:U:H2'	1:2:554:C:H6	1.73	0.54
1:2:707:A:O2'	1:2:708:A:H5'	2.08	0.54
1:2:1734:A:C2	1:2:1736:U:H1'	2.42	0.54
5:A:93:ASN:HB3	5:A:96:ARG:HB3	1.90	0.54
14:J:228:LEU:CD2	14:J:238:THR:HG23	2.37	0.54
14:J:284:ASN:HB2	32:b:46:LEU:HD21	1.90	0.54
36:f:75:ARG:HH11	36:f:75:ARG:HG3	1.73	0.54
38:h:338:PRO:HG2	38:h:385:ASN:ND2	2.22	0.54
1:2:466:A:C2'	1:2:467:G:H5'	2.38	0.54
1:2:915:G:C2	1:2:916:A:C4	2.96	0.54
1:2:1743:A:C3'	1:2:1744:C:H4'	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:35:ARG:HB3	25:U:48:ILE:CG2	2.34	0.54
7:C:83:PRO:O	7:C:87:MET:HG3	2.08	0.54
7:C:175:LEU:HD23	7:C:175:LEU:O	2.08	0.54
7:C:183:LEU:HD13	8:D:71:ILE:HD11	1.90	0.54
35:e:224:GLU:OE1	35:e:224:GLU:HA	2.06	0.54
38:h:311:ILE:HA	38:h:314:ILE:HG22	1.90	0.54
1:2:317:U:H4'	1:2:318:U:OP1	2.07	0.53
1:2:341:C:O2'	1:2:342:U:H5'	2.08	0.53
1:2:837:U:HO2'	25:U:61:ARG:HG2	1.72	0.53
1:2:1734:A:H1'	1:2:1737:A:C2	2.43	0.53
7:C:130:ARG:HD2	7:C:138:MET:HE2	1.91	0.53
14:J:284:ASN:HB3	32:b:46:LEU:HD23	1.83	0.53
26:V:56:PRO:HG3	26:V:65:MET:SD	2.47	0.53
26:V:115:ARG:HD2	26:V:115:ARG:C	2.33	0.53
38:h:103:MET:HE1	38:h:132:LEU:HD22	1.90	0.53
1:2:155:U:O2'	30:Z:51:LYS:HD2	2.09	0.53
18:N:328:GLU:HA	18:N:328:GLU:OE2	2.07	0.53
1:2:716:C:H5"	1:2:717:A:OP2	2.08	0.53
1:2:1762:U:H3'	1:2:1763:U:C5'	2.37	0.53
2:5:71:G:O2'	2:5:72:C:H5'	2.08	0.53
14:J:210:THR:HG22	14:J:216:VAL:HA	1.89	0.53
36:f:67:ALA:HB3	36:f:68:PRO:HD3	1.90	0.53
38:h:251:LEU:HD23	38:h:256:PHE:HE1	1.74	0.53
38:h:260:MET:HG2	38:h:293:SER:CB	2.33	0.53
39:i:321:VAL:HG11	39:i:341:TRP:HD1	1.73	0.53
41:l:279:ARG:HD3	41:l:281:PHE:HE2	1.73	0.53
1:2:1703:G:H3'	1:2:1704:A:H8	1.74	0.53
1:2:1711:A:H2'	1:2:1712:U:O4'	2.08	0.53
7:C:260:LEU:CD2	8:D:181:LEU:HD12	2.35	0.53
36:f:264:LEU:C	36:f:264:LEU:HD13	2.33	0.53
38:h:169:ARG:HH12	38:h:175:ASN:HB3	1.74	0.53
38:h:302:HIS:CD2	38:h:360:ASP:HB2	2.43	0.53
39:i:129:LEU:HD23	39:i:129:LEU:O	2.09	0.53
39:i:151:PRO:HB2	39:i:163:TRP:HZ2	1.73	0.53
39:i:334:PRO:HD2	39:i:369:LYS:CE	2.38	0.53
41:l:252:ASP:O	41:l:256:LYS:HG2	2.07	0.53
7:C:210:LEU:HD12	8:D:87:VAL:CG2	2.38	0.53
20:P:84:GLN:HG2	20:P:85:ALA:N	2.24	0.53
7:C:174:ILE:O	7:C:178:LYS:HB2	2.09	0.53
8:D:364:VAL:HG22	8:D:386:MET:SD	2.49	0.53
12:H:227:GLY:C	12:H:230:ARG:HG2	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:355:THR:HG21	12:H:394:MET:SD	2.49	0.53
39:i:134:LYS:HG2	39:i:158:PHE:HE2	1.74	0.53
1:2:426:A:O2'	7:C:122:GLN:HG2	2.08	0.53
1:2:1684:G:N2	1:2:1788:U:H1'	2.24	0.53
2:5:29:C:H3'	2:5:29:C:OP2	2.09	0.53
7:C:25:LEU:HD13	7:C:29:VAL:HG11	1.90	0.53
7:C:289:LEU:HD13	35:e:150:SER:HB2	1.90	0.53
25:U:62:LYS:HZ1	25:U:103:MET:HE3	1.72	0.53
38:h:206:MET:HG3	38:h:240:TYR:CE2	2.44	0.53
39:i:363:ASN:HD22	39:i:366:ALA:HB2	1.71	0.53
41:l:529:TRP:CH2	41:l:561:GLU:HB2	2.44	0.53
41:l:529:TRP:HE1	41:l:557:VAL:HG23	1.73	0.53
2:5:76:C:H2'	2:5:77:A:C8	2.44	0.53
7:C:307:ARG:NH1	7:C:307:ARG:HB3	2.24	0.53
10:F:38:ARG:HH12	10:F:109:LYS:HA	1.74	0.53
26:V:127:GLU:C	26:V:127:GLU:OE2	2.52	0.53
31:a:105:LEU:HD23	31:a:105:LEU:H	1.73	0.53
39:i:108:MET:HA	39:i:108:MET:CE	2.37	0.53
39:i:129:LEU:HA	39:i:132:VAL:HG12	1.91	0.53
39:i:305:GLU:HA	39:i:305:GLU:OE2	2.09	0.53
5:A:35:ARG:HD3	40:k:14:PHE:CG	2.44	0.53
8:D:314:LYS:O	8:D:318:LYS:HD3	2.08	0.53
20:P:29:LEU:HD23	20:P:30:TYR:CE2	2.44	0.53
36:f:195:TYR:HE1	39:i:275:LYS:HD2	1.74	0.53
38:h:130:GLN:O	38:h:134:ARG:HG3	2.09	0.53
1:2:243:U:H2'	1:2:244:U:O2	2.09	0.53
1:2:1801:A:O2'	1:2:1802:A:H5'	2.09	0.53
5:A:50:LEU:HD12	5:A:50:LEU:O	2.08	0.53
8:D:217:LEU:HD11	39:i:207:ILE:HD11	1.90	0.53
25:U:53:ASP:HA	25:U:56:VAL:CG2	2.39	0.53
26:V:182:GLU:HA	26:V:185:ILE:HD12	1.91	0.53
38:h:226:ARG:HB3	38:h:226:ARG:CZ	2.39	0.53
1:2:1142:A:N6	41:l:478:VAL:HG21	2.24	0.52
1:2:1737:A:H2'	1:2:1738:G:N3	2.25	0.52
2:5:11:A:C2	2:5:12:G:H1'	2.44	0.52
7:C:222:SER:O	7:C:226:GLU:HG2	2.09	0.52
10:F:44:ARG:HD3	10:F:49:LEU:HD11	1.91	0.52
27:W:167:LYS:HD3	27:W:167:LYS:N	2.24	0.52
27:W:215:VAL:HG22	27:W:216:LYS:HG2	1.91	0.52
30:Z:84:ILE:O	30:Z:84:ILE:HG13	2.09	0.52
39:i:108:MET:HE2	39:i:112:VAL:HG23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:360:ARG:HG3	39:i:367:TYR:CE1	2.45	0.52
1:2:888:G:H2'	1:2:889:U:H6	1.73	0.52
7:C:287:LEU:HD22	8:D:178:LEU:CD2	2.40	0.52
8:D:187:LEU:CD1	39:i:244:ARG:HH21	2.21	0.52
8:D:221:LEU:O	8:D:221:LEU:HD22	2.10	0.52
8:D:303:ILE:HG23	8:D:304:LEU:HD23	1.90	0.52
10:F:58:LYS:NZ	10:F:60:ILE:HG12	2.24	0.52
1:2:904:U:H2'	1:2:905:C:C6	2.44	0.52
1:2:1703:G:H3'	1:2:1704:A:C8	2.44	0.52
2:5:28:U:H3	2:5:44:A:N6	2.07	0.52
25:U:59:PHE:HA	25:U:62:LYS:NZ	2.25	0.52
31:a:381:ILE:O	31:a:385:ILE:HG22	2.09	0.52
35:e:179:SER:O	35:e:180:TYR:HB3	2.09	0.52
36:f:192:LEU:CD2	36:f:196:LEU:HD23	2.34	0.52
1:2:212:G:O2'	1:2:213:C:H5'	2.08	0.52
1:2:845:U:H2'	1:2:846:G:C8	2.44	0.52
2:5:45:A:H2'	2:5:46:G:C1'	2.39	0.52
7:C:242:LEU:HD22	7:C:297:PHE:HB3	1.92	0.52
19:O:102:PRO:HB2	19:O:111:VAL:CG1	2.40	0.52
35:e:233:LEU:HD13	35:e:233:LEU:C	2.34	0.52
38:h:190:LEU:HD21	38:h:224:VAL:CG2	2.39	0.52
38:h:219:GLY:CA	38:h:252:ARG:HH21	2.22	0.52
4:8:261:LYS:O	4:8:262:LEU:HD12	2.09	0.52
4:8:263:MET:HE3	4:8:263:MET:H	1.74	0.52
5:A:156:VAL:CG1	5:A:172:ILE:HD13	2.39	0.52
7:C:199:PHE:CG	8:D:121:ILE:HD11	2.45	0.52
7:C:204:THR:HG22	8:D:116:GLU:HG2	1.91	0.52
27:W:472:MET:O	27:W:476:VAL:HG23	2.10	0.52
36:f:144:MET:O	36:f:165:THR:HG23	2.09	0.52
36:f:306:LYS:HE2	36:f:306:LYS:CA	2.39	0.52
38:h:268:ASP:HB3	38:h:271:SER:OG	2.09	0.52
38:h:308:ALA:HA	38:h:311:ILE:HG12	1.90	0.52
39:i:130:LEU:HD23	39:i:131:ILE:N	2.25	0.52
1:2:80:U:H2'	1:2:81:U:H6	1.75	0.52
1:2:1336:U:H2'	1:2:1337:U:H6	1.75	0.52
5:A:156:VAL:HG12	5:A:172:ILE:HD13	1.92	0.52
8:D:329:LYS:HG3	8:D:332:ARG:HH22	1.75	0.52
8:D:329:LYS:CD	8:D:329:LYS:H	2.22	0.52
14:J:195:ILE:HD12	14:J:211:ASP:O	2.10	0.52
36:f:75:ARG:HG3	36:f:75:ARG:NH1	2.24	0.52
36:f:157:ILE:HA	36:f:162:ARG:CD	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:239:LEU:HD13	39:i:239:LEU:C	2.35	0.52
1:2:272:U:O2'	20:P:13:MET:HE3	2.09	0.52
1:2:1336:U:H2'	1:2:1337:U:C6	2.45	0.52
5:A:20:ARG:HD2	40:k:20:MET:CE	2.40	0.52
6:B:96:ARG:HG2	6:B:97:TRP:H	1.74	0.52
7:C:165:GLU:OE2	7:C:165:GLU:HA	2.10	0.52
38:h:153:GLN:HA	38:h:156:LYS:HG2	1.91	0.52
38:h:189:LEU:HD22	38:h:205:VAL:HB	1.90	0.52
38:h:199:SER:O	38:h:202:MET:HG3	2.10	0.52
41:l:546:LEU:HD22	41:l:550:SER:HB2	1.92	0.52
1:2:929:C:H2'	1:2:930:A:H8	1.74	0.52
7:C:179:ILE:O	7:C:184:LEU:HB2	2.10	0.52
7:C:212:LEU:CD1	35:e:243:ARG:HG3	2.40	0.52
25:U:50:LEU:HB3	25:U:52:GLU:OE2	2.10	0.52
25:U:51:PRO:HB2	25:U:90:LEU:HD21	1.92	0.52
36:f:176:GLN:OE1	36:f:176:GLN:HA	2.10	0.52
6:B:359:LEU:HD22	6:B:411:TYR:HB2	1.92	0.52
12:H:212:GLU:HB3	12:H:216:LYS:NZ	2.24	0.52
26:V:126:GLU:OE1	26:V:126:GLU:HA	2.09	0.52
36:f:179:PHE:HZ	36:f:339:SER:HB3	1.73	0.52
38:h:169:ARG:NH2	38:h:176:VAL:H	2.08	0.52
39:i:321:VAL:O	39:i:325:LEU:CD2	2.58	0.52
1:2:517:C:H2'	1:2:518:A:C8	2.45	0.52
1:2:629:G:H2'	1:2:630:C:H6	1.74	0.52
1:2:1113:U:H2'	1:2:1114:G:C8	2.45	0.52
1:2:1700:U:H2'	1:2:1701:C:C6	2.45	0.52
16:L:114:CYS:HB2	22:R:198:GLU:HG2	1.91	0.52
20:P:15:LYS:HA	20:P:44:ASP:O	2.09	0.52
22:R:206:LYS:NZ	22:R:208:HIS:CE1	2.78	0.52
32:b:62:SER:O	32:b:66:GLN:HG2	2.10	0.52
34:d:62:THR:HB	34:d:63:GLU:OE2	2.10	0.52
36:f:82:GLU:OE2	39:i:208:ARG:HG3	2.09	0.52
38:h:189:LEU:C	38:h:189:LEU:HD23	2.34	0.52
1:2:241:U:H2'	1:2:242:G:H8	1.75	0.51
1:2:516:C:C5	1:2:528:G:H5'	2.45	0.51
1:2:1723:U:H3'	1:2:1724:U:H6	1.74	0.51
5:A:76:PHE:CE1	5:A:185:VAL:HG11	2.45	0.51
20:P:88:ALA:O	20:P:91:LEU:HB2	2.11	0.51
38:h:260:MET:CE	38:h:275:VAL:HG13	2.40	0.51
2:5:23:A:H5"	2:5:24:C:C5	2.46	0.51
2:5:47:A:H3'	2:5:48:U:C5	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:93:ARG:HH22	8:D:96:GLU:HG2	1.75	0.51
38:h:232:ASP:HA	38:h:262:PHE:HZ	1.75	0.51
1:2:80:U:O2'	1:2:81:U:H5'	2.11	0.51
1:2:553:U:H2'	1:2:554:C:C6	2.44	0.51
1:2:822:U:H1'	11:G:15:ASN:HD22	1.75	0.51
2:5:60:A:O2'	2:5:61:U:H5'	2.11	0.51
8:D:172:GLN:OE1	8:D:172:GLN:HA	2.08	0.51
26:V:61:ASP:O	26:V:65:MET:HG3	2.10	0.51
36:f:181:PRO:O	36:f:185:ALA:HB3	2.10	0.51
36:f:290:VAL:HG21	36:f:299:LYS:HD2	1.91	0.51
41:l:503:MET:HE2	41:l:503:MET:HA	1.93	0.51
1:2:921:G:O2'	1:2:1842:U:OP1	2.29	0.51
1:2:997:G:H22	1:2:1029:C:H5	1.58	0.51
2:5:10:G:H5'	2:5:10:G:C8	2.46	0.51
7:C:67:ILE:CG2	7:C:350:LEU:HD12	2.40	0.51
12:H:266:GLU:HA	12:H:269:ASN:HD22	1.75	0.51
23:S:89:LYS:CE	32:b:19:LEU:HG	2.40	0.51
31:a:220:LYS:HD2	31:a:224:LYS:HE2	1.92	0.51
36:f:230:VAL:HG22	36:f:252:TYR:HB3	1.92	0.51
38:h:151:CYS:HA	38:h:154:VAL:HG12	1.93	0.51
38:h:197:LYS:CE	38:h:230:GLU:HG3	2.40	0.51
41:l:240:LEU:HA	41:l:243:LYS:HD2	1.92	0.51
1:2:172:A:H5'	1:2:173:A:C5'	2.37	0.51
1:2:793:C:O2'	1:2:794:U:H5'	2.10	0.51
1:2:1384:A:O2'	41:l:485:ARG:HD3	2.10	0.51
1:2:1711:A:O2'	1:2:1712:U:H5'	2.11	0.51
2:5:49:U:OP2	2:5:60:A:H5'	2.10	0.51
7:C:213:LYS:HG3	7:C:213:LYS:O	2.10	0.51
21:Q:243:GLN:HA	21:Q:246:GLU:OE1	2.11	0.51
22:R:132:MET:HE2	22:R:134:ARG:HB2	1.91	0.51
28:X:401:PRO:HD2	31:a:365:LEU:HD22	1.92	0.51
39:i:100:PHE:CD1	39:i:173:VAL:HG11	2.46	0.51
1:2:74:A:O2'	1:2:75:C:H5'	2.11	0.51
1:2:747:C:H2'	1:2:748:G:O4'	2.10	0.51
8:D:329:LYS:H	8:D:329:LYS:CE	2.24	0.51
22:R:56:GLY:O	22:R:79:PHE:HA	2.10	0.51
26:V:128:ARG:NE	26:V:132:GLN:HE21	2.08	0.51
28:X:492:VAL:HG12	28:X:511:MET:HE1	1.92	0.51
38:h:206:MET:O	38:h:209:LEU:HG	2.10	0.51
39:i:286:GLU:OE2	39:i:288:SER:HB3	2.11	0.51
41:l:211:TYR:OH	41:l:246:LYS:HE3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:441:U:O2	1:2:441:U:H3'	2.10	0.51
1:2:516:C:H5	1:2:528:G:H5'	1.75	0.51
1:2:763:A:H2'	1:2:764:A:C8	2.45	0.51
1:2:790:A:H2'	1:2:791:C:C6	2.46	0.51
5:A:73:ASN:OD1	5:A:75:LEU:HB2	2.11	0.51
6:B:171:LYS:HD3	6:B:174:ARG:HH12	1.74	0.51
12:H:219:LYS:CD	25:U:127:LEU:HD11	2.39	0.51
4:8:211:LEU:HD13	4:8:212:GLU:O	2.10	0.51
7:C:221:ARG:O	7:C:225:GLN:HG3	2.11	0.51
7:C:254:ARG:HH22	39:i:226:ASP:CA	2.11	0.51
14:J:193:ALA:HB2	21:Q:247:TYR:CE1	2.46	0.51
25:U:84:VAL:HG13	25:U:88:ARG:HH21	1.75	0.51
27:W:468:ASN:HB3	27:W:471:GLU:HB2	1.92	0.51
36:f:358:ARG:HB3	36:f:358:ARG:NH1	2.26	0.51
37:g:615:ARG:HH11	37:g:618:GLU:HG3	1.76	0.51
38:h:353:VAL:CG1	38:h:357:LEU:HD13	2.41	0.51
39:i:425:LEU:HG	39:i:429:TYR:CE2	2.46	0.51
6:B:449:ALA:HB2	6:B:539:ILE:HG22	1.93	0.51
19:O:12:CYS:SG	19:O:15:ARG:HB2	2.51	0.51
36:f:157:ILE:O	36:f:162:ARG:HD3	2.11	0.51
38:h:110:TRP:HH2	38:h:153:GLN:CB	2.24	0.51
39:i:352:TRP:HB3	39:i:380:PHE:CE1	2.46	0.51
1:2:177:G:H2'	1:2:178:U:C6	2.46	0.51
1:2:226:A:O2'	1:2:227:A:H5'	2.10	0.51
1:2:467:G:H2'	1:2:468:U:C6	2.45	0.51
6:B:290:ALA:HB3	6:B:318:ASN:HD22	1.76	0.51
7:C:172:LYS:O	7:C:176:VAL:HB	2.11	0.51
19:O:23:THR:HG22	19:O:33:HIS:HB2	1.93	0.51
27:W:372:THR:HB	27:W:375:SER:HB3	1.92	0.51
38:h:304:PRO:HB3	38:h:364:MET:HE3	1.92	0.51
1:2:81:U:O2'	1:2:82:C:H5'	2.10	0.50
1:2:160:A:H2'	1:2:161:A:C1'	2.41	0.50
1:2:1095:C:H2'	1:2:1096:G:O4'	2.12	0.50
1:2:1720:C:C2	1:2:1721:A:C8	2.98	0.50
27:W:189:ARG:HH12	27:W:205:PRO:HB3	1.75	0.50
38:h:194:LEU:HD22	38:h:230:GLU:CD	2.36	0.50
1:2:759:G:H2'	1:2:760:C:C6	2.46	0.50
1:2:1481:C:H2'	1:2:1482:U:H6	1.77	0.50
4:8:158:ARG:O	4:8:161:ALA:HB3	2.12	0.50
12:H:219:LYS:HB3	25:U:124:LEU:CD2	2.41	0.50
36:f:264:LEU:HD13	36:f:264:LEU:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:562:C:H4'	15:K:4:PHE:CZ	2.46	0.50
4:8:122:LEU:HD23	4:8:136:ILE:CD1	2.42	0.50
8:D:138:GLU:CG	8:D:141:ARG:HD2	2.42	0.50
12:H:247:ASP:C	12:H:247:ASP:OD1	2.54	0.50
21:Q:192:ILE:HD11	23:S:50:SER:O	2.11	0.50
28:X:469:GLU:O	28:X:473:ILE:HG12	2.11	0.50
38:h:194:LEU:C	38:h:194:LEU:HD13	2.36	0.50
38:h:226:ARG:HB3	38:h:226:ARG:NH1	2.26	0.50
38:h:342:LEU:HD11	38:h:353:VAL:CG1	2.42	0.50
39:i:286:GLU:O	39:i:287:LEU:HD23	2.12	0.50
1:2:236:A:OP1	1:2:236:A:H4'	2.11	0.50
1:2:298:A:H5"	1:2:300:G:O4'	2.12	0.50
1:2:1686:U:H2'	1:2:1687:U:H6	1.72	0.50
5:A:32:TYR:HD1	40:k:1:MET:SD	2.33	0.50
7:C:246:PHE:CD2	8:D:212:ARG:HD3	2.47	0.50
8:D:148:SER:O	8:D:149:ASP:HB2	2.11	0.50
35:e:233:LEU:HD12	35:e:235:ARG:H	1.77	0.50
36:f:310:PRO:HG3	36:f:373:LEU:HD22	1.93	0.50
38:h:194:LEU:CD2	38:h:227:ILE:HG12	2.42	0.50
1:2:522:G:H2'	1:2:523:C:C6	2.47	0.50
1:2:814:G:O2'	1:2:815:A:H5'	2.11	0.50
1:2:825:G:O2'	1:2:826:C:H5'	2.12	0.50
1:2:1604:C:H5"	12:H:427:TRP:HE3	1.76	0.50
1:2:1685:G:H2'	1:2:1685:G:N3	2.25	0.50
7:C:257:LEU:CD2	8:D:194:MET:CE	2.79	0.50
7:C:285:SER:O	7:C:289:LEU:HG	2.11	0.50
7:C:325:THR:HG21	7:C:327:LYS:HZ2	1.76	0.50
14:J:190:GLU:OE1	14:J:190:GLU:N	2.43	0.50
20:P:46:THR:O	20:P:46:THR:HG22	2.12	0.50
20:P:58:ASP:OD1	20:P:72:ALA:HB2	2.11	0.50
21:Q:248:GLU:OE1	21:Q:251:ASP:HB2	2.12	0.50
25:U:76:ALA:O	40:k:13:ILE:HA	2.11	0.50
38:h:329:GLU:O	38:h:332:LYS:HB2	2.11	0.50
1:2:211:G:O2'	1:2:212:G:H5'	2.10	0.50
1:2:224:A:H5"	1:2:225:G:OP2	2.11	0.50
1:2:788:A:H1'	1:2:790:A:N7	2.26	0.50
2:5:10:G:H2'	2:5:11:A:C8	2.46	0.50
7:C:252:MET:HE1	7:C:290:TYR:CB	2.41	0.50
8:D:187:LEU:HD13	39:i:244:ARG:NH2	2.24	0.50
22:R:175:ARG:HB3	22:R:182:HIS:HB3	1.93	0.50
23:S:93:ILE:CG2	32:b:86:LEU:HD21	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:260:MET:HG3	38:h:272:LEU:HD11	1.94	0.50
39:i:168:GLU:O	39:i:172:THR:HG23	2.12	0.50
39:i:420:LEU:HD12	39:i:421:THR:N	2.27	0.50
8:D:318:LYS:N	8:D:318:LYS:HD2	2.27	0.50
8:D:509:ARG:HG2	35:e:273:MET:O	2.12	0.50
38:h:333:LEU:O	38:h:338:PRO:HD3	2.11	0.50
41:l:398:MET:HG2	41:l:403:PRO:HD2	1.93	0.50
1:2:1524:A:H8	31:a:338:LYS:NZ	2.09	0.50
1:2:1567:G:N2	1:2:1594:A:H2	2.10	0.50
1:2:1704:A:H2	1:2:1706:C:H41	1.59	0.50
1:2:1767:G:H2'	1:2:1768:A:H5"	1.93	0.50
2:5:12:G:C2	2:5:13:G:H1'	2.47	0.50
2:5:26:C:O2	2:5:26:C:H2'	2.11	0.50
36:f:65:LEU:HA	36:f:69:MET:HE2	1.93	0.50
41:l:217:VAL:HG11	41:l:237:LEU:HD11	1.94	0.50
1:2:1724:U:O2	1:2:1724:U:H2'	2.11	0.50
1:2:1754:U:O2'	1:2:1755:G:H5'	2.12	0.50
4:8:200:LEU:HD23	4:8:201:ALA:N	2.26	0.50
4:8:220:LEU:O	4:8:224:THR:HG23	2.12	0.50
7:C:251:ARG:NH1	7:C:252:MET:HA	2.26	0.50
8:D:157:TRP:O	8:D:161:ARG:HG2	2.11	0.50
1:2:546:G:H2'	1:2:547:U:O4'	2.12	0.49
1:2:1706:C:HO2'	1:2:1707:A:P	2.35	0.49
7:C:341:HIS:HB2	7:C:343:ILE:HD12	1.94	0.49
26:V:159:GLU:OE1	26:V:159:GLU:HA	2.11	0.49
39:i:391:ILE:HG23	39:i:428:MET:SD	2.51	0.49
1:2:379:G:H2'	1:2:380:G:C8	2.46	0.49
1:2:763:A:H2'	1:2:764:A:H8	1.77	0.49
5:A:83:THR:HG23	5:A:193:THR:OG1	2.13	0.49
25:U:77:PHE:HE1	40:k:13:ILE:HG12	1.76	0.49
25:U:84:VAL:HG13	25:U:88:ARG:NH2	2.27	0.49
38:h:159:VAL:CG2	38:h:192:TYR:HD2	2.24	0.49
39:i:240:ASP:HB3	39:i:244:ARG:NH2	2.27	0.49
1:2:750:C:H3'	1:2:750:C:O2	2.12	0.49
1:2:1719:G:H2'	1:2:1720:C:H6	1.77	0.49
1:2:1721:A:H5'	1:2:1722:C:OP2	2.13	0.49
6:B:366:LYS:HE3	28:X:334:PHE:O	2.12	0.49
7:C:53:LYS:O	7:C:56:LYS:HG2	2.13	0.49
7:C:312:ILE:HD12	7:C:312:ILE:C	2.36	0.49
8:D:436:GLN:HG3	8:D:445:TYR:CE2	2.47	0.49
14:J:189:LEU:HD21	21:Q:248:GLU:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:V:60:LYS:O	26:V:63:GLU:HG2	2.12	0.49
35:e:281:ILE:H	35:e:281:ILE:HD12	1.78	0.49
38:h:349:ASP:O	38:h:353:VAL:HG23	2.12	0.49
1:2:1667:G:H2'	1:2:1668:U:H6	1.76	0.49
1:2:1797:G:H2'	1:2:1798:G:C8	2.44	0.49
2:5:53:G:H2'	2:5:54:G:C8	2.43	0.49
5:A:20:ARG:CD	40:k:20:MET:HE3	2.42	0.49
7:C:97:ILE:HD11	7:C:354:SER:HB3	1.93	0.49
20:P:88:ALA:HA	20:P:91:LEU:CD1	2.36	0.49
22:R:206:LYS:HZ1	22:R:208:HIS:CE1	2.30	0.49
36:f:358:ARG:HD2	36:f:364:PHE:CD1	2.47	0.49
39:i:321:VAL:O	39:i:324:LYS:HG2	2.12	0.49
1:2:1075:U:H5"	1:2:1078:U:C5	2.44	0.49
1:2:1096:G:H5'	5:A:115:LYS:HG2	1.94	0.49
7:C:25:LEU:CD1	7:C:29:VAL:HG11	2.42	0.49
7:C:148:HIS:ND1	7:C:148:HIS:O	2.45	0.49
7:C:256:LEU:HB2	7:C:286:SER:HB2	1.94	0.49
9:E:30:VAL:HG21	9:E:69:MET:SD	2.52	0.49
30:Z:98:ILE:CD1	30:Z:110:PRO:HG3	2.40	0.49
36:f:273:TYR:CD1	36:f:286:MET:HG3	2.47	0.49
1:2:706:G:O2'	1:2:707:A:H5'	2.13	0.49
4:8:173:PRO:HA	4:8:219:LEU:HD13	1.94	0.49
5:A:110:SER:O	5:A:111:TYR:C	2.55	0.49
5:A:158:ALA:HB3	5:A:172:ILE:CD1	2.41	0.49
5:A:197:VAL:HG12	12:H:258:VAL:HG13	1.93	0.49
10:F:4:LEU:HD21	10:F:47:ILE:HD12	1.95	0.49
30:Z:53:LEU:HD12	30:Z:53:LEU:O	2.12	0.49
36:f:111:ILE:HD12	36:f:116:THR:HG22	1.94	0.49
36:f:355:ILE:O	36:f:359:LEU:HB2	2.12	0.49
36:f:408:TYR:CD2	39:i:187:LYS:HA	2.47	0.49
38:h:251:LEU:HG	38:h:255:THR:HG23	1.93	0.49
39:i:300:HIS:O	39:i:304:GLU:HG2	2.13	0.49
1:2:408:A:H3'	1:2:409:U:H6	1.76	0.49
1:2:466:A:O2'	1:2:467:G:H5'	2.12	0.49
8:D:138:GLU:HG3	8:D:141:ARG:CD	2.43	0.49
15:K:74:LEU:HD21	15:K:80:VAL:CG1	2.42	0.49
18:N:306:LYS:O	18:N:310:VAL:HG23	2.12	0.49
25:U:91:GLU:HA	25:U:94:LYS:CG	2.42	0.49
34:d:97:LYS:HG3	34:d:102:LEU:HB2	1.95	0.49
1:2:591:U:H2'	1:2:592:C:C6	2.48	0.49
1:2:1675:C:H2'	1:2:1676:U:O4'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:9:A:C2	2:5:46:G:H3'	2.48	0.49
2:5:17:U:H3'	2:5:17:U:P	2.53	0.49
38:h:122:ILE:HG13	38:h:123:SER:N	2.28	0.49
38:h:381:GLU:HA	38:h:384:LYS:HB2	1.94	0.49
1:2:386:U:H5	1:2:412:A:N1	2.10	0.49
8:D:158:ASP:HA	8:D:161:ARG:NE	2.28	0.49
26:V:119:GLU:OE1	26:V:119:GLU:HA	2.12	0.49
35:e:233:LEU:CD1	35:e:235:ARG:H	2.25	0.49
36:f:174:GLU:OE2	36:f:181:PRO:HG3	2.13	0.49
36:f:321:ARG:HA	36:f:324:ARG:HD2	1.95	0.49
39:i:425:LEU:HD23	39:i:425:LEU:C	2.37	0.49
1:2:356:G:H2'	1:2:357:A:H8	1.78	0.49
2:5:43:G:H3'	2:5:44:A:O4'	2.12	0.49
2:5:69:C:C2	2:5:70:C:C5	3.01	0.49
5:A:194:LYS:HE3	12:H:260:GLY:HA3	1.95	0.49
7:C:97:ILE:HB	7:C:98:PRO:HD3	1.94	0.49
8:D:93:ARG:HH12	8:D:96:GLU:CB	2.26	0.49
11:G:118:ARG:HB2	11:G:120:VAL:HG12	1.94	0.49
14:J:251:LYS:HB2	14:J:282:TYR:CD1	2.48	0.49
26:V:104:VAL:HA	26:V:107:ARG:HG2	1.95	0.49
36:f:81:GLU:HA	36:f:138:LYS:HE3	1.94	0.49
36:f:277:ASP:OD2	39:i:121:LYS:HE2	2.13	0.49
36:f:378:LYS:HA	36:f:381:VAL:HG22	1.95	0.49
36:f:409:PHE:HD1	39:i:187:LYS:CE	2.25	0.49
1:2:145:U:C2	1:2:146:U:C5	3.01	0.48
1:2:1138:G:C8	1:2:1139:A:C8	3.01	0.48
7:C:171:TYR:HA	7:C:174:ILE:HG22	1.95	0.48
8:D:252:ASN:OD1	25:U:22:ARG:HB2	2.12	0.48
19:O:75:ARG:CZ	19:O:75:ARG:HB3	2.41	0.48
36:f:164:ALA:HB1	36:f:168:THR:HG21	1.95	0.48
36:f:257:TYR:CD2	36:f:258:PRO:HD2	2.47	0.48
36:f:289:GLU:HG2	36:f:295:ASN:ND2	2.28	0.48
38:h:314:ILE:HD11	38:h:318:TYR:OH	2.13	0.48
39:i:356:ILE:HD11	39:i:380:PHE:HE1	1.78	0.48
1:2:499:C:H2'	1:2:500:C:H6	1.78	0.48
1:2:739:G:H2'	1:2:740:U:H6	1.77	0.48
1:2:1806:G:H1'	1:2:1827:MA6:H2	1.94	0.48
6:B:380:ILE:HB	6:B:384:LYS:HZ2	1.77	0.48
7:C:260:LEU:HD12	7:C:283:TYR:CZ	2.48	0.48
23:S:77:LEU:HD13	23:S:81:ILE:HG23	1.95	0.48
26:V:167:LEU:C	26:V:167:LEU:HD13	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:299:LYS:HE2	36:f:299:LYS:CA	2.43	0.48
36:f:347:VAL:HG11	36:f:380:MET:HB3	1.95	0.48
39:i:132:VAL:O	39:i:136:VAL:HG12	2.12	0.48
39:i:282:ILE:HG12	39:i:283:TYR:CD2	2.48	0.48
1:2:1710:G:H2'	1:2:1711:A:H8	1.79	0.48
2:5:69:C:H2'	2:5:70:C:H6	1.78	0.48
6:B:174:ARG:NH2	28:X:366:ARG:HD3	2.27	0.48
14:J:268:PHE:CE2	23:S:44:GLN:HB2	2.48	0.48
36:f:127:TYR:HB3	36:f:398:LEU:HD21	1.95	0.48
41:l:460:GLU:HA	41:l:463:GLU:HG2	1.93	0.48
8:D:76:ALA:O	8:D:79:VAL:HG22	2.13	0.48
21:Q:206:GLN:OE1	21:Q:206:GLN:HA	2.12	0.48
25:U:92:LEU:C	25:U:97:ILE:HG22	2.38	0.48
30:Z:49:LYS:HD3	30:Z:49:LYS:N	2.29	0.48
30:Z:102:ASP:C	30:Z:102:ASP:OD1	2.56	0.48
32:b:37:MET:O	32:b:41:LEU:HG	2.14	0.48
36:f:170:LEU:HD22	36:f:171:ALA:N	2.28	0.48
38:h:171:LEU:O	38:h:171:LEU:HD12	2.12	0.48
39:i:177:MET:O	39:i:180:GLU:HG2	2.13	0.48
1:2:775:C:O2'	1:2:776:G:H5'	2.13	0.48
1:2:839:C:O2'	1:2:840:U:O5'	2.31	0.48
8:D:369:LYS:HG3	8:D:382:TYR:CE2	2.49	0.48
36:f:290:VAL:O	36:f:294:GLY:HA2	2.14	0.48
38:h:292:PHE:CE1	38:h:333:LEU:HD11	2.49	0.48
39:i:130:LEU:HD21	39:i:158:PHE:HE1	1.74	0.48
41:l:355:PHE:HA	41:l:358:GLU:OE1	2.14	0.48
41:l:440:PRO:HB2	41:l:445:TYR:CE2	2.47	0.48
1:2:11:A:H5"	1:2:12:A:H5'	1.94	0.48
1:2:414:C:O2'	1:2:415:A:H5'	2.13	0.48
1:2:428:U:O2'	1:2:429:G:H5'	2.13	0.48
1:2:1625:A:N3	1:2:1625:A:H2'	2.28	0.48
1:2:1691:C:O2	1:2:1691:C:H2'	2.13	0.48
1:2:1748:G:H2'	1:2:1749:A:N9	2.29	0.48
7:C:325:THR:HB	7:C:326:PRO:C	2.38	0.48
16:L:135:ALA:HB3	16:L:139:LYS:HE3	1.96	0.48
23:S:93:ILE:HG23	32:b:86:LEU:CD2	2.44	0.48
31:a:101:ILE:O	31:a:105:LEU:HD23	2.14	0.48
36:f:96:LYS:HA	36:f:96:LYS:HD2	1.65	0.48
36:f:356:ARG:HD2	36:f:356:ARG:C	2.38	0.48
38:h:192:TYR:HA	38:h:195:GLU:CG	2.43	0.48
38:h:343:LYS:HZ3	38:h:387:ALA:HB1	1.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:253:VAL:HG12	39:i:254:GLU:HG3	1.95	0.48
39:i:386:ASP:O	39:i:389:LYS:HB2	2.14	0.48
1:2:719:A:H5"	1:2:720:A:OP2	2.13	0.48
1:2:1668:U:H2'	1:2:1669:C:O4'	2.13	0.48
8:D:464:MET:HE1	8:D:491:LEU:HG	1.96	0.48
12:H:254:ASP:OD1	12:H:256:GLN:HG3	2.13	0.48
14:J:262:VAL:CG2	14:J:275:ILE:HD11	2.43	0.48
27:W:189:ARG:NH1	27:W:205:PRO:HB3	2.29	0.48
35:e:148:ARG:O	35:e:152:VAL:HG12	2.14	0.48
36:f:310:PRO:CB	36:f:373:LEU:HD22	2.44	0.48
38:h:112:LEU:HD13	38:h:112:LEU:O	2.13	0.48
41:l:140:ASP:HA	41:l:173:ASN:HD21	1.78	0.48
1:2:161:A:C2'	1:2:162:C:H4'	2.43	0.48
1:2:1553:A:H5"	12:H:341:MET:HE1	1.96	0.48
7:C:344:ARG:HG2	7:C:344:ARG:NH1	2.28	0.48
13:I:145:TRP:CD1	13:I:145:TRP:H	2.30	0.48
14:J:197:HIS:O	14:J:207:VAL:HA	2.14	0.48
16:L:45:LEU:HD13	16:L:74:ALA:HA	1.96	0.48
32:b:82:HIS:O	32:b:86:LEU:HD23	2.12	0.48
36:f:175:VAL:HG12	36:f:308:ALA:CB	2.44	0.48
36:f:337:ARG:HD2	36:f:388:ALA:CB	2.44	0.48
38:h:189:LEU:HD21	38:h:201:LEU:HG	1.96	0.48
38:h:262:PHE:O	38:h:265:LYS:HB2	2.13	0.48
1:2:151:A:O2'	1:2:153:A:H1'	2.14	0.48
2:5:7:G:H4'	2:5:8:U:OP2	2.14	0.48
6:B:305:GLU:O	6:B:309:ARG:HG2	2.14	0.48
6:B:382:LYS:HE3	31:a:110:LEU:HG	1.94	0.48
6:B:444:SER:OG	6:B:446:TYR:HD1	1.97	0.48
22:R:20:SER:HA	22:R:23:LEU:HD23	1.96	0.48
34:d:64:LEU:HD21	34:d:81:PHE:HE2	1.78	0.48
35:e:287:VAL:O	35:e:291:ILE:HG13	2.14	0.48
36:f:408:TYR:HD2	39:i:187:LYS:HA	1.78	0.48
37:g:607:PHE:CD1	37:g:608:PRO:HD2	2.41	0.48
37:g:607:PHE:CE2	37:g:637:PRO:HD2	2.48	0.48
38:h:190:LEU:CD2	38:h:223:LEU:HB3	2.44	0.48
38:h:192:TYR:O	38:h:195:GLU:HG3	2.14	0.48
38:h:341:VAL:HG23	38:h:342:LEU:HD13	1.96	0.48
1:2:177:G:H2'	1:2:178:U:H6	1.78	0.48
1:2:674:U:H2'	1:2:675:U:H6	1.78	0.48
1:2:1726:U:N3	1:2:1744:C:N4	2.30	0.48
5:A:112:SER:O	5:A:113:PRO:C	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:J:244:GLU:C	14:J:244:GLU:OE1	2.57	0.48
27:W:129:VAL:HG13	27:W:133:LYS:HB3	1.95	0.48
28:X:347:LYS:HD2	28:X:347:LYS:HA	1.51	0.48
28:X:350:ASP:HA	28:X:353:MET:HE3	1.96	0.48
36:f:157:ILE:HB	36:f:158:PRO:HD3	1.96	0.48
38:h:236:LEU:O	38:h:240:TYR:HB2	2.14	0.48
39:i:181:ARG:CZ	39:i:182:LYS:HB2	2.43	0.48
1:2:192:G:O2'	1:2:193:A:H5'	2.14	0.47
1:2:929:C:C2	1:2:930:A:C8	3.02	0.47
1:2:1825:2MG:HM21	1:2:1828:MA6:N7	2.29	0.47
14:J:196:ILE:CD1	14:J:209:VAL:HG23	2.44	0.47
23:S:77:LEU:HD13	23:S:81:ILE:CG2	2.44	0.47
25:U:54:PRO:HG2	25:U:55:TYR:CD1	2.48	0.47
26:V:183:LYS:O	26:V:187:GLU:HG2	2.14	0.47
35:e:151:ARG:HG2	35:e:151:ARG:NH1	2.23	0.47
36:f:261:THR:O	36:f:261:THR:CG2	2.61	0.47
38:h:170:ALA:HA	38:h:179:LEU:HD13	1.95	0.47
41:l:469:LYS:HD3	41:l:470:LYS:HG3	1.95	0.47
1:2:674:U:H2'	1:2:675:U:C6	2.48	0.47
1:2:915:G:N1	1:2:916:A:C4	2.82	0.47
1:2:1721:A:H2'	1:2:1721:A:N3	2.29	0.47
5:A:20:ARG:HA	5:A:20:ARG:NE	2.28	0.47
7:C:157:ASN:C	7:C:157:ASN:OD1	2.57	0.47
8:D:300:ARG:HA	8:D:303:ILE:HG22	1.96	0.47
38:h:331:LYS:CE	38:h:335:ASN:HD21	2.27	0.47
1:2:1137:G:C8	1:2:1138:G:C2	3.01	0.47
2:5:27:A:H61	2:5:45:A:H61	1.62	0.47
10:F:81:ARG:NH2	32:b:65:MET:HG2	2.29	0.47
12:H:218:GLU:HG2	12:H:219:LYS:N	2.29	0.47
15:K:49:LEU:O	15:K:51:LYS:HE3	2.14	0.47
23:S:95:ILE:HA	23:S:98:VAL:HG12	1.96	0.47
28:X:497:LYS:HB2	28:X:497:LYS:HE3	1.59	0.47
30:Z:86:LEU:HD22	30:Z:87:TYR:O	2.14	0.47
36:f:66:SER:OG	36:f:69:MET:HG3	2.14	0.47
38:h:353:VAL:O	38:h:357:LEU:HB2	2.14	0.47
39:i:133:GLU:CA	39:i:136:VAL:HG12	2.44	0.47
41:l:487:TYR:HB3	41:l:492:GLU:O	2.14	0.47
41:l:523:CYS:O	41:l:527:LEU:HD23	2.13	0.47
1:2:1754:U:C2'	1:2:1755:G:H5'	2.44	0.47
8:D:78:ARG:CZ	8:D:78:ARG:HB3	2.44	0.47
8:D:191:TYR:HA	8:D:194:MET:HG3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:244:GLU:C	12:H:245:MET:HE3	2.39	0.47
25:U:56:VAL:HG11	25:U:83:ARG:HA	1.97	0.47
34:d:49:ILE:H	34:d:49:ILE:CD1	2.27	0.47
36:f:299:LYS:O	36:f:303:LYS:HG3	2.14	0.47
38:h:194:LEU:HD23	38:h:227:ILE:CG1	2.45	0.47
1:2:976:A:H5'	1:2:977:C:OP2	2.15	0.47
1:2:1499:A:H2'	1:2:1500:C:C6	2.50	0.47
14:J:282:TYR:CD2	14:J:291:PRO:HG3	2.49	0.47
14:J:311:LYS:HB2	23:S:62:HIS:ND1	2.30	0.47
15:K:44:LYS:H	15:K:44:LYS:CD	2.13	0.47
27:W:168:GLU:OE2	27:W:473:ARG:HB2	2.13	0.47
29:Y:6:LEU:O	29:Y:10:VAL:HG23	2.14	0.47
35:e:233:LEU:HD11	35:e:235:ARG:CZ	2.44	0.47
38:h:117:ARG:HA	38:h:117:ARG:NE	2.30	0.47
38:h:234:TRP:CE3	38:h:266:ARG:HD2	2.50	0.47
38:h:263:ALA:HB3	38:h:272:LEU:CD1	2.43	0.47
38:h:329:GLU:HA	38:h:332:LYS:HG2	1.97	0.47
1:2:1734:A:H2	1:2:1736:U:H1'	1.79	0.47
7:C:173:GLU:OE2	7:C:178:LYS:HD2	2.15	0.47
10:F:103:TYR:HD1	10:F:103:TYR:O	1.97	0.47
11:G:9:ALA:HB1	11:G:26:LEU:HD13	1.96	0.47
14:J:201:LEU:HB2	14:J:204:ASN:O	2.14	0.47
22:R:33:LEU:HD21	22:R:79:PHE:HD1	1.79	0.47
25:U:79:PRO:HG3	40:k:11:GLY:CA	2.44	0.47
25:U:80:ASP:HB3	25:U:81:PRO:CD	2.44	0.47
36:f:240:ASP:OD1	36:f:240:ASP:O	2.32	0.47
39:i:309:ARG:O	39:i:350:VAL:HG11	2.14	0.47
1:2:161:A:H3'	1:2:162:C:C5'	2.45	0.47
1:2:265:A:C2	1:2:301:A:C5	3.03	0.47
1:2:333:C:O2'	1:2:334:A:H5'	2.14	0.47
1:2:499:C:H2'	1:2:500:C:C6	2.50	0.47
1:2:571:A:H5'	1:2:571:A:C8	2.44	0.47
1:2:893:A:H8	1:2:893:A:OP2	1.98	0.47
1:2:1567:G:H21	1:2:1594:A:H2	1.59	0.47
1:2:1722:C:O2	1:2:1722:C:H2'	2.13	0.47
1:2:1754:U:H4'	38:h:141:ARG:CD	2.44	0.47
1:2:1830:C:H2'	1:2:1831:U:C6	2.49	0.47
2:5:9:A:H3'	2:5:10:G:C5'	2.45	0.47
2:5:11:A:C4	2:5:12:G:H1'	2.50	0.47
2:5:45:A:H2'	2:5:46:G:O4'	2.14	0.47
6:B:399:MET:HE3	31:a:102:ILE:HG23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:I:224:LEU:HD23	31:a:289:PRO:HG2	1.95	0.47
14:J:198:ILE:HD12	14:J:198:ILE:N	2.29	0.47
35:e:168:LEU:HA	35:e:171:VAL:HG22	1.97	0.47
39:i:384:ILE:CG2	39:i:415:ILE:HG12	2.45	0.47
1:2:408:A:H3'	1:2:409:U:C6	2.49	0.47
1:2:1029:C:H2'	1:2:1030:U:H5"	1.97	0.47
3:6:35:U:C3'	3:6:36:A:H5"	2.45	0.47
4:8:268:ILE:HD12	4:8:268:ILE:O	2.15	0.47
5:A:76:PHE:O	5:A:80:VAL:HG23	2.14	0.47
7:C:256:LEU:HD11	7:C:287:LEU:HD23	1.97	0.47
7:C:311:ARG:HH11	7:C:311:ARG:HG3	1.80	0.47
8:D:324:HIS:ND1	8:D:324:HIS:O	2.48	0.47
9:E:22:LEU:HD23	9:E:88:LEU:HD21	1.97	0.47
10:F:103:TYR:O	10:F:103:TYR:CD1	2.68	0.47
21:Q:243:GLN:CD	21:Q:243:GLN:N	2.72	0.47
27:W:163:GLU:HG2	27:W:167:LYS:HZ1	1.80	0.47
36:f:195:TYR:CE1	39:i:275:LYS:HD2	2.50	0.47
38:h:151:CYS:HA	38:h:154:VAL:CG1	2.44	0.47
41:l:289:CYS:O	41:l:293:LEU:HG	2.15	0.47
1:2:590:A:H2'	1:2:591:U:H6	1.78	0.47
1:2:598:G:H2'	1:2:599:A:H8	1.80	0.47
1:2:1502:A:C4	1:2:1560:C:N4	2.83	0.47
1:2:1742:C:H2'	1:2:1743:A:C1'	2.45	0.47
2:5:27:A:H61	2:5:45:A:N6	2.13	0.47
2:5:68:C:C2	2:5:69:C:C5	3.02	0.47
5:A:20:ARG:O	5:A:39:THR:HG22	2.15	0.47
6:B:473:LYS:HD2	6:B:473:LYS:C	2.40	0.47
25:U:80:ASP:HB3	25:U:81:PRO:HD2	1.96	0.47
1:2:446:C:O2'	1:2:447:U:H5'	2.15	0.47
4:8:211:LEU:HD12	4:8:216:LEU:CD2	2.43	0.47
5:A:61:ALA:HB2	5:A:196:PHE:CD2	2.50	0.47
8:D:89:LYS:O	8:D:93:ARG:HG2	2.15	0.47
8:D:329:LYS:H	8:D:329:LYS:HD3	1.80	0.47
14:J:209:VAL:HG12	14:J:218:CYS:O	2.15	0.47
26:V:167:LEU:HD13	26:V:171:GLN:HG3	1.97	0.47
27:W:449:ARG:HH21	27:W:452:VAL:HG11	1.79	0.47
37:g:570:MET:HG2	37:g:575:PHE:HB2	1.97	0.47
1:2:384:U:H5"	1:2:385:C:OP1	2.15	0.46
1:2:1767:G:C2'	1:2:1768:A:H5"	2.46	0.46
2:5:14:A:H3'	2:5:15:A:C8	2.43	0.46
7:C:311:ARG:HG3	7:C:311:ARG:NH1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:E:2:PRO:HA	9:E:70:MET:HE1	1.97	0.46
9:E:3:LEU:HD23	9:E:96:HIS:CG	2.50	0.46
19:O:99:ASP:C	19:O:99:ASP:OD1	2.58	0.46
28:X:423:VAL:HG22	28:X:428:ILE:HG21	1.96	0.46
39:i:368:LEU:O	39:i:372:GLU:HG2	2.15	0.46
41:l:529:TRP:CD2	41:l:558:LYS:HD2	2.51	0.46
1:2:395:G:H5"	19:O:6:ARG:HB2	1.98	0.46
1:2:987:A:C2	17:M:68:LYS:HE2	2.51	0.46
1:2:1344:U:H2'	1:2:1345:U:C6	2.50	0.46
2:5:15:A:C2	2:5:60:A:C2	3.03	0.46
5:A:35:ARG:HD3	40:k:14:PHE:CB	2.45	0.46
5:A:87:ILE:HD12	5:A:196:PHE:CG	2.50	0.46
6:B:410:PRO:HG3	28:X:369:PRO:HG3	1.97	0.46
8:D:214:ILE:CD1	8:D:243:VAL:HG11	2.45	0.46
14:J:298:THR:HG22	21:Q:228:GLY:HA2	1.96	0.46
36:f:323:GLY:HA2	36:f:326:GLN:HG2	1.97	0.46
36:f:345:LYS:HG2	36:f:349:GLY:HA2	1.97	0.46
39:i:129:LEU:O	39:i:132:VAL:HG12	2.15	0.46
39:i:221:ARG:HG3	39:i:224:MET:HE3	1.97	0.46
1:2:134:A:O2'	1:2:135:A:H5'	2.16	0.46
1:2:386:U:O2	1:2:386:U:H2'	2.14	0.46
1:2:834:C:O2'	1:2:835:U:H5'	2.15	0.46
1:2:1833:U:H2'	1:2:1834:G:H8	1.79	0.46
5:A:135:VAL:HA	5:A:157:VAL:O	2.15	0.46
11:G:106:PRO:HD2	11:G:120:VAL:CG2	2.46	0.46
12:H:230:ARG:NH2	25:U:78:ILE:HB	2.30	0.46
25:U:110:TYR:HA	25:U:113:GLU:CG	2.45	0.46
36:f:408:TYR:HD2	39:i:187:LYS:HG3	1.80	0.46
38:h:225:PHE:HE2	38:h:251:LEU:HD21	1.80	0.46
38:h:287:THR:HA	38:h:318:TYR:OH	2.15	0.46
39:i:101:LEU:HD22	39:i:132:VAL:HG23	1.98	0.46
1:2:215:A:H2'	1:2:216:A:C8	2.50	0.46
1:2:811:A:H4'	1:2:813:C:C5	2.50	0.46
1:2:1110:C:H1'	1:2:1442:A:C4	2.51	0.46
2:5:8:U:O2	2:5:22:A:H2	1.98	0.46
2:5:56:U:H2'	2:5:58:G:OP2	2.16	0.46
6:B:96:ARG:HH12	28:X:327:GLU:HB2	1.81	0.46
6:B:371:LEU:HD23	6:B:375:LYS:HZ3	1.80	0.46
8:D:329:LYS:HD3	8:D:329:LYS:N	2.30	0.46
8:D:516:LEU:O	35:e:282:LYS:HE2	2.15	0.46
14:J:262:VAL:HG11	14:J:271:LYS:CG	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:90:LEU:HD23	36:f:141:ILE:HB	1.96	0.46
36:f:179:PHE:CZ	36:f:339:SER:HB3	2.49	0.46
38:h:173:LYS:HD2	38:h:212:ASN:HA	1.97	0.46
41:l:155:LEU:HD21	41:l:180:TRP:CZ3	2.51	0.46
1:2:557:A:H4'	1:2:558:A:H3'	1.96	0.46
1:2:1731:A:P	38:h:252:ARG:HH22	2.38	0.46
2:5:9:A:H3'	2:5:10:G:H5'	1.98	0.46
2:5:15:A:H2	2:5:60:A:C2	2.33	0.46
2:5:24:C:H41	2:5:47:A:N6	2.13	0.46
6:B:372:GLY:H	6:B:375:LYS:HE3	1.80	0.46
12:H:244:GLU:H	12:H:244:GLU:CD	2.24	0.46
16:L:138:LYS:HA	16:L:138:LYS:HD2	1.70	0.46
22:R:175:ARG:HA	22:R:183:VAL:O	2.15	0.46
28:X:419:LYS:HE3	28:X:434:TRP:CD1	2.50	0.46
35:e:182:LYS:HB2	35:e:185:GLU:OE2	2.16	0.46
38:h:190:LEU:CD2	38:h:224:VAL:HG23	2.45	0.46
38:h:277:LYS:HG2	38:h:281:GLU:OE2	2.15	0.46
1:2:216:A:H2'	1:2:217:A:C8	2.51	0.46
1:2:993:G:H2'	1:2:994:A:H8	1.79	0.46
1:2:1317:A:H2'	1:2:1318:A:C8	2.51	0.46
6:B:284:ARG:NH1	31:a:201:GLU:HG2	2.31	0.46
14:J:259:VAL:HG11	21:Q:245:PHE:CE1	2.51	0.46
15:K:44:LYS:HD2	15:K:44:LYS:N	2.22	0.46
20:P:22:ASP:OD2	20:P:35:LYS:HD2	2.15	0.46
27:W:449:ARG:NH2	27:W:452:VAL:HG11	2.29	0.46
35:e:151:ARG:HH11	35:e:151:ARG:CG	2.21	0.46
36:f:83:ASN:HD22	36:f:86:ILE:HD11	1.80	0.46
1:2:144:U:H2'	1:2:145:U:H6	1.80	0.46
1:2:611:G:H2'	1:2:612:U:C6	2.50	0.46
1:2:686:G:O2'	1:2:687:G:H5'	2.15	0.46
1:2:733:C:H2'	1:2:734:U:H6	1.80	0.46
1:2:1318:A:H2'	1:2:1319:A:O4'	2.15	0.46
12:H:224:VAL:C	12:H:225:ILE:HG13	2.41	0.46
23:S:89:LYS:HE3	32:b:19:LEU:CG	2.41	0.46
26:V:179:LYS:HA	26:V:179:LYS:HD3	1.58	0.46
1:2:1698:C:C2'	1:2:1699:A:H5'	2.46	0.46
1:2:1699:A:H2'	1:2:1700:U:H6	1.81	0.46
5:A:35:ARG:CB	25:U:48:ILE:HG22	2.39	0.46
5:A:200:GLN:O	5:A:200:GLN:HG3	2.14	0.46
30:Z:86:LEU:HD23	30:Z:87:TYR:H	1.80	0.46
39:i:120:ASP:OD2	39:i:122:LYS:HB2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:175:LYS:HD3	39:i:175:LYS:HA	1.52	0.46
1:2:78:U:H1'	1:2:79:G:H5'	1.98	0.46
1:2:629:G:H2'	1:2:630:C:C6	2.51	0.46
2:5:2:G:C2'	2:5:3:C:H5'	2.46	0.46
2:5:42:U:H2'	2:5:43:G:H8	1.81	0.46
5:A:9:GLN:HE21	5:A:9:GLN:CA	2.11	0.46
18:N:314:PHE:CZ	26:V:168:LEU:HD23	2.51	0.46
22:R:35:ILE:HG22	22:R:104:VAL:HG22	1.98	0.46
27:W:442:TYR:CD1	27:W:447:LEU:HD12	2.51	0.46
31:a:89:TYR:HB2	31:a:97:ALA:HB3	1.98	0.46
39:i:350:VAL:O	39:i:353:ILE:HG12	2.16	0.46
1:2:365:G:H3'	1:2:365:G:N3	2.32	0.46
1:2:631:U:O2'	1:2:632:U:H5'	2.15	0.46
1:2:1412:C:H2'	1:2:1413:A:C8	2.51	0.46
1:2:1710:G:H2'	1:2:1711:A:C8	2.51	0.46
1:2:1763:U:H5'	1:2:1764:A:H5'	1.98	0.46
5:A:141:ARG:HH21	5:A:165:PRO:HD3	1.78	0.46
6:B:399:MET:HE3	31:a:102:ILE:CG2	2.46	0.46
7:C:117:LEU:HD13	7:C:123:ALA:HA	1.98	0.46
7:C:229:LEU:O	7:C:229:LEU:HD12	2.16	0.46
9:E:39:GLU:OE1	9:E:41:LYS:HD2	2.15	0.46
31:a:165:LYS:HB2	31:a:165:LYS:HE2	1.59	0.46
36:f:205:GLN:HG2	36:f:304:GLN:HE22	1.81	0.46
39:i:108:MET:HE3	39:i:108:MET:O	2.14	0.46
41:l:375:PHE:CD2	41:l:394:LEU:HD11	2.51	0.46
1:2:134:A:H2'	1:2:135:A:C8	2.51	0.45
1:2:147:U:H2'	1:2:148:U:C6	2.51	0.45
1:2:1799:U:O2'	1:2:1800:G:H5'	2.15	0.45
2:5:64:U:O2'	2:5:65:G:H5'	2.16	0.45
8:D:189:GLU:O	8:D:192:LYS:HB2	2.16	0.45
8:D:191:TYR:C	8:D:194:MET:HB2	2.41	0.45
11:G:5:ILE:HG13	11:G:6:LEU:N	2.30	0.45
12:H:219:LYS:O	25:U:124:LEU:HD21	2.15	0.45
31:a:120:GLU:HA	31:a:123:ASP:OD2	2.16	0.45
37:g:639:TYR:CD1	37:g:640:ILE:HG13	2.51	0.45
38:h:169:ARG:HG3	38:h:169:ARG:NH1	2.28	0.45
1:2:1669:C:H1'	4:8:178:LYS:CD	2.46	0.45
6:B:147:ARG:HB3	28:X:508:TYR:CZ	2.51	0.45
6:B:371:LEU:HD23	6:B:375:LYS:NZ	2.30	0.45
7:C:234:LYS:HE3	7:C:234:LYS:HB2	1.59	0.45
8:D:131:GLN:HA	8:D:134:LYS:HZ3	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:H:247:ASP:HA	12:H:250:ILE:CG1	2.46	0.45
15:K:8:ILE:HG12	20:P:27:ASN:OD1	2.16	0.45
29:Y:69:ARG:O	29:Y:73:GLU:OE2	2.35	0.45
37:g:564:LEU:HD11	37:g:598:PHE:HA	1.98	0.45
38:h:202:MET:HE1	38:h:228:CYS:N	2.31	0.45
41:l:468:ALA:O	41:l:472:HIS:HB2	2.17	0.45
1:2:142:U:H2'	1:2:143:U:C6	2.52	0.45
1:2:147:U:O2'	1:2:148:U:H5'	2.16	0.45
1:2:244:U:O2	1:2:244:U:O4'	2.35	0.45
1:2:379:G:O2'	1:2:380:G:H5'	2.15	0.45
1:2:1651:C:H2'	1:2:1652:C:C6	2.51	0.45
6:B:361:ASN:HA	6:B:364:ARG:HH12	1.81	0.45
6:B:484:GLY:HA3	6:B:509:LYS:O	2.16	0.45
7:C:320:GLU:HG3	35:e:222:LEU:CD1	2.47	0.45
10:F:124:SER:HA	10:F:127:ARG:HD3	1.98	0.45
12:H:310:GLY:HA3	12:H:378:ALA:O	2.16	0.45
14:J:188:ASN:OD1	21:Q:250:ILE:HG12	2.16	0.45
15:K:40:ARG:HH11	15:K:52:ILE:CD1	2.29	0.45
31:a:197:LYS:HG3	31:a:198:GLU:N	2.31	0.45
38:h:82:PRO:HG3	38:h:124:PHE:CE2	2.52	0.45
39:i:341:TRP:CH2	39:i:355:LEU:HB2	2.51	0.45
41:l:529:TRP:CZ2	41:l:558:LYS:HA	2.52	0.45
6:B:383:PHE:O	6:B:383:PHE:HD1	2.00	0.45
7:C:204:THR:CB	8:D:116:GLU:HG2	2.47	0.45
8:D:249:PHE:CE1	8:D:390:ASN:HB2	2.52	0.45
8:D:362:VAL:HG21	8:D:413:TYR:HE1	1.81	0.45
10:F:39:PRO:HB2	10:F:44:ARG:HD2	1.98	0.45
19:O:22:ALA:O	19:O:34:ILE:HB	2.16	0.45
23:S:65:LYS:HB2	23:S:68:GLU:OE1	2.16	0.45
35:e:172:LYS:NZ	35:e:172:LYS:HB3	2.32	0.45
36:f:281:GLU:OE1	36:f:281:GLU:N	2.49	0.45
39:i:103:ARG:CG	39:i:173:VAL:HG22	2.45	0.45
1:2:470:C:H5"	34:d:74:ARG:HD3	1.97	0.45
1:2:1828:MA6:H8	1:2:1828:MA6:H5"	1.99	0.45
6:B:380:ILE:HB	6:B:384:LYS:HZ1	1.81	0.45
7:C:72:THR:HG21	7:C:85:THR:OG1	2.17	0.45
8:D:161:ARG:HH11	8:D:161:ARG:HG3	1.80	0.45
12:H:245:MET:HG2	39:i:291:LYS:HZ2	1.81	0.45
14:J:289:GLN:HG3	21:Q:252:ASP:CG	2.42	0.45
31:a:96:ASP:OD1	31:a:97:ALA:N	2.49	0.45
39:i:321:VAL:O	39:i:325:LEU:HD22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:324:LYS:HG3	39:i:325:LEU:HD22	1.97	0.45
41:l:311:PHE:CE1	41:l:319:GLU:HB2	2.52	0.45
41:l:529:TRP:HH2	41:l:561:GLU:HB2	1.81	0.45
1:2:476:C:O2	1:2:476:C:O4'	2.34	0.45
1:2:1384:A:H1'	41:l:481:HIS:NE2	2.32	0.45
1:2:1739:U:H2'	1:2:1740:C:C6	2.51	0.45
2:5:6:G:N3	2:5:6:G:H2'	2.31	0.45
7:C:178:LYS:O	7:C:182:LYS:HB3	2.16	0.45
19:O:102:PRO:HB2	19:O:111:VAL:HG11	1.98	0.45
25:U:53:ASP:N	25:U:54:PRO:HD2	2.31	0.45
27:W:236:LEU:HD12	27:W:236:LEU:HA	1.78	0.45
27:W:413:ARG:NH1	27:W:417:PRO:HG3	2.31	0.45
38:h:190:LEU:HD23	38:h:223:LEU:CB	2.43	0.45
41:l:214:TRP:CH2	41:l:253:VAL:HG22	2.51	0.45
1:2:341:C:H2'	1:2:342:U:C6	2.52	0.45
1:2:1698:C:O2'	1:2:1699:A:H5'	2.16	0.45
1:2:1761:C:O2'	1:2:1764:A:H8	2.00	0.45
4:8:237:GLU:OE1	4:8:239:ASP:OD1	2.34	0.45
5:A:100:LEU:HD21	5:A:127:PRO:HD3	1.98	0.45
5:A:150:ALA:CB	5:A:171:LYS:HE3	2.47	0.45
7:C:49:LYS:HG2	7:C:53:LYS:HE2	1.99	0.45
9:E:31:TYR:HE2	26:V:178:PRO:HA	1.81	0.45
11:G:70:ASP:HB3	11:G:129:TYR:CZ	2.52	0.45
12:H:225:ILE:HA	12:H:228:PRO:CA	2.46	0.45
23:S:95:ILE:HG22	40:k:26:MET:CE	2.44	0.45
29:Y:84:ARG:O	29:Y:84:ARG:HG2	2.17	0.45
35:e:354:VAL:HG21	35:e:362:ARG:CZ	2.47	0.45
36:f:189:LEU:HD12	36:f:190:SER:N	2.31	0.45
1:2:460:U:O2	1:2:460:U:H2'	2.16	0.45
1:2:1134:U:C2'	1:2:1135:A:H5'	2.46	0.45
1:2:1502:A:H62	1:2:1561:A:N6	2.15	0.45
1:2:1729:G:H2'	1:2:1730:U:H6	1.81	0.45
5:A:128:THR:CG2	8:D:305:LEU:HD13	2.46	0.45
8:D:231:ILE:HG22	8:D:235:LYS:HE2	1.99	0.45
9:E:22:LEU:O	9:E:26:ILE:HG13	2.17	0.45
9:E:48:LEU:HB3	21:Q:220:GLY:O	2.16	0.45
12:H:245:MET:HB3	39:i:292:TRP:CH2	2.52	0.45
25:U:42:ASN:C	25:U:42:ASN:OD1	2.60	0.45
25:U:98:SER:HB2	25:U:101:ASP:OD2	2.17	0.45
30:Z:59:PHE:CE1	38:h:176:VAL:HG13	2.52	0.45
31:a:356:HIS:HB2	31:a:359:GLU:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:60:LEU:HD21	34:d:83:ILE:HD11	1.99	0.45
35:e:306:ARG:HB3	35:e:306:ARG:CZ	2.47	0.45
36:f:105:LEU:HB3	36:f:106:PRO:HD3	1.97	0.45
39:i:397:GLU:HB3	39:i:399:HIS:CE1	2.52	0.45
41:l:198:LEU:HD22	41:l:233:ILE:HG23	1.98	0.45
41:l:276:LEU:HD22	41:l:284:TRP:HE3	1.82	0.45
41:l:452:TYR:CB	41:l:461:ALA:HB2	2.47	0.45
1:2:901:A:H2'	1:2:902:A:H8	1.82	0.45
1:2:1003:C:H2'	1:2:1004:C:H6	1.81	0.45
2:5:15:A:H2	2:5:60:A:N3	2.13	0.45
5:A:9:GLN:NE2	5:A:9:GLN:CA	2.75	0.45
9:E:7:MET:HE3	9:E:64:LEU:HD11	1.99	0.45
27:W:413:ARG:H	27:W:413:ARG:HG2	1.51	0.45
27:W:439:CYS:SG	27:W:458:TRP:HB2	2.57	0.45
1:2:403:G:H2'	1:2:404:C:C6	2.52	0.45
1:2:1441:G:P	12:H:395:ARG:HH12	2.40	0.45
1:2:1800:G:H5"	15:K:44:LYS:HZ1	1.79	0.45
1:2:1813:G:H5"	1:2:1814:G:H5'	1.98	0.45
2:5:68:C:H2'	2:5:69:C:H6	1.82	0.45
6:B:78:ARG:HD2	6:B:80:ARG:NH2	2.32	0.45
7:C:161:ILE:HD13	7:C:161:ILE:HA	1.87	0.45
8:D:82:ASP:O	8:D:86:GLU:HG3	2.16	0.45
10:F:57:ILE:HD13	10:F:92:ILE:HD11	1.99	0.45
12:H:247:ASP:HA	12:H:250:ILE:HD11	1.98	0.45
14:J:258:VAL:O	14:J:293:VAL:HG22	2.17	0.45
18:N:397:TYR:CZ	18:N:401:LEU:HD11	2.52	0.45
25:U:101:ASP:O	25:U:105:VAL:HG12	2.17	0.45
28:X:494:LEU:HD23	29:Y:29:MET:HE2	1.99	0.45
36:f:80:TRP:HA	36:f:86:ILE:HD12	1.99	0.45
1:2:44:C:C2'	1:2:45:U:H5'	2.47	0.44
1:2:428:U:HO2'	1:2:429:G:H5'	1.82	0.44
1:2:467:G:H2'	1:2:468:U:H6	1.82	0.44
1:2:617:A:OP2	1:2:617:A:H8	1.99	0.44
2:5:67:C:C2	2:5:68:C:C5	3.05	0.44
8:D:218:MET:O	8:D:222:LYS:HG2	2.17	0.44
12:H:428:VAL:O	12:H:429:LYS:C	2.59	0.44
22:R:34:TYR:HB3	22:R:106:VAL:O	2.18	0.44
31:a:103:GLU:O	31:a:107:GLN:NE2	2.44	0.44
32:b:72:LYS:HB2	32:b:74:LYS:NZ	2.32	0.44
34:d:42:ILE:N	34:d:43:PRO:HD2	2.32	0.44
34:d:45:PHE:O	34:d:49:ILE:HD12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:127:TYR:HD2	36:f:398:LEU:CD2	2.30	0.44
38:h:113:ILE:O	38:h:157:THR:HG21	2.17	0.44
39:i:103:ARG:CD	39:i:173:VAL:HG22	2.46	0.44
41:l:394:LEU:O	41:l:398:MET:HB3	2.18	0.44
1:2:177:G:C1'	1:2:373:G:H5'	2.47	0.44
1:2:275:U:O2'	1:2:276:U:H5'	2.18	0.44
1:2:696:A:H62	4:8:148:LYS:HG3	1.81	0.44
5:A:60:LEU:HD23	5:A:60:LEU:HA	1.80	0.44
6:B:282:GLN:H	6:B:282:GLN:CD	2.24	0.44
8:D:243:VAL:HG23	8:D:244:GLU:OE1	2.16	0.44
9:E:89:LEU:O	9:E:90:ARG:HG2	2.17	0.44
21:Q:230:LYS:H	21:Q:230:LYS:HG2	1.60	0.44
27:W:155:PRO:HG3	27:W:277:PHE:HB2	1.99	0.44
32:b:76:TRP:HZ2	32:b:82:HIS:CE1	2.35	0.44
38:h:192:TYR:O	38:h:192:TYR:HD1	2.00	0.44
38:h:251:LEU:CG	38:h:255:THR:HG21	2.46	0.44
38:h:337:TRP:N	38:h:338:PRO:HD2	2.32	0.44
38:h:358:LYS:O	38:h:362:PRO:HG2	2.17	0.44
39:i:141:ARG:HB3	39:i:146:LYS:NZ	2.33	0.44
1:2:274:G:O2'	1:2:275:U:H5'	2.17	0.44
1:2:1146:A:H2'	1:2:1147:A:H8	1.81	0.44
1:2:1715:C:O2'	1:2:1716:C:H5'	2.17	0.44
7:C:213:LYS:O	7:C:213:LYS:CG	2.65	0.44
7:C:307:ARG:HB3	7:C:307:ARG:HH11	1.81	0.44
9:E:89:LEU:C	9:E:90:ARG:HG2	2.42	0.44
13:I:166:LEU:HD21	13:I:173:LYS:HD2	2.00	0.44
15:K:50:ARG:HG3	15:K:90:LEU:HD21	1.99	0.44
25:U:53:ASP:O	25:U:56:VAL:HG23	2.17	0.44
28:X:448:MET:HE3	28:X:448:MET:HB3	1.78	0.44
36:f:325:PHE:HB3	39:i:103:ARG:NH2	2.32	0.44
39:i:312:LYS:NZ	39:i:312:LYS:HB3	2.32	0.44
39:i:341:TRP:CH2	39:i:355:LEU:HD22	2.52	0.44
1:2:37:A:C2'	1:2:38:G:H5'	2.46	0.44
1:2:169:G:H2'	1:2:170:C:C6	2.53	0.44
1:2:1504:G:H2'	1:2:1505:G:H8	1.82	0.44
2:5:11:A:C5	2:5:12:G:C8	3.05	0.44
5:A:50:LEU:HD13	5:A:188:PHE:CD1	2.53	0.44
6:B:370:LEU:HD23	6:B:370:LEU:HA	1.64	0.44
7:C:252:MET:HE1	7:C:290:TYR:N	2.33	0.44
7:C:255:ASN:HD21	35:e:146:ASP:CG	2.24	0.44
12:H:230:ARG:NH2	25:U:79:PRO:CD	2.79	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:U:77:PHE:CD1	40:k:13:ILE:HG12	2.53	0.44
30:Z:87:TYR:HB2	30:Z:92:HIS:O	2.17	0.44
31:a:187:GLY:HA3	31:a:193:LEU:HD23	2.00	0.44
34:d:54:GLU:O	34:d:57:VAL:HG23	2.17	0.44
36:f:323:GLY:HA2	36:f:326:GLN:CG	2.47	0.44
36:f:389:THR:HG21	36:f:397:GLU:CG	2.47	0.44
41:l:396:LEU:HA	41:l:399:ILE:HG22	1.99	0.44
1:2:164:A:O2'	1:2:165:A:H5'	2.16	0.44
1:2:1692:C:H2'	1:2:1693:C:H6	1.82	0.44
1:2:1773:U:C2'	1:2:1774:A:OP1	2.66	0.44
30:Z:60:LEU:HD13	30:Z:67:TYR:CD2	2.51	0.44
32:b:83:LEU:HA	32:b:86:LEU:CD2	2.47	0.44
36:f:356:ARG:HA	36:f:360:VAL:HB	2.00	0.44
38:h:229:HIS:HD2	38:h:262:PHE:HB2	1.82	0.44
41:l:143:SER:HB2	41:l:146:PHE:HB3	1.99	0.44
1:2:592:C:O2'	1:2:593:G:H5'	2.18	0.44
1:2:1770:G:H3'	1:2:1771:C:C4'	2.45	0.44
6:B:494:LYS:HD3	6:B:494:LYS:HA	1.74	0.44
12:H:216:LYS:HG3	25:U:127:LEU:HD13	1.99	0.44
14:J:191:THR:HG22	21:Q:246:GLU:OE1	2.18	0.44
23:S:77:LEU:O	23:S:77:LEU:HD13	2.18	0.44
30:Z:63:TRP:NE1	38:h:137:LEU:HD12	2.32	0.44
34:d:97:LYS:HB2	34:d:97:LYS:HE3	1.51	0.44
35:e:243:ARG:HB3	35:e:243:ARG:CZ	2.47	0.44
36:f:226:ARG:HD3	36:f:254:ASP:OD1	2.16	0.44
38:h:229:HIS:CD2	38:h:261:GLU:HG3	2.53	0.44
39:i:128:LEU:HD12	39:i:129:LEU:N	2.32	0.44
39:i:312:LYS:HE2	39:i:345:LEU:O	2.18	0.44
1:2:82:C:OP2	1:2:82:C:H6	2.01	0.44
1:2:767:A:H2'	1:2:768:U:C6	2.53	0.44
1:2:1138:G:H8	41:l:513:ASP:OD2	2.00	0.44
4:8:106:VAL:HG12	4:8:107:SER:N	2.32	0.44
7:C:37:ILE:H	7:C:37:ILE:CD1	2.29	0.44
26:V:181:LEU:HD11	26:V:185:ILE:HD11	2.00	0.44
28:X:381:ASP:O	28:X:385:MET:HG3	2.17	0.44
31:a:110:LEU:HD23	31:a:110:LEU:HA	1.85	0.44
35:e:189:MET:HG2	35:e:209:TYR:CE1	2.52	0.44
36:f:279:VAL:O	36:f:283:ILE:HG23	2.17	0.44
38:h:227:ILE:O	38:h:231:THR:HG23	2.18	0.44
41:l:330:LYS:O	41:l:331:GLU:HG3	2.18	0.44
1:2:598:G:O2'	1:2:599:A:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1318:A:C2	1:2:1319:A:H1'	2.53	0.44
1:2:1571:G:H2'	1:2:1572:U:C6	2.52	0.44
1:2:1796:G:H2'	1:2:1797:G:H8	1.82	0.44
2:5:74:U:H2'	2:5:75:C:O4'	2.18	0.44
6:B:41:TYR:CZ	6:B:45:ILE:HD11	2.53	0.44
8:D:189:GLU:HG2	8:D:193:TRP:NE1	2.32	0.44
9:E:48:LEU:HD12	9:E:59:HIS:O	2.17	0.44
9:E:76:ASN:HB2	9:E:93:LEU:HD23	2.00	0.44
25:U:122:LYS:HE2	25:U:122:LYS:N	2.33	0.44
36:f:267:ILE:HG13	36:f:271:ASP:OD2	2.17	0.44
36:f:311:LEU:HA	36:f:311:LEU:HD23	1.72	0.44
39:i:334:PRO:HD2	39:i:369:LYS:NZ	2.33	0.44
41:l:356:ALA:HB1	41:l:378:VAL:HG22	2.00	0.44
41:l:423:LEU:HD23	41:l:423:LEU:HA	1.76	0.44
1:2:253:C:O2'	1:2:254:U:H5'	2.18	0.44
1:2:1728:U:O2'	1:2:1729:G:H8	2.01	0.44
6:B:204:THR:HG23	6:B:207:PHE:H	1.82	0.44
7:C:327:LYS:HE2	35:e:225:ASP:OD2	2.18	0.44
22:R:65:ASN:HD22	22:R:72:ARG:CZ	2.31	0.44
36:f:157:ILE:HD13	36:f:217:LEU:HD22	2.00	0.44
38:h:117:ARG:HH12	38:h:160:ARG:NH1	2.16	0.44
38:h:189:LEU:CD2	38:h:205:VAL:HB	2.48	0.44
38:h:353:VAL:HG13	38:h:357:LEU:HD13	1.99	0.44
41:l:386:ARG:HH12	41:l:419:LYS:HG2	1.82	0.44
41:l:523:CYS:HB3	41:l:553:LEU:HD22	2.00	0.44
1:2:129:A:C5	1:2:150:A:C2	3.06	0.43
1:2:325:A:C2	1:2:326:U:C6	3.06	0.43
1:2:1839:G:H2'	1:2:1840:A:C8	2.53	0.43
5:A:3:LEU:HD23	39:i:299:ILE:CD1	2.48	0.43
6:B:96:ARG:NH1	28:X:327:GLU:HB2	2.33	0.43
6:B:376:VAL:O	6:B:380:ILE:HG23	2.18	0.43
6:B:466:SER:O	6:B:470:ILE:HG13	2.18	0.43
8:D:127:LYS:HE2	8:D:127:LYS:HB3	1.83	0.43
14:J:201:LEU:HD23	14:J:201:LEU:N	2.33	0.43
22:R:35:ILE:HD13	22:R:38:LEU:HD11	2.00	0.43
23:S:93:ILE:HG21	32:b:86:LEU:HD21	2.00	0.43
26:V:112:GLU:O	26:V:115:ARG:HG3	2.17	0.43
34:d:59:ARG:HH11	34:d:59:ARG:CG	2.31	0.43
35:e:354:VAL:O	35:e:355:SER:HB3	2.18	0.43
36:f:189:LEU:HD13	36:f:320:ILE:HD12	1.98	0.43
36:f:389:THR:CG2	36:f:397:GLU:HB2	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:81:ASP:HB2	38:h:82:PRO:CD	2.40	0.43
38:h:88:GLU:OE1	38:h:88:GLU:CA	2.66	0.43
1:2:633:U:O2'	1:2:634:C:H5'	2.18	0.43
1:2:857:A:H2'	1:2:858:A:C8	2.53	0.43
1:2:1054:U:H2'	1:2:1055:C:C6	2.53	0.43
6:B:213:LYS:HA	6:B:213:LYS:HD2	1.69	0.43
8:D:152:LEU:HD23	8:D:152:LEU:H	1.83	0.43
8:D:177:LEU:HD21	8:D:197:LEU:CA	2.48	0.43
8:D:214:ILE:HD11	8:D:243:VAL:HG11	1.99	0.43
12:H:270:LEU:HD12	12:H:270:LEU:HA	1.83	0.43
14:J:189:LEU:CD2	21:Q:248:GLU:HA	2.48	0.43
15:K:87:VAL:O	15:K:87:VAL:HG13	2.18	0.43
25:U:85:TYR:O	25:U:89:VAL:HG12	2.18	0.43
28:X:346:LYS:HZ3	28:X:347:LYS:HD3	1.83	0.43
30:Z:80:GLU:HA	30:Z:80:GLU:OE2	2.18	0.43
36:f:328:LEU:HD13	36:f:328:LEU:O	2.18	0.43
37:g:554:ILE:HG22	37:g:559:GLY:HA3	1.99	0.43
38:h:242:LYS:HE3	38:h:242:LYS:HB3	1.89	0.43
39:i:341:TRP:CZ3	39:i:355:LEU:HD22	2.53	0.43
1:2:78:U:O2'	1:2:79:G:H8	2.02	0.43
1:2:226:A:H1'	1:2:241:U:HO2'	1.80	0.43
1:2:354:C:C2	1:2:355:G:C8	3.06	0.43
1:2:1716:C:H2'	1:2:1717:C:H6	1.83	0.43
1:2:1802:A:H1'	1:2:1803:G:P	2.58	0.43
2:5:11:A:H2'	2:5:12:G:C4'	2.47	0.43
5:A:165:PRO:HB2	5:A:167:GLU:HG2	2.01	0.43
6:B:96:ARG:O	6:B:100:THR:HG23	2.17	0.43
6:B:332:LEU:HD21	31:a:193:LEU:HB3	2.00	0.43
14:J:251:LYS:HD2	14:J:251:LYS:O	2.19	0.43
19:O:23:THR:HG22	19:O:33:HIS:CA	2.47	0.43
30:Z:101:LYS:O	30:Z:102:ASP:OD1	2.37	0.43
36:f:160:MET:HG2	36:f:161:PHE:CZ	2.53	0.43
36:f:273:TYR:CG	36:f:286:MET:HG3	2.53	0.43
36:f:278:THR:O	36:f:282:ILE:HG12	2.18	0.43
36:f:298:CYS:HA	36:f:301:THR:HG22	2.01	0.43
38:h:150:LEU:O	38:h:150:LEU:HD13	2.19	0.43
39:i:429:TYR:HB3	39:i:434:ASN:O	2.17	0.43
1:2:683:A:C2	1:2:700:A:C5	3.06	0.43
1:2:733:C:H2'	1:2:734:U:C6	2.54	0.43
1:2:1701:C:C2'	1:2:1702:G:C8	2.98	0.43
2:5:10:G:H2'	2:5:11:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:28:U:H3	2:5:44:A:H61	1.66	0.43
9:E:21:ASP:OD1	9:E:21:ASP:C	2.62	0.43
12:H:219:LYS:HB3	25:U:124:LEU:HD22	2.00	0.43
12:H:245:MET:N	12:H:245:MET:SD	2.91	0.43
19:O:106:MET:SD	35:e:320:CYS:HB2	2.58	0.43
23:S:77:LEU:HD13	23:S:77:LEU:C	2.44	0.43
25:U:69:VAL:HG13	25:U:78:ILE:HD12	2.00	0.43
35:e:257:ARG:HD3	35:e:259:PHE:O	2.18	0.43
38:h:311:ILE:HD12	38:h:368:LEU:HD21	1.97	0.43
38:h:353:VAL:O	38:h:357:LEU:HD13	2.18	0.43
41:l:239:ALA:HB2	41:l:271:LEU:HD13	2.01	0.43
1:2:150:A:H3'	1:2:151:A:C8	2.54	0.43
1:2:781:G:O2'	1:2:782:G:H5'	2.19	0.43
1:2:1740:C:O2	1:2:1740:C:H2'	2.17	0.43
12:H:224:VAL:O	12:H:225:ILE:HB	2.18	0.43
14:J:268:PHE:HE2	23:S:44:GLN:HB2	1.82	0.43
25:U:15:LEU:HB3	25:U:21:THR:CG2	2.45	0.43
25:U:79:PRO:CB	40:k:11:GLY:HA2	2.47	0.43
27:W:101:ARG:HB3	27:W:170:TRP:CZ3	2.54	0.43
27:W:147:GLU:OE1	27:W:147:GLU:N	2.51	0.43
36:f:160:MET:HG2	36:f:161:PHE:CE2	2.53	0.43
36:f:317:LEU:HD23	36:f:317:LEU:C	2.44	0.43
39:i:321:VAL:O	39:i:325:LEU:HD23	2.18	0.43
41:l:423:LEU:HD13	41:l:452:TYR:CD1	2.54	0.43
1:2:57:U:O2'	1:2:58:A:H2'	2.19	0.43
1:2:158:A:H2'	1:2:159:G:O4'	2.18	0.43
1:2:550:U:N3	1:2:551:C:C5	2.87	0.43
1:2:991:A:H2'	1:2:992:U:H6	1.83	0.43
1:2:1065:U:OP1	8:D:411:LYS:HG2	2.19	0.43
1:2:1699:A:H2'	1:2:1700:U:C6	2.52	0.43
5:A:147:LEU:HD22	5:A:147:LEU:H	1.82	0.43
6:B:361:ASN:HA	6:B:364:ARG:NH1	2.33	0.43
7:C:260:LEU:HD23	8:D:181:LEU:CD1	2.40	0.43
9:E:43:PHE:HB2	9:E:64:LEU:HB3	2.00	0.43
11:G:103:VAL:HG12	11:G:105:THR:HG23	2.01	0.43
14:J:263:ASN:C	14:J:263:ASN:OD1	2.62	0.43
23:S:64:ILE:HG22	23:S:69:LYS:HG3	1.99	0.43
30:Z:53:LEU:HD12	30:Z:53:LEU:C	2.43	0.43
30:Z:62:ASN:O	30:Z:63:TRP:HB2	2.17	0.43
31:a:392:GLN:C	31:a:392:GLN:OE1	2.61	0.43
38:h:171:LEU:HD21	38:h:208:LEU:HB2	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:337:TRP:O	38:h:341:VAL:HG13	2.18	0.43
39:i:240:ASP:O	39:i:244:ARG:HG3	2.18	0.43
39:i:322:MET:HG3	39:i:323:GLU:N	2.33	0.43
39:i:425:LEU:HA	39:i:428:MET:HG2	1.99	0.43
41:l:155:LEU:HD21	41:l:180:TRP:HZ3	1.83	0.43
41:l:493:TYR:O	41:l:497:LEU:HG	2.17	0.43
1:2:13:A:H2'	1:2:14:G:O4'	2.19	0.43
1:2:440:A:OP2	1:2:441:U:H6	2.02	0.43
1:2:1166:U:H2'	1:2:1167:U:C6	2.54	0.43
4:8:90:ILE:HD11	4:8:122:LEU:HB3	2.01	0.43
7:C:224:MET:HA	7:C:227:GLU:HG2	2.00	0.43
8:D:381:ARG:HH21	8:D:401:LYS:CE	2.32	0.43
17:M:91:LYS:O	17:M:95:LYS:HG3	2.19	0.43
25:U:55:TYR:CD1	25:U:55:TYR:N	2.87	0.43
30:Z:122:LYS:HG2	30:Z:123:TYR:N	2.33	0.43
36:f:190:SER:HG	36:f:324:ARG:HG2	1.81	0.43
38:h:184:ALA:O	38:h:187:HIS:HB3	2.18	0.43
41:l:360:LEU:HD13	41:l:375:PHE:CE2	2.54	0.43
1:2:609:U:O2	1:2:609:U:H2'	2.19	0.43
1:2:997:G:H1	1:2:1029:C:H41	1.64	0.43
1:2:1731:A:C3'	1:2:1732:A:H5"	2.49	0.43
1:2:1822:A:H2'	1:2:1823:G:C8	2.54	0.43
6:B:184:TYR:O	6:B:188:VAL:HG12	2.19	0.43
8:D:218:MET:CE	35:e:168:LEU:HD23	2.46	0.43
12:H:216:LYS:HE3	25:U:127:LEU:HB3	1.99	0.43
12:H:301:ASP:OD1	12:H:302:GLU:N	2.51	0.43
14:J:282:TYR:CE2	14:J:291:PRO:HG3	2.54	0.43
18:N:313:TYR:CE1	26:V:168:LEU:HD21	2.54	0.43
19:O:52:MET:HG3	19:O:53:GLY:N	2.33	0.43
27:W:163:GLU:O	27:W:167:LYS:HE2	2.19	0.43
31:a:179:LYS:O	31:a:183:ILE:HG22	2.19	0.43
35:e:334:ILE:HD12	35:e:334:ILE:N	2.33	0.43
36:f:90:LEU:HA	36:f:141:ILE:O	2.18	0.43
37:g:602:MET:HG2	37:g:603:THR:N	2.33	0.43
38:h:95:ASP:HA	38:h:98:ASN:OD1	2.19	0.43
1:2:848:G:OP2	1:2:864:U:H5	2.01	0.43
1:2:950:U:O2	1:2:952:A:H8	2.02	0.43
4:8:137:VAL:HG22	4:8:138:LYS:N	2.34	0.43
6:B:147:ARG:HB3	28:X:508:TYR:CE2	2.54	0.43
6:B:465:ARG:HD2	6:B:470:ILE:HG12	2.00	0.43
13:I:136:SER:HB2	13:I:211:GLY:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:O:4:ARG:NH2	19:O:70:SER:HA	2.33	0.43
27:W:162:ILE:HG12	27:W:221:ILE:HG12	2.00	0.43
28:X:440:GLU:O	28:X:444:GLU:HG2	2.19	0.43
38:h:332:LYS:HA	38:h:332:LYS:HD3	1.85	0.43
41:l:531:LYS:N	41:l:531:LYS:HD2	2.33	0.43
1:2:486:C:H2'	1:2:487:U:C6	2.54	0.43
2:5:22:A:C6	2:5:47:A:H1'	2.54	0.43
5:A:76:PHE:CD1	5:A:185:VAL:HG11	2.54	0.43
7:C:114:LEU:O	7:C:115:HIS:HB2	2.19	0.43
24:T:62:LYS:HB3	24:T:62:LYS:HE3	1.90	0.43
25:U:59:PHE:HE1	25:U:63:HIS:HE1	1.67	0.43
30:Z:69:MET:HG2	30:Z:81:ILE:HD11	2.01	0.43
38:h:156:LYS:O	38:h:159:VAL:HG12	2.19	0.43
38:h:169:ARG:HH12	38:h:175:ASN:CB	2.32	0.43
38:h:288:LEU:HD11	38:h:326:LEU:CD2	2.49	0.43
39:i:130:LEU:HD23	39:i:131:ILE:HG12	1.99	0.43
39:i:400:ILE:HG12	39:i:434:ASN:OD1	2.19	0.43
39:i:415:ILE:HG13	39:i:416:PHE:N	2.34	0.43
1:2:79:G:C4'	1:2:80:U:OP1	2.67	0.42
1:2:549:U:H2'	1:2:550:U:H6	1.84	0.42
1:2:1767:G:H2'	1:2:1768:A:C4'	2.49	0.42
2:5:69:C:H2'	2:5:70:C:C6	2.53	0.42
6:B:367:CYS:HA	6:B:370:LEU:HB2	2.00	0.42
6:B:369:ASN:ND2	28:X:338:ASN:HA	2.34	0.42
12:H:245:MET:HE3	12:H:245:MET:N	2.34	0.42
22:R:35:ILE:HD12	22:R:35:ILE:O	2.18	0.42
25:U:50:LEU:HD13	25:U:83:ARG:CZ	2.49	0.42
1:2:1749:A:H5"	1:2:1750:C:OP2	2.19	0.42
7:C:311:ARG:HD2	35:e:251:PHE:O	2.20	0.42
8:D:150:SER:O	8:D:151:GLU:HB2	2.20	0.42
25:U:54:PRO:HA	25:U:57:ARG:NH2	2.34	0.42
26:V:141:LYS:HE3	26:V:141:LYS:HB3	1.53	0.42
38:h:194:LEU:HD22	38:h:230:GLU:OE2	2.19	0.42
39:i:108:MET:CE	39:i:111:LYS:HB2	2.49	0.42
39:i:181:ARG:HD2	39:i:181:ARG:C	2.44	0.42
39:i:196:MET:HE3	39:i:196:MET:HB3	1.85	0.42
39:i:353:ILE:HA	39:i:356:ILE:HD12	2.01	0.42
41:l:411:ASN:HB3	41:l:443:TYR:CD2	2.54	0.42
1:2:280:U:H2'	1:2:282:A:OP2	2.20	0.42
1:2:592:C:H2'	1:2:593:G:C8	2.55	0.42
1:2:640:C:C2	1:2:641:A:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8:123:VAL:N	4:8:136:ILE:HD11	2.12	0.42
7:C:126:LEU:HD13	7:C:131:ARG:HE	1.83	0.42
19:O:107:THR:HG1	19:O:109:ARG:HG2	1.84	0.42
31:a:377:LYS:HD3	31:a:377:LYS:HA	1.77	0.42
34:d:66:ASP:OD1	34:d:66:ASP:C	2.61	0.42
35:e:177:ARG:NH1	35:e:179:SER:HB2	2.35	0.42
35:e:334:ILE:CG2	35:e:335:THR:N	2.82	0.42
39:i:127:MET:HE3	39:i:127:MET:CA	2.48	0.42
1:2:490:A:H2'	1:2:491:G:C8	2.54	0.42
1:2:915:G:C6	1:2:916:A:C6	3.08	0.42
1:2:1669:C:H1'	4:8:178:LYS:HD3	2.01	0.42
8:D:130:LYS:HG2	8:D:134:LYS:CE	2.48	0.42
23:S:53:GLU:OE2	23:S:57:LYS:HE3	2.19	0.42
23:S:64:ILE:HD12	23:S:64:ILE:N	2.34	0.42
23:S:96:LYS:HG3	40:k:26:MET:HE3	2.02	0.42
31:a:220:LYS:HB3	31:a:220:LYS:HE3	1.77	0.42
36:f:127:TYR:HD2	36:f:398:LEU:HD22	1.84	0.42
36:f:170:LEU:HD13	36:f:170:LEU:C	2.44	0.42
36:f:408:TYR:CD2	39:i:187:LYS:HG3	2.54	0.42
39:i:125:ASP:HA	39:i:128:LEU:HD21	2.00	0.42
41:l:517:LYS:HE2	41:l:517:LYS:HB2	1.79	0.42
1:2:200:C:O2	1:2:200:C:O4'	2.36	0.42
1:2:478:U:H5"	34:d:92:LEU:HD13	2.02	0.42
1:2:498:G:H2'	1:2:499:C:C6	2.55	0.42
1:2:732:U:H2'	1:2:733:C:H6	1.84	0.42
1:2:1065:U:P	8:D:411:LYS:HE3	2.59	0.42
1:2:1633:G:O3'	12:H:371:GLY:HA3	2.20	0.42
2:5:22:A:H5'	2:5:23:A:P	2.60	0.42
4:8:86:LEU:HG	4:8:87:ASN:H	1.84	0.42
7:C:262:LEU:HD13	7:C:262:LEU:C	2.43	0.42
8:D:343:GLU:O	8:D:347:LEU:HD13	2.20	0.42
12:H:266:GLU:O	12:H:269:ASN:HB2	2.18	0.42
23:S:63:HIS:C	23:S:64:ILE:HD12	2.45	0.42
27:W:235:TRP:CD2	27:W:350:PRO:HB2	2.54	0.42
31:a:401:MET:H	31:a:401:MET:CE	2.32	0.42
32:b:17:GLY:O	32:b:18:ASN:C	2.63	0.42
35:e:334:ILE:HG22	35:e:335:THR:N	2.34	0.42
35:e:334:ILE:O	35:e:354:VAL:O	2.36	0.42
36:f:105:LEU:HD12	36:f:105:LEU:HA	1.78	0.42
36:f:290:VAL:HG21	36:f:299:LYS:CD	2.49	0.42
37:g:567:LEU:HB2	37:g:568:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:194:LEU:HD22	38:h:230:GLU:OE1	2.20	0.42
1:2:67:A:H1'	1:2:373:G:N2	2.34	0.42
1:2:392:A:C2	1:2:480:A:C6	3.07	0.42
1:2:1379:C:H5	1:2:1381:C:C2	2.38	0.42
5:A:150:ALA:HB3	5:A:171:LYS:HE3	2.01	0.42
6:B:521:TYR:HA	6:B:537:VAL:O	2.20	0.42
7:C:227:GLU:O	7:C:231:ARG:HG3	2.20	0.42
7:C:238:GLU:HG2	7:C:239:LYS:N	2.35	0.42
8:D:325:THR:CG2	8:D:329:LYS:HB2	2.50	0.42
20:P:73:GLU:HG2	20:P:74:ILE:N	2.35	0.42
25:U:92:LEU:O	25:U:97:ILE:HG22	2.20	0.42
27:W:118:PRO:HB3	27:W:436:GLU:HG2	2.01	0.42
38:h:156:LYS:C	38:h:159:VAL:HG12	2.45	0.42
38:h:182:SER:C	38:h:214:LEU:HD21	2.44	0.42
38:h:183:VAL:HG21	38:h:217:GLN:NE2	2.34	0.42
38:h:251:LEU:HD23	38:h:256:PHE:CE1	2.55	0.42
39:i:230:TYR:C	39:i:230:TYR:CD1	2.97	0.42
39:i:239:LEU:HD13	39:i:239:LEU:O	2.20	0.42
41:l:267:LYS:HE2	41:l:271:LEU:HD11	2.01	0.42
41:l:375:PHE:CE2	41:l:394:LEU:HD11	2.55	0.42
41:l:410:PHE:HE1	41:l:432:LEU:HD22	1.84	0.42
1:2:253:C:H2'	1:2:254:U:O4'	2.19	0.42
1:2:352:C:C2	1:2:353:C:C5	3.08	0.42
1:2:366:G:H2'	1:2:367:G:H8	1.84	0.42
1:2:731:C:H2'	1:2:732:U:H6	1.85	0.42
1:2:915:G:N1	1:2:916:A:N3	2.67	0.42
1:2:1665:C:O5'	1:2:1665:C:H6	2.02	0.42
1:2:1754:U:H4'	38:h:141:ARG:HD3	2.02	0.42
8:D:75:GLU:O	8:D:79:VAL:HG13	2.19	0.42
8:D:329:LYS:CD	8:D:329:LYS:N	2.82	0.42
8:D:342:GLU:C	8:D:342:GLU:OE2	2.63	0.42
16:L:119:ARG:HD2	16:L:119:ARG:HA	1.85	0.42
18:N:360:LEU:HD12	18:N:378:MET:HE1	2.00	0.42
23:S:84:ILE:HD12	23:S:84:ILE:HA	1.95	0.42
25:U:67:LYS:HA	25:U:67:LYS:HD2	1.60	0.42
26:V:34:HIS:CD2	26:V:34:HIS:C	2.98	0.42
31:a:85:ARG:H	31:a:85:ARG:HG2	1.58	0.42
31:a:371:LEU:HD23	31:a:371:LEU:HA	1.87	0.42
38:h:83:THR:O	38:h:86:VAL:HG22	2.20	0.42
38:h:112:LEU:HD13	38:h:112:LEU:C	2.45	0.42
39:i:282:ILE:HG23	39:i:282:ILE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:915:G:C6	1:2:916:A:C5	3.08	0.42
1:2:1384:A:H2'	1:2:1385:A:C8	2.53	0.42
1:2:1502:A:H62	1:2:1561:A:H61	1.68	0.42
5:A:197:VAL:HG12	12:H:258:VAL:CG1	2.50	0.42
6:B:383:PHE:C	6:B:383:PHE:CD1	2.97	0.42
6:B:399:MET:HE2	6:B:399:MET:HA	2.02	0.42
8:D:221:LEU:O	8:D:221:LEU:HD13	2.19	0.42
8:D:314:LYS:HD2	8:D:314:LYS:HA	1.81	0.42
9:E:2:PRO:HA	9:E:70:MET:CE	2.50	0.42
21:Q:226:THR:HG23	21:Q:230:LYS:O	2.20	0.42
28:X:505:ASP:HA	28:X:508:TYR:CE2	2.54	0.42
32:b:83:LEU:O	32:b:86:LEU:HG	2.20	0.42
35:e:243:ARG:HB3	35:e:243:ARG:HH11	1.81	0.42
36:f:385:PHE:N	36:f:385:PHE:CD1	2.87	0.42
37:g:564:LEU:HD12	37:g:567:LEU:HD12	2.01	0.42
38:h:225:PHE:N	38:h:225:PHE:CD1	2.87	0.42
39:i:147:VAL:HG12	39:i:170:SER:HB3	2.01	0.42
1:2:146:U:C2	1:2:147:U:C5	3.08	0.42
1:2:1594:A:H2'	1:2:1595:A:O4'	2.19	0.42
1:2:1698:C:N4	1:2:1774:A:H61	2.18	0.42
1:2:1792:A:C2'	1:2:1793:C:H5'	2.50	0.42
2:5:14:A:C8	2:5:23:A:C5	3.08	0.42
6:B:96:ARG:HE	6:B:96:ARG:HB2	1.47	0.42
9:E:41:LYS:HA	26:V:188:ALA:HB1	2.02	0.42
9:E:53:LYS:HD2	9:E:54:LYS:O	2.19	0.42
30:Z:98:ILE:HD11	30:Z:110:PRO:CG	2.47	0.42
36:f:126:LEU:HD11	36:f:151:CYS:SG	2.60	0.42
38:h:229:HIS:NE2	38:h:261:GLU:HG3	2.34	0.42
38:h:269:THR:CG2	38:h:300:LEU:HD23	2.46	0.42
38:h:274:LYS:O	38:h:278:LEU:HG	2.19	0.42
38:h:298:PHE:CE2	38:h:310:VAL:HG21	2.55	0.42
38:h:298:PHE:HE2	38:h:310:VAL:HG21	1.84	0.42
41:l:371:GLY:O	41:l:403:PRO:HG3	2.19	0.42
41:l:457:MET:HE3	41:l:457:MET:HB3	1.88	0.42
1:2:65:G:H2'	1:2:66:C:C6	2.55	0.42
1:2:403:G:H2'	1:2:404:C:H6	1.85	0.42
1:2:762:A:H2'	1:2:763:A:O5'	2.20	0.42
1:2:920:G:H4'	1:2:1812:A:N7	2.35	0.42
2:5:23:A:C5'	2:5:24:C:H5	2.32	0.42
8:D:305:LEU:HD12	8:D:309:ASN:OD1	2.20	0.42
10:F:91:TRP:CD2	10:F:128:LYS:HD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:G:3:ARG:HD2	11:G:75:THR:HA	2.02	0.42
12:H:224:VAL:O	12:H:225:ILE:CB	2.67	0.42
19:O:93:ARG:HE	19:O:93:ARG:HB3	1.66	0.42
28:X:343:LYS:HG2	28:X:346:LYS:NZ	2.35	0.42
32:b:26:LEU:O	32:b:28:ASN:N	2.52	0.42
35:e:257:ARG:HG3	35:e:258:GLU:N	2.35	0.42
39:i:325:LEU:HD13	39:i:337:LEU:HD22	2.02	0.42
41:l:221:GLY:HA2	41:l:229:LEU:HD11	2.02	0.42
1:2:302:U:C2	1:2:303:G:C8	3.07	0.41
1:2:593:G:OP2	1:2:593:G:H8	2.02	0.41
1:2:691:A:H2'	1:2:692:A:O4'	2.20	0.41
1:2:806:C:C4	1:2:807:C:C5	3.08	0.41
1:2:817:G:O2'	1:2:818:A:H5'	2.20	0.41
1:2:1388:A:O2'	1:2:1389:A:H8	2.01	0.41
2:5:68:C:H2'	2:5:69:C:C6	2.55	0.41
2:5:72:C:C4	2:5:73:A:C8	3.08	0.41
7:C:93:ARG:CD	7:C:98:PRO:HG2	2.30	0.41
9:E:70:MET:HE2	18:N:318:ASN:HB3	2.02	0.41
12:H:429:LYS:HD2	12:H:429:LYS:HA	1.67	0.41
14:J:261:LYS:HA	14:J:296:GLU:O	2.19	0.41
25:U:46:LYS:HE2	25:U:46:LYS:HB2	1.89	0.41
25:U:95:ASN:HA	39:i:389:LYS:HG2	2.01	0.41
26:V:33:HIS:HB2	26:V:35:ARG:NE	2.19	0.41
27:W:318:LEU:HD23	27:W:318:LEU:HA	1.90	0.41
36:f:166:ASP:OD1	36:f:166:ASP:C	2.63	0.41
39:i:101:LEU:O	39:i:105:VAL:HG23	2.20	0.41
39:i:324:LYS:CD	39:i:337:LEU:HD21	2.50	0.41
41:l:251:PHE:CE1	41:l:284:TRP:HB3	2.54	0.41
41:l:305:GLY:HA3	41:l:338:PHE:CD2	2.55	0.41
1:2:916:A:C2	1:2:917:C:C2	3.08	0.41
1:2:1652:C:H5'	32:b:15:LYS:HA	2.01	0.41
1:2:1846:U:H2'	1:2:1847:C:C6	2.55	0.41
2:5:65:G:C2'	2:5:66:U:O4'	2.66	0.41
4:8:130:LYS:HB3	4:8:131:PRO:HD3	2.01	0.41
5:A:9:GLN:HG3	12:H:236:ILE:HD12	2.02	0.41
7:C:212:LEU:HD11	35:e:243:ARG:HG3	2.02	0.41
7:C:346:LYS:HB3	7:C:346:LYS:HE2	1.74	0.41
8:D:304:LEU:HD13	8:D:350:LYS:HG3	2.02	0.41
10:F:75:VAL:HG13	10:F:148:TRP:HH2	1.84	0.41
14:J:293:VAL:HG23	14:J:294:TYR:HD1	1.85	0.41
18:N:315:HIS:ND1	18:N:316:PRO:HD2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:X:364:CYS:O	28:X:368:LEU:HB2	2.20	0.41
31:a:153:LEU:HA	31:a:153:LEU:HD23	1.81	0.41
39:i:99:GLU:HG3	39:i:100:PHE:N	2.35	0.41
39:i:277:LYS:HE3	39:i:279:LYS:HD2	2.01	0.41
39:i:325:LEU:HD12	39:i:328:LEU:HD11	2.02	0.41
41:l:539:MET:SD	41:l:544:LEU:HB2	2.61	0.41
1:2:273:G:C4'	20:P:13:MET:HE2	2.49	0.41
1:2:549:U:C2	1:2:550:U:C5	3.08	0.41
1:2:1063:C:H2'	1:2:1064:G:C8	2.55	0.41
1:2:1679:G:C6	1:2:1791:G:C6	3.08	0.41
1:2:1702:G:H5'	1:2:1703:G:OP1	2.20	0.41
1:2:1739:U:H2'	1:2:1740:C:H6	1.85	0.41
2:5:45:A:H2'	2:5:46:G:H1'	2.02	0.41
5:A:139:ALA:HB3	5:A:140:GLU:OE2	2.20	0.41
7:C:257:LEU:CG	8:D:194:MET:CE	2.98	0.41
8:D:187:LEU:HD22	39:i:240:ASP:CB	2.50	0.41
11:G:105:THR:HG22	11:G:121:GLY:C	2.45	0.41
12:H:388:GLN:HE21	12:H:388:GLN:HB3	1.55	0.41
31:a:98:LEU:HA	31:a:101:ILE:HG12	2.02	0.41
36:f:127:TYR:HE2	36:f:336:TYR:CA	2.32	0.41
36:f:176:GLN:OE1	36:f:176:GLN:CA	2.68	0.41
36:f:378:LYS:HA	36:f:381:VAL:CG2	2.50	0.41
38:h:237:LEU:HD11	38:h:262:PHE:HD2	1.85	0.41
38:h:320:ASP:O	38:h:323:LYS:HG2	2.20	0.41
39:i:104:PHE:HE2	39:i:131:ILE:HG22	1.83	0.41
40:k:1:MET:HE3	40:k:1:MET:HB3	1.77	0.41
1:2:1489:C:H4'	1:2:1490:A:OP1	2.20	0.41
1:2:1706:C:O2'	1:2:1707:A:P	2.78	0.41
2:5:49:U:H4'	2:5:51:C:P	2.60	0.41
7:C:166:ILE:CD1	7:C:326:PRO:HG3	2.51	0.41
7:C:233:LYS:HB3	7:C:238:GLU:OE1	2.20	0.41
12:H:229:ASP:O	12:H:230:ARG:C	2.64	0.41
15:K:114:ARG:NH2	15:K:121:LYS:HG3	2.35	0.41
18:N:340:GLU:H	18:N:340:GLU:HG2	1.65	0.41
27:W:190:ILE:HD12	27:W:207:LYS:HG3	2.01	0.41
30:Z:58:GLN:CG	38:h:176:VAL:HG12	2.46	0.41
35:e:244:LEU:HD12	35:e:244:LEU:O	2.20	0.41
38:h:206:MET:HB3	38:h:240:TYR:OH	2.21	0.41
38:h:361:ILE:N	38:h:362:PRO:CD	2.84	0.41
40:k:18:ARG:O	40:k:21:GLN:HG3	2.20	0.41
1:2:392:A:C2	1:2:393:A:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:411:C:H2'	1:2:412:A:H8	1.86	0.41
1:2:558:A:C5	8:D:478:ILE:HD13	2.55	0.41
1:2:672:A:H2'	1:2:673:U:H6	1.85	0.41
1:2:1014:A:H2'	1:2:1015:C:C6	2.56	0.41
1:2:1692:C:H2'	1:2:1693:C:C6	2.56	0.41
1:2:1766:U:H2'	1:2:1767:G:C8	2.56	0.41
5:A:4:HIS:O	5:A:7:VAL:HG22	2.21	0.41
7:C:231:ARG:NH2	7:C:308:ARG:HE	2.19	0.41
12:H:247:ASP:HA	12:H:250:ILE:HG12	2.02	0.41
13:I:162:LEU:HD12	13:I:179:PHE:O	2.21	0.41
18:N:298:PRO:HB2	18:N:300:TYR:CE2	2.56	0.41
21:Q:243:GLN:CD	21:Q:243:GLN:H	2.28	0.41
30:Z:69:MET:SD	30:Z:81:ILE:HD11	2.59	0.41
36:f:308:ALA:HB3	36:f:313:LEU:HD11	2.03	0.41
37:g:621:MET:SD	37:g:653:MET:HB2	2.60	0.41
38:h:89:LEU:HB3	38:h:112:LEU:HD23	2.01	0.41
38:h:110:TRP:HH2	38:h:153:GLN:HB3	1.84	0.41
38:h:194:LEU:HD13	38:h:194:LEU:O	2.21	0.41
41:l:405:PRO:HB2	41:l:410:PHE:HE2	1.85	0.41
1:2:53:U:H2'	1:2:54:G:H8	1.84	0.41
1:2:377:U:H2'	1:2:378:G:H8	1.84	0.41
1:2:491:G:H2'	1:2:492:G:N7	2.34	0.41
1:2:599:A:H2'	1:2:600:A:H8	1.85	0.41
1:2:946:G:C6	1:2:1492:A:C6	3.08	0.41
1:2:1089:C:H2'	1:2:1090:U:C6	2.56	0.41
1:2:1469:G:OP1	29:Y:77:LYS:HE2	2.21	0.41
1:2:1768:A:H2'	1:2:1769:C:C5'	2.46	0.41
1:2:1770:G:H3'	1:2:1771:C:C5'	2.50	0.41
2:5:9:A:C2	2:5:46:G:H5"	2.56	0.41
36:f:393:ASP:OD2	36:f:396:SER:HB3	2.20	0.41
38:h:204:GLU:OE1	38:h:208:LEU:CD2	2.67	0.41
39:i:402:ASP:HA	39:i:405:ARG:NE	2.15	0.41
41:l:529:TRP:HE1	41:l:557:VAL:CG2	2.33	0.41
1:2:1013:A:H2	1:2:1482:U:H1'	1.86	0.41
1:2:1742:C:H3'	1:2:1743:A:C8	2.56	0.41
2:5:29:C:H6	2:5:29:C:H2'	1.69	0.41
8:D:308:LEU:HD22	8:D:344:ARG:HD3	2.01	0.41
9:E:22:LEU:CD2	9:E:88:LEU:HD21	2.50	0.41
14:J:225:LEU:HD12	14:J:228:LEU:HD13	2.03	0.41
28:X:467:ASN:HB3	28:X:497:LYS:HD3	2.02	0.41
34:d:104:LYS:CG	34:d:105:PRO:HD2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:192:LEU:H	36:f:192:LEU:HD12	1.86	0.41
36:f:227:LEU:HB3	36:f:231:GLU:OE1	2.21	0.41
36:f:353:GLU:HG2	36:f:367:LYS:O	2.20	0.41
38:h:86:VAL:HA	38:h:112:LEU:HD22	2.03	0.41
38:h:226:ARG:O	38:h:229:HIS:HB3	2.19	0.41
38:h:343:LYS:HD3	38:h:343:LYS:HA	1.57	0.41
39:i:174:LEU:O	39:i:178:GLU:HG2	2.21	0.41
39:i:180:GLU:HG3	39:i:181:ARG:N	2.35	0.41
1:2:221:C:C2’	1:2:222:G:H5’	2.50	0.41
1:2:289:A:O2’	1:2:290:C:H5’	2.21	0.41
1:2:687:G:H2’	1:2:688:U:C6	2.56	0.41
1:2:923:C:H5”	32:b:14:ARG:NH2	2.34	0.41
1:2:1507:A:H2’	1:2:1508:A:C8	2.55	0.41
1:2:1728:U:H4’	38:h:153:GLN:HE22	1.86	0.41
1:2:1784:G:N3	1:2:1784:G:H2’	2.34	0.41
2:5:24:C:H6	2:5:24:C:O5’	2.02	0.41
6:B:482:VAL:HG12	6:B:484:GLY:H	1.86	0.41
6:B:529:ARG:HG2	6:B:530:TYR:CD1	2.55	0.41
7:C:169:SER:O	7:C:173:GLU:HB3	2.21	0.41
7:C:212:LEU:HD22	35:e:248:TYR:HE1	1.85	0.41
7:C:320:GLU:O	7:C:328:ALA:HA	2.21	0.41
12:H:224:VAL:HG12	12:H:225:ILE:N	2.30	0.41
12:H:427:TRP:CZ3	12:H:429:LYS:HD2	2.55	0.41
18:N:302:LEU:HD23	18:N:302:LEU:HA	1.87	0.41
23:S:27:ILE:HD12	23:S:47:MET:SD	2.61	0.41
25:U:79:PRO:HG3	40:k:11:GLY:HA2	2.02	0.41
31:a:167:MET:HE2	31:a:167:MET:HB2	1.88	0.41
38:h:296:LYS:HE3	38:h:333:LEU:CG	2.44	0.41
39:i:125:ASP:HA	39:i:128:LEU:HD23	2.02	0.41
1:2:17:G:H5”	8:D:481:ARG:HD3	2.02	0.41
1:2:178:U:O2’	1:2:179:G:H5’	2.21	0.41
1:2:547:U:H2’	1:2:548:G:H8	1.85	0.41
1:2:689:G:C6	3:6:34:A:C4	3.09	0.41
1:2:701:U:O2	1:2:701:U:H2’	2.21	0.41
1:2:759:G:H2’	1:2:760:C:H6	1.86	0.41
1:2:1319:A:H4’	1:2:1320:A:OP1	2.21	0.41
1:2:1726:U:C4	1:2:1744:C:N4	2.83	0.41
1:2:1752:U:C2	1:2:1753:U:C5	3.09	0.41
2:5:5:G:H2’	2:5:6:G:C8	2.56	0.41
2:5:20:U:H5	4:8:128:ASP:OD1	2.04	0.41
2:5:71:G:C4	2:5:72:C:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8:146:LYS:HA	4:8:149:VAL:HG22	2.03	0.41
5:A:50:LEU:HD13	5:A:188:PHE:HD1	1.85	0.41
5:A:141:ARG:HD3	5:A:141:ARG:N	2.36	0.41
6:B:187:VAL:O	6:B:191:ILE:HG12	2.21	0.41
6:B:393:ILE:HD13	28:X:359:GLY:HA3	2.03	0.41
6:B:474:ILE:O	6:B:478:ILE:HG12	2.21	0.41
7:C:325:THR:N	7:C:326:PRO:HA	2.35	0.41
8:D:160:GLU:OE2	8:D:160:GLU:HA	2.18	0.41
8:D:361:ASP:O	8:D:388:CYS:HA	2.21	0.41
12:H:269:ASN:HA	12:H:272:ARG:HH11	1.86	0.41
13:I:170:HIS:ND1	13:I:171:VAL:HG22	2.36	0.41
14:J:200:LEU:O	14:J:201:LEU:HD23	2.21	0.41
19:O:91:MET:HB3	34:d:100:LEU:CD1	2.51	0.41
21:Q:188:THR:HG22	21:Q:194:VAL:CG1	2.51	0.41
23:S:81:ILE:C	23:S:81:ILE:HD12	2.46	0.41
27:W:105:LEU:HD23	27:W:105:LEU:HA	1.87	0.41
27:W:125:THR:CG2	27:W:143:PHE:HA	2.51	0.41
27:W:293:ILE:HD13	27:W:324:MET:HE1	2.02	0.41
30:Z:97:GLY:O	30:Z:110:PRO:HB3	2.21	0.41
35:e:151:ARG:NH1	35:e:151:ARG:CG	2.80	0.41
36:f:111:ILE:HD11	36:f:116:THR:HG22	1.99	0.41
36:f:161:PHE:C	36:f:162:ARG:HG3	2.46	0.41
36:f:273:TYR:CD1	36:f:286:MET:HE3	2.56	0.41
36:f:280:GLU:H	36:f:280:GLU:CD	2.27	0.41
37:g:580:ASP:HA	37:g:583:MET:HG3	2.03	0.41
38:h:308:ALA:HA	38:h:311:ILE:CG1	2.50	0.41
40:k:4:MET:O	40:k:8:SER:HB3	2.21	0.41
1:2:267:G:O2'	1:2:268:U:H5'	2.21	0.41
1:2:700:A:C5	1:2:701:U:C5	3.09	0.41
1:2:849:G:C2'	1:2:850:C:H5'	2.51	0.41
1:2:1713:C:O2	1:2:1713:C:H2'	2.21	0.41
2:5:39:A:C2'	2:5:40:C:H5'	2.51	0.41
4:8:238:ALA:C	4:8:239:ASP:OD1	2.64	0.41
7:C:119:THR:HB	7:C:121:PRO:HD2	2.02	0.41
7:C:212:LEU:HD23	7:C:212:LEU:HA	1.83	0.41
7:C:260:LEU:O	7:C:264:LYS:HB3	2.21	0.41
7:C:312:ILE:CD1	35:e:252:PHE:HD1	2.30	0.41
8:D:156:ASP:OD1	8:D:156:ASP:O	2.39	0.41
8:D:242:LEU:HD12	39:i:205:ILE:HD11	2.03	0.41
9:E:28:LYS:HD2	9:E:28:LYS:C	2.46	0.41
11:G:49:PHE:HA	11:G:61:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:135:SER:OG	27:W:137:LYS:HG2	2.21	0.41
36:f:266:LYS:O	36:f:270:ILE:HD12	2.21	0.41
38:h:122:ILE:O	38:h:125:LEU:HB3	2.21	0.41
38:h:343:LYS:HZ1	38:h:387:ALA:HB1	1.82	0.41
39:i:108:MET:CE	39:i:112:VAL:HG23	2.50	0.41
39:i:177:MET:HG2	39:i:177:MET:H	1.62	0.41
41:l:238:ILE:HD13	41:l:272:THR:OG1	2.20	0.41
41:l:529:TRP:CZ2	41:l:557:VAL:C	2.99	0.41
1:2:8:U:O2	1:2:8:U:H2'	2.21	0.40
1:2:344:A:H2'	1:2:345:G:O4'	2.21	0.40
1:2:558:A:C6	8:D:478:ILE:HD13	2.56	0.40
1:2:732:U:H2'	1:2:733:C:C6	2.55	0.40
1:2:921:G:N2	32:b:13:GLY:O	2.53	0.40
1:2:1576:C:H2'	1:2:1577:U:C6	2.55	0.40
4:8:122:LEU:HD23	4:8:136:ILE:HD13	2.03	0.40
6:B:427:LEU:HD23	6:B:427:LEU:HA	1.79	0.40
7:C:63:LEU:HD13	8:D:466:LEU:CD2	2.51	0.40
7:C:262:LEU:O	7:C:265:ARG:HG3	2.21	0.40
8:D:116:GLU:O	8:D:117:ASP:C	2.64	0.40
8:D:260:ILE:O	8:D:260:ILE:HG22	2.20	0.40
8:D:261:GLU:CG	8:D:261:GLU:O	2.69	0.40
9:E:33:LYS:N	9:E:33:LYS:HD2	2.37	0.40
11:G:39:ILE:HD11	11:G:109:ILE:HG22	2.02	0.40
15:K:42:PRO:HD3	15:K:48:ALA:O	2.20	0.40
25:U:4:MET:HE1	25:U:15:LEU:HG	2.03	0.40
25:U:67:LYS:HB3	25:U:69:VAL:HG23	2.02	0.40
30:Z:58:GLN:HB2	30:Z:63:TRP:CZ3	2.55	0.40
35:e:176:ALA:O	35:e:256:ASP:O	2.39	0.40
38:h:109:LEU:HD22	38:h:132:LEU:HD13	2.02	0.40
38:h:342:LEU:HD11	38:h:353:VAL:HG12	2.03	0.40
38:h:385:ASN:HB2	38:h:388:LEU:HD12	2.01	0.40
39:i:100:PHE:HD1	39:i:173:VAL:HG11	1.86	0.40
39:i:325:LEU:CD1	39:i:337:LEU:HD22	2.51	0.40
41:l:529:TRP:HZ2	41:l:557:VAL:HB	1.85	0.40
1:2:304:C:O2'	1:2:305:U:H5'	2.21	0.40
1:2:1567:G:N2	1:2:1594:A:C2	2.87	0.40
1:2:1821:U:H2'	1:2:1822:A:C8	2.57	0.40
2:5:38:G:H2'	2:5:39:A:O4'	2.21	0.40
6:B:288:ARG:HB3	31:a:213:LEU:HG	2.03	0.40
8:D:306:GLU:N	8:D:306:GLU:OE1	2.54	0.40
15:K:123:LYS:HA	15:K:123:LYS:HD3	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:33:LEU:HD21	22:R:79:PHE:CD1	2.55	0.40
27:W:131:LEU:HA	27:W:134:LEU:CD2	2.52	0.40
32:b:83:LEU:HA	32:b:86:LEU:HD23	2.03	0.40
36:f:347:VAL:O	36:f:347:VAL:HG12	2.21	0.40
38:h:239:LYS:O	38:h:243:LYS:HG3	2.21	0.40
1:2:609:U:H3	1:2:625:G:H22	1.69	0.40
1:2:733:C:C2	1:2:734:U:C5	3.09	0.40
1:2:1846:U:H4'	23:S:79:ARG:CZ	2.51	0.40
6:B:411:TYR:CE2	6:B:412:ARG:HD3	2.56	0.40
6:B:481:ARG:HD3	31:a:154:GLU:CD	2.46	0.40
7:C:252:MET:C	7:C:252:MET:SD	3.04	0.40
7:C:341:HIS:CE1	7:C:348:LEU:HD22	2.57	0.40
8:D:437:THR:CG2	8:D:493:ALA:HB2	2.51	0.40
12:H:298:ARG:HH21	12:H:300:VAL:HG21	1.86	0.40
19:O:97:GLU:OE2	19:O:97:GLU:HA	2.20	0.40
38:h:209:LEU:HD11	38:h:216:LEU:CD2	2.50	0.40
38:h:361:ILE:CG2	38:h:362:PRO:CD	2.96	0.40
39:i:289:ASP:OD1	39:i:290:PRO:HD2	2.21	0.40
41:l:424:ASP:O	41:l:428:GLU:HG2	2.22	0.40
1:2:476:C:C5	19:O:88:MET:HG2	2.57	0.40
1:2:611:G:H2'	1:2:612:U:H6	1.85	0.40
1:2:959:A:C4	2:5:35:C:H4'	2.57	0.40
1:2:1669:C:O2	1:2:1670:A:C8	2.74	0.40
1:2:1801:A:P	1:2:1801:A:H8	2.45	0.40
1:2:1822:A:H2'	1:2:1823:G:H8	1.86	0.40
6:B:67:LYS:HD2	28:X:385:MET:HE3	2.04	0.40
7:C:221:ARG:CD	35:e:250:GLU:OE1	2.69	0.40
7:C:253:LYS:HD3	7:C:290:TYR:OH	2.21	0.40
8:D:437:THR:HG22	8:D:493:ALA:HB2	2.03	0.40
10:F:58:LYS:HZ2	10:F:60:ILE:HG12	1.85	0.40
10:F:91:TRP:CD1	10:F:128:LYS:HZ3	2.38	0.40
12:H:241:ILE:HD12	12:H:241:ILE:HA	1.87	0.40
12:H:269:ASN:HA	12:H:272:ARG:NH1	2.36	0.40
14:J:229:LYS:HA	14:J:229:LYS:HD3	1.87	0.40
25:U:92:LEU:HB3	25:U:97:ILE:HG22	2.02	0.40
27:W:101:ARG:HB3	27:W:170:TRP:HZ3	1.86	0.40
36:f:199:TYR:HB2	36:f:270:ILE:HG23	2.02	0.40
36:f:278:THR:HB	36:f:280:GLU:OE2	2.22	0.40
38:h:168:LYS:HE2	38:h:204:GLU:HG2	2.03	0.40
41:l:442:VAL:HG22	41:l:475:LEU:HD23	2.04	0.40
41:l:457:MET:HE3	41:l:460:GLU:OE1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1412:C:H2'	1:2:1413:A:H8	1.87	0.40
1:2:1420:A:C2	1:2:1444:G:C4	3.09	0.40
1:2:1683:U:H2'	1:2:1684:G:O4'	2.22	0.40
1:2:1701:C:C3'	1:2:1702:G:H8	2.34	0.40
1:2:1802:A:H1'	1:2:1803:G:OP1	2.21	0.40
2:5:42:U:H2'	2:5:43:G:C8	2.56	0.40
5:A:9:GLN:CG	12:H:236:ILE:HG13	2.52	0.40
7:C:37:ILE:N	7:C:37:ILE:CD1	2.85	0.40
7:C:257:LEU:CD1	8:D:194:MET:HE2	2.50	0.40
8:D:196:LYS:HA	8:D:196:LYS:HD3	1.67	0.40
10:F:98:LYS:O	10:F:101:ILE:HG22	2.22	0.40
26:V:181:LEU:CD1	26:V:185:ILE:HD11	2.51	0.40
32:b:61:LEU:O	32:b:64:CYS:HB3	2.21	0.40
36:f:120:LYS:HG2	36:f:340:LEU:CD1	2.51	0.40
36:f:369:ASP:CB	36:f:370:PRO:HD3	2.23	0.40
36:f:376:VAL:HA	36:f:380:MET:HE1	2.02	0.40
38:h:109:LEU:HG	38:h:113:ILE:HD11	2.03	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	
4	8	184/520 (35%)	154 (84%)	29 (16%)	1 (0%)	24	52
5	A	202/212 (95%)	193 (96%)	8 (4%)	1 (0%)	24	52
6	B	457/554 (82%)	428 (94%)	28 (6%)	1 (0%)	43	70
7	C	329/362 (91%)	324 (98%)	5 (2%)	0	100	100
8	D	413/501 (82%)	393 (95%)	18 (4%)	2 (0%)	24	52
9	E	99/138 (72%)	98 (99%)	1 (1%)	0	100	100
10	F	146/157 (93%)	136 (93%)	9 (6%)	1 (1%)	18	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	G	126/129 (98%)	124 (98%)	2 (2%)	0	100	100
12	H	208/383 (54%)	197 (95%)	10 (5%)	1 (0%)	24	52
13	I	111/228 (49%)	107 (96%)	4 (4%)	0	100	100
14	J	125/304 (41%)	120 (96%)	5 (4%)	0	100	100
15	K	122/125 (98%)	116 (95%)	6 (5%)	0	100	100
16	L	108/154 (70%)	103 (95%)	5 (5%)	0	100	100
17	M	99/155 (64%)	98 (99%)	1 (1%)	0	100	100
18	N	114/414 (28%)	113 (99%)	1 (1%)	0	100	100
19	O	108/136 (79%)	107 (99%)	1 (1%)	0	100	100
20	P	89/110 (81%)	88 (99%)	1 (1%)	0	100	100
21	Q	88/237 (37%)	87 (99%)	1 (1%)	0	100	100
22	R	162/212 (76%)	155 (96%)	7 (4%)	0	100	100
23	S	73/100 (73%)	73 (100%)	0	0	100	100
24	T	48/94 (51%)	44 (92%)	4 (8%)	0	100	100
25	U	125/192 (65%)	122 (98%)	3 (2%)	0	100	100
26	V	162/193 (84%)	158 (98%)	4 (2%)	0	100	100
27	W	376/483 (78%)	369 (98%)	7 (2%)	0	100	100
28	X	202/496 (41%)	191 (95%)	8 (4%)	3 (2%)	8	28
29	Y	96/102 (94%)	95 (99%)	1 (1%)	0	100	100
30	Z	78/153 (51%)	74 (95%)	4 (5%)	0	100	100
31	a	311/424 (73%)	297 (96%)	14 (4%)	0	100	100
32	b	75/80 (94%)	65 (87%)	7 (9%)	3 (4%)	2	11
33	c	24/128 (19%)	24 (100%)	0	0	100	100
34	d	76/110 (69%)	75 (99%)	1 (1%)	0	100	100
35	e	244/383 (64%)	232 (95%)	11 (4%)	1 (0%)	30	57
36	f	375/410 (92%)	357 (95%)	18 (5%)	0	100	100
37	g	101/668 (15%)	96 (95%)	5 (5%)	0	100	100
38	h	308/384 (80%)	302 (98%)	6 (2%)	0	100	100
39	i	332/725 (46%)	326 (98%)	6 (2%)	0	100	100
40	k	26/153 (17%)	22 (85%)	4 (15%)	0	100	100
41	l	440/576 (76%)	432 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	6762/10885 (62%)	6495 (96%)	253 (4%)	14 (0%)	44 70

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	H	225	ILE
32	b	27	GLY
32	b	87	THR
4	8	266	ILE
32	b	18	ASN
35	e	180	TYR
28	X	461	VAL
5	A	113	PRO
6	B	409	ILE
8	D	352	ARG
28	X	428	ILE
28	X	458	PRO
8	D	260	ILE
10	F	2	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	8	164/461 (36%)	160 (98%)	4 (2%)	43 66
5	A	177/182 (97%)	173 (98%)	4 (2%)	44 66
6	B	421/492 (86%)	409 (97%)	12 (3%)	37 62
7	C	312/343 (91%)	305 (98%)	7 (2%)	45 67
8	D	370/444 (83%)	364 (98%)	6 (2%)	55 72
9	E	90/126 (71%)	87 (97%)	3 (3%)	33 60
10	F	124/124 (100%)	123 (99%)	1 (1%)	73 79
11	G	112/113 (99%)	110 (98%)	2 (2%)	51 70
12	H	175/320 (55%)	168 (96%)	7 (4%)	28 56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	I	104/197 (53%)	101 (97%)	3 (3%)	37	62
14	J	108/256 (42%)	101 (94%)	7 (6%)	15	40
15	K	106/107 (99%)	105 (99%)	1 (1%)	70	78
16	L	93/128 (73%)	89 (96%)	4 (4%)	26	53
17	M	90/137 (66%)	88 (98%)	2 (2%)	45	67
18	N	107/362 (30%)	107 (100%)	0	100	100
19	O	93/117 (80%)	92 (99%)	1 (1%)	65	76
20	P	78/95 (82%)	77 (99%)	1 (1%)	61	74
21	Q	75/203 (37%)	73 (97%)	2 (3%)	39	64
22	R	141/180 (78%)	134 (95%)	7 (5%)	22	49
23	S	68/90 (76%)	67 (98%)	1 (2%)	57	73
24	T	44/79 (56%)	43 (98%)	1 (2%)	44	66
25	U	109/170 (64%)	108 (99%)	1 (1%)	70	78
26	V	147/173 (85%)	143 (97%)	4 (3%)	39	64
27	W	328/410 (80%)	321 (98%)	7 (2%)	47	68
28	X	174/395 (44%)	170 (98%)	4 (2%)	44	66
29	Y	84/86 (98%)	83 (99%)	1 (1%)	63	75
30	Z	65/119 (55%)	64 (98%)	1 (2%)	57	73
31	a	252/375 (67%)	248 (98%)	4 (2%)	55	72
32	b	68/71 (96%)	67 (98%)	1 (2%)	57	73
33	c	25/116 (22%)	25 (100%)	0	100	100
34	d	65/93 (70%)	64 (98%)	1 (2%)	57	73
35	e	226/339 (67%)	224 (99%)	2 (1%)	70	78
36	f	321/351 (92%)	312 (97%)	9 (3%)	38	63
37	g	92/597 (15%)	89 (97%)	3 (3%)	33	60
38	h	271/337 (80%)	265 (98%)	6 (2%)	45	67
39	i	297/629 (47%)	293 (99%)	4 (1%)	61	74
40	k	21/109 (19%)	20 (95%)	1 (5%)	23	50
41	l	378/492 (77%)	371 (98%)	7 (2%)	50	69
All	All	5975/9418 (63%)	5843 (98%)	132 (2%)	45	67

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	8	171	PHE
4	8	193	SER
4	8	209	LYS
4	8	247	VAL
5	A	77	ASP
5	A	119	ARG
5	A	122	LYS
5	A	140	GLU
6	B	100	THR
6	B	172	LEU
6	B	296	LEU
6	B	312	HIS
6	B	320	LEU
6	B	327	LYS
6	B	333	PHE
6	B	363	LEU
6	B	419	GLU
6	B	436	LEU
6	B	445	VAL
6	B	510	THR
7	C	110	ILE
7	C	148	HIS
7	C	184	LEU
7	C	224	MET
7	C	234	LYS
7	C	256	LEU
7	C	261	PHE
8	D	314	LYS
8	D	324	HIS
8	D	344	ARG
8	D	348	THR
8	D	503	VAL
8	D	517	LEU
9	E	13	ILE
9	E	36	VAL
9	E	54	LYS
10	F	146	ARG
11	G	68	VAL
11	G	79	ASP
12	H	341	MET
12	H	354	GLU
12	H	358	LEU
12	H	381	LEU

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Mol	Chain	Res	Type
12	H	388	GLN
12	H	428	VAL
12	H	429	LYS
13	I	138	ASP
13	I	194	SER
13	I	226	MET
14	J	189	LEU
14	J	192	ASN
14	J	205	THR
14	J	210	THR
14	J	240	ASP
14	J	262	VAL
14	J	266	THR
15	K	89	ASP
16	L	33	ARG
16	L	47	THR
16	L	104	SER
16	L	111	GLU
17	M	99	LEU
17	M	157	VAL
19	O	75	ARG
20	P	61	ARG
21	Q	226	THR
21	Q	227	MET
22	R	22	MET
22	R	35	ILE
22	R	143	ASP
22	R	148	LYS
22	R	151	ASN
22	R	189	GLU
22	R	207	LYS
23	S	48	GLN
24	T	68	SER
25	U	63	HIS
26	V	33	HIS
26	V	116	LEU
26	V	153	THR
26	V	173	SER
27	W	273	ASP
27	W	279	GLU
27	W	316	SER
27	W	339	LEU

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Mol	Chain	Res	Type
27	W	400	VAL
27	W	419	VAL
27	W	455	GLU
28	X	335	VAL
28	X	348	MET
28	X	352	ILE
28	X	394	MET
29	Y	7	LYS
30	Z	84	ILE
31	a	107	GLN
31	a	152	GLU
31	a	183	ILE
31	a	217	LEU
32	b	65	MET
34	d	53	VAL
35	e	172	LYS
35	e	281	ILE
36	f	44	SER
36	f	105	LEU
36	f	148	THR
36	f	165	THR
36	f	210	VAL
36	f	256	VAL
36	f	267	ILE
36	f	283	ILE
36	f	346	THR
37	g	583	MET
37	g	610	ILE
37	g	633	LEU
38	h	113	ILE
38	h	150	LEU
38	h	220	THR
38	h	260	MET
38	h	273	TRP
38	h	374	ARG
39	i	130	LEU
39	i	158	PHE
39	i	204	GLU
39	i	443	GLU
40	k	13	ILE
41	l	244	LEU
41	l	380	HIS

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Mol	Chain	Res	Type
41	l	436	ARG
41	l	469	LYS
41	l	504	ASP
41	l	549	ILE
41	l	566	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	9	GLN
5	A	71	ASN
6	B	64	HIS
6	B	244	ASN
6	B	318	ASN
6	B	516	ASN
6	B	517	GLN
7	C	135	ASN
7	C	255	ASN
7	C	349	ASN
8	D	168	ASN
10	F	37	HIS
11	G	15	ASN
11	G	50	GLN
17	M	74	HIS
22	R	101	ASN
22	R	208	HIS
25	U	107	ASN
26	V	171	GLN
27	W	360	ASN
27	W	426	ASN
29	Y	28	HIS
30	Z	58	GLN
32	b	42	ASN
32	b	78	ASN
36	f	180	HIS
37	g	573	HIS
38	h	115	ASN
38	h	143	HIS
38	h	177	HIS
38	h	285	GLN
38	h	335	ASN
38	h	344	HIS

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Mol	Chain	Res	Type
39	i	394	HIS
39	i	412	GLN
40	k	21	GLN
41	l	501	ASN
41	l	545	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1592/1601 (99%)	275 (17%)	19 (1%)
2	5	76/77 (98%)	39 (51%)	6 (7%)
3	6	4/5 (80%)	4 (100%)	0
All	All	1672/1683 (99%)	318 (19%)	25 (1%)

All (318) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	6	A
1	2	12	A
1	2	17	G
1	2	30	G
1	2	37	A
1	2	38	G
1	2	39	G
1	2	40	A
1	2	47	G
1	2	55	C
1	2	56	U
1	2	59	A
1	2	76	G
1	2	79	G
1	2	80	U
1	2	82	C
1	2	83	U
1	2	150	A
1	2	151	A
1	2	152	G
1	2	153	A
1	2	154	G
1	2	156	U
1	2	157	G

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Mol	Chain	Res	Type
1	2	161	A
1	2	162	C
1	2	163	A
1	2	184	A
1	2	185	G
1	2	195	U
1	2	203	A
1	2	206	G
1	2	210	G
1	2	214	U
1	2	215	A
1	2	224	A
1	2	225	G
1	2	226	A
1	2	233	G
1	2	237	G
1	2	245	U
1	2	264	U
1	2	266	G
1	2	270	G
1	2	285	G
1	2	286	C
1	2	298	A
1	2	308	G
1	2	317	U
1	2	318	U
1	2	347	C
1	2	351	G
1	2	363	A
1	2	364	C
1	2	365	G
1	2	370	G
1	2	371	C
1	2	373	G
1	2	386	U
1	2	391	C
1	2	392	A
1	2	401	A
1	2	403	G
1	2	409	U
1	2	416	A
1	2	420	U

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Mol	Chain	Res	Type
1	2	421	G
1	2	425	G
1	2	430	A
1	2	432	G
1	2	440	A
1	2	441	U
1	2	442	U
1	2	443	C
1	2	444	C
1	2	450	U
1	2	451	A
1	2	469	G
1	2	470	C
1	2	471	G
1	2	479	G
1	2	480	A
1	2	492	G
1	2	494	A
1	2	495	G
1	2	507	A
1	2	509	C
1	2	516	C
1	2	522	G
1	2	525	G7M
1	2	528	G
1	2	530	A
1	2	531	A
1	2	545	A
1	2	557	A
1	2	560	G
1	2	566	G
1	2	571	A
1	2	572	A
1	2	573	G
1	2	574	G
1	2	575	G
1	2	594	G
1	2	617	A
1	2	649	U
1	2	661	A
1	2	684	G
1	2	698	G

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Mol	Chain	Res	Type
1	2	699	G
1	2	717	A
1	2	718	A
1	2	720	A
1	2	744	U
1	2	745	A
1	2	751	G
1	2	762	A
1	2	763	A
1	2	773	A
1	2	789	U
1	2	790	A
1	2	811	A
1	2	813	C
1	2	836	A
1	2	837	U
1	2	838	U
1	2	839	C
1	2	840	U
1	2	846	G
1	2	865	A
1	2	866	A
1	2	893	A
1	2	907	A
1	2	919	G
1	2	920	G
1	2	921	G
1	2	926	G
1	2	927	C
1	2	928	A
1	2	935	G
1	2	953	U
1	2	962	A
1	2	964	G
1	2	968	A
1	2	969	G
1	2	970	A
1	2	986	G
1	2	998	A
1	2	999	G
1	2	1002	A
1	2	1007	A

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Mol	Chain	Res	Type
1	2	1029	C
1	2	1030	U
1	2	1031	U
1	2	1037	C
1	2	1057	U
1	2	1079	U
1	2	1081	G
1	2	1086	G
1	2	1087	U
1	2	1093	A
1	2	1112	U
1	2	1116	G
1	2	1117	U
1	2	1118	U
1	2	1122	C
1	2	1123	A
1	2	1125	A
1	2	1127	A
1	2	1135	A
1	2	1136	A
1	2	1137	G
1	2	1140	G
1	2	1141	A
1	2	1143	A
1	2	1316	A
1	2	1320	A
1	2	1321	A
1	2	1379	C
1	2	1380	U
1	2	1386	A
1	2	1387	C
1	2	1388	A
1	2	1389	A
1	2	1391	C
1	2	1392	A
1	2	1395	A
1	2	1402	G
1	2	1407	G
1	2	1420	A
1	2	1422	U
1	2	1431	U
1	2	1432	A

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Mol	Chain	Res	Type
1	2	1450	G
1	2	1459	A
1	2	1460	A
1	2	1468	U
1	2	1475	U
1	2	1476	A
1	2	1490	A
1	2	1491	C
1	2	1492	A
1	2	1494	G
1	2	1501	A
1	2	1504	G
1	2	1511	A
1	2	1515	U
1	2	1516	G
1	2	1521	G
1	2	1523	A
1	2	1541	G
1	2	1542	A
1	2	1543	A
1	2	1561	A
1	2	1564	U
1	2	1581	A
1	2	1582	C
1	2	1600	G
1	2	1602	A
1	2	1615	G
1	2	1626	U
1	2	1632	G
1	2	1647	G
1	2	1659	C
1	2	1694	G
1	2	1702	G
1	2	1703	G
1	2	1706	C
1	2	1707	A
1	2	1714	A
1	2	1721	A
1	2	1722	C
1	2	1723	U
1	2	1724	U
1	2	1725	C

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Mol	Chain	Res	Type
1	2	1727	G
1	2	1728	U
1	2	1729	G
1	2	1731	A
1	2	1732	A
1	2	1735	C
1	2	1736	U
1	2	1738	G
1	2	1740	C
1	2	1743	A
1	2	1744	C
1	2	1745	A
1	2	1746	A
1	2	1747	A
1	2	1750	C
1	2	1751	U
1	2	1753	U
1	2	1760	U
1	2	1762	U
1	2	1763	U
1	2	1764	A
1	2	1765	U
1	2	1766	U
1	2	1768	A
1	2	1769	C
1	2	1770	G
1	2	1771	C
1	2	1772	A
1	2	1774	A
1	2	1784	G
1	2	1801	A
1	2	1802	A
1	2	1803	G
1	2	1812	A
1	2	1826	G
1	2	1828	MA6
1	2	1829	C
1	2	1838	G
1	2	1839	G
1	2	1846	U
1	2	1848	C
2	5	5	G

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Mol	Chain	Res	Type
2	5	6	G
2	5	7	G
2	5	8	U
2	5	9	A
2	5	10	G
2	5	11	A
2	5	12	G
2	5	15	A
2	5	17	U
2	5	18	G
2	5	19	G
2	5	20	U
2	5	21	C
2	5	22	A
2	5	23	A
2	5	24	C
2	5	25	U
2	5	27	A
2	5	28	U
2	5	29	C
2	5	30	A
2	5	31	G
2	5	32	G
2	5	33	C
2	5	34	U
2	5	41	C
2	5	42	U
2	5	44	A
2	5	45	A
2	5	46	G
2	5	47	A
2	5	48	U
2	5	49	U
2	5	50	A
2	5	52	A
2	5	54	G
2	5	65	G
2	5	66	U
3	6	35	U
3	6	36	A
3	6	37	U
3	6	38	G

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	79	G
1	2	225	G
1	2	317	U
1	2	450	U
1	2	491	G
1	2	493	A
1	2	571	A
1	2	998	A
1	2	1117	U
1	2	1319	A
1	2	1430	A
1	2	1600	G
1	2	1701	C
1	2	1705	C
1	2	1706	C
1	2	1726	U
1	2	1769	C
1	2	1802	A
1	2	1845	A
2	5	7	G
2	5	9	A
2	5	28	U
2	5	29	C
2	5	32	G
2	5	41	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	MA6	2	1827	1	23,26,27	0.27	0	34,38,41	0.75	1 (2%)
1	G7M	2	525	1	23,26,27	0.70	1 (4%)	35,39,42	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	2MG	2	1825	1	23,26,27	0.50	0	32,38,41	0.52	0
1	UR3	2	1807	1	19,22,23	0.30	0	26,32,35	0.67	0
1	4OC	2	1664	1	20,23,24	0.35	0	26,32,35	0.44	0
1	MA6	2	1828	1	23,26,27	0.29	0	34,38,41	0.68	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	2	1827	1	-	0/11/29/30	0/3/3/3
1	G7M	2	525	1	-	2/7/25/26	0/3/3/3
1	2MG	2	1825	1	-	0/9/27/28	0/3/3/3
1	UR3	2	1807	1	-	0/7/25/26	0/2/2/2
1	4OC	2	1664	1	-	0/9/29/30	0/2/2/2
1	MA6	2	1828	1	-	2/11/29/30	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	525	G7M	C8-N7	2.45	1.37	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2	1827	MA6	C2-N1-C6	2.85	118.47	111.75
1	2	1828	MA6	C2-N1-C6	2.78	118.32	111.75

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	525	G7M	C3'-C4'-C5'-O5'
1	2	525	G7M	O4'-C4'-C5'-O5'
1	2	1828	MA6	C4'-C5'-O5'-P
1	2	1828	MA6	C3'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	1827	MA6	1	0
1	2	1825	2MG	1	0
1	2	1828	MA6	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
42	ATP	W	501	-	29,33,33	0.49	0	44,52,52	0.54	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
42	ATP	W	501	-	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

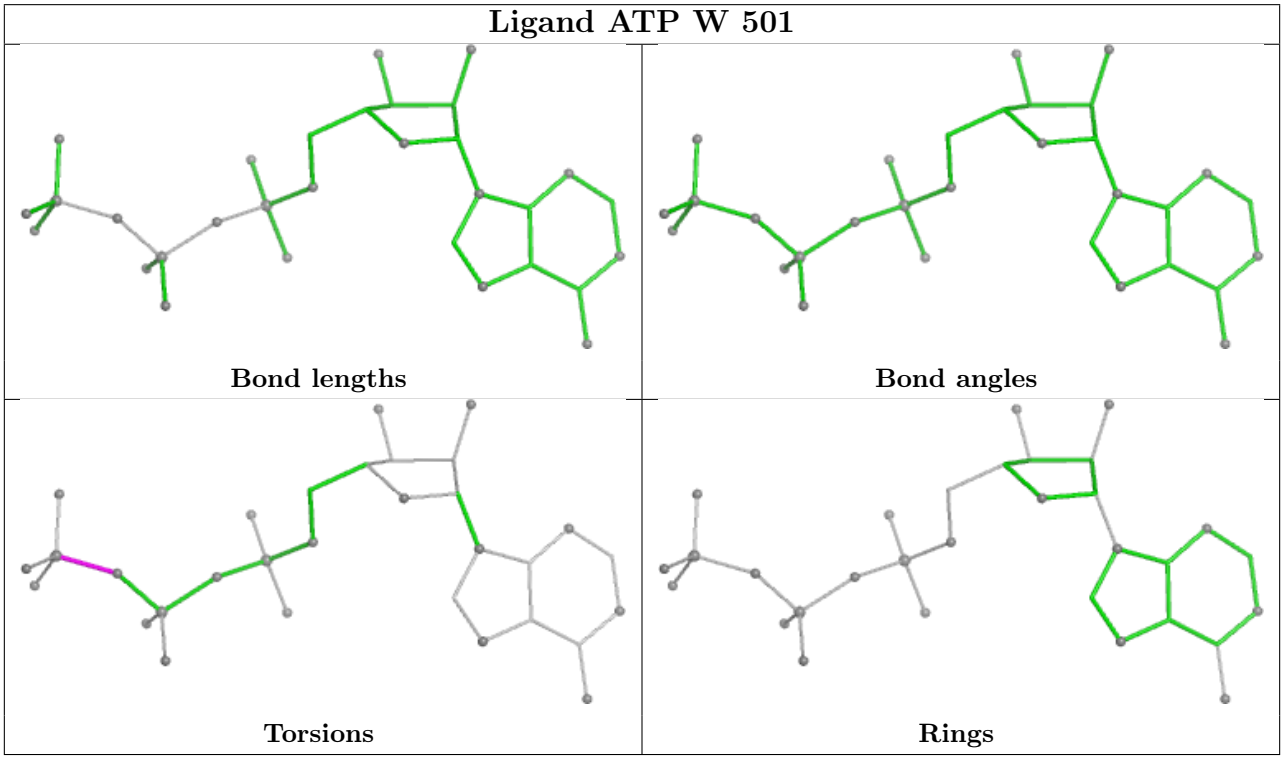
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
42	W	501	ATP	PB-O3B-PG-O1G
42	W	501	ATP	PB-O3B-PG-O2G
42	W	501	ATP	PB-O3B-PG-O3G

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	7
4	8	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1147:A	O3'	1164:U	P	23.26
1	2	1330:A	O3'	1335:U	P	18.29
1	2	1167:U	O3'	1314:A	P	18.25
1	2	83:U	O3'	129:A	P	17.64
1	2	137:A	O3'	142:U	P	13.88
1	2	1345:U	O3'	1376:A	P	13.72
1	8	158:ARG	C	159:ALA	N	5.89
1	8	249:HIS	C	250:ALA	N	3.71
1	2	1824:G	O3'	1825:2MG	P	2.92

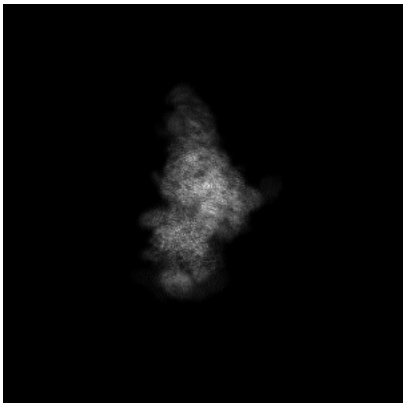
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-56197. These allow visual inspection of the internal detail of the map and identification of artifacts.

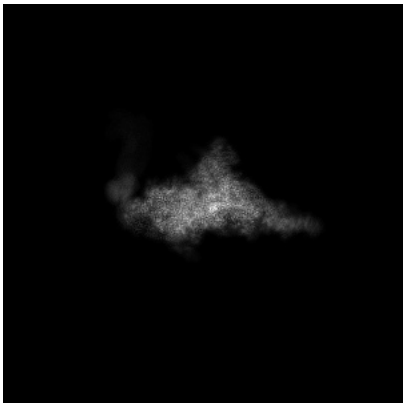
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

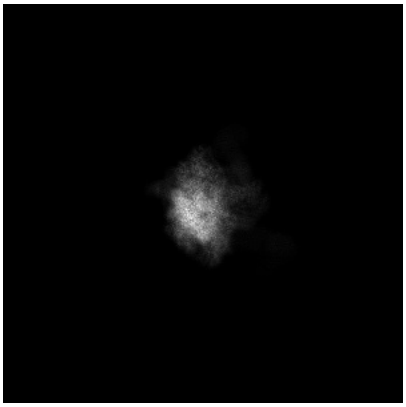
6.1.1 Primary map



X



Y

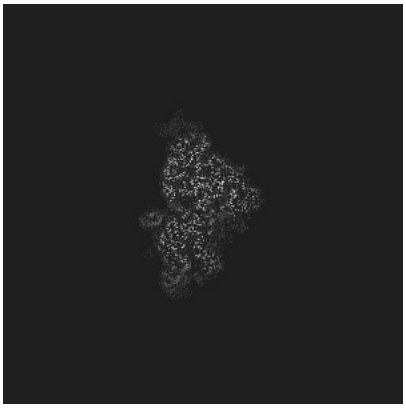


Z

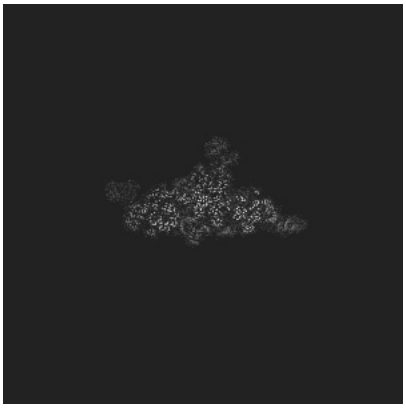
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map



X Index: 350



Y Index: 350

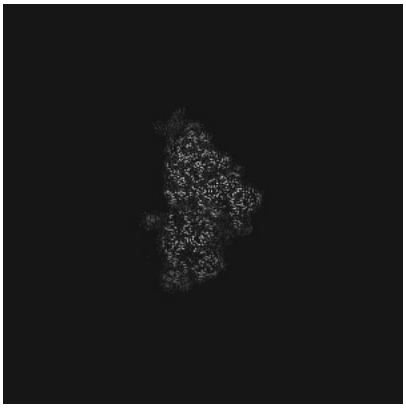


Z Index: 350

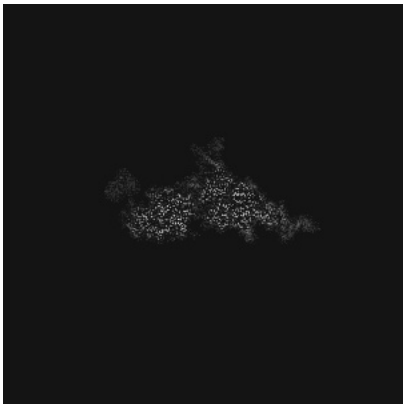
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

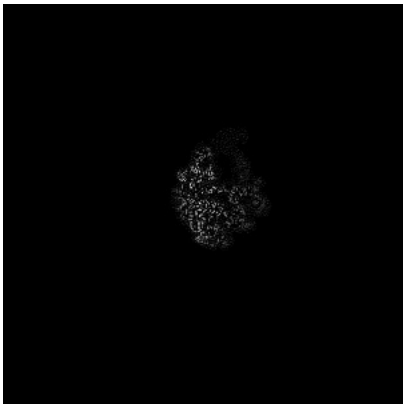
6.3.1 Primary map



X Index: 343



Y Index: 334

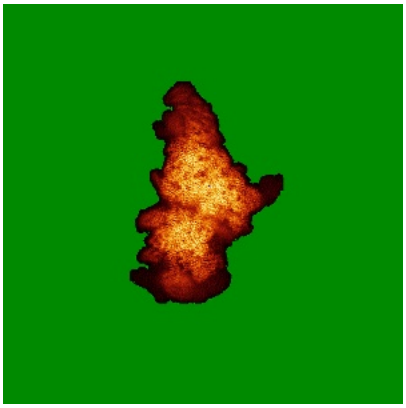


Z Index: 369

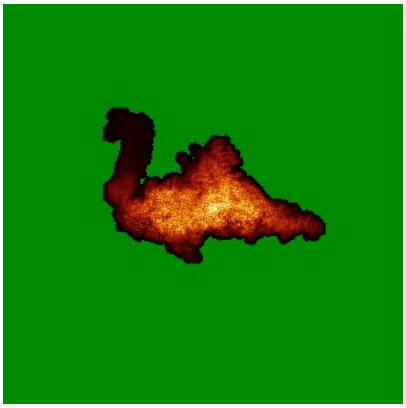
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

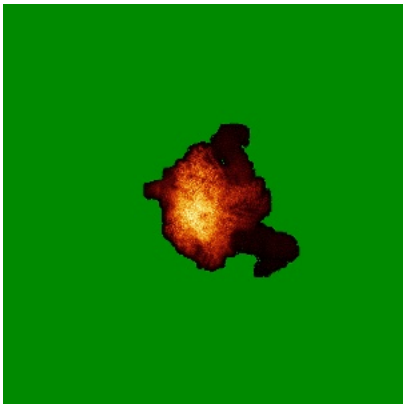
6.4.1 Primary map



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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.24. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

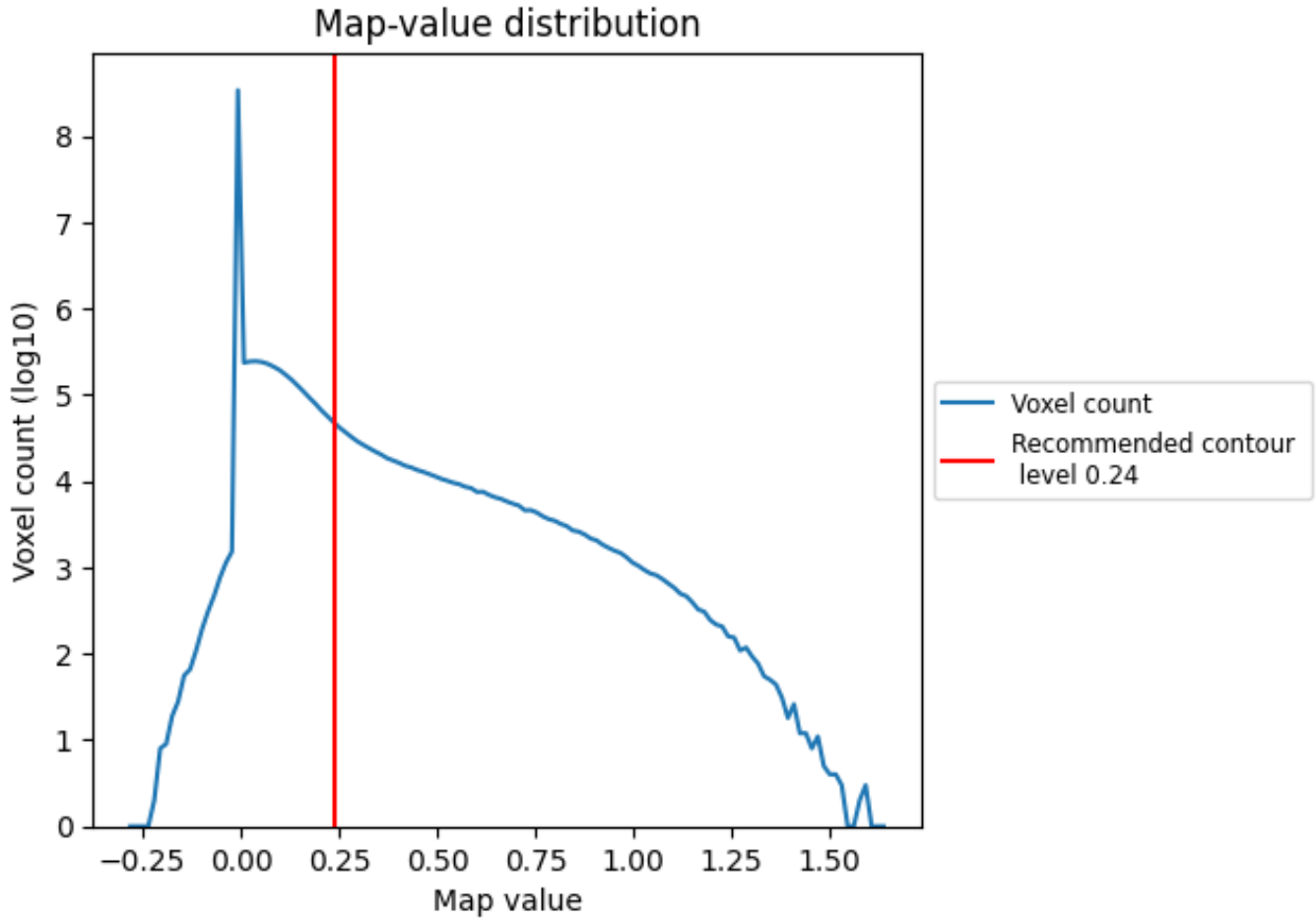
6.6 Mask visualisation (i)

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

7 Map analysis

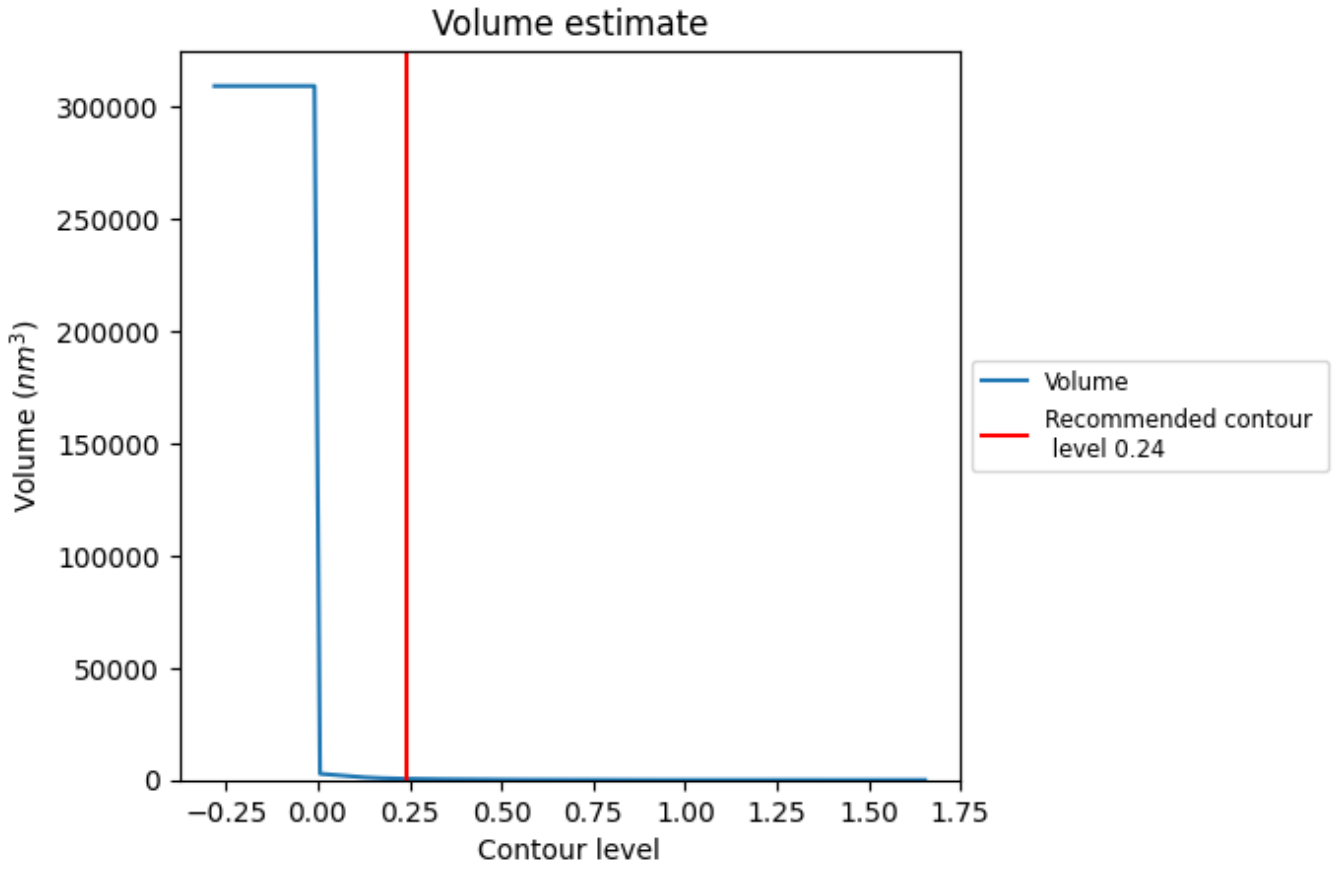
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

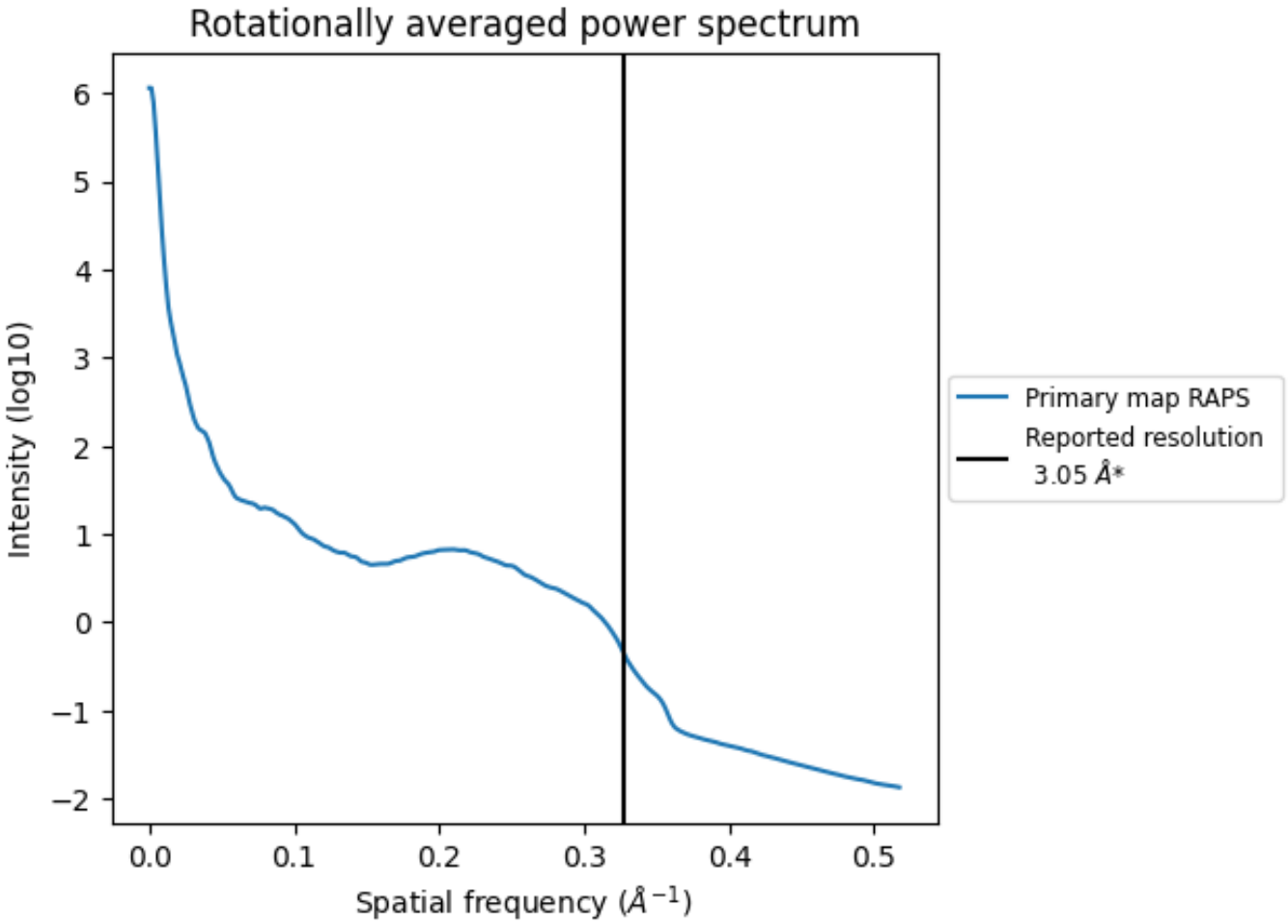
7.2 Volume estimate



The volume at the recommended contour level is 515 nm^3; this corresponds to an approximate mass of 465 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.328 Å^{-1}

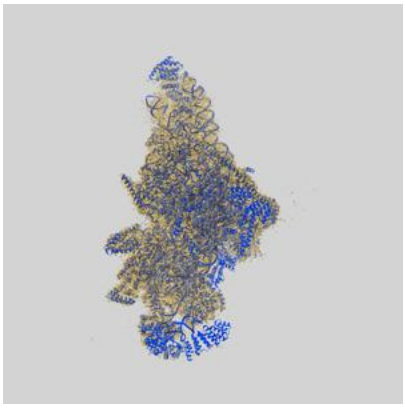
8 Fourier-Shell correlation

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

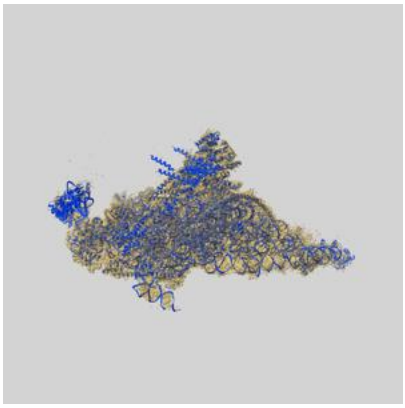
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-56197 and PDB model 9TRT. Per-residue inclusion information can be found in section 3 on page 12.

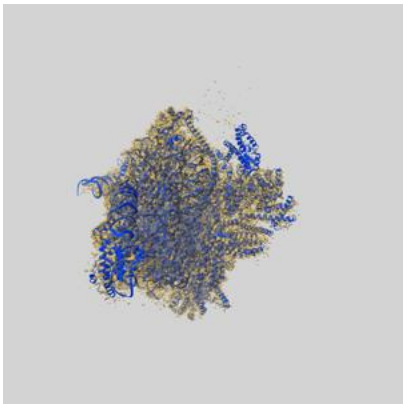
9.1 Map-model overlay



X



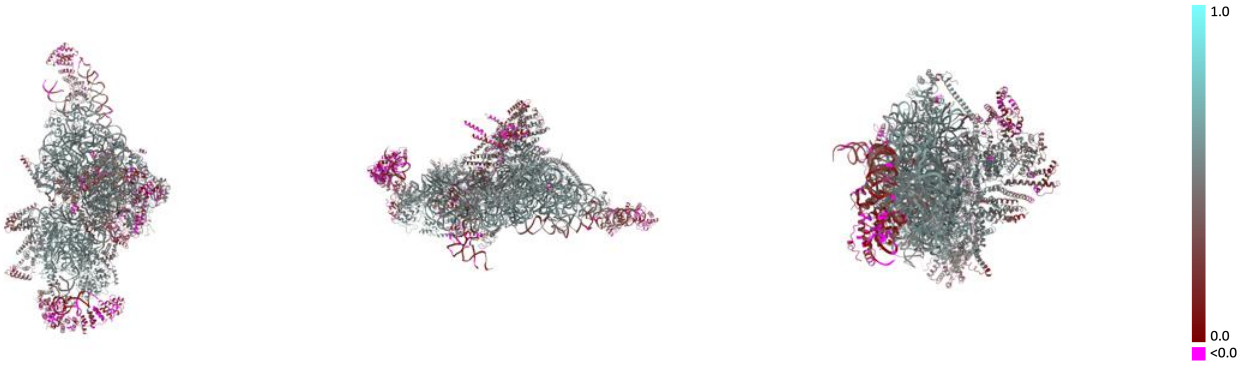
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.24 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.

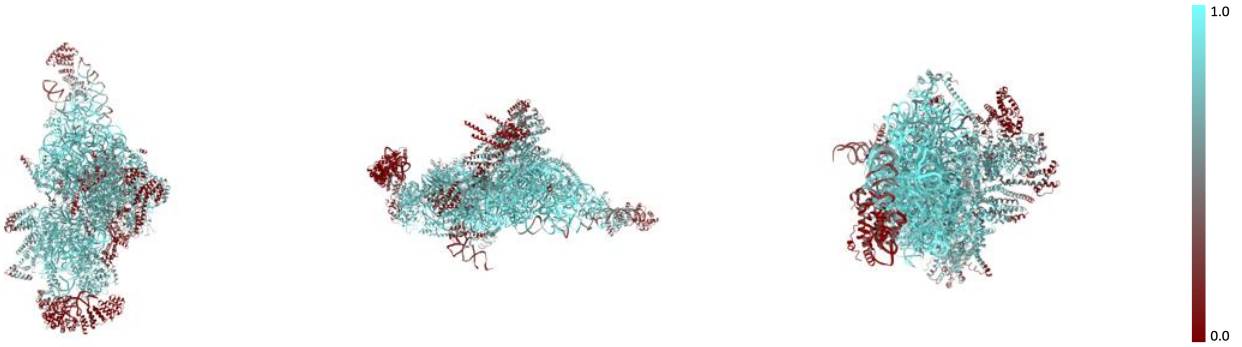
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

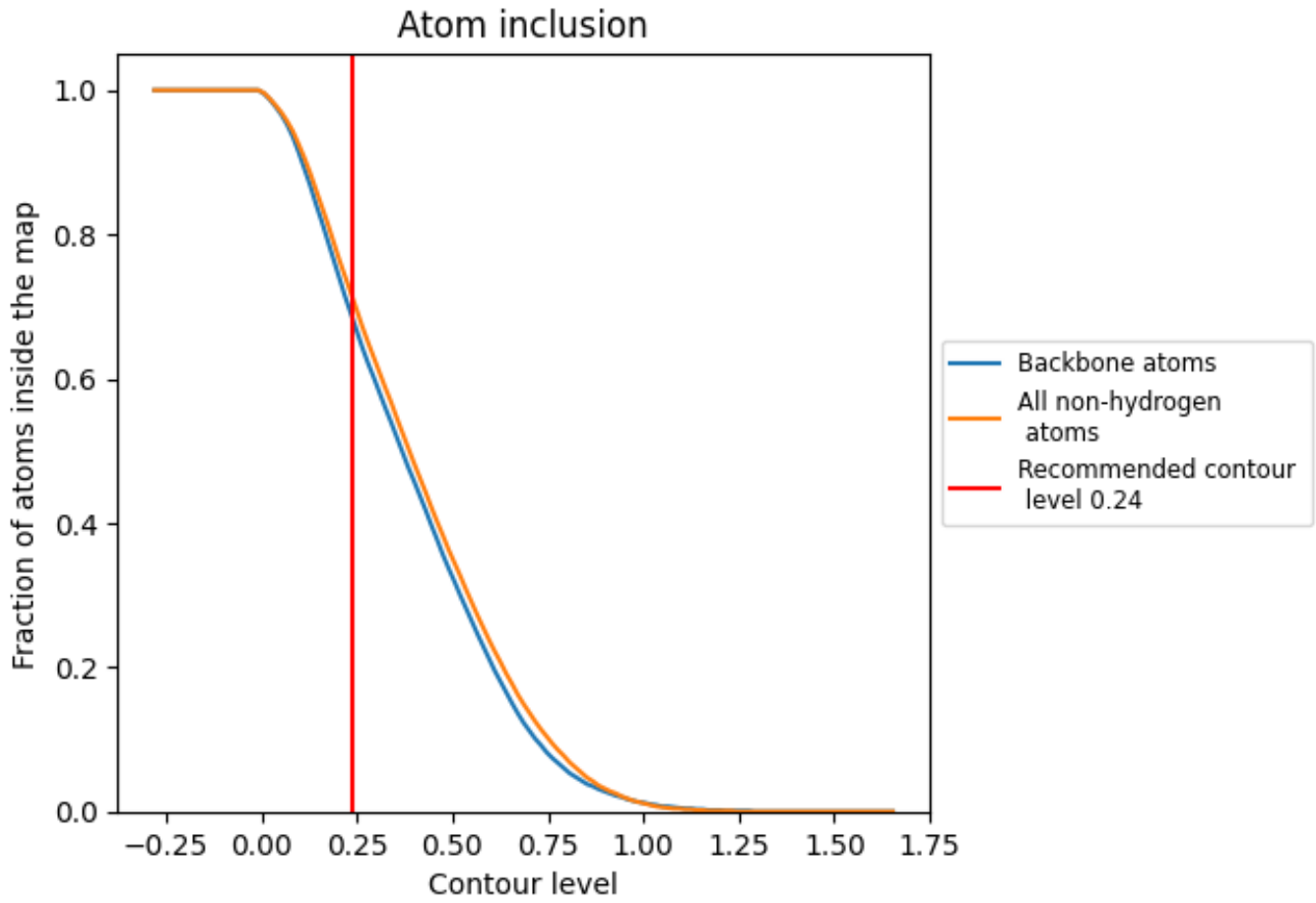
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.24).

9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 71% 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 (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7090	0.4460
2	0.8750	0.4950
5	0.3930	0.1840
6	0.4210	0.3350
8	0.4060	0.2720
A	0.7760	0.5220
B	0.7280	0.4760
C	0.8060	0.5130
D	0.6960	0.4640
E	0.7990	0.5090
F	0.1660	0.3850
G	0.8740	0.5520
H	0.6560	0.4510
I	0.9000	0.5770
J	0.7060	0.4420
K	0.8640	0.5430
L	0.8310	0.5570
M	0.9120	0.5780
N	0.8060	0.5210
O	0.9150	0.5550
P	0.8230	0.5370
Q	0.7570	0.5100
R	0.4650	0.3310
S	0.6160	0.4380
T	0.9190	0.5780
U	0.3270	0.3040
V	0.7190	0.4890
W	0.7980	0.5320
X	0.7480	0.4980
Y	0.7960	0.5330
Z	0.7570	0.4500
a	0.7040	0.4710
b	0.0300	0.1640
c	0.7890	0.5020
d	0.8040	0.5030



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Chain	Atom inclusion	Q-score
e	0.8080	0.5130
f	0.6360	0.4490
g	0.0060	0.0930
h	0.2940	0.1950
i	0.2440	0.2460
k	0.3260	0.3700
l	0.1080	0.1350