



Full wwPDB EM Validation Report ⓘ

Oct 1, 2024 – 10:38 AM JST

PDB ID : 6ID1
EMDB ID : EMD-9647
Title : Cryo-EM structure of a human intron lariat spliceosome after Prp43 loaded (ILS2 complex) at 2.9 angstrom resolution
Authors : Zhang, X.; Zhan, X.; Yan, C.; Shi, Y.
Deposited on : 2018-09-07
Resolution : 2.86 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.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

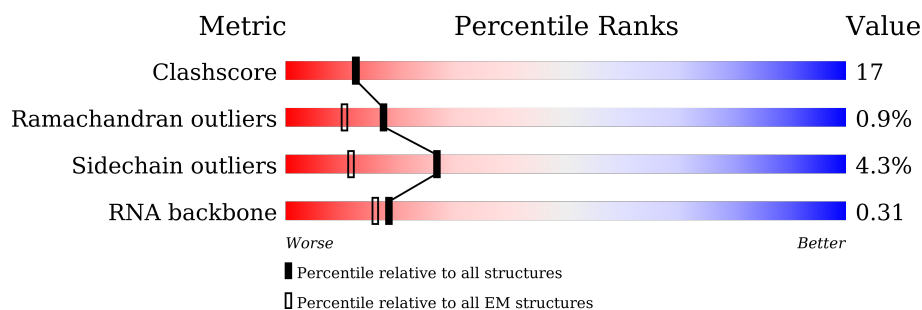
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 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.



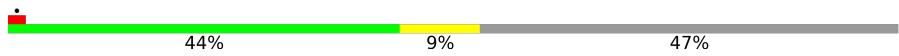

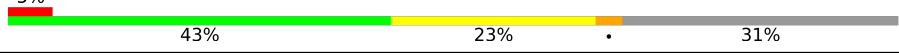
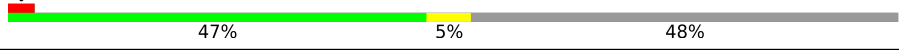


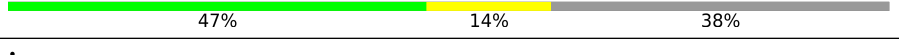


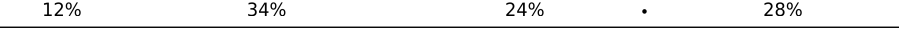
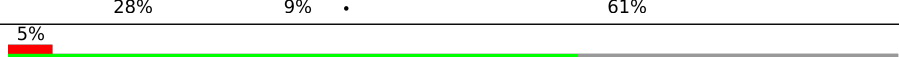


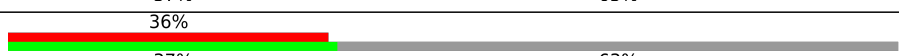
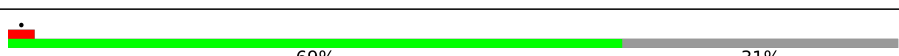







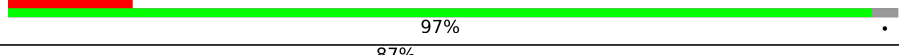


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	2335	
2	B	117	
3	C	972	
4	E	357	
5	F	107	
6	J	848	
7	L	802	

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Mol	Chain	Length	Quality of chain
8	M	243	
9	N	144	
10	O	420	
11	P	229	
12	R	536	
13	S	166	
14	T	514	
15	W	579	
16	G	272	
17	H	188	
18	U	894	
19	a	126	
19	h	126	
20	b	231	
20	i	231	
21	c	119	
21	j	119	
22	d	118	
22	k	118	
23	f	86	
23	m	86	
24	e	92	
24	l	92	
25	g	76	
25	n	76	

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Mol	Chain	Length	Quality of chain
26	q	504	
26	r	504	
26	s	504	
26	t	504	
27	K	225	
28	I	855	
29	Q	1485	
30	y	301	
31	o	255	
32	p	225	
33	V	795	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	GTP	C	1500	-	-	X	-

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 79882 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1981	Total	C	N	O	S	0	0
			16477	10621	2883	2902	71		

- Molecule 2 is a RNA chain called U5snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	98	Total	C	N	O	P	0	0
			2060	923	341	698	98		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	888	Total	C	N	O	S	0	0
			7022	4494	1172	1322	34		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	303	Total	C	N	O	S	0	0
			2366	1487	415	451	13		

- Molecule 5 is a RNA chain called U6snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	97	Total	C	N	O	P	0	0
			2075	928	381	669	97		

- Molecule 6 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	568	Total	C	N	O	S	0	0
			3817	2379	717	715	6		

- Molecule 7 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	475	Total	C	N	O	S	0	0
			3369	2094	634	635	6		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	130	Total	C	N	O	S	0	0
			1098	684	204	208	2		

- Molecule 9 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	143	Total	C	N	O	S	0	0
			1184	746	217	209	12		

- Molecule 10 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	290	Total	C	N	O	S	0	0
			2340	1469	415	436	20		

- Molecule 11 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	118	Total	C	N	O	S	0	0
			985	601	194	188	2		

- Molecule 12 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	R	272	Total	C	N	O	P	S	0	0
			2165	1357	393	401	2	12		

- Molecule 13 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	S	159	Total	C	N	O	S	0	0
			1236	787	215	227	7		

- Molecule 14 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	T	317	Total	C	N	O	S	0	0
			2496	1574	453	461	8		

- Molecule 15 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	158	Total	C	N	O	S	0	0
			1276	803	217	252	4		

- Molecule 16 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	68	Total	C	N	O	P	0	0
			1201	529	148	456	68		

- Molecule 17 is a RNA chain called U2snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	136	Total	C	N	O	P	0	0
			2884	1289	496	963	136		

- Molecule 18 is a protein called CWF19-like protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	347	Total	C	N	O	S	0	0
			2864	1817	496	529	22		

- Molecule 19 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	a	81	Total	C	N	O	0	0
			399	237	81	81		
19	h	80	Total	C	N	O	0	0
			393	233	80	80		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	b	86	Total	C	N	O	0	0
			424	252	86	86		
20	i	86	Total	C	N	O	0	0
			424	252	86	86		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	c	82	Total	C	N	O	0	0
			406	242	82	82		
21	j	82	Total	C	N	O	0	0
			406	242	82	82		

- Molecule 22 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	d	97	Total	C	N	O	0	0
			480	286	97	97		
22	k	85	Total	C	N	O	0	0
			422	252	85	85		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	f	74	Total	C	N	O	0	0
			361	213	74	74		
23	m	74	Total	C	N	O	0	0
			361	213	74	74		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	e	79	Total	C	N	O	0	0
			391	233	79	79		
24	l	79	Total	C	N	O	0	0
			391	233	79	79		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	g	74	Total	C	N	O	0	0
			363	215	74	74		
25	n	67	Total	C	N	O	0	0
			329	195	67	67		

- Molecule 26 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	q	132	Total	C	N	O	0	0
			659	395	132	132		
26	r	131	Total	C	N	O	0	0
			654	392	131	131		
26	s	67	Total	C	N	O	0	0
			335	201	67	67		
26	t	67	Total	C	N	O	0	0
			335	201	67	67		

- Molecule 27 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	152	Total	C	N	O	S	0	0
			980	612	177	189	2		

- Molecule 28 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	I	576	Total	C	N	O	S	0	0
			2875	1716	579	579	1		

- Molecule 29 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	Q	1322	Total	C	N	O	0	0
			6554	3910	1322	1322		

- Molecule 30 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	y	79	Total	C	N	O	0	0
			390	232	79	79		

- Molecule 31 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	o	162	Total	C	N	O	0	0
			804	480	162	162		

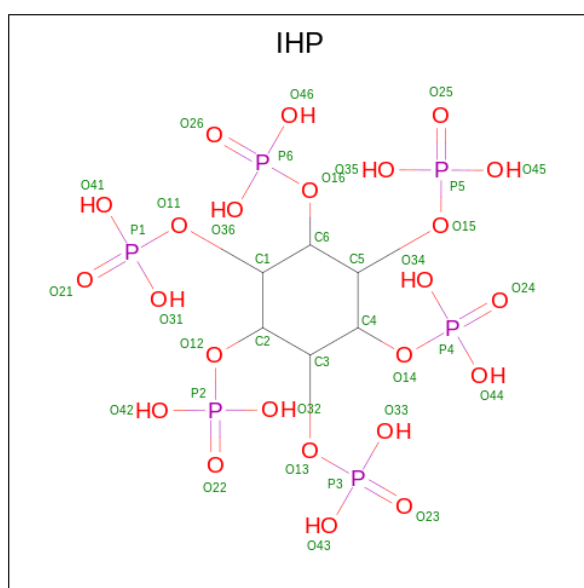
- Molecule 32 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	p	94	Total	C	N	O	0	0
			464	276	94	94		

- Molecule 33 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15.

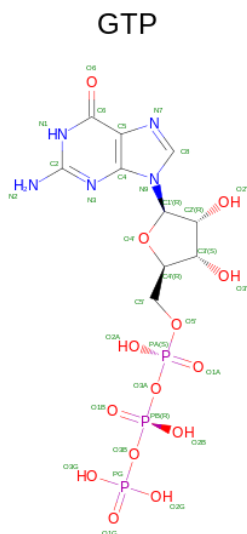
Mol	Chain	Residues	Atoms				AltConf	Trace
33	V	663	Total	C	N	O	0	0
			3285	1959	663	663		

- Molecule 34 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				AltConf
34	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 35 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
35	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	C	1	Total 1	Mg 1	0
36	F	6	Total 6	Mg 6	0

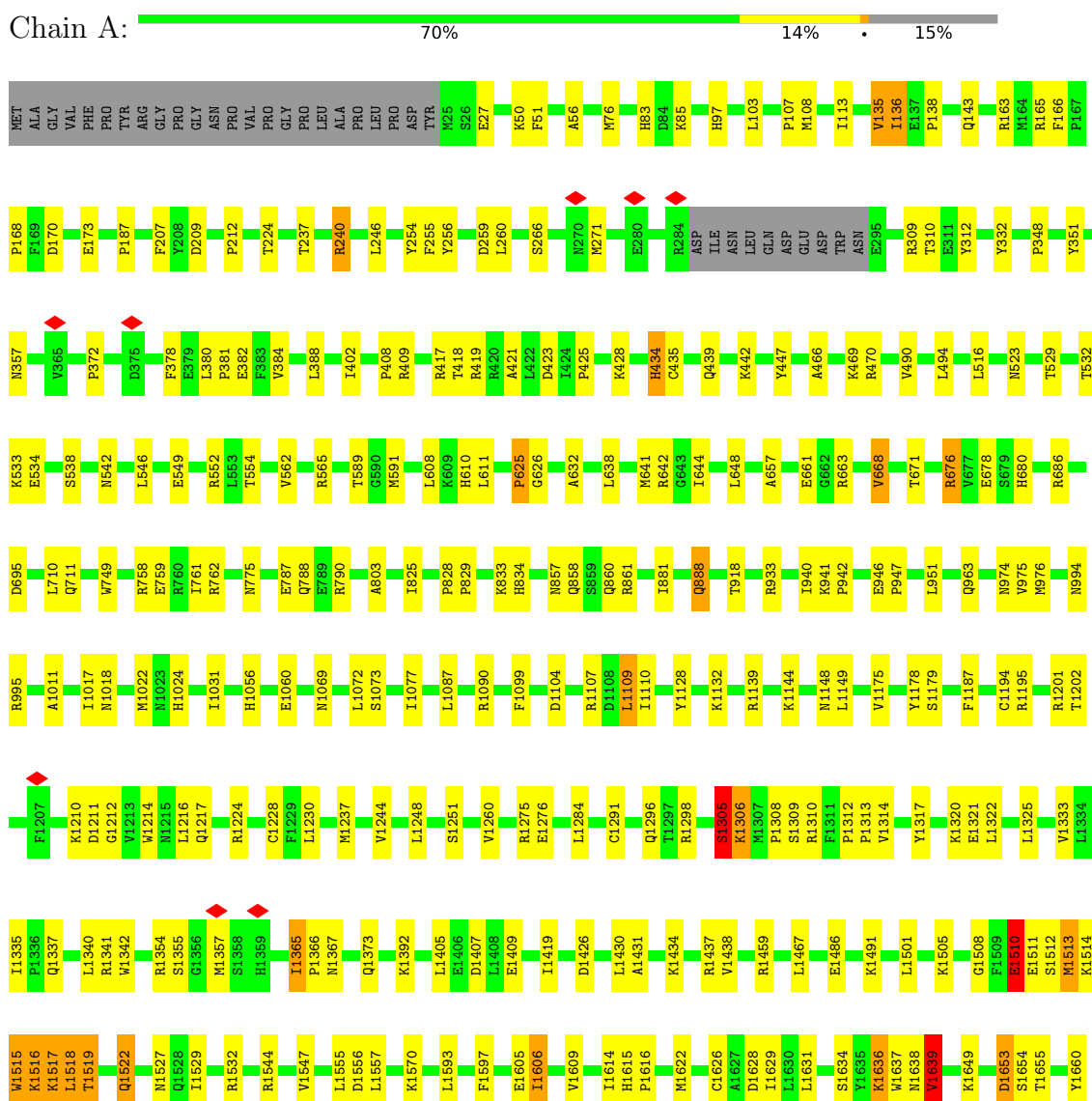
- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

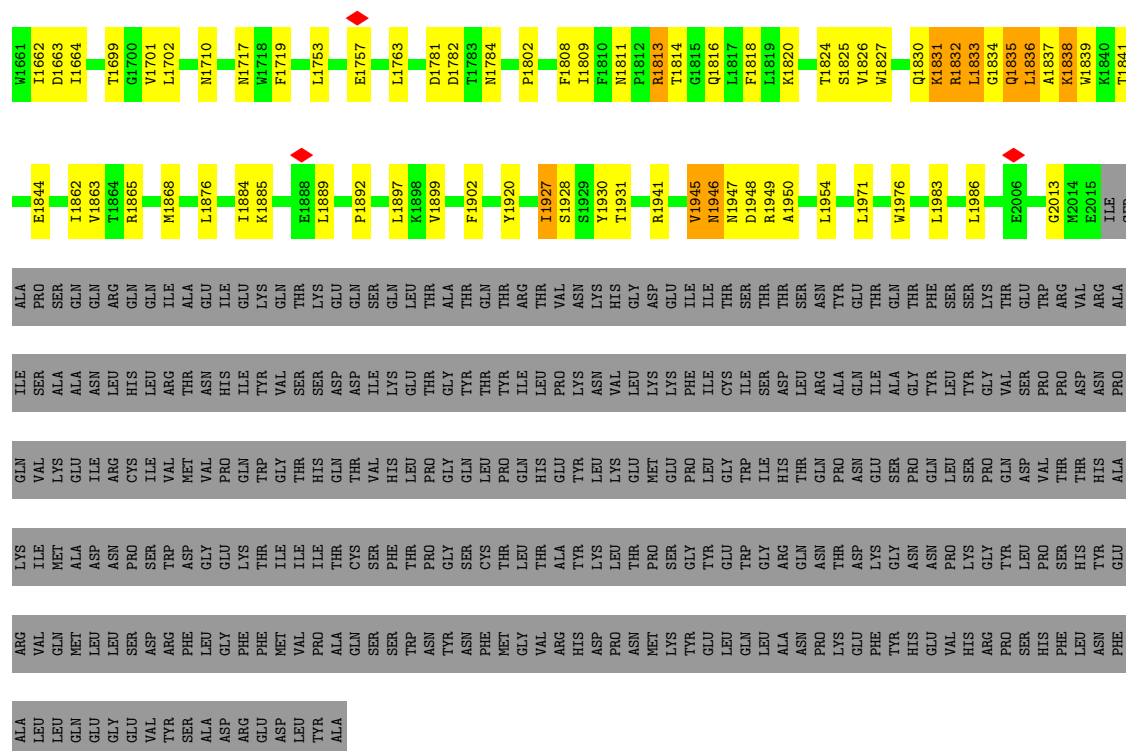
Mol	Chain	Residues	Atoms		AltConf
37	N	3	Total 3	Zn 3	0
37	O	3	Total 3	Zn 3	0
37	U	1	Total 1	Zn 1	0

3 Residue-property plots

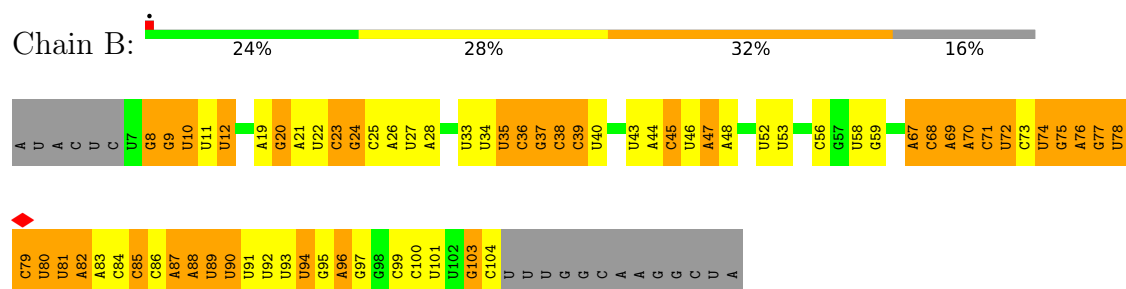
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Pre-mRNA-processing-splicing factor 8

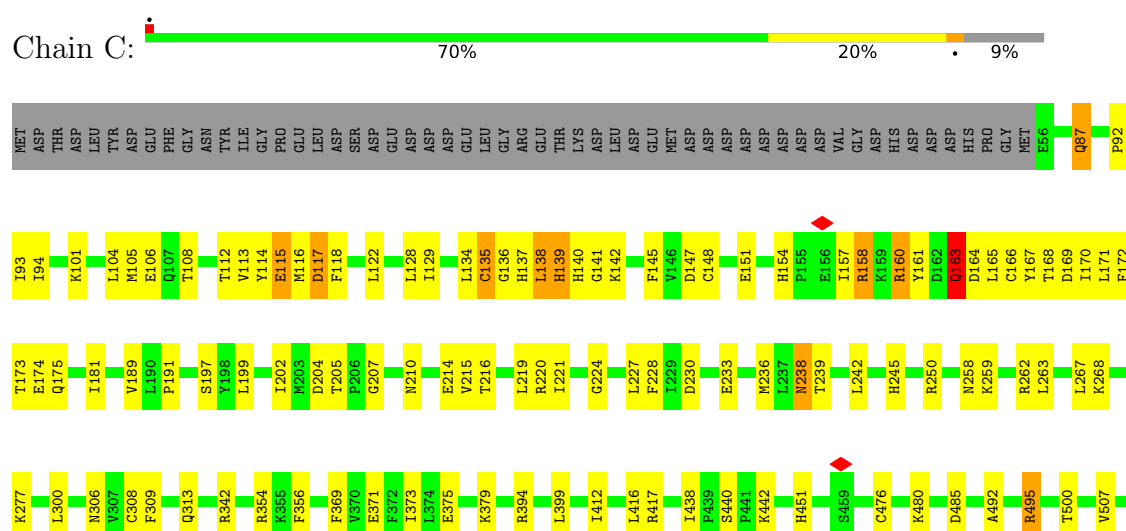


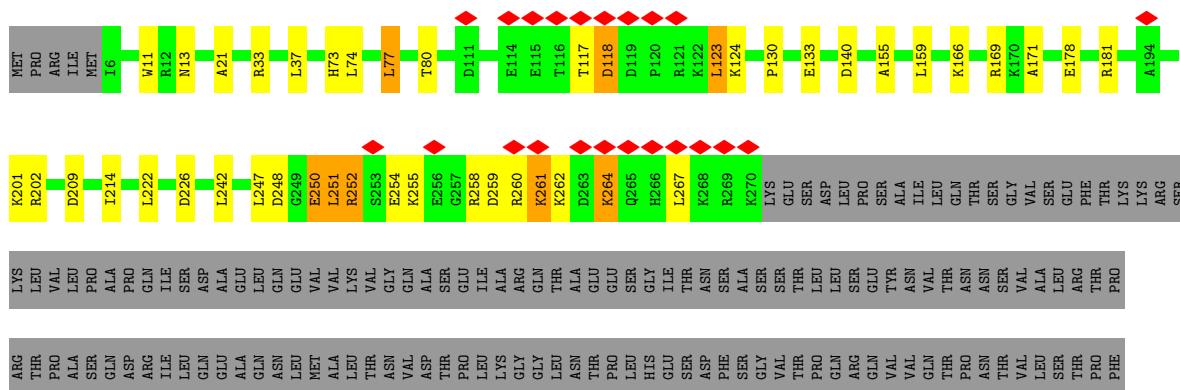


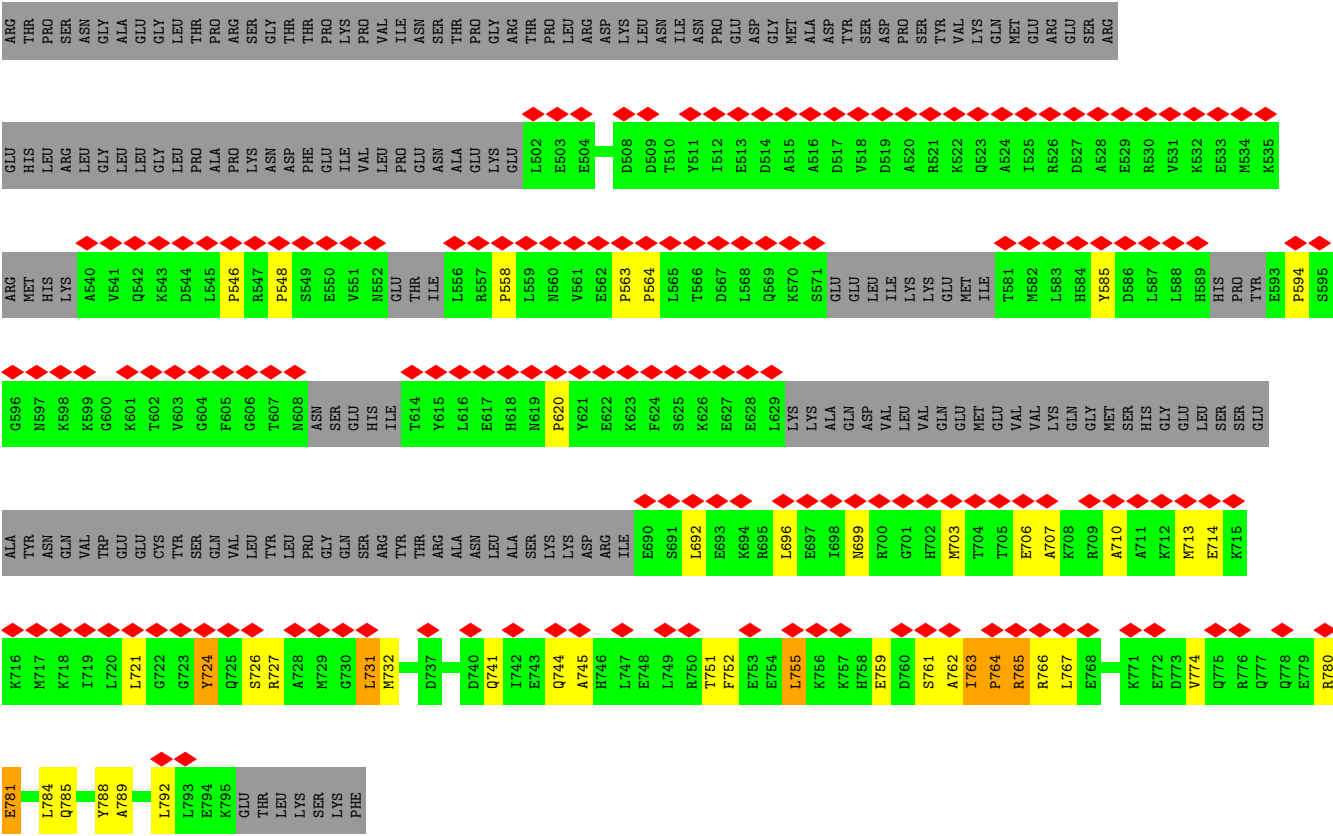
• Molecule 2: U5snRNA



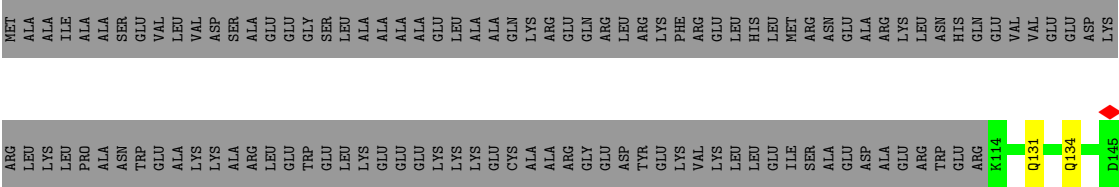
• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component



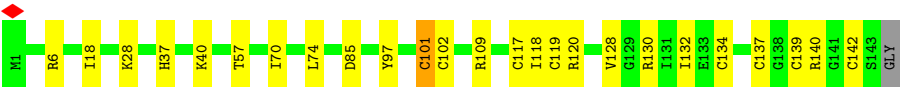
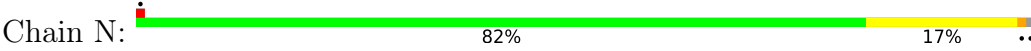




• Molecule 8: Pre-mRNA-splicing factor SYF2



• Molecule 9: Protein BUD31 homolog



• Molecule 10: Pre-mRNA-splicing factor RBM22



PRO
SER
ASP
SER
SER
ARG
PRO
LYS
GLU
HIS
GLU
HIS
GLY
LYS
LYS
ARG
ARG
LYS
GLU

• Molecule 13: Peptidyl-prolyl cis-trans isomerase-like 1

Chain S: 

MET
ALA
ALA
ILE
PRO
PRO
ASP
SR
Y15
T18
S19
M20
L25
E26
N38
E41
B44
M49
G50
T51
K52
R55
I56
I57
M61
I62
Q63
R72
G73
G74
A75
S76
D84
D89
L90
K91
P92
T93
L98
N102
A103
G104
P105
D106
T107
N108

• Molecule 14: Pleiotropic regulator 1

Chain T: 

MET
VAL
GLU
GLN
VAL
GLN
HIS
HIS
THR
LEU
VAL
PHE
SER
TYR
VAL
LEU
HIS
LYS
ARG
GLN
THR
TYR
HIS
ASP
MET
PHE
VAL
GLY
ALA
ASP
ASN
GLY
VAL
PRO
VAL
PRO
GLU
ASP
GLY
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THR
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TYR
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ALA
GLY
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LEU
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GLY
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SER
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GLY
ILE
VAL
HIS
LEU
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PRO
THR
GLU

LYS
ALA
PRO
T184
V190
R198
R199
I200
E213
P214
G215
N216
Q217
W218
F219
V220
K239
R250
V254
S255
T256
L261
H261
E266
V270
W273
N278
Y284
H285
H297
P298
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T369
K372
K373
S374
V375
R376
V379
L380
H381
P382
R383
F387
G390
S391
P392
D393
N394
I395
W398
K399
F400
F405
I406
I415
I416
M417
T418
L419
T420
A431
W439
N446

A467
Q472
I486
I487
V488
E498
T499
H500
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VAL
TRP
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• Molecule 15: Pre-mRNA-processing factor 17

Chain W: 

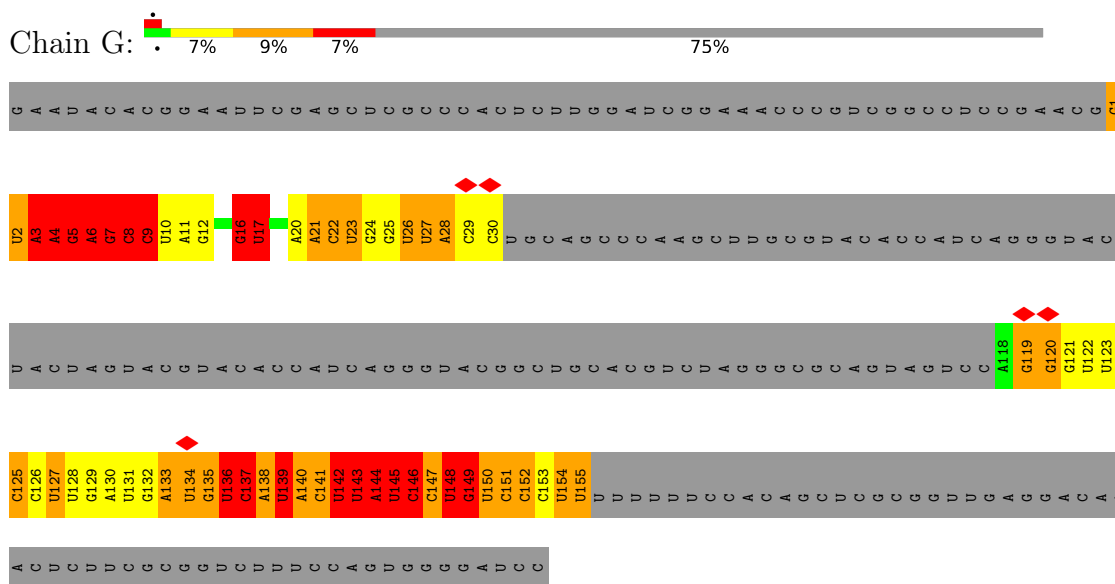
MET
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ILE
ALA
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ALA
ALA
TYR
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SER
GLY
GLY
LYS
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SER
SER
ASP
ASP
GLY
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SER
PRO
LEU
ALA
ALA
ASP
SER
SER
MET
HIS
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PRO
SER
PRO
SER
SER
SER
PRO
LEU
ALA
ALA
VAL
ASP
SER
ALA
PRO
GLU
VAL

ALA
VAL
GLU
ASP
LEU
GLU
THR
GLY
V70
V76
K77
N82
P83
F86
T87
M88
F89
N97
R100
Q103
R108
L111
A118
H119
I120
M124
R130
L139
D140
P141
S142
L143
D144
N145
H146
Q147
V148
S149
A150
K151
Y152
I153
A159
G164

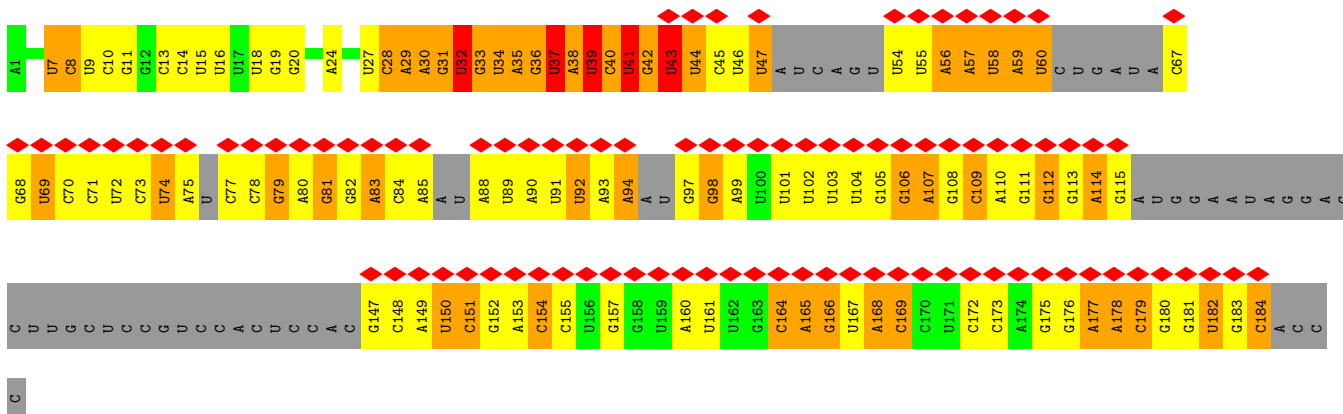
I189
L193
D204
D205
P208
L216
L219
K225
K226
K227
GLU
GLN
GLU
GLU
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ALA
VAL
VAL
ARG
GLY
PHE
PRO
LEU
GLU
GLU
THR
ILE
HIS
HIS
LEU
VAL
LYS
GLY
SER
CYS
MET
ASP
GLN
GLY
ILE
LYS
SER
TRP
GLU
TYR
VAL
ARG
GLY
GLY
THR
PHE
ILE
GLY
HIS

ASP	ASP	CYS	ASP	VAL	SER
GLY	GLY	GLN	PHE	ALA	LYS
LEU	LEU	VAL	ASP	GLY	ALA
ILE	ILE	ASP	TYR	MET	VAL
LYS	LYS	PHE	ILE	SER	ARG
LEU	LEU	SER	ALA	ASP	ILE
TRP	TRP	PRO	GLU	LYS	CYS
ASP	ASP	ASP	PRO	LYS	PHE
		MET	SER	ILE	ASN
		SER	MET	VAL	THR
		TYR	HIS	GLN	ALA
		VAL	SER	TRP	GLY
		ILE	MET	ASP	THR
		SER	PRO	ILE	GLY
		GLY	ALA	ARG	THR
		ASP	VAL	SER	ALA
		GLY	LEU	GLY	SER
		ASN	LEU	GLU	THR
		GLY	SER	ILE	ALA
		LYS	PRO	VAL	ALA
		LEU	ASN	GLN	TYR
		ASN	GLY	GLU	ASP
		ILE	LYS	TVR	ARG
		TRP	TRP	ASP	TVR
		ASP	LEU	ARG	LEU
		TRP	ALA	HIS	LYS
		LYS	CYS	LEU	LEU
		THR	GLN	GLY	TRP
		THR	SER	ALA	ASP
		LYS	MET	VAL	THR
		LEU	ASP	ASN	GLU
		TYR	ASN	THR	THR
		SER	GLN	ILE	GLY
		ARG	ILE	VAL	CYS
		PHE	LEU	PHE	ILE
		LYS	ILE	VAL	ILE
		ALA	PHE	ASP	SER
		HIS	GLY	GLU	ARG
		ASP	ALA	ASN	PHE
		LYS	GLN	ARG	THR
		VAL	ASN	ARG	ASN
		CYS	ARG	PHE	ARG
		ILE	PHE	VAL	LYS
		GLY	ARG	SER	VAL
		ALA	LEU	THR	PRO
		VAL	ASN	SER	TVR
		TRP	LYS	ASP	CYS
		HIS	LYS	ASP	VAL
		PRO	LYS	LYS	LYS
		HIS	ILE	SER	PHE
		GLU	PHE	LEU	ASN
		THR	LYS	ARG	PRO
		SER	GLY	VAL	ASP
		LYS	HIS	TRP	GLU
		VAL	MET	GLU	ASP
		ILE	VAL	TRP	LYS
		THR	ALA	ASP	GLN
		CYS	GLY	ILE	ASN
		GLY	TVR	LEU	ASN
		TRP	ALA	VAL	PHE

- Molecule 16: pre-mRNA



- Molecule 17: U2snRNA



- Molecule 18: CWF19-like protein 2

[illegible][illegible]

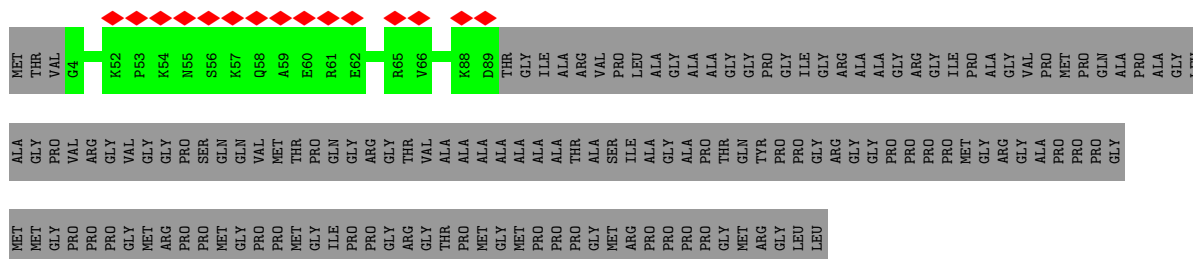
- Chain a: 5% 64% 36%

[illegible]

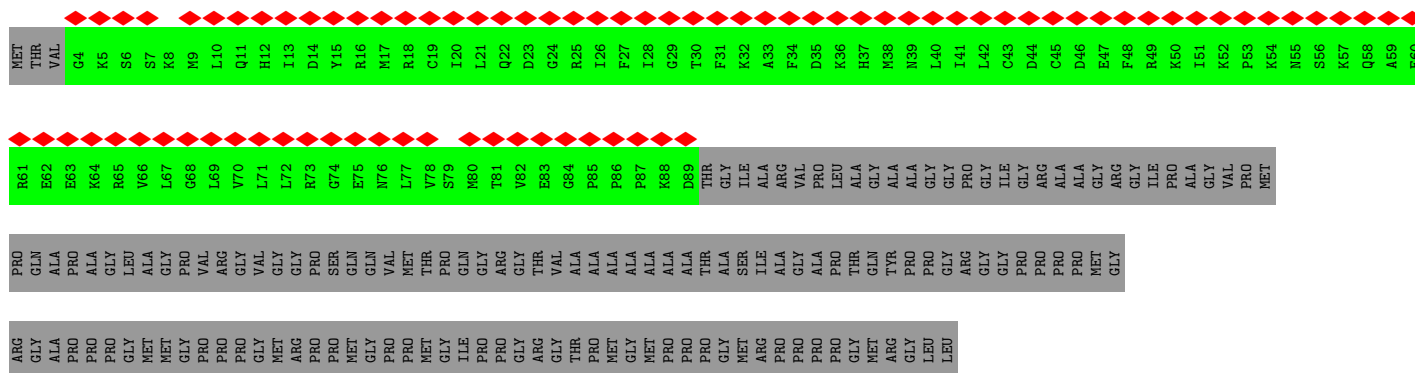
- Chain h:  63% 37%

MET	SER	I	LE
G4	V6	P6	I7
K8	V9	L10	H11
E12	A13	E14	G15
H16	I17	V18	T19
C20	E21	T22	N23
T24	G25	E26	V27
Y28	R29	G30	K31
L32	I33	E34	A35
D37	N38	M39	X40
C41	Q42	M43	S44
N45	I46	T47	V48
T49	Y50	R51	D52
G53	R54	V55	A56
Q57	L58	E59	F60

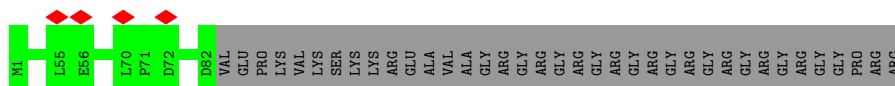
- Molecule 20: Small nuclear ribonucleoprotein-associated protein



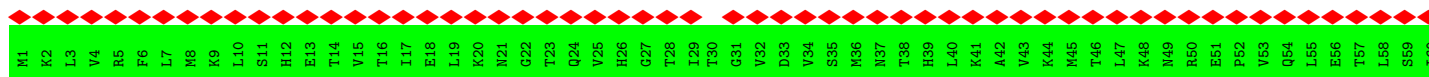
- Molecule 20: Small nuclear ribonucleoprotein-associated protein



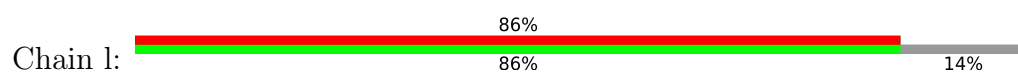
- Molecule 21: Small nuclear ribonucleoprotein Sm D1



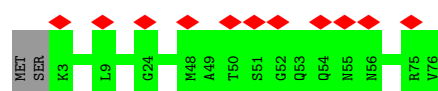
- Molecule 21: Small nuclear ribonucleoprotein Sm D1



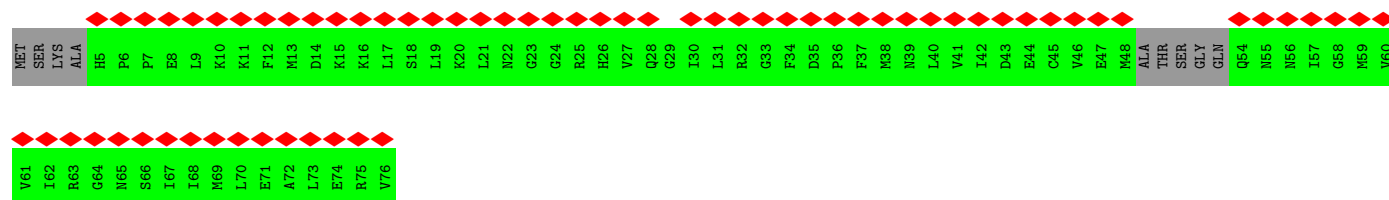
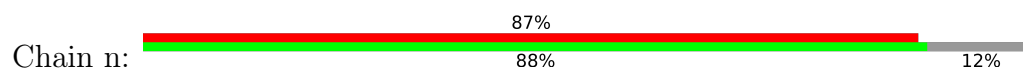




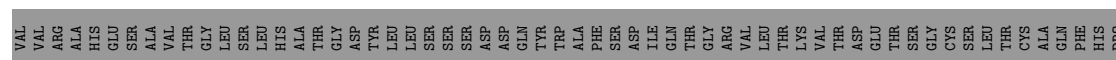
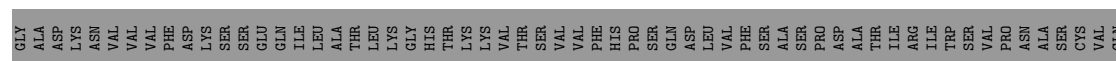
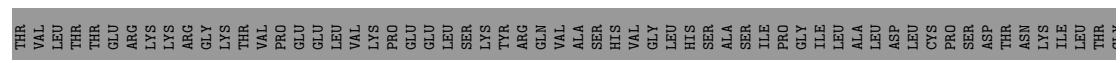
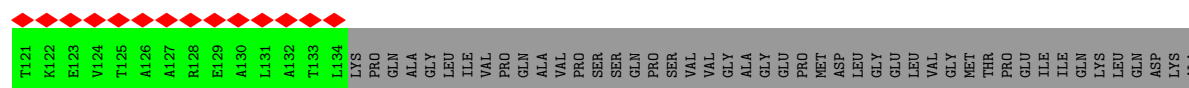
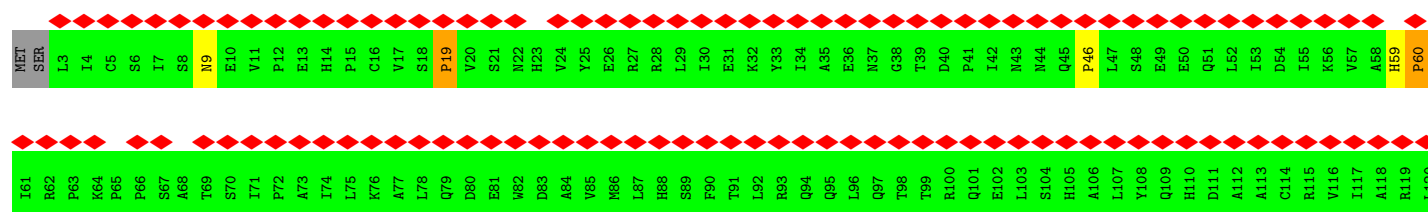
• Molecule 25: Small nuclear ribonucleoprotein G



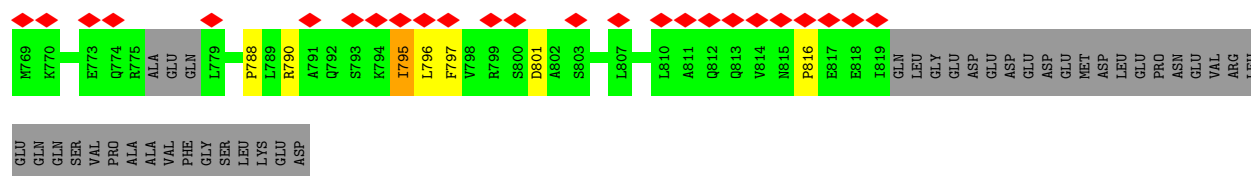
• Molecule 25: Small nuclear ribonucleoprotein G



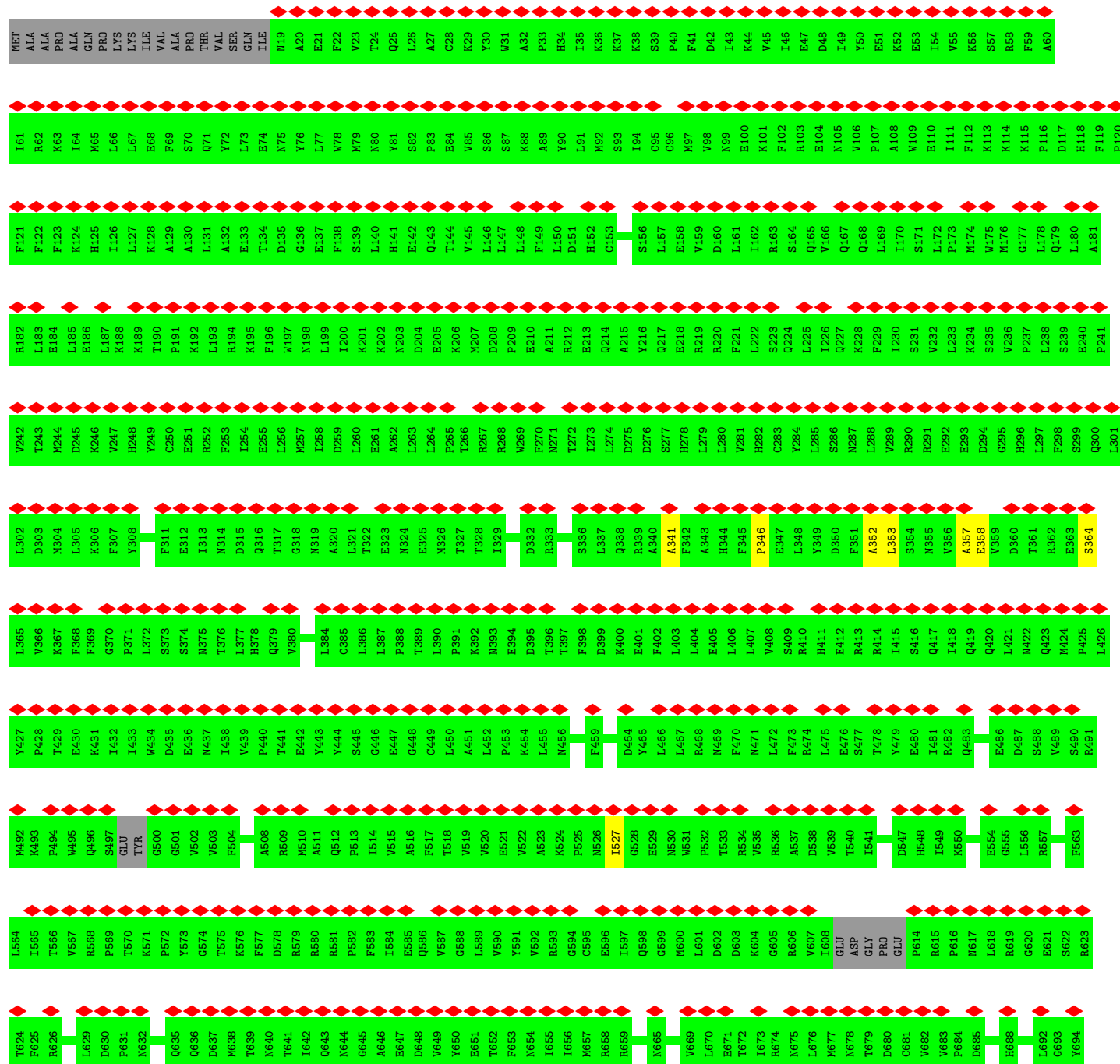
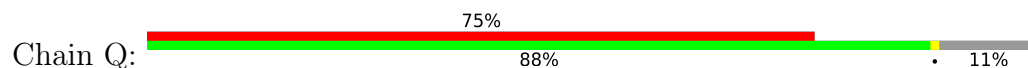
• Molecule 26: Pre-mRNA-processing factor 19








• Molecule 29: RNA helicase aquarius





Chain V:  76% 81% 17%

MET	LEU	L181	L241	Y303	D363	E425	Y485	L546	E612	N672	E732
SER	ARG	P122	E244	F304	E364	T426	T486	A547	A613	L673	W733
LYS	ALA	H123	A245	D305	A365	S427	E487	A548	K614	P674	V734
ARG	THR	T124	A246	N306	C366	L428	K488	L549	M615	R675	L735
HIS	ASN	P125	M246	N307	C367	T429	A489	M550	R616	R676	W736
LEU	ALA	R126	N247	C308	K368	L430	Y490	D551	F617	S677	T737
ASP	MET	Y127	D248	L309	I369	D431	K491	D552	A618	T678	E738
GLY	ILE	Y128	P249	L310	K370	G432	T492	G553	H619	D679	F739
LEU	ASP	D129	V188	T311	R371	V433	E493	D554	F620	F680	W740
ASP	ALA	I130	A189	T312	E372	V434	M494	L555	D621	T681	L741
TYR	GLY	L131	C190	P313	Y373	F435	Q495	T556	G622	S682	T742
PRO	LEU	L132	E252	G314	D374	V436	D496	E557	D623	R683	W743
SER	PRO	K132	R253	G315	D375	L437	M497	L558	H624	D684	K744
GLY	PRO	P133	Q192	T316	L376	D438	T498	G559	L625	Y685	W745
LYS	LEU	R134	P193	T317	D377	P439	Y499	S560	T626	Y686	W746
ARG	ALA	K135	R194	H317	G377	G440	P500	M561	L627	L687	W747
ALA	SER	L136	R195	P318	P378	F441	E501	H562	L628	M688	W748
GLY	HIS	Q136	V196	V319	E379	A442	E502	A563	N629	I689	W749
THR	SER	Y137	A197	E320	V380	K443	L503	E564	V630	R690	W750
ASP	ALA	P138	L259	I321	G381	Q444	R504	F565	W631	K691	W751
GLY	HIS	V139	M199	F322	K384	K445	B505	P566	H632	A692	W752
LYS	SER	W140	S200	Y323	L385	V446	S506	P569	A633	A693	W753
ASP	THR	E141	V201	T324	I386	Y447	S508	P575	F634	V694	K754
ASP	SER	Y142	A202	P325	L387	M448	S509	P576	K635	T695	W755
ARG	ALA	K143	Q203	P326	P387	P449	W510	Q577	Q636	G696	W756
ASP	HIS	D144	R204	E326	L388	P450	V511	A577	L576	L697	W757
ASP	SER	R145	V205	P327	Y389	R450	W512	A578	M637	L698	W758
ASP	THR	F146	A206	E328	S390	L451	L512	S579	H638	M699	W759
GLU	SER	T147	D207	R329	T391	R452	L513	C579	E639	Q700	W760
ASP	HIS	Y148	E208	D330	L392	A453	L514	D580	S640	V701	W761
LYS	SER	I149	M209	Y331	L393	E454	K515	W581	V641	A702	W762
ASP	ALA	L150	D210	L332	P393	E455	K516	M582	Q642	W703	W763
ASP	SER	V151	V211	E333	P394	L456	L517	C583	W643	W704	W764
ARG	THR	R152	M212	A334	Q395	L457	G518	S584	C644	L704	W765
ASP	HIS	H153	L213	A335	Q396	V458	G519	S585	W645	W705	W766
GLU	ALA	Q154	G214	I336	K399	T459	L519	M586	D646	R706	W767
ASP	GLY	S155	Q215	R337	L400	T459	D520	S587	E586	W707	W768
GLY	ALA	F156	E216	T338	F401	L461	D521	V587	L461	F648	W769
ASP	GLY	V157	G217	V339	E402	S462	L522	L588	L463	W709	W770
ASP	HIS	L158	V218	I340	P403	K463	V523	S589	N650	W710	W771
GLU	SER	V159	G218	Q341	P404	A464	H524	T591	V651	L711	W772
GLU	LEU	E160	Q282	R342	A405	S465	D525	A592	R652	T712	W773
ARG	PRO	G160	R283	H343	P406	A466	F525	A593	L654	W713	W774
GLN	GLN	T162	S284	N344	K407	Q467	F527	M593	G653	W714	W775
LYS	LYS	G163	D285	C345	K408	Q468	M528	L594	L654	D715	W776
LYS	GLU	S164	E224	L286	Q409	Q469	D529	S595	M655	W716	W777
LYS	GLU	G165	D225	K287	M410	R469	P530	V596	S656	A657	W778
LYS	GLU	K166	C226	V288	G411	A470	P531	W597	D658	W718	W779
LYS	LEU	T167	S227	L289	G412	G471	A532	Q598	D659	W719	W780
LYS	PRO	T168	S228	E349	A413	R472	P533	C599	V660	W720	W781
LYS	LYS	Q169	A229	D351	L414	A473	E534	F600	T535	R661	W782
LYS	LYS	P171	K230	L352	R415	G474	L536	V601	L721	Q662	W783
LYS	LYS	W170	T231	L353	K416	T476	M537	P603	H602	Q663	W784
LYS	LYS	W173	T233	L295	V417	R477	R538	T604	L664	L664	W785
LYS	LYS	C174	L233	D296	V418	P478	A539	E605	S665	R666	W786
LYS	LYS	V175	Y235	A297	V419	G479	L540	A606	W607	K607	W787
LYS	LYS	E176	M236	G358	T421	K480	E541	L542	C481	F482	W788
LYS	LYS	Y177	T237	Q359	N422	F482	L543	M544	W608	K608	W789
LYS	LYS	M178	D238	E361	L423	R483	L544	A609	D669	W670	W790
LYS	LYS	R179	G239	I362	A424	L484	Y545	P671	W731	W731	W791

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	499840	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.577	Depositor
Minimum map value	-0.264	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.338, 1.338, 1.338	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, IHP, ZN, MG, SEP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.33	0/16926	0.61	7/22947 (0.0%)
2	B	0.43	1/2296 (0.0%)	0.88	0/3569
3	C	0.30	0/7181	0.62	3/9758 (0.0%)
4	E	0.42	0/2420	0.69	0/3281
5	F	0.56	4/2323 (0.2%)	1.11	13/3619 (0.4%)
6	J	0.33	0/3863	0.55	6/5250 (0.1%)
7	L	0.39	2/3401 (0.1%)	0.59	10/4570 (0.2%)
8	M	0.27	0/1119	0.55	1/1497 (0.1%)
9	N	1.19	7/1210 (0.6%)	0.76	0/1622
10	O	0.38	0/2390	0.62	1/3227 (0.0%)
11	P	0.30	0/1000	0.54	0/1330
12	R	0.32	0/2186	0.69	3/2937 (0.1%)
13	S	0.29	0/1268	0.57	1/1714 (0.1%)
14	T	0.42	1/2562 (0.0%)	0.69	0/3492
15	W	0.30	0/1306	0.60	1/1760 (0.1%)
16	G	0.89	10/1327 (0.8%)	1.60	40/2053 (1.9%)
17	H	0.58	9/3214 (0.3%)	0.99	9/4989 (0.2%)
18	U	0.33	0/2928	0.68	3/3928 (0.1%)
19	a	0.47	0/397	0.61	0/549
19	h	0.47	0/391	0.61	0/540
20	b	0.51	0/423	0.72	0/587
20	i	0.50	0/423	0.73	0/587
21	c	0.58	0/405	0.73	0/563
21	j	0.57	0/405	0.73	0/563
22	d	0.69	0/479	0.85	0/666
22	k	0.70	0/420	0.85	0/583
23	f	0.75	0/360	0.82	0/497
23	m	0.75	0/360	0.81	0/497
24	e	0.66	0/390	0.80	0/542
24	l	0.64	0/390	0.80	0/542
25	g	0.54	0/362	0.71	0/501
25	n	0.53	0/327	0.72	0/451

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	q	0.35	0/658	0.58	3/919 (0.3%)
26	r	0.33	0/653	0.59	3/912 (0.3%)
26	s	0.27	0/334	0.37	0/466
26	t	0.31	0/334	0.38	0/466
27	K	1.05	9/982 (0.9%)	0.69	5/1318 (0.4%)
28	I	0.35	0/2858	0.61	11/3948 (0.3%)
29	Q	0.22	0/6545	0.43	0/9115
30	y	0.29	0/389	0.73	0/540
31	o	0.64	0/803	1.49	4/1119 (0.4%)
32	p	0.62	0/463	1.26	0/643
33	V	0.66	0/3284	0.75	0/4578
All	All	0.45	43/81755 (0.1%)	0.72	124/113235 (0.1%)

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
1	A	0	10
3	C	0	3
5	F	0	1
6	J	0	1
7	L	0	2
11	P	0	1
12	R	0	1
14	T	0	2
15	W	0	2
16	G	0	8
18	U	0	2
22	d	0	1
22	k	0	1
29	Q	0	1
33	V	0	1
All	All	0	37

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	K	106	CYS	CB-SG	-23.11	1.43	1.82
9	N	101	CYS	CB-SG	-16.04	1.54	1.82
9	N	137	CYS	CB-SG	-12.01	1.61	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	N	119	CYS	CB-SG	-10.98	1.63	1.82
9	N	142	CYS	CB-SG	-9.64	1.65	1.82
5	F	34	G	O3'-P	9.08	1.72	1.61
27	K	183	SER	CB-OG	8.27	1.53	1.42
7	L	726	SER	CB-OG	8.16	1.52	1.42
27	K	187	SER	CB-OG	7.93	1.52	1.42
27	K	190	SER	CB-OG	7.88	1.52	1.42
9	N	117	CYS	CB-SG	-7.29	1.69	1.82
16	G	145	U	O3'-P	7.22	1.69	1.61
16	G	149	G	C1'-N9	-7.21	1.36	1.46
9	N	134	CYS	CB-SG	-7.19	1.70	1.82
14	T	306	CYS	CB-SG	-7.09	1.70	1.82
16	G	4	A	C5'-C4'	6.93	1.59	1.51
17	H	58	U	C1'-N1	6.88	1.59	1.48
17	H	60	U	C1'-N1	6.86	1.59	1.48
2	B	103	G	C1'-N9	-6.85	1.37	1.46
5	F	42	C	C3'-O3'	6.78	1.51	1.42
9	N	102	CYS	CB-SG	-6.54	1.71	1.82
7	L	724	TYR	CB-CG	-6.52	1.41	1.51
27	K	93	SER	CB-OG	6.47	1.50	1.42
17	H	184	C	C1'-N1	6.42	1.58	1.48
17	H	151	C	C1'-N1	6.38	1.58	1.48
16	G	146	C	O3'-P	-6.35	1.53	1.61
27	K	43	TYR	CB-CG	-6.18	1.42	1.51
16	G	137	C	C1'-N1	6.05	1.57	1.48
27	K	40	THR	CB-OG1	5.70	1.54	1.43
16	G	4	A	O5'-C5'	5.60	1.53	1.44
17	H	43	U	C1'-N1	5.44	1.56	1.48
5	F	35	A	C3'-O3'	5.41	1.49	1.42
17	H	39	U	C1'-N1	5.40	1.56	1.48
16	G	136	U	C1'-N1	5.39	1.56	1.48
17	H	41	U	C1'-N1	5.39	1.56	1.48
17	H	37	U	C1'-N1	5.36	1.56	1.48
16	G	139	U	C1'-N1	5.35	1.56	1.48
17	H	32	U	C1'-N1	5.33	1.56	1.48
27	K	30	GLU	CB-CG	-5.32	1.42	1.52
5	F	35	A	O5'-C5'	5.32	1.52	1.44
16	G	3	A	O3'-P	-5.25	1.54	1.61
16	G	142	U	C3'-O3'	5.23	1.49	1.42
27	K	186	VAL	CA-CB	-5.11	1.44	1.54

All (124) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	G	4	A	O4'-C1'-N9	18.63	123.10	108.20
16	G	3	A	N9-C1'-C2'	13.62	131.71	114.00
16	G	8	C	N1-C1'-C2'	10.36	127.47	114.00
5	F	35	A	C4'-C3'-O3'	10.21	133.43	113.00
16	G	143	U	N1-C1'-C2'	9.61	126.49	114.00
16	G	142	U	N1-C1'-C2'	9.29	126.07	114.00
16	G	9	C	O4'-C1'-N1	9.12	115.50	108.20
16	G	17	U	N1-C2-O2	9.02	129.11	122.80
16	G	7	G	O4'-C4'-C3'	-8.92	95.08	104.00
5	F	42	C	C2'-C3'-O3'	8.80	128.85	109.50
27	K	90	PRO	CA-CB-CG	8.66	121.25	104.80
16	G	4	A	C5'-C4'-O4'	8.51	119.32	109.10
16	G	146	C	O5'-P-OP1	-8.42	98.12	105.70
16	G	3	A	O4'-C1'-N9	-8.38	101.49	108.20
16	G	17	U	N3-C2-O2	-8.23	116.44	122.20
16	G	145	U	O4'-C4'-C3'	-7.85	96.15	104.00
16	G	142	U	O4'-C1'-N1	7.83	114.47	108.20
8	M	168	LEU	CA-CB-CG	7.81	133.26	115.30
16	G	17	U	C2-N1-C1'	7.74	126.99	117.70
16	G	148	U	C2'-C3'-O3'	7.72	126.48	109.50
1	A	434	HIS	C-N-CA	7.57	140.64	121.70
16	G	5	G	N9-C4-C5	-7.57	102.37	105.40
12	R	132	LEU	CA-CB-CG	7.49	132.53	115.30
1	A	1763	LEU	CA-CB-CG	7.33	132.16	115.30
17	H	58	U	OP2-P-O3'	7.27	121.19	105.20
17	H	57	A	OP2-P-O3'	7.25	121.15	105.20
17	H	59	A	OP2-P-O3'	7.19	121.03	105.20
17	H	56	A	OP2-P-O3'	7.17	120.99	105.20
16	G	144	A	C2'-C3'-O3'	7.13	125.19	109.50
16	G	142	U	C3'-C2'-C1'	-6.83	96.04	101.50
16	G	145	U	C2'-C3'-O3'	6.82	124.62	113.70
17	H	59	A	O3'-P-O5'	-6.80	91.08	104.00
12	R	268	LEU	CA-CB-CG	6.80	130.94	115.30
17	H	57	A	O3'-P-O5'	-6.77	91.14	104.00
17	H	56	A	O3'-P-O5'	-6.76	91.16	104.00
17	H	58	U	O3'-P-O5'	-6.72	91.22	104.00
1	A	1109	LEU	CA-CB-CG	6.70	130.71	115.30
16	G	5	G	C8-N9-C4	-6.69	103.72	106.40
16	G	145	U	P-O3'-C3'	6.62	127.64	119.70
26	q	46	PRO	N-CA-CB	6.59	111.21	103.30
27	K	90	PRO	N-CA-CB	6.58	111.20	103.30
16	G	144	A	C2-N3-C4	6.56	113.88	110.60
16	G	148	U	C4'-C3'-O3'	-6.56	95.63	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	44	G	O4'-C1'-N9	6.48	113.38	108.20
26	r	46	PRO	N-CA-CB	6.45	111.04	103.30
1	A	1467	LEU	CA-CB-CG	6.44	130.12	115.30
26	q	60	PRO	N-CA-CB	6.41	110.99	103.30
16	G	8	C	C2-N1-C1'	6.41	125.85	118.80
5	F	37	C	O4'-C4'-C3'	-6.38	97.62	104.00
27	K	78	PRO	N-CA-CB	6.33	110.90	103.30
28	I	589	PRO	N-CA-CB	6.31	110.88	103.30
31	o	5	THR	N-CA-CB	-6.30	98.33	110.30
18	U	818	LEU	CA-CB-CG	6.29	129.77	115.30
16	G	146	C	O5'-P-OP2	6.28	118.24	110.70
28	I	475	PRO	N-CA-CB	6.22	110.76	103.30
27	K	107	VAL	CA-CB-CG1	6.20	120.20	110.90
16	G	9	C	C2-N1-C1'	-6.18	112.00	118.80
28	I	162	PRO	N-CA-CB	6.09	110.61	103.30
16	G	144	A	N3-C4-C5	-6.07	122.55	126.80
28	I	788	PRO	N-CA-CB	6.07	110.59	103.30
7	L	558	PRO	N-CA-CB	6.07	110.58	103.30
28	I	177	PRO	N-CA-CB	6.06	110.58	103.30
7	L	546	PRO	N-CA-CB	6.05	110.56	103.30
6	J	523	PRO	N-CA-CB	6.03	110.54	103.30
16	G	4	A	P-O5'-C5'	6.03	130.55	120.90
7	L	123	LEU	CA-CB-CG	5.98	129.05	115.30
7	L	594	PRO	N-CA-CB	5.94	110.43	103.30
28	I	160	PRO	N-CA-CB	5.93	110.42	103.30
6	J	637	PRO	N-CA-CB	5.92	110.40	103.30
28	I	518	PRO	N-CA-CB	5.91	110.39	103.30
7	L	563	PRO	N-CA-CB	5.90	110.39	103.30
28	I	816	PRO	N-CA-CB	5.90	110.38	103.30
26	r	19	PRO	N-CA-CB	5.89	110.37	103.30
26	q	19	PRO	N-CA-CB	5.89	110.36	103.30
16	G	3	A	C3'-C2'-C1'	-5.88	96.80	101.50
1	A	1510	GLU	N-CA-C	-5.87	95.16	111.00
6	J	488	PRO	N-CA-CB	5.86	110.33	103.30
16	G	4	A	C5'-C4'-C3'	5.83	125.33	116.00
1	A	260	LEU	CA-CB-CG	5.83	128.71	115.30
16	G	8	C	C6-N1-C1'	-5.83	113.81	120.80
7	L	548	PRO	N-CA-CB	5.82	110.28	103.30
31	o	27	ARG	CB-CA-C	-5.82	98.77	110.40
16	G	3	A	C4-N9-C1'	-5.81	115.84	126.30
6	J	566	PRO	N-CA-CB	5.78	110.23	103.30
16	G	16	G	P-O3'-C3'	5.76	126.61	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	620	PRO	N-CA-CB	5.75	110.20	103.30
7	L	564	PRO	N-CA-CB	5.73	110.17	103.30
5	F	36	A	C8-N9-C1'	-5.73	117.39	127.70
5	F	52	U	N3-C2-O2	-5.72	118.20	122.20
6	J	522	PRO	N-CA-CB	5.70	110.14	103.30
5	F	52	U	N1-C2-O2	5.67	126.77	122.80
7	L	77	LEU	CA-CB-CG	5.67	128.33	115.30
28	I	588	PRO	N-CA-CB	5.61	110.03	103.30
26	r	60	PRO	N-CA-CB	5.59	110.01	103.30
5	F	42	C	C3'-C2'-C1'	5.59	105.97	101.50
5	F	36	A	C4-N9-C1'	5.55	136.30	126.30
31	o	58	ASP	N-CA-CB	-5.55	100.60	110.60
7	L	774	VAL	CA-CB-CG2	5.54	119.21	110.90
5	F	33	G	P-O3'-C3'	5.54	126.35	119.70
28	I	761	PRO	N-CA-CB	5.53	109.94	103.30
17	H	13	C	N1-C2-O2	5.53	122.22	118.90
16	G	142	U	C2-N1-C1'	-5.50	111.10	117.70
27	K	93	SER	N-CA-CB	-5.50	102.25	110.50
28	I	625	PRO	N-CA-CB	5.47	109.86	103.30
3	C	758	LEU	CA-CB-CG	5.46	127.85	115.30
16	G	142	U	C4'-C3'-C2'	-5.45	97.15	102.60
1	A	1305	SER	C-N-CA	5.42	135.25	121.70
10	O	28	LEU	CA-CB-CG	5.40	127.72	115.30
18	U	820	TYR	CA-CB-CG	5.40	123.67	113.40
12	R	171	LEU	CA-CB-CG	5.34	127.58	115.30
3	C	105	MET	CA-CB-CG	5.33	122.36	113.30
31	o	47	ILE	N-CA-CB	5.33	123.05	110.80
13	S	106	ASP	CB-CG-OD1	5.32	123.09	118.30
3	C	87	GLN	CA-CB-CG	5.31	125.07	113.40
16	G	4	A	O4'-C1'-C2'	-5.29	100.51	105.80
16	G	17	U	C5-C6-N1	5.20	125.30	122.70
16	G	144	A	N3-C4-N9	5.17	131.53	127.40
5	F	50	A	P-O3'-C3'	5.15	125.89	119.70
5	F	38	G	N9-C1'-C2'	5.15	120.70	114.00
16	G	3	A	O3'-P-O5'	5.15	113.78	104.00
6	J	220	LEU	CA-CB-CG	5.12	127.08	115.30
5	F	45	A	C4-N9-C1'	5.11	135.50	126.30
15	W	146	HIS	N-CA-C	-5.07	97.31	111.00
18	U	792	SER	C-N-CA	5.00	134.21	121.70

There are no chirality outliers.

All (37) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	PRO	Peptide
1	A	1305	SER	Peptide
1	A	135	VAL	Peptide
1	A	1555	LEU	Peptide
1	A	1606	ILE	Peptide
1	A	1638	ASN	Peptide
1	A	1639	VAL	Peptide
1	A	1653	ASP	Peptide
1	A	166	PHE	Peptide
1	A	1920	TYR	Peptide
3	C	559	ILE	Peptide
3	C	560	VAL	Peptide
3	C	93	ILE	Peptide
5	F	38	G	Sidechain
16	G	143	U	Sidechain
16	G	145	U	Sidechain
16	G	146	C	Sidechain
16	G	3	A	Sidechain
16	G	4	A	Sidechain
16	G	5	G	Sidechain
16	G	6	A	Sidechain
16	G	9	C	Sidechain
6	J	240	THR	Peptide
7	L	117	THR	Peptide
7	L	118	ASP	Peptide
11	P	204	GLN	Peptide
29	Q	846	GLU	Peptide
12	R	168	ALA	Peptide
14	T	342	GLU	Peptide
14	T	405	PHE	Peptide
18	U	578	MET	Peptide
18	U	818	LEU	Peptide
33	V	374	ASP	Peptide
15	W	204	ASP	Peptide
15	W	76	VAL	Peptide
22	d	112	ASN	Peptide
22	k	112	ASN	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16477	0	16462	280	0
2	B	2060	0	1044	98	0
3	C	7022	0	7046	168	0
4	E	2366	0	2303	421	0
5	F	2075	0	1048	127	0
6	J	3817	0	2912	46	0
7	L	3369	0	2929	157	0
8	M	1098	0	1082	19	0
9	N	1184	0	1189	15	0
10	O	2340	0	2316	193	0
11	P	985	0	965	6	0
12	R	2165	0	2214	74	0
13	S	1236	0	1210	31	0
14	T	2496	0	2446	47	0
15	W	1276	0	1221	66	0
16	G	1201	0	609	232	0
17	H	2884	0	1461	279	0
18	U	2864	0	2814	146	0
19	a	399	0	173	0	0
19	h	393	0	170	0	0
20	b	424	0	179	0	0
20	i	424	0	179	0	0
21	c	406	0	170	0	0
21	j	406	0	170	0	0
22	d	480	0	200	0	0
22	k	422	0	175	0	0
23	f	361	0	158	0	0
23	m	361	0	158	0	0
24	e	391	0	163	0	0
24	l	391	0	163	0	0
25	g	363	0	160	0	0
25	n	329	0	138	0	0
26	q	659	0	296	0	0
26	r	654	0	294	0	0
26	s	335	0	168	0	0
26	t	335	0	168	0	0
27	K	980	0	741	158	0
28	I	2875	0	1374	82	0
29	Q	6554	0	2828	23	0
30	y	390	0	190	0	0
31	o	804	0	350	0	0
32	p	464	0	205	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	V	3285	0	1442	5	0
34	A	36	0	6	2	0
35	C	32	0	12	9	0
36	C	1	0	0	0	0
36	F	6	0	0	0	0
37	N	3	0	0	0	0
37	O	3	0	0	0	0
37	U	1	0	0	0	0
All	All	79882	0	61701	2254	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 17.

All (2254) 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)
10:O:155:PRO:HG3	12:R:188:PHE:CD1	1.21	1.62
16:G:120:G:H2'	29:Q:1019:SER:CB	1.24	1.60
6:J:658:ARG:HA	6:J:667:ILE:CB	1.39	1.53
6:J:496:ASP:CB	6:J:536:LEU:H	1.23	1.51
10:O:260:THR:HG23	10:O:273:GLN:CB	1.32	1.50
17:H:34:U:C5'	18:U:662:ILE:HG12	1.44	1.44
27:K:19:PHE:CE1	27:K:175:GLY:HA3	1.58	1.39
16:G:134:U:H2'	16:G:135:G:C8	1.56	1.39
27:K:19:PHE:CZ	27:K:175:GLY:HA3	1.58	1.38
10:O:155:PRO:CG	12:R:188:PHE:CD1	2.08	1.37
7:L:713:MET:HB2	27:K:124:LEU:CD2	1.55	1.36
10:O:155:PRO:CG	12:R:188:PHE:HD1	1.35	1.36
4:E:74:PHE:HA	4:E:81:LEU:CD2	1.52	1.36
4:E:84:ALA:CB	4:E:90:ILE:HD13	1.54	1.35
4:E:65:HIS:ND1	4:E:69:VAL:HG22	1.40	1.35
16:G:147:C:P	18:U:659:LYS:HD3	1.65	1.33
4:E:307:ARG:NH1	15:W:143:LEU:HD13	1.42	1.33
28:I:200:LEU:CB	28:I:207:GLU:CB	2.08	1.31
7:L:703:MET:CG	27:K:113:GLN:CG	2.06	1.31
28:I:756:VAL:CB	28:I:764:SER:CB	2.09	1.31
1:A:534:GLU:HG3	5:F:38:G:OP1	1.28	1.30
15:W:150:ALA:O	15:W:151:LYS:HD2	1.23	1.29
18:U:626:MET:HE2	18:U:643:LYS:NZ	1.43	1.29
16:G:120:G:C2'	29:Q:1019:SER:CB	2.08	1.29
27:K:131:GLY:O	27:K:135:TRP:HB2	1.23	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:54:U:H2'	17:H:55:U:C6	1.67	1.29
6:J:587:LYS:CB	6:J:593:ARG:CB	2.12	1.27
4:E:336:HIS:ND1	4:E:337:PRO:HD2	1.51	1.26
28:I:365:ALA:HA	28:I:372:ARG:CB	1.65	1.25
4:E:74:PHE:CA	4:E:81:LEU:HD21	1.66	1.25
4:E:82:ALA:CB	4:E:92:LEU:CD2	2.16	1.24
4:E:90:ILE:CD1	4:E:112:VAL:HG11	1.68	1.24
17:H:35:A:H5''	18:U:658:ARG:NH2	1.49	1.23
15:W:147:GLN:O	15:W:148:VAL:HG12	1.35	1.23
28:I:408:ASN:CB	29:Q:353:LEU:CB	2.17	1.23
4:E:82:ALA:HB2	4:E:92:LEU:CD2	1.69	1.22
28:I:172:PHE:CB	28:I:199:ARG:CB	2.18	1.22
2:B:8:G:H8	2:B:75:G:N1	1.37	1.22
4:E:88:ARG:HG2	4:E:110:GLY:O	1.34	1.22
16:G:147:C:OP1	18:U:659:LYS:HD3	1.37	1.22
4:E:321:TYR:OH	4:E:356:ILE:HG23	1.36	1.21
5:F:42:C:O2'	5:F:43:A:H5'	1.37	1.21
16:G:152:C:H2'	16:G:153:C:C6	1.74	1.21
3:C:157:ILE:HG23	3:C:158:ARG:HG2	1.23	1.20
17:H:153:A:H2'	17:H:154:C:C5'	1.72	1.20
1:A:1946:ASN:CG	1:A:1986:LEU:HD23	1.60	1.19
4:E:131:LYS:HG2	4:E:152:SER:O	1.40	1.19
4:E:65:HIS:CE1	4:E:69:VAL:HG22	1.78	1.18
27:K:19:PHE:CE2	27:K:172:LEU:HA	1.78	1.18
10:O:283:ALA:O	10:O:287:SER:HB3	1.43	1.18
4:E:76:PRO:CG	4:E:121:GLY:HA3	1.75	1.17
17:H:34:U:P	18:U:662:ILE:HD13	1.83	1.17
10:O:260:THR:CG2	10:O:273:GLN:CB	2.21	1.17
28:I:790:ARG:CB	28:I:801:ASP:CB	2.23	1.17
4:E:84:ALA:HB1	4:E:90:ILE:HD13	1.24	1.17
4:E:65:HIS:ND1	4:E:69:VAL:CG2	2.07	1.16
16:G:147:C:OP1	18:U:659:LYS:CD	1.93	1.16
5:F:43:A:H1'	16:G:4:A:N6	1.58	1.16
17:H:35:A:C5'	18:U:658:ARG:HH21	1.58	1.16
27:K:18:TYR:CD1	27:K:168:LYS:HG2	1.81	1.15
17:H:153:A:H2'	17:H:154:C:H5'	1.18	1.15
17:H:83:A:H2'	17:H:84:C:H6	1.10	1.14
17:H:7:U:C4	17:H:8:C:N4	2.16	1.14
16:G:150:U:H6	16:G:150:U:H5''	1.13	1.13
4:E:76:PRO:HG2	4:E:121:GLY:CA	1.77	1.13
6:J:773:ARG:CB	6:J:790:THR:CB	2.26	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:I:374:ILE:CB	29:Q:357:ALA:CB	2.25	1.12
6:J:496:ASP:CB	6:J:536:LEU:N	2.09	1.12
7:L:707:ALA:HB2	27:K:117:GLN:OE1	1.44	1.12
17:H:34:U:H5'	18:U:662:ILE:CG1	1.77	1.12
4:E:62:LEU:HB2	4:E:351:LEU:HB2	1.26	1.12
27:K:19:PHE:CZ	27:K:175:GLY:CA	2.31	1.12
1:A:466:ALA:HA	2:B:20:G:N2	1.63	1.12
28:I:374:ILE:CB	29:Q:357:ALA:HB2	1.80	1.12
1:A:466:ALA:CA	2:B:20:G:H21	1.61	1.11
5:F:44:G:N2	16:G:3:A:N6	1.98	1.11
7:L:710:ALA:CB	27:K:120:ARG:HD3	1.79	1.11
16:G:152:C:C2	16:G:153:C:C5	2.38	1.11
7:L:710:ALA:HB1	27:K:120:ARG:HD3	1.14	1.11
7:L:780:ARG:HB2	27:K:188:LEU:HD21	1.26	1.11
4:E:307:ARG:NH1	15:W:143:LEU:CD1	2.13	1.11
10:O:260:THR:HG23	10:O:273:GLN:HB3	1.28	1.11
4:E:129:THR:HG22	4:E:153:PHE:HD2	1.06	1.11
4:E:59:ILE:HD12	15:W:82:ASN:HD21	1.12	1.10
6:J:658:ARG:CA	6:J:667:ILE:CB	2.29	1.10
4:E:84:ALA:HB2	4:E:90:ILE:HG23	1.22	1.10
4:E:90:ILE:HD11	4:E:112:VAL:HG11	1.30	1.10
7:L:731:LEU:HB2	27:K:142:LEU:HD23	1.26	1.10
4:E:108:HIS:ND1	4:E:128:SER:HB2	1.64	1.10
17:H:83:A:H2'	17:H:84:C:C6	1.85	1.10
4:E:131:LYS:HG2	4:E:152:SER:C	1.72	1.09
18:U:626:MET:CE	18:U:643:LYS:NZ	2.15	1.09
4:E:82:ALA:HB2	4:E:92:LEU:HD22	1.20	1.09
17:H:27:U:O2'	17:H:28:C:H5'	1.51	1.09
1:A:1517:LYS:CD	1:A:1522:GLN:HG2	1.82	1.08
17:H:69:U:H2'	17:H:70:C:C6	1.88	1.08
4:E:75:HIS:HB2	4:E:80:THR:O	1.53	1.08
16:G:145:U:C6	16:G:145:U:H5'	1.89	1.08
17:H:154:C:O2'	17:H:155:C:H5'	1.52	1.08
18:U:626:MET:CE	18:U:643:LYS:HZ1	1.65	1.08
2:B:77:G:N7	2:B:80:U:C5	2.22	1.08
4:E:307:ARG:HH12	15:W:143:LEU:CD1	1.66	1.08
5:F:37:C:H2'	5:F:38:G:H5'	1.30	1.07
7:L:710:ALA:HA	27:K:124:LEU:CD2	1.84	1.07
7:L:713:MET:HB3	27:K:124:LEU:HG	1.30	1.07
15:W:147:GLN:O	15:W:148:VAL:CG1	2.02	1.07
1:A:1517:LYS:HD2	1:A:1522:GLN:CG	1.82	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:43:A:C1'	16:G:4:A:H61	1.68	1.07
7:L:762:ALA:HB1	27:K:14:ASP:OD1	1.51	1.07
17:H:182:U:O2'	17:H:183:G:H5'	1.54	1.06
17:H:93:A:O2'	17:H:94:A:H5'	1.55	1.06
7:L:780:ARG:CB	27:K:188:LEU:HD21	1.86	1.06
16:G:5:G:C4	16:G:6:A:C8	2.44	1.06
1:A:51:PHE:CZ	4:E:66:GLU:CG	2.38	1.05
4:E:55:LEU:HG	4:E:96:TYR:OH	1.56	1.05
5:F:37:C:C2'	5:F:38:G:H5'	1.85	1.05
17:H:179:C:H2'	17:H:180:G:H8	1.20	1.05
10:O:223:LEU:HG	10:O:285:GLU:HA	1.10	1.05
4:E:82:ALA:CB	4:E:92:LEU:HD23	1.86	1.05
4:E:84:ALA:HB2	4:E:90:ILE:HD13	1.38	1.05
3:C:166:CYS:SG	3:C:536:ARG:NE	2.28	1.05
10:O:155:PRO:CA	12:R:188:PHE:HE1	1.69	1.05
17:H:69:U:O2'	17:H:70:C:H5'	1.57	1.05
17:H:153:A:C2'	17:H:154:C:H5'	1.85	1.05
28:I:465:ARG:CB	28:I:543:ARG:NH2	2.20	1.04
4:E:65:HIS:CD2	4:E:91:LEU:HD11	1.92	1.04
4:E:94:ASN:O	4:E:99:CYS:HA	1.56	1.04
4:E:125:PHE:CE2	4:E:159:PRO:HB3	1.93	1.04
5:F:44:G:C2	16:G:3:A:N6	2.26	1.04
10:O:260:THR:HG23	10:O:273:GLN:HB2	1.08	1.04
17:H:92:U:H2'	17:H:93:A:H8	1.20	1.04
4:E:266:PRO:HG2	7:L:785:GLN:HB2	1.39	1.04
17:H:69:U:H2'	17:H:70:C:H6	1.19	1.03
3:C:165:LEU:O	3:C:169:ASP:HB3	1.57	1.03
10:O:155:PRO:N	12:R:188:PHE:HE1	1.54	1.03
7:L:713:MET:HB2	27:K:124:LEU:HD23	1.35	1.03
10:O:256:GLY:HA2	12:R:70:ALA:CB	1.89	1.03
28:I:343:LEU:CB	29:Q:527:ILE:CB	2.37	1.03
16:G:134:U:C2'	16:G:135:G:C8	2.40	1.03
2:B:75:G:C5	2:B:76:A:N7	2.26	1.02
18:U:548:LEU:HD22	18:U:661:ALA:CB	1.87	1.02
4:E:108:HIS:CE1	4:E:128:SER:HB2	1.93	1.02
4:E:129:THR:HG22	4:E:153:PHE:CD2	1.94	1.02
10:O:260:THR:CG2	10:O:273:GLN:HB3	1.87	1.02
10:O:245:GLU:OE2	10:O:261:ILE:HG21	1.59	1.01
16:G:6:A:C6	16:G:7:G:C5	2.48	1.01
17:H:34:U:C5'	18:U:662:ILE:CG1	2.34	1.01
5:F:92:A:C2	5:F:93:G:C5	2.48	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:108:G:H2'	17:H:109:C:C6	1.94	1.01
4:E:54:SER:CB	4:E:355:GLU:OE2	2.09	1.01
4:E:108:HIS:CE1	4:E:128:SER:CB	2.43	1.01
1:A:466:ALA:HA	2:B:20:G:H21	0.84	1.01
27:K:19:PHE:CE1	27:K:175:GLY:CA	2.44	1.01
1:A:51:PHE:HZ	4:E:66:GLU:HG3	1.25	1.00
7:L:710:ALA:HA	27:K:124:LEU:HD23	1.40	1.00
10:O:229:LYS:HG3	10:O:277:ARG:NH1	1.75	1.00
17:H:34:U:OP1	18:U:662:ILE:HD13	1.57	1.00
1:A:1946:ASN:CB	1:A:1986:LEU:HD23	1.91	1.00
4:E:298:SER:C	4:E:314:THR:HB	1.82	1.00
28:I:343:LEU:CA	29:Q:527:ILE:CB	2.40	1.00
4:E:65:HIS:CD2	4:E:91:LEU:CD1	2.44	1.00
7:L:713:MET:HB2	27:K:124:LEU:HD21	1.44	0.99
4:E:54:SER:CB	4:E:355:GLU:CD	2.31	0.99
7:L:767:LEU:HD21	27:K:177:LYS:HB2	1.41	0.99
10:O:229:LYS:CD	10:O:277:ARG:HH12	1.76	0.99
16:G:144:A:H5''	16:G:144:A:N3	1.78	0.99
1:A:51:PHE:CZ	4:E:66:GLU:HB3	1.98	0.99
10:O:223:LEU:CG	10:O:285:GLU:HA	1.93	0.99
1:A:1946:ASN:CG	1:A:1986:LEU:CD2	2.31	0.99
4:E:125:PHE:HE2	4:E:159:PRO:CB	1.76	0.99
7:L:767:LEU:CD2	27:K:177:LYS:HB2	1.92	0.98
4:E:84:ALA:CB	4:E:90:ILE:CD1	2.41	0.98
10:O:155:PRO:N	12:R:188:PHE:CE1	2.31	0.98
10:O:234:LEU:HD11	10:O:274:PHE:CE2	1.98	0.98
10:O:155:PRO:HG3	12:R:188:PHE:CE1	1.99	0.98
4:E:321:TYR:OH	4:E:356:ILE:CG2	2.12	0.98
6:J:773:ARG:CB	6:J:787:LYS:HA	1.93	0.97
2:B:67:A:H4'	2:B:68:C:C4	2.00	0.97
10:O:234:LEU:HD11	10:O:274:PHE:CZ	1.99	0.97
2:B:77:G:N7	2:B:80:U:H5	1.59	0.97
7:L:692:LEU:CB	27:K:107:VAL:HG11	1.94	0.97
17:H:83:A:O2'	17:H:84:C:H5'	1.63	0.97
27:K:131:GLY:O	27:K:135:TRP:CB	2.13	0.97
7:L:731:LEU:CB	27:K:142:LEU:HD23	1.95	0.97
7:L:710:ALA:HB1	27:K:120:ARG:CD	1.94	0.97
16:G:150:U:H5''	16:G:150:U:C6	2.00	0.97
16:G:152:C:H3'	16:G:153:C:C5	2.00	0.97
17:H:54:U:H2'	17:H:55:U:H6	1.03	0.97
10:O:149:LYS:HE3	10:O:290:LYS:HZ2	1.29	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1514:LYS:NZ	1:A:1529:ILE:HD11	1.80	0.96
4:E:54:SER:HB2	4:E:355:GLU:CD	1.85	0.96
7:L:713:MET:CB	27:K:124:LEU:CD2	2.43	0.96
28:I:176:SER:CB	28:I:196:ALA:HB1	1.95	0.96
1:A:1827:TRP:HH2	1:A:1837:ALA:HB2	1.29	0.96
10:O:220:MET:HG2	10:O:221:PRO:HD2	1.45	0.96
7:L:713:MET:CB	27:K:124:LEU:HG	1.95	0.96
16:G:152:C:C2'	16:G:153:C:C5	2.49	0.96
4:E:119:THR:CG2	4:E:161:ARG:HB3	1.96	0.96
10:O:223:LEU:HD13	10:O:223:LEU:H	1.30	0.95
16:G:152:C:C4	16:G:153:C:N4	2.34	0.95
28:I:374:ILE:CB	29:Q:357:ALA:HB3	1.95	0.95
10:O:155:PRO:CG	12:R:188:PHE:CE1	2.49	0.95
3:C:538:HIS:HE1	3:C:551:LEU:CD1	1.79	0.95
17:H:56:A:N6	17:H:92:U:C4	2.34	0.95
1:A:1518:LEU:O	1:A:1519:THR:OG1	1.85	0.95
4:E:298:SER:HA	4:E:314:THR:HG21	1.47	0.95
7:L:759:GLU:OE1	27:K:17:PRO:HD2	1.65	0.95
4:E:78:GLY:HA3	4:E:336:HIS:HE1	1.31	0.95
5:F:36:A:N1	16:G:10:U:N3	2.15	0.95
10:O:245:GLU:OE2	10:O:261:ILE:CG2	2.14	0.95
17:H:83:A:C4	17:H:84:C:C5	2.55	0.95
7:L:764:PRO:O	7:L:765:ARG:CG	2.14	0.94
16:G:148:U:H6	16:G:148:U:H5'	1.30	0.94
16:G:148:U:N3	17:H:30:A:C2	2.36	0.94
7:L:707:ALA:HB2	27:K:117:GLN:CD	1.88	0.94
12:R:232:SEP:HB3	14:T:372:LYS:HE3	1.48	0.94
16:G:27:U:O2'	16:G:28:A:O5'	1.86	0.94
17:H:27:U:C2'	17:H:28:C:H5'	1.96	0.94
17:H:147:G:C6	17:H:148:C:N4	2.36	0.94
1:A:1518:LEU:O	1:A:1519:THR:CB	2.16	0.94
16:G:120:G:H2'	29:Q:1019:SER:CA	1.97	0.94
4:E:118:ASN:HD22	4:E:119:THR:H	1.10	0.94
7:L:780:ARG:HB2	27:K:188:LEU:CD2	1.97	0.94
4:E:59:ILE:HD12	15:W:82:ASN:ND2	1.83	0.93
17:H:93:A:C2'	17:H:94:A:H5'	1.97	0.93
17:H:35:A:C5'	18:U:658:ARG:NH2	2.23	0.93
4:E:119:THR:CG2	4:E:161:ARG:CB	2.47	0.93
4:E:298:SER:HA	4:E:314:THR:CG2	1.99	0.93
3:C:142:LYS:HG2	3:C:228:PHE:HD2	1.34	0.93
4:E:95:VAL:HG13	4:E:353:MET:CE	1.99	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:731:LEU:HB2	27:K:142:LEU:CD2	1.99	0.93
10:O:229:LYS:CG	10:O:277:ARG:HH12	1.82	0.93
5:F:36:A:C2	16:G:10:U:O2	2.22	0.93
17:H:56:A:N6	17:H:92:U:N3	2.17	0.93
29:Q:358:GLU:O	29:Q:364:SER:CB	2.16	0.93
10:O:260:THR:N	10:O:273:GLN:HB3	1.83	0.92
16:G:152:C:H2'	16:G:153:C:C5	2.03	0.92
4:E:99:CYS:SG	4:E:353:MET:SD	2.67	0.92
4:E:307:ARG:HH11	15:W:143:LEU:HD22	1.33	0.92
17:H:57:A:N6	17:H:91:U:H3	1.68	0.92
7:L:699:ASN:HA	27:K:114:LEU:HB2	1.50	0.92
16:G:152:C:C5	16:G:153:C:N4	2.37	0.92
10:O:259:ARG:HG2	10:O:275:ALA:N	1.84	0.92
2:B:75:G:C6	2:B:76:A:N7	2.37	0.92
4:E:271:GLU:OE2	4:E:273:CYS:SG	2.28	0.92
6:J:604:PRO:HA	6:J:607:LYS:N	1.83	0.92
4:E:66:GLU:CA	4:E:87:ASP:OD2	2.18	0.92
7:L:710:ALA:O	27:K:124:LEU:HD21	1.69	0.92
16:G:152:C:H2'	16:G:153:C:H6	1.32	0.92
7:L:767:LEU:HD22	27:K:177:LYS:CB	2.00	0.92
5:F:38:G:C2	5:F:39:A:C5	2.58	0.91
5:F:44:G:N1	16:G:2:U:C5	2.38	0.91
4:E:298:SER:O	4:E:314:THR:HB	1.70	0.91
7:L:732:MET:N	27:K:142:LEU:HD21	1.86	0.91
18:U:811:ARG:HH11	18:U:811:ARG:HG3	1.36	0.91
10:O:253:TYR:CE1	13:S:93:THR:OG1	2.24	0.91
17:H:34:U:O2'	17:H:35:A:C8	2.23	0.91
4:E:78:GLY:HA3	4:E:336:HIS:CE1	2.05	0.91
17:H:172:C:O2'	17:H:173:C:H5'	1.71	0.91
17:H:106:G:N2	17:H:107:A:C2	2.39	0.91
16:G:146:C:OP1	18:U:658:ARG:HD2	1.68	0.91
16:G:134:U:H2'	16:G:135:G:N7	1.84	0.90
10:O:155:PRO:CD	12:R:188:PHE:CE1	2.53	0.90
10:O:223:LEU:HG	10:O:285:GLU:CA	2.00	0.90
17:H:179:C:H2'	17:H:180:G:C8	2.05	0.90
3:C:142:LYS:HG2	3:C:228:PHE:CD2	2.05	0.90
17:H:179:C:O2'	17:H:180:G:H5'	1.69	0.90
4:E:65:HIS:HD2	4:E:91:LEU:HD11	1.30	0.90
16:G:146:C:H1'	16:G:147:C:C6	2.07	0.90
1:A:534:GLU:CG	5:F:38:G:OP1	2.16	0.90
4:E:82:ALA:HB1	4:E:92:LEU:CD2	1.97	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:325:GLY:O	4:E:352:TYR:CE2	2.25	0.90
17:H:92:U:H2'	17:H:93:A:C8	2.05	0.90
7:L:731:LEU:CB	27:K:142:LEU:CD2	2.50	0.90
17:H:35:A:H5'	18:U:658:ARG:HH21	1.37	0.90
27:K:19:PHE:CE2	27:K:172:LEU:CA	2.55	0.90
4:E:76:PRO:HG2	4:E:121:GLY:HA3	0.91	0.89
4:E:125:PHE:HE2	4:E:159:PRO:HB3	1.27	0.89
2:B:70:A:N3	2:B:70:A:H5''	1.87	0.89
4:E:92:LEU:O	4:E:101:ASN:HA	1.72	0.89
28:I:465:ARG:CB	28:I:543:ARG:HH22	1.79	0.89
10:O:256:GLY:HA2	12:R:70:ALA:HB3	1.52	0.89
16:G:6:A:H2'	16:G:7:G:C1'	2.02	0.89
3:C:158:ARG:HA	3:C:158:ARG:NH2	1.88	0.89
10:O:259:ARG:CG	10:O:274:PHE:C	2.40	0.89
18:U:666:ARG:HH21	18:U:666:ARG:HG2	1.36	0.89
27:K:135:TRP:O	27:K:136:LYS:CG	2.21	0.89
5:F:44:G:N1	16:G:2:U:C4	2.41	0.89
10:O:234:LEU:O	10:O:271:PHE:HA	1.72	0.89
4:E:124:LEU:HD12	4:E:125:PHE:N	1.86	0.89
10:O:259:ARG:H	10:O:274:PHE:HA	1.34	0.89
16:G:27:U:C2'	16:G:28:A:O5'	2.19	0.89
1:A:51:PHE:CZ	4:E:66:GLU:CB	2.57	0.88
7:L:767:LEU:HD22	27:K:177:LYS:HB3	1.55	0.88
16:G:152:C:C2'	16:G:153:C:C6	2.55	0.88
17:H:182:U:H2'	17:H:183:G:H8	1.36	0.88
5:F:44:G:C6	16:G:2:U:C5	2.61	0.88
15:W:150:ALA:O	15:W:151:LYS:CD	2.18	0.88
16:G:21:A:H4'	16:G:22:C:OP1	1.71	0.88
17:H:150:U:H2'	17:H:151:C:H6	1.37	0.88
10:O:260:THR:HG23	10:O:273:GLN:CG	2.03	0.88
16:G:147:C:P	18:U:659:LYS:CD	2.59	0.88
28:I:520:ILE:O	28:I:524:TYR:N	2.06	0.88
1:A:51:PHE:CZ	4:E:66:GLU:HG3	2.04	0.88
4:E:54:SER:HB3	4:E:355:GLU:OE2	1.72	0.88
16:G:2:U:N3	18:U:625:PHE:CD2	2.41	0.88
17:H:147:G:C2	17:H:148:C:C4	2.62	0.88
1:A:1522:GLN:HA	1:A:1522:GLN:NE2	1.87	0.88
2:B:8:G:C8	2:B:75:G:N1	2.26	0.88
3:C:690:GLU:O	3:C:788:LYS:HB3	1.74	0.88
16:G:144:A:H5''	16:G:144:A:C4	2.09	0.88
4:E:336:HIS:ND1	4:E:337:PRO:CD	2.37	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:307:ARG:HH12	15:W:143:LEU:HD13	0.74	0.87
10:O:253:TYR:HE1	13:S:93:THR:OG1	1.57	0.87
28:I:343:LEU:HA	29:Q:527:ILE:CB	2.02	0.87
10:O:155:PRO:CD	12:R:188:PHE:CD1	2.57	0.87
16:G:146:C:O2'	16:G:147:C:C6	2.27	0.87
4:E:131:LYS:HA	4:E:154:VAL:HG23	1.56	0.87
5:F:36:A:N1	16:G:10:U:C2	2.43	0.87
16:G:148:U:O2	16:G:149:G:N2	2.08	0.87
4:E:95:VAL:HG13	4:E:353:MET:HE3	1.57	0.87
27:K:19:PHE:HE2	27:K:172:LEU:HA	1.36	0.87
4:E:62:LEU:CB	4:E:351:LEU:HB2	2.04	0.87
4:E:326:HIS:HD2	4:E:330:ILE:HG12	1.38	0.87
7:L:727:ARG:O	7:L:731:LEU:HD23	1.73	0.87
3:C:160:ARG:NH1	3:C:160:ARG:O	2.08	0.87
17:H:8:C:H2'	17:H:9:U:C6	2.10	0.86
17:H:33:G:O3'	18:U:662:ILE:HD13	1.73	0.86
7:L:731:LEU:HB3	27:K:142:LEU:HG	1.55	0.86
1:A:51:PHE:HZ	4:E:66:GLU:CG	1.79	0.86
4:E:90:ILE:HD11	4:E:112:VAL:CG1	2.05	0.86
4:E:257:ASN:HB2	15:W:149:SER:CB	2.05	0.86
16:G:5:G:N3	16:G:6:A:N7	2.22	0.86
5:F:44:G:N2	16:G:3:A:C6	2.43	0.86
18:U:548:LEU:HD22	18:U:661:ALA:HB2	1.57	0.86
17:H:98:G:O2'	17:H:99:A:H5'	1.76	0.86
17:H:151:C:H2'	17:H:152:G:C8	2.11	0.86
16:G:6:A:C5	16:G:7:G:N7	2.44	0.86
28:I:520:ILE:O	28:I:524:TYR:CB	2.23	0.86
16:G:152:C:C3'	16:G:153:C:C5	2.58	0.86
4:E:62:LEU:HD13	4:E:93:TRP:CD2	2.11	0.85
4:E:131:LYS:CG	4:E:152:SER:O	2.23	0.85
7:L:724:TYR:CG	27:K:135:TRP:CG	2.64	0.85
16:G:152:C:C3'	16:G:153:C:H5	1.89	0.85
4:E:257:ASN:HB2	15:W:149:SER:HB3	1.58	0.85
7:L:252:ARG:HG2	7:L:252:ARG:HH11	1.41	0.85
16:G:152:C:C2	16:G:153:C:C4	2.63	0.85
18:U:668:LEU:HD12	18:U:668:LEU:O	1.77	0.85
7:L:767:LEU:CD2	27:K:177:LYS:CB	2.53	0.85
4:E:93:TRP:HA	4:E:101:ASN:HA	1.58	0.85
4:E:116:HIS:O	4:E:124:LEU:HD13	1.76	0.85
4:E:54:SER:HA	4:E:355:GLU:OE2	1.76	0.85
7:L:710:ALA:CB	27:K:120:ARG:CD	2.55	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:260:THR:H	10:O:273:GLN:HB3	1.41	0.84
16:G:6:A:H2'	16:G:7:G:H1'	1.58	0.84
4:E:307:ARG:HH11	15:W:143:LEU:CD2	1.90	0.84
4:E:84:ALA:HB2	4:E:90:ILE:CD1	2.02	0.84
10:O:155:PRO:CA	12:R:188:PHE:CE1	2.58	0.84
17:H:74:U:H2'	17:H:75:A:H8	1.40	0.84
1:A:50:LYS:HB2	4:E:88:ARG:HH12	1.42	0.84
17:H:8:C:H2'	17:H:9:U:H6	1.41	0.84
4:E:115:LEU:HD22	4:E:126:SER:HB3	1.60	0.84
17:H:55:U:C4	17:H:93:A:N6	2.46	0.84
4:E:54:SER:CA	4:E:355:GLU:OE2	2.25	0.84
7:L:710:ALA:O	27:K:124:LEU:CD2	2.26	0.84
10:O:149:LYS:HE3	10:O:290:LYS:NZ	1.92	0.84
16:G:134:U:H4'	16:G:135:G:OP1	1.78	0.84
16:G:146:C:O2'	16:G:147:C:O5'	1.94	0.84
17:H:7:U:C4	17:H:8:C:C4	2.65	0.84
7:L:692:LEU:HB3	27:K:107:VAL:CB	2.08	0.83
10:O:259:ARG:HG2	10:O:274:PHE:C	1.98	0.83
16:G:144:A:N7	18:U:624:LYS:NZ	2.25	0.83
4:E:108:HIS:ND1	4:E:128:SER:CB	2.42	0.83
5:F:35:A:O2'	5:F:36:A:OP1	1.95	0.83
16:G:148:U:N3	17:H:30:A:H2	1.77	0.83
4:E:108:HIS:CE1	4:E:128:SER:HB3	2.11	0.83
15:W:147:GLN:C	15:W:148:VAL:CG1	2.44	0.83
28:I:521:VAL:O	28:I:527:PHE:CB	2.27	0.83
4:E:116:HIS:CE1	4:E:158:TYR:CD1	2.67	0.82
4:E:162:ARG:NH2	4:E:203:ASP:O	2.12	0.82
7:L:713:MET:CB	27:K:124:LEU:CG	2.57	0.82
17:H:166:G:N2	17:H:166:G:OP2	2.11	0.82
4:E:66:GLU:N	4:E:87:ASP:OD2	2.11	0.82
10:O:283:ALA:O	10:O:287:SER:CB	2.26	0.82
1:A:1514:LYS:HZ2	1:A:1529:ILE:HD11	1.39	0.82
16:G:6:A:C6	16:G:7:G:C6	2.67	0.82
4:E:129:THR:CG2	4:E:153:PHE:HD2	1.91	0.82
4:E:266:PRO:HG2	7:L:785:GLN:CB	2.09	0.82
10:O:234:LEU:CD1	10:O:274:PHE:CZ	2.61	0.82
10:O:235:TYR:HD2	10:O:301:LYS:HB2	1.44	0.82
15:W:146:HIS:O	15:W:148:VAL:HG13	1.80	0.82
28:I:749:SER:O	28:I:753:THR:N	2.13	0.82
4:E:66:GLU:CB	4:E:87:ASP:OD2	2.28	0.82
4:E:88:ARG:CG	4:E:110:GLY:O	2.24	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:44:G:C8	16:G:1:G:N2	2.48	0.82
27:K:19:PHE:CD2	27:K:172:LEU:HA	2.13	0.82
4:E:78:GLY:CA	4:E:336:HIS:HE1	1.93	0.81
7:L:692:LEU:CA	27:K:107:VAL:HG11	2.10	0.81
16:G:150:U:H6	16:G:150:U:C5'	1.92	0.81
27:K:19:PHE:HE2	27:K:172:LEU:CA	1.92	0.81
4:E:84:ALA:HB2	4:E:90:ILE:CG2	2.07	0.81
4:E:243:LEU:CD1	4:E:247:GLY:HA2	2.10	0.81
5:F:37:C:H2'	5:F:38:G:C5'	2.10	0.81
4:E:59:ILE:CD1	15:W:82:ASN:HD21	1.92	0.81
10:O:260:THR:O	10:O:273:GLN:N	2.13	0.81
17:H:151:C:H2'	17:H:152:G:H8	1.45	0.81
4:E:59:ILE:CD1	15:W:82:ASN:ND2	2.44	0.81
7:L:692:LEU:HB3	27:K:107:VAL:CG1	2.10	0.81
12:R:184:GLN:HE21	12:R:184:GLN:HA	1.46	0.81
1:A:1946:ASN:HD22	1:A:1949:ARG:HB3	1.44	0.81
4:E:118:ASN:HD22	4:E:119:THR:N	1.79	0.81
10:O:260:THR:CG2	10:O:273:GLN:CG	2.58	0.81
17:H:33:G:O5'	18:U:666:ARG:NE	2.14	0.81
17:H:105:G:H2'	17:H:106:G:H5''	1.61	0.81
4:E:57:ALA:O	4:E:355:GLU:CB	2.29	0.81
4:E:78:GLY:CA	4:E:336:HIS:CE1	2.64	0.80
4:E:83:SER:O	4:E:91:LEU:N	2.14	0.80
16:G:125:C:OP2	16:G:125:C:H4'	1.78	0.80
17:H:154:C:H2'	17:H:155:C:C6	2.16	0.80
4:E:116:HIS:CE1	4:E:158:TYR:CE1	2.69	0.80
17:H:34:U:H5''	18:U:662:ILE:HG12	0.81	0.80
4:E:269:PRO:O	4:E:270:LYS:HB3	1.81	0.80
16:G:148:U:H3	17:H:30:A:H2	1.25	0.80
17:H:153:A:H2'	17:H:154:C:H5''	1.62	0.80
5:F:92:A:N1	5:F:93:G:C6	2.50	0.80
16:G:152:C:H3'	16:G:153:C:H5	1.41	0.80
16:G:5:G:C4	16:G:6:A:N7	2.49	0.80
27:K:125:GLU:O	27:K:129:GLN:HB2	1.81	0.80
7:L:763:ILE:CB	7:L:764:PRO:HD2	2.12	0.80
17:H:79:G:H2'	17:H:80:A:H8	1.46	0.80
17:H:172:C:H2'	17:H:173:C:C6	2.17	0.80
2:B:77:G:O6	2:B:80:U:C4	2.35	0.79
5:F:90:G:N2	17:H:8:C:O2	2.15	0.79
16:G:148:U:C2	17:H:30:A:H2	1.98	0.79
2:B:8:G:C8	2:B:75:G:C6	2.69	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:46:U:O4	2:B:47:A:N6	2.16	0.79
10:O:224:ASP:O	10:O:302:TRP:NE1	2.15	0.79
4:E:111:ALA:O	4:E:113:MET:N	2.15	0.79
28:I:463:PRO:O	28:I:464:ALA:HB2	1.82	0.79
16:G:152:C:N1	16:G:153:C:C5	2.49	0.79
2:B:75:G:C5	2:B:76:A:C8	2.71	0.79
4:E:65:HIS:CD2	4:E:91:LEU:HD12	2.17	0.79
4:E:115:LEU:CD2	4:E:126:SER:HB3	2.13	0.79
4:E:149:GLY:O	4:E:177:LYS:NZ	2.16	0.79
17:H:54:U:C2'	17:H:55:U:H6	1.92	0.79
5:F:42:C:HO2'	5:F:43:A:H5'	1.46	0.79
10:O:229:LYS:HD2	10:O:277:ARG:HH12	1.47	0.79
17:H:172:C:H2'	17:H:173:C:H6	1.46	0.78
28:I:325:VAL:O	28:I:328:GLU:CB	2.31	0.78
17:H:101:U:H5''	17:H:102:U:H5'	1.64	0.78
4:E:123:MET:HB3	4:E:125:PHE:HE1	1.47	0.78
4:E:125:PHE:CE2	4:E:159:PRO:CB	2.60	0.78
10:O:229:LYS:HD2	10:O:277:ARG:NH1	1.99	0.78
16:G:7:G:H2'	16:G:7:G:N3	1.97	0.78
17:H:153:A:C2'	17:H:154:C:C5'	2.52	0.78
4:E:266:PRO:CG	7:L:785:GLN:HB2	2.12	0.78
7:L:763:ILE:CB	7:L:764:PRO:CD	2.61	0.78
16:G:148:U:H5'	16:G:148:U:C6	2.18	0.78
1:A:888:GLN:N	1:A:888:GLN:HE21	1.81	0.78
1:A:1517:LYS:HB2	1:A:1517:LYS:NZ	1.98	0.78
4:E:69:VAL:CG1	4:E:345:ALA:HB1	2.14	0.78
28:I:545:ILE:HG12	28:I:546:SER:N	1.97	0.78
17:H:147:G:C4	17:H:148:C:C5	2.72	0.78
4:E:118:ASN:ND2	4:E:119:THR:H	1.81	0.77
7:L:713:MET:HB2	27:K:124:LEU:CG	2.15	0.77
17:H:7:U:O4	17:H:8:C:N4	2.16	0.77
2:B:35:U:C5'	2:B:35:U:H6	1.98	0.77
17:H:33:G:O3'	18:U:662:ILE:CD1	2.32	0.77
17:H:34:U:P	18:U:662:ILE:CD1	2.72	0.77
4:E:84:ALA:CB	4:E:90:ILE:HG23	2.11	0.77
7:L:699:ASN:CG	27:K:114:LEU:HB3	2.05	0.77
16:G:9:C:H2'	16:G:10:U:C6	2.20	0.77
4:E:326:HIS:CE1	4:E:352:TYR:HD2	2.02	0.77
7:L:710:ALA:CA	27:K:124:LEU:CD2	2.61	0.77
17:H:150:U:H2'	17:H:151:C:C6	2.17	0.77
7:L:692:LEU:HB3	27:K:107:VAL:HG11	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:710:ALA:HA	27:K:124:LEU:HD22	1.66	0.77
17:H:83:A:C6	17:H:84:C:N4	2.52	0.77
17:H:183:G:H2'	17:H:184:C:H6	1.49	0.77
4:E:55:LEU:CG	4:E:96:TYR:OH	2.32	0.77
17:H:154:C:HO2'	17:H:155:C:H5'	1.50	0.77
17:H:69:U:C2	17:H:70:C:C5	2.73	0.77
1:A:1827:TRP:CH2	1:A:1837:ALA:HB2	2.18	0.77
10:O:256:GLY:HA2	12:R:70:ALA:HB2	1.67	0.76
5:F:36:A:C5'	5:F:36:A:H8	1.99	0.76
10:O:259:ARG:HB2	10:O:273:GLN:C	2.05	0.76
10:O:259:ARG:HG3	10:O:274:PHE:C	2.05	0.76
16:G:9:C:O2'	16:G:10:U:O4'	2.03	0.76
2:B:75:G:N7	2:B:76:A:N7	2.33	0.76
16:G:151:C:O2'	16:G:152:C:H5''	1.84	0.76
7:L:692:LEU:O	27:K:107:VAL:HG13	1.84	0.76
10:O:229:LYS:CG	10:O:277:ARG:NH1	2.43	0.76
18:U:626:MET:CE	18:U:643:LYS:HZ2	1.97	0.76
28:I:465:ARG:CB	28:I:543:ARG:CZ	2.64	0.76
4:E:108:HIS:HD2	4:E:136:TRP:HH2	1.33	0.76
17:H:177:A:H5''	17:H:178:A:OP1	1.84	0.76
4:E:147:LEU:N	4:E:147:LEU:HD23	2.01	0.76
4:E:165:GLN:O	4:E:166:LEU:HD23	1.85	0.76
27:K:19:PHE:CZ	27:K:175:GLY:C	2.59	0.76
5:F:42:C:O2'	5:F:43:A:C5'	2.28	0.75
5:F:38:G:N3	5:F:39:A:C8	2.54	0.75
7:L:759:GLU:OE1	27:K:171:GLN:NE2	2.19	0.75
18:U:655:GLU:HA	18:U:658:ARG:HG2	1.67	0.75
4:E:82:ALA:CA	4:E:92:LEU:HD23	2.16	0.75
3:C:115:GLU:OE1	3:C:189:VAL:HG23	1.85	0.75
5:F:36:A:N1	16:G:10:U:O2	2.20	0.75
16:G:120:G:C2'	29:Q:1019:SER:CA	2.59	0.75
27:K:19:PHE:CD1	27:K:175:GLY:HA3	2.19	0.75
1:A:532:THR:HB	16:G:3:A:O5'	1.85	0.75
2:B:8:G:N7	2:B:75:G:O6	2.18	0.75
4:E:78:GLY:O	4:E:336:HIS:CE1	2.39	0.75
18:U:626:MET:HE2	18:U:643:LYS:HZ1	0.71	0.75
27:K:19:PHE:CE2	27:K:175:GLY:HA3	2.18	0.75
5:F:42:C:H2'	5:F:43:A:C8	2.21	0.75
7:L:699:ASN:CG	27:K:111:MET:HA	2.06	0.75
10:O:149:LYS:CE	10:O:290:LYS:HZ2	2.00	0.75
1:A:417:ARG:NH2	2:B:59:G:OP1	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:160:ARG:HH11	3:C:160:ARG:HG3	1.52	0.75
7:L:759:GLU:HG2	27:K:167:ARG:HD2	1.68	0.75
3:C:538:HIS:CE1	3:C:551:LEU:CD1	2.67	0.75
6:J:642:SER:CB	6:J:650:GLU:HA	2.17	0.74
7:L:731:LEU:HB3	27:K:142:LEU:CG	2.15	0.74
17:H:93:A:O2'	17:H:94:A:C5'	2.33	0.74
1:A:51:PHE:CE1	4:E:66:GLU:HB3	2.22	0.74
2:B:8:G:C8	2:B:75:G:O6	2.40	0.74
2:B:77:G:O6	2:B:80:U:O4	2.05	0.74
18:U:548:LEU:CD2	18:U:661:ALA:HB1	2.18	0.74
5:F:44:G:C2	16:G:2:U:C4	2.75	0.74
7:L:692:LEU:HA	27:K:107:VAL:HG11	1.69	0.74
16:G:6:A:C4	16:G:7:G:C8	2.75	0.74
17:H:80:A:H2'	17:H:81:G:H8	1.51	0.74
17:H:93:A:H2'	17:H:94:A:H5'	1.67	0.74
18:U:548:LEU:CD2	18:U:661:ALA:CB	2.65	0.74
10:O:220:MET:HG2	10:O:221:PRO:CD	2.16	0.74
18:U:550:ARG:CB	18:U:660:LYS:HD3	2.17	0.74
1:A:1836:LEU:HD11	18:U:549:VAL:HG11	1.70	0.74
4:E:75:HIS:CD2	4:E:80:THR:HG22	2.22	0.74
5:F:37:C:C3'	5:F:38:G:H5'	2.17	0.74
18:U:548:LEU:HD22	18:U:661:ALA:HB1	1.69	0.74
27:K:130:HIS:O	27:K:134:ALA:HB3	1.86	0.74
2:B:81:U:O2'	2:B:82:A:OP2	2.04	0.74
4:E:119:THR:CG2	4:E:161:ARG:HB2	2.16	0.74
4:E:231:MET:HB3	4:E:262:TRP:CZ3	2.22	0.74
4:E:109:SER:C	4:E:130:ASP:OD2	2.26	0.74
4:E:251:LEU:HG	4:E:291:CYS:SG	2.28	0.74
10:O:234:LEU:CD1	10:O:274:PHE:HZ	2.01	0.74
4:E:119:THR:HG21	4:E:161:ARG:HB2	1.68	0.74
6:J:493:ALA:HB1	6:J:499:ARG:CB	2.18	0.74
3:C:832:TYR:HE1	3:C:901:PHE:HB2	1.51	0.74
4:E:162:ARG:NH2	4:E:204:THR:HA	2.01	0.74
10:O:260:THR:CG2	10:O:273:GLN:HB2	2.03	0.74
7:L:707:ALA:CB	27:K:117:GLN:OE1	2.32	0.74
4:E:265:ARG:H	4:E:272:ARG:NH2	1.86	0.73
1:A:1517:LYS:HB2	1:A:1517:LYS:HZ3	1.54	0.73
4:E:266:PRO:HB3	7:L:788:TYR:HB3	1.70	0.73
7:L:713:MET:HB3	27:K:124:LEU:CG	2.14	0.73
17:H:147:G:N3	17:H:148:C:C5	2.56	0.73
28:I:720:ILE:O	28:I:721:LYS:CB	2.34	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:147:ASP:OD2	3:C:164:ASP:HB3	1.87	0.73
3:C:139:HIS:HA	35:C:1500:GTP:O3B	1.89	0.73
27:K:18:TYR:CD1	27:K:168:LYS:CG	2.68	0.73
27:K:123:ASN:O	27:K:127:MET:N	2.20	0.73
5:F:44:G:C8	16:G:1:G:C2	2.76	0.73
17:H:114:A:H2'	17:H:115:G:H8	1.53	0.73
2:B:9:G:H2'	2:B:9:G:N3	2.04	0.73
5:F:43:A:H1'	16:G:4:A:H61	0.73	0.73
18:U:811:ARG:HG3	18:U:811:ARG:NH1	1.99	0.73
4:E:257:ASN:OD1	15:W:149:SER:CB	2.37	0.73
7:L:752:PHE:HA	7:L:755:LEU:HB2	1.71	0.73
3:C:160:ARG:NH1	3:C:160:ARG:HG3	2.03	0.73
4:E:75:HIS:CB	4:E:80:THR:O	2.35	0.72
4:E:66:GLU:C	4:E:87:ASP:OD2	2.27	0.72
4:E:277:PHE:HE2	4:E:300:ILE:CD1	2.01	0.72
5:F:41:A:H61	16:G:6:A:H61	1.35	0.72
7:L:759:GLU:OE1	27:K:17:PRO:CD	2.36	0.72
15:W:147:GLN:C	15:W:148:VAL:HG13	2.08	0.72
16:G:152:C:N3	16:G:153:C:C4	2.57	0.72
4:E:115:LEU:HD22	4:E:126:SER:CB	2.18	0.72
16:G:2:U:C4	18:U:625:PHE:HD2	2.07	0.72
1:A:942:PRO:HB2	1:A:1438:VAL:HG22	1.70	0.72
17:H:55:U:O4	17:H:93:A:N6	2.22	0.72
4:E:243:LEU:HD11	4:E:247:GLY:HA2	1.71	0.72
4:E:248:SER:HB2	4:E:249:TYR:CD1	2.24	0.72
10:O:258:ILE:HG22	10:O:274:PHE:CD1	2.24	0.72
16:G:2:U:N3	18:U:625:PHE:HD2	1.85	0.72
16:G:146:C:H1'	16:G:147:C:N1	2.03	0.72
4:E:119:THR:HG22	4:E:161:ARG:HB3	1.71	0.72
1:A:1522:GLN:HA	1:A:1522:GLN:HE21	1.52	0.72
4:E:69:VAL:HG12	4:E:345:ALA:HB1	1.72	0.72
10:O:155:PRO:HA	12:R:188:PHE:HE1	1.54	0.72
10:O:252:PHE:O	10:O:255:PHE:HD2	1.73	0.72
2:B:8:G:H8	2:B:75:G:C6	2.04	0.72
28:I:545:ILE:O	28:I:547:LEU:N	2.22	0.72
4:E:108:HIS:HD2	4:E:136:TRP:CH2	2.07	0.72
10:O:149:LYS:HZ1	10:O:290:LYS:NZ	1.87	0.72
10:O:243:ILE:HG22	10:O:294:ASN:OD1	1.89	0.72
17:H:34:U:H5'	18:U:662:ILE:HG12	1.67	0.72
17:H:98:G:O2'	17:H:99:A:C5'	2.38	0.72
17:H:160:A:O2'	17:H:161:U:H5'	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:38:G:H2'	5:F:39:A:H8	1.54	0.71
1:A:1802:PRO:HG2	1:A:1824:THR:CG2	2.19	0.71
10:O:223:LEU:HD13	10:O:223:LEU:N	2.05	0.71
27:K:115:GLU:HA	27:K:115:GLU:OE2	1.90	0.71
4:E:92:LEU:O	4:E:101:ASN:CA	2.37	0.71
16:G:6:A:N6	16:G:7:G:C6	2.59	0.71
17:H:182:U:H2'	17:H:183:G:C8	2.23	0.71
28:I:545:ILE:C	28:I:547:LEU:H	1.92	0.71
1:A:1927:ILE:HG22	1:A:1931:THR:HB	1.73	0.71
2:B:96:A:C6	2:B:97:G:C5	2.78	0.71
4:E:266:PRO:CB	7:L:788:TYR:HB3	2.20	0.71
10:O:224:ASP:HB3	10:O:225:PRO:HD2	1.72	0.71
10:O:258:ILE:HG22	10:O:274:PHE:HD1	1.55	0.71
16:G:120:G:C2'	29:Q:1019:SER:N	2.54	0.71
5:F:40:U:C4	5:F:41:A:N6	2.59	0.71
2:B:77:G:C5	2:B:80:U:H5	2.08	0.71
17:H:54:U:C2'	17:H:55:U:C6	2.63	0.71
3:C:139:HIS:HB3	35:C:1500:GTP:O3G	1.90	0.71
17:H:33:G:OP1	18:U:666:ARG:NH1	2.23	0.71
17:H:154:C:O2'	17:H:155:C:C5'	2.34	0.71
5:F:92:A:C2	5:F:93:G:C4	2.78	0.71
12:R:232:SEP:HB3	14:T:372:LYS:CE	2.18	0.71
2:B:77:G:C5	2:B:80:U:C5	2.79	0.70
4:E:63:SER:O	4:E:93:TRP:HZ3	1.73	0.70
4:E:124:LEU:O	4:E:136:TRP:HD1	1.73	0.70
3:C:158:ARG:HA	3:C:158:ARG:HH21	1.54	0.70
10:O:234:LEU:HD11	10:O:274:PHE:HE2	1.56	0.70
10:O:260:THR:CA	10:O:273:GLN:HB3	2.21	0.70
16:G:6:A:C5	16:G:7:G:C8	2.80	0.70
16:G:5:G:C2	16:G:6:A:C5	2.78	0.70
28:I:365:ALA:CA	28:I:372:ARG:CB	2.59	0.70
7:L:703:MET:HA	27:K:117:GLN:HG3	1.71	0.70
16:G:147:C:OP2	18:U:659:LYS:HD3	1.90	0.70
16:G:148:U:H6	16:G:148:U:C5'	2.01	0.70
17:H:109:C:O2'	17:H:110:A:H5'	1.91	0.70
4:E:95:VAL:HG13	4:E:353:MET:HE1	1.72	0.70
4:E:114:GLU:HG3	4:E:156:SER:OG	1.90	0.70
7:L:731:LEU:HB3	27:K:142:LEU:CD2	2.20	0.70
27:K:17:PRO:HG3	27:K:167:ARG:NH1	2.07	0.70
28:I:742:ALA:O	28:I:746:LEU:N	2.24	0.70
1:A:1811:ASN:HD22	1:A:1816:GLN:HB3	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:71:CYS:SG	4:E:115:LEU:HB2	2.31	0.70
16:G:6:A:N9	16:G:7:G:C8	2.60	0.70
17:H:147:G:N1	17:H:148:C:C4	2.60	0.70
6:J:604:PRO:CA	6:J:607:LYS:N	2.54	0.70
10:O:288:PHE:CD1	10:O:289:ASN:OD1	2.45	0.70
28:I:585:ASP:O	28:I:588:PRO:N	2.25	0.70
5:F:92:A:N1	5:F:93:G:C5	2.60	0.70
4:E:115:LEU:CD2	4:E:126:SER:CB	2.70	0.69
10:O:149:LYS:HZ1	10:O:290:LYS:CG	2.04	0.69
10:O:259:ARG:HG3	10:O:274:PHE:O	1.92	0.69
27:K:19:PHE:HE2	27:K:172:LEU:C	1.95	0.69
4:E:277:PHE:HE2	4:E:300:ILE:HD13	1.56	0.69
5:F:34:G:C4	5:F:35:A:C8	2.80	0.69
5:F:81:C:H6	5:F:81:C:C5'	2.04	0.69
16:G:27:U:H2'	16:G:28:A:O5'	1.91	0.69
16:G:120:G:C1'	29:Q:1019:SER:CB	2.70	0.69
17:H:34:U:O2'	17:H:35:A:H8	1.75	0.69
17:H:179:C:C2	17:H:180:G:N7	2.60	0.69
4:E:67:GLY:N	4:E:87:ASP:OD2	2.25	0.69
4:E:82:ALA:HA	4:E:92:LEU:HD23	1.73	0.69
10:O:223:LEU:N	10:O:223:LEU:HD22	2.06	0.69
18:U:550:ARG:HB2	18:U:660:LYS:HD3	1.75	0.69
4:E:287:ASN:O	4:E:289:LEU:HD23	1.92	0.69
5:F:81:C:H6	5:F:81:C:H5''	1.55	0.69
4:E:108:HIS:HE1	4:E:128:SER:CB	2.04	0.69
4:E:257:ASN:CB	15:W:149:SER:HB3	2.21	0.69
17:H:83:A:C2	17:H:84:C:C4	2.81	0.69
17:H:80:A:C2'	17:H:81:G:H5'	2.23	0.69
17:H:113:G:C2'	17:H:114:A:H5'	2.22	0.69
1:A:1514:LYS:HZ3	1:A:1529:ILE:HD11	1.57	0.69
7:L:692:LEU:CB	27:K:107:VAL:CG1	2.67	0.69
16:G:145:U:H5'	16:G:145:U:N1	2.06	0.69
4:E:62:LEU:HD13	4:E:93:TRP:CE3	2.27	0.69
6:J:592:ALA:H	6:J:595:ALA:HB3	1.56	0.69
10:O:149:LYS:CE	10:O:290:LYS:NZ	2.53	0.69
10:O:262:THR:HB	10:O:271:PHE:HB2	1.75	0.69
16:G:146:C:H3'	16:G:146:C:P	2.33	0.69
1:A:1946:ASN:ND2	1:A:1986:LEU:CD2	2.54	0.69
4:E:54:SER:HB2	4:E:355:GLU:OE1	1.91	0.69
4:E:209:ILE:HG21	4:E:250:LEU:CD1	2.23	0.69
4:E:313:ASP:HA	4:E:320:LEU:HD11	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:3:A:O2'	16:G:4:A:OP2	2.11	0.69
17:H:147:G:C2	17:H:148:C:C5	2.81	0.69
27:K:17:PRO:HG3	27:K:167:ARG:HH12	1.58	0.69
27:K:19:PHE:HD2	27:K:171:GLN:C	1.96	0.69
1:A:51:PHE:CZ	4:E:66:GLU:HG2	2.27	0.69
7:L:762:ALA:CB	27:K:14:ASP:OD1	2.37	0.69
3:C:139:HIS:HB2	35:C:1500:GTP:H5''	1.75	0.68
7:L:780:ARG:HB3	27:K:188:LEU:HD21	1.75	0.68
5:F:44:G:C6	16:G:2:U:C4	2.81	0.68
2:B:77:G:N7	2:B:80:U:C4	2.61	0.68
4:E:119:THR:HG23	4:E:161:ARG:HB3	1.73	0.68
4:E:132:THR:OG1	4:E:148:LYS:HG2	1.94	0.68
16:G:22:C:H1'	16:G:23:U:OP1	1.93	0.68
16:G:147:C:H5'	18:U:659:LYS:NZ	2.09	0.68
5:F:82:A:H5''	5:F:82:A:H8	1.58	0.68
18:U:655:GLU:O	18:U:658:ARG:HG3	1.94	0.68
7:L:699:ASN:CA	27:K:114:LEU:HB2	2.24	0.68
27:K:18:TYR:CG	27:K:168:LYS:HG2	2.27	0.68
4:E:62:LEU:CD1	4:E:93:TRP:CD2	2.77	0.68
1:A:113:ILE:HG21	9:N:6:ARG:HE	1.58	0.68
2:B:35:U:H6	2:B:35:U:H5''	1.57	0.68
1:A:1210:LYS:HG3	1:A:1212:GLY:H	1.59	0.67
4:E:111:ALA:HB3	4:E:129:THR:OG1	1.93	0.67
6:J:223:TYR:OH	7:L:248:ASP:CG	2.31	0.67
17:H:57:A:N6	17:H:91:U:N3	2.35	0.67
2:B:23:C:O2'	2:B:24:G:H3'	1.93	0.67
4:E:78:GLY:C	4:E:336:HIS:CE1	2.67	0.67
16:G:22:C:C1'	16:G:23:U:OP1	2.41	0.67
17:H:147:G:N1	17:H:148:C:N4	2.42	0.67
1:A:1836:LEU:HD11	18:U:549:VAL:CG1	2.24	0.67
4:E:55:LEU:O	4:E:57:ALA:N	2.27	0.67
17:H:54:U:C4	17:H:93:A:N6	2.62	0.67
1:A:1836:LEU:CD1	18:U:549:VAL:HG11	2.23	0.67
5:F:44:G:C8	16:G:1:G:N1	2.63	0.67
7:L:692:LEU:CA	27:K:107:VAL:CG1	2.72	0.67
5:F:36:A:H2	16:G:10:U:O2	1.71	0.67
16:G:148:U:H3'	16:G:149:G:H5''	1.76	0.67
4:E:61:LEU:HD13	4:E:352:TYR:CE1	2.30	0.67
4:E:82:ALA:HB1	4:E:92:LEU:HD21	1.74	0.67
4:E:125:PHE:CD2	4:E:159:PRO:HB3	2.29	0.67
17:H:153:A:C3'	17:H:154:C:H5'	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:I:790:ARG:CB	28:I:797:PHE:O	2.43	0.67
4:E:246:GLU:HB2	4:E:248:SER:OG	1.95	0.67
7:L:252:ARG:HG2	7:L:252:ARG:NH1	2.10	0.67
28:I:403:LYS:O	28:I:405:TYR:N	2.27	0.67
28:I:463:PRO:O	28:I:464:ALA:CB	2.42	0.67
10:O:149:LYS:NZ	10:O:290:LYS:NZ	2.43	0.67
4:E:266:PRO:HG2	7:L:785:GLN:CA	2.25	0.67
10:O:149:LYS:HZ1	10:O:290:LYS:CE	2.07	0.67
1:A:1605:GLU:HB3	1:A:1637:TRP:HE1	1.58	0.66
4:E:264:VAL:HA	4:E:272:ARG:HH21	1.58	0.66
10:O:292:ILE:HG12	10:O:297:ARG:HA	1.77	0.66
4:E:264:VAL:HA	4:E:272:ARG:NH2	2.10	0.66
16:G:119:G:O2'	29:Q:1021:LEU:CB	2.43	0.66
17:H:147:G:H2'	17:H:148:C:C6	2.31	0.66
17:H:183:G:H2'	17:H:184:C:C6	2.30	0.66
4:E:298:SER:O	4:E:314:THR:N	2.27	0.66
10:O:247:ASP:N	10:O:247:ASP:OD1	2.25	0.66
27:K:128:SER:O	27:K:132:CYS:N	2.25	0.66
28:I:172:PHE:CB	28:I:199:ARG:C	2.64	0.66
4:E:58:PRO:HD2	4:E:59:ILE:H	1.61	0.66
4:E:250:LEU:HD23	4:E:250:LEU:O	1.93	0.66
13:S:56:ILE:HG12	13:S:62:ILE:HG23	1.78	0.66
1:A:1809:ILE:HB	1:A:1818:PHE:HB2	1.76	0.66
4:E:54:SER:CB	4:E:355:GLU:OE1	2.43	0.66
2:B:96:A:O2'	2:B:97:G:H5'	1.95	0.66
5:F:34:G:H2'	5:F:35:A:O5'	1.96	0.66
2:B:96:A:C6	2:B:97:G:C6	2.84	0.66
5:F:82:A:H62	12:R:258:LYS:NZ	1.94	0.66
7:L:759:GLU:CG	27:K:171:GLN:HE22	2.08	0.66
27:K:19:PHE:HD2	27:K:172:LEU:N	1.94	0.66
28:I:790:ARG:CB	28:I:801:ASP:CA	2.74	0.66
17:H:83:A:O2'	17:H:84:C:C5'	2.42	0.66
14:T:216:ASN:HD21	14:T:472:GLN:H	1.44	0.65
27:K:119:VAL:O	27:K:123:ASN:N	2.27	0.65
1:A:1832:ARG:HA	1:A:1832:ARG:NE	2.08	0.65
14:T:261:LEU:HB3	14:T:273:TRP:HB2	1.78	0.65
7:L:692:LEU:HA	27:K:107:VAL:CG1	2.27	0.65
10:O:240:GLY:HA3	10:O:296:ARG:HH12	1.60	0.65
4:E:139:GLU:HG3	4:E:140:THR:HG23	1.78	0.65
4:E:321:TYR:CE1	4:E:356:ILE:HD13	2.31	0.65
7:L:706:GLU:HB2	27:K:117:GLN:HB3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:220:MET:CG	10:O:221:PRO:HD2	2.24	0.65
6:J:223:TYR:HH	7:L:248:ASP:CG	1.99	0.65
7:L:759:GLU:CG	27:K:167:ARG:HD2	2.26	0.65
2:B:8:G:H8	2:B:75:G:H1	0.71	0.65
1:A:1836:LEU:CD2	18:U:547:ILE:HG21	2.27	0.65
16:G:6:A:C5	16:G:7:G:C5	2.84	0.65
17:H:8:C:O2'	17:H:9:U:H5'	1.96	0.65
29:Q:341:ALA:HB1	29:Q:352:ALA:HB2	1.79	0.65
1:A:1214:TRP:HB2	1:A:1228:CYS:HB3	1.78	0.65
4:E:234:HIS:HA	4:E:256:ASP:OD2	1.96	0.65
7:L:242:LEU:HD21	7:L:247:LEU:HD21	1.79	0.65
1:A:1802:PRO:HG2	1:A:1824:THR:HG21	1.77	0.65
4:E:125:PHE:HE2	4:E:159:PRO:HB2	1.61	0.65
7:L:201:LYS:HB2	16:G:8:C:OP1	1.97	0.65
17:H:7:U:N3	17:H:8:C:C4	2.65	0.65
17:H:43:U:O2'	17:H:44:U:C5	2.47	0.65
17:H:80:A:C2	17:H:81:G:C5	2.84	0.65
1:A:888:GLN:OE1	7:L:130:PRO:HG3	1.97	0.64
4:E:326:HIS:CD2	4:E:330:ILE:HG12	2.28	0.64
10:O:259:ARG:CG	10:O:275:ALA:N	2.55	0.64
16:G:148:U:O2	17:H:30:A:H2	1.79	0.64
1:A:1518:LEU:HD21	17:H:29:A:N6	2.13	0.64
4:E:74:PHE:HA	4:E:81:LEU:HD21	0.70	0.64
4:E:74:PHE:CA	4:E:81:LEU:CD2	2.45	0.64
27:K:18:TYR:CG	27:K:168:LYS:HA	2.32	0.64
7:L:696:LEU:HA	27:K:110:SER:OG	1.96	0.64
16:G:6:A:N7	16:G:7:G:N7	2.45	0.64
16:G:22:C:H1'	16:G:23:U:P	2.38	0.64
17:H:7:U:C5	17:H:8:C:N4	2.64	0.64
5:F:36:A:C8	5:F:36:A:H3'	2.32	0.64
12:R:193:LYS:CB	15:W:145:ASN:HD21	2.10	0.64
3:C:137:HIS:CD2	3:C:236:MET:HB3	2.32	0.64
4:E:73:LYS:O	4:E:81:LEU:HD22	1.98	0.64
5:F:36:A:C8	5:F:36:A:C3'	2.80	0.64
10:O:221:PRO:HA	10:O:222:ARG:NH2	2.12	0.64
27:K:19:PHE:CD2	27:K:172:LEU:CA	2.80	0.64
1:A:1946:ASN:ND2	1:A:1949:ARG:HB3	2.11	0.64
4:E:307:ARG:NH1	15:W:143:LEU:HD22	2.08	0.64
12:R:189:ASN:HD22	12:R:189:ASN:C	2.01	0.64
18:U:626:MET:HE1	18:U:643:LYS:HZ2	1.62	0.64
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1831:LYS:O	1:A:1831:LYS:NZ	2.24	0.64
4:E:92:LEU:O	4:E:101:ASN:CB	2.46	0.64
1:A:1662:ILE:HA	1:A:1701:VAL:O	1.98	0.64
3:C:832:TYR:CD1	3:C:900:VAL:O	2.51	0.64
4:E:130:ASP:C	4:E:131:LYS:HG3	2.19	0.64
4:E:307:ARG:NH1	15:W:143:LEU:CD2	2.61	0.64
4:E:326:HIS:CE1	4:E:352:TYR:CD2	2.85	0.64
6:J:223:TYR:OH	7:L:248:ASP:OD2	2.16	0.64
17:H:27:U:O2'	17:H:28:C:C5'	2.39	0.64
1:A:1518:LEU:O	1:A:1519:THR:HB	1.97	0.63
1:A:1570:LYS:HE2	18:U:637:ASP:HB3	1.80	0.63
1:A:1839:TRP:NE1	18:U:557:VAL:O	2.31	0.63
3:C:112:THR:HG23	3:C:115:GLU:HG3	1.80	0.63
4:E:54:SER:HB3	4:E:355:GLU:CD	2.10	0.63
10:O:149:LYS:NZ	10:O:290:LYS:CG	2.61	0.63
10:O:276:THR:HG23	10:O:279:ALA:H	1.62	0.63
4:E:90:ILE:HD12	4:E:112:VAL:HG11	1.75	0.63
4:E:108:HIS:CD2	4:E:136:TRP:CH2	2.86	0.63
12:R:184:GLN:HA	12:R:184:GLN:NE2	2.13	0.63
17:H:80:A:N3	17:H:81:G:C8	2.66	0.63
18:U:666:ARG:HG2	18:U:666:ARG:NH2	2.09	0.63
1:A:761:ILE:HD12	1:A:775:ASN:HD22	1.62	0.63
1:A:940:ILE:HD12	1:A:1090:ARG:HH21	1.62	0.63
3:C:832:TYR:CE1	3:C:901:PHE:HB2	2.33	0.63
4:E:82:ALA:HB1	4:E:92:LEU:HD23	1.71	0.63
16:G:145:U:H1'	16:G:146:C:H5'	1.81	0.63
1:A:50:LYS:HB2	4:E:88:ARG:NH1	2.12	0.63
16:G:5:G:N2	16:G:6:A:H62	1.97	0.63
2:B:37:G:N2	2:B:45:C:O2	2.26	0.63
10:O:87:ASP:HB3	10:O:91:GLY:H	1.64	0.63
17:H:74:U:H2'	17:H:75:A:C8	2.28	0.63
17:H:83:A:C2	17:H:84:C:N3	2.66	0.63
4:E:57:ALA:O	4:E:355:GLU:HB3	1.99	0.63
15:W:97:ASN:HD21	15:W:100:ARG:HH21	1.47	0.63
16:G:152:C:C4	16:G:153:C:C4	2.86	0.63
4:E:134:ALA:HB1	4:E:143:ARG:HD2	1.80	0.62
10:O:149:LYS:NZ	10:O:290:LYS:HG3	2.14	0.62
2:B:74:U:O4	2:B:76:A:N6	2.32	0.62
4:E:178:LEU:HD11	4:E:222:LEU:CD2	2.29	0.62
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.80	0.62
4:E:178:LEU:HD21	4:E:208:ILE:CD1	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:178:LEU:CD1	4:E:222:LEU:CD2	2.77	0.62
5:F:36:A:H8	5:F:36:A:O5'	1.81	0.62
10:O:27:CYS:SG	10:O:66:LYS:NZ	2.72	0.62
16:G:146:C:C1'	16:G:147:C:C6	2.80	0.62
17:H:8:C:O2'	17:H:9:U:C5'	2.47	0.62
17:H:83:A:C6	17:H:84:C:C4	2.86	0.62
1:A:1928:SER:OG	1:A:1930:TYR:CD1	2.52	0.62
5:F:45:A:C2	18:U:625:PHE:CE1	2.88	0.62
4:E:298:SER:O	4:E:314:THR:CB	2.44	0.62
9:N:139:CYS:SG	9:N:140:ARG:N	2.72	0.62
16:G:152:C:C2'	16:G:153:C:H5	2.00	0.62
1:A:1515:TRP:CE3	1:A:1515:TRP:HA	2.34	0.62
1:A:1515:TRP:HA	1:A:1515:TRP:HE3	1.64	0.62
3:C:618:THR:HB	3:C:630:LEU:HB2	1.81	0.62
4:E:235:ALA:HB3	4:E:256:ASP:HB2	1.82	0.62
7:L:764:PRO:O	7:L:765:ARG:CB	2.48	0.62
3:C:117:ASP:N	3:C:117:ASP:OD1	2.31	0.62
10:O:239:LEU:O	10:O:243:ILE:HD11	2.00	0.62
16:G:6:A:C8	16:G:7:G:C8	2.88	0.62
1:A:888:GLN:OE1	7:L:130:PRO:CG	2.48	0.62
4:E:153:PHE:O	4:E:171:SER:HB2	2.00	0.61
10:O:235:TYR:HD1	10:O:271:PHE:HE1	1.46	0.61
10:O:272:ILE:CG2	10:O:274:PHE:CE1	2.83	0.61
17:H:30:A:O2'	17:H:31:G:C8	2.52	0.61
17:H:83:A:C2	17:H:84:C:C2	2.88	0.61
17:H:112:G:H2'	17:H:113:G:H8	1.65	0.61
1:A:1342:TRP:HB2	1:A:1486:GLU:HG3	1.81	0.61
4:E:69:VAL:HG12	4:E:69:VAL:O	2.00	0.61
17:H:98:G:H5''	17:H:104:U:P	2.40	0.61
28:I:795:ILE:O	28:I:795:ILE:HG22	1.99	0.61
6:J:741:THR:O	6:J:745:CYS:CB	2.48	0.61
3:C:141:GLY:N	35:C:1500:GTP:O2B	2.34	0.61
7:L:267:LEU:HD23	7:L:267:LEU:C	2.21	0.61
7:L:713:MET:CB	27:K:124:LEU:HD21	2.21	0.61
10:O:155:PRO:HD3	12:R:188:PHE:CD1	2.35	0.61
14:T:350:HIS:HA	14:T:374:SER:HB2	1.82	0.61
16:G:3:A:H1'	16:G:4:A:O5'	2.00	0.61
16:G:7:G:C2	16:G:8:C:H1'	2.36	0.61
1:A:469:LYS:NZ	2:B:59:G:O6	2.33	0.61
1:A:1941:ARG:O	1:A:1945:VAL:HG22	2.01	0.61
3:C:666:VAL:HG13	3:C:824:THR:HG23	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:108:HIS:CD2	4:E:136:TRP:HH2	2.17	0.61
4:E:116:HIS:HE1	4:E:158:TYR:CE1	2.17	0.61
16:G:120:G:C1'	29:Q:1019:SER:CA	2.78	0.61
28:I:399:VAL:O	28:I:399:VAL:HG13	2.00	0.61
7:L:710:ALA:CA	27:K:124:LEU:HD22	2.26	0.61
7:L:759:GLU:OE2	7:L:759:GLU:HA	2.01	0.61
16:G:120:G:H2'	29:Q:1019:SER:N	2.14	0.61
17:H:69:U:H2'	17:H:70:C:C5	2.35	0.61
18:U:814:VAL:HG11	18:U:820:TYR:HB3	1.83	0.61
1:A:1892:PRO:HD3	1:A:1941:ARG:HH21	1.66	0.61
3:C:160:ARG:O	3:C:160:ARG:HG3	1.99	0.61
4:E:93:TRP:HA	4:E:101:ASN:CA	2.30	0.61
2:B:71:C:H6	2:B:71:C:H5''	1.66	0.61
7:L:784:LEU:CB	27:K:195:ILE:CB	2.78	0.61
2:B:103:G:O2'	2:B:104:C:H5'	2.00	0.61
4:E:58:PRO:CD	4:E:59:ILE:H	2.14	0.61
4:E:325:GLY:O	4:E:352:TYR:HE2	1.83	0.61
5:F:36:A:C8	5:F:36:A:C4'	2.84	0.61
17:H:154:C:H2'	17:H:155:C:H6	1.65	0.61
3:C:160:ARG:HH11	3:C:160:ARG:CG	2.14	0.60
10:O:259:ARG:N	10:O:273:GLN:O	2.34	0.60
1:A:788:GLN:HG2	1:A:1024:HIS:HB3	1.83	0.60
1:A:1508:GLY:O	1:A:1511:GLU:HG3	2.01	0.60
10:O:234:LEU:HD11	10:O:274:PHE:HZ	1.59	0.60
17:H:147:G:H2'	17:H:148:C:H6	1.65	0.60
18:U:620:ARG:NH2	18:U:643:LYS:O	2.34	0.60
1:A:1516:LYS:NZ	1:A:1516:LYS:HA	2.16	0.60
4:E:124:LEU:HD12	4:E:124:LEU:C	2.21	0.60
4:E:233:GLY:O	4:E:260:ARG:NH2	2.33	0.60
7:L:707:ALA:HB2	27:K:117:GLN:NE2	2.16	0.60
7:L:781:GLU:HG2	27:K:191:LYS:CG	2.30	0.60
10:O:235:TYR:CD2	10:O:301:LYS:HB2	2.33	0.60
18:U:579:VAL:HG22	18:U:646:GLU:HB2	1.83	0.60
4:E:298:SER:CA	4:E:314:THR:HB	2.31	0.60
10:O:72:GLN:OE1	10:O:82:GLN:NE2	2.34	0.60
17:H:34:U:OP1	18:U:662:ILE:CD1	2.44	0.60
28:I:285:THR:CB	28:I:288:THR:CB	2.79	0.60
1:A:663:ARG:HH22	5:F:63:C:H3'	1.66	0.60
7:L:267:LEU:HD23	7:L:267:LEU:O	2.01	0.60
12:R:182:SER:O	12:R:182:SER:OG	2.18	0.60
16:G:146:C:H3'	16:G:146:C:OP2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:692:LEU:CG	27:K:107:VAL:HG11	2.31	0.60
10:O:221:PRO:HB2	10:O:289:ASN:ND2	2.17	0.60
16:G:147:C:OP2	18:U:659:LYS:HB2	2.01	0.60
18:U:868:SER:HB2	18:U:872:GLN:H	1.66	0.60
28:I:405:TYR:O	28:I:409:GLY:N	2.34	0.60
3:C:137:HIS:HA	3:C:238:ASN:HB3	1.83	0.60
4:E:61:LEU:HD13	4:E:352:TYR:CD1	2.37	0.60
16:G:120:G:O2'	29:Q:1019:SER:N	2.35	0.60
17:H:58:U:O4	17:H:90:A:N1	2.34	0.60
1:A:1144:LYS:HE2	1:A:1148:ASN:HD21	1.66	0.60
3:C:113:VAL:HG23	3:C:113:VAL:O	2.00	0.60
10:O:234:LEU:CD1	10:O:274:PHE:CE2	2.82	0.60
17:H:93:A:C2'	17:H:94:A:C5'	2.79	0.60
27:K:117:GLN:HA	27:K:117:GLN:HE21	1.66	0.60
1:A:695:ASP:OD2	14:T:376:ARG:NH2	2.35	0.60
10:O:222:ARG:CZ	10:O:222:ARG:H	2.15	0.60
17:H:79:G:H2'	17:H:80:A:C8	2.34	0.60
27:K:19:PHE:CD2	27:K:171:GLN:C	2.75	0.60
1:A:1636:LYS:HB2	1:A:1655:THR:HB	1.84	0.59
2:B:72:U:O5'	2:B:72:U:H6	1.86	0.59
3:C:168:THR:HG22	3:C:168:THR:O	2.02	0.59
4:E:313:ASP:HB2	4:E:320:LEU:HD21	1.82	0.59
16:G:26:U:H2'	16:G:27:U:H5''	1.82	0.59
4:E:66:GLU:HB2	4:E:87:ASP:OD2	2.02	0.59
16:G:6:A:H3'	16:G:7:G:H8	1.65	0.59
3:C:538:HIS:HE1	3:C:551:LEU:HD11	1.62	0.59
5:F:45:A:N3	18:U:625:PHE:CE1	2.69	0.59
5:F:82:A:H5''	5:F:82:A:C8	2.37	0.59
10:O:251:HIS:CE1	10:O:291:LEU:HD11	2.38	0.59
14:T:314:ILE:HD12	14:T:324:HIS:HB2	1.84	0.59
16:G:5:G:N2	16:G:6:A:N6	2.50	0.59
17:H:113:G:H2'	17:H:114:A:H5'	1.83	0.59
4:E:116:HIS:CD2	4:E:157:CYS:O	2.56	0.59
4:E:128:SER:OG	4:E:130:ASP:OD1	2.11	0.59
17:H:7:U:C2	17:H:8:C:C5	2.91	0.59
27:K:128:SER:O	27:K:132:CYS:CB	2.50	0.59
3:C:678:THR:OG1	3:C:680:ASN:O	2.20	0.59
4:E:81:LEU:O	4:E:92:LEU:HA	2.03	0.59
4:E:93:TRP:CZ2	4:E:351:LEU:CD1	2.86	0.59
3:C:210:ASN:HB3	3:C:636:TYR:HB2	1.85	0.59
16:G:2:U:C4	18:U:625:PHE:CD2	2.88	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:97:G:H8	17:H:97:G:OP2	1.84	0.59
18:U:668:LEU:HD12	18:U:668:LEU:C	2.22	0.59
1:A:425:PRO:HB2	1:A:428:LYS:HB2	1.84	0.59
2:B:77:G:C6	2:B:80:U:O4	2.56	0.59
3:C:160:ARG:HH11	3:C:160:ARG:C	2.04	0.59
17:H:182:U:HO2'	17:H:183:G:H5'	1.66	0.59
18:U:550:ARG:CB	18:U:660:LYS:CD	2.81	0.59
27:K:128:SER:O	27:K:132:CYS:HB2	2.01	0.59
28:I:464:ALA:O	28:I:467:ALA:N	2.35	0.59
10:O:149:LYS:HZ1	10:O:290:LYS:HG3	1.67	0.59
12:R:78:ARG:HG3	12:R:79:LYS:HG2	1.83	0.59
5:F:36:A:C5'	5:F:36:A:C8	2.85	0.59
5:F:78:A:O2'	11:P:6:ARG:NH1	2.35	0.59
5:F:90:G:N1	5:F:91:A:C6	2.70	0.59
10:O:260:THR:CG2	10:O:273:GLN:OE1	2.50	0.59
13:S:18:THR:HG22	13:S:159:ILE:HG12	1.85	0.59
16:G:1:G:O2'	16:G:2:U:OP1	2.17	0.59
4:E:131:LYS:HD3	4:E:151:THR:C	2.23	0.58
16:G:147:C:OP1	18:U:659:LYS:HD2	1.97	0.58
16:G:147:C:H2'	16:G:148:U:H5''	1.85	0.58
17:H:54:U:O2'	17:H:55:U:H5'	2.03	0.58
28:I:465:ARG:CB	28:I:543:ARG:NH1	2.66	0.58
1:A:995:ARG:HG3	12:R:291:LEU:HD13	1.85	0.58
1:A:1631:LEU:HB2	1:A:1660:TYR:HB3	1.86	0.58
4:E:243:LEU:HD12	4:E:247:GLY:HA2	1.85	0.58
12:R:234:SER:O	12:R:235:ARG:C	2.42	0.58
17:H:80:A:C4	17:H:81:G:N7	2.71	0.58
17:H:83:A:N3	17:H:84:C:C6	2.71	0.58
17:H:172:C:O2'	17:H:173:C:C5'	2.48	0.58
1:A:1431:ALA:O	1:A:1434:LYS:NZ	2.36	0.58
5:F:84:A:H62	6:J:241:VAL:HG13	1.68	0.58
10:O:15:TRP:HE1	11:P:26:LEU:HB2	1.66	0.58
18:U:550:ARG:HB3	18:U:660:LYS:HD3	1.84	0.58
1:A:348:PRO:HG2	1:A:351:TYR:HB3	1.85	0.58
1:A:1865:ARG:NH1	18:U:726:ASP:OD2	2.36	0.58
3:C:693:GLU:H	3:C:696:LEU:HD12	1.68	0.58
7:L:37:LEU:HD11	7:L:155:ALA:HA	1.84	0.58
10:O:288:PHE:CE1	10:O:289:ASN:OD1	2.56	0.58
12:R:101:ILE:O	12:R:104:GLN:NE2	2.36	0.58
4:E:90:ILE:CD1	4:E:112:VAL:CG1	2.61	0.58
2:B:96:A:N6	2:B:97:G:C6	2.71	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:125:PHE:HB3	4:E:135:VAL:HG22	1.86	0.58
7:L:73:HIS:O	7:L:77:LEU:HB2	2.02	0.58
8:M:166:SER:O	13:S:141:ARG:NH2	2.37	0.58
1:A:857:ASN:OD1	1:A:860:GLN:NE2	2.36	0.58
4:E:65:HIS:ND1	4:E:69:VAL:HG23	2.13	0.58
11:P:13:ARG:HH12	14:T:330:THR:HA	1.69	0.58
2:B:20:G:H4'	2:B:20:G:OP1	2.02	0.58
10:O:240:GLY:HA3	10:O:296:ARG:HH22	1.68	0.58
1:A:1784:ASN:HD22	1:A:1897:LEU:HD12	1.69	0.58
4:E:77:ASN:OD1	4:E:79:SER:OG	2.20	0.58
4:E:257:ASN:CB	15:W:149:SER:CB	2.81	0.58
13:S:92:PHE:H	13:S:123:ASP:HB3	1.69	0.58
2:B:10:U:O2	2:B:67:A:N6	2.37	0.58
3:C:692:LEU:O	3:C:786:ASN:ND2	2.37	0.58
4:E:66:GLU:OE1	4:E:66:GLU:HA	2.04	0.58
4:E:178:LEU:HD21	4:E:208:ILE:HD13	1.85	0.58
17:H:97:G:H2'	17:H:97:G:N3	2.18	0.58
3:C:168:THR:OG1	3:C:204:ASP:OD2	2.13	0.57
5:F:49:G:OP1	7:L:33:ARG:NH2	2.36	0.57
5:F:81:C:C5'	5:F:81:C:C6	2.86	0.57
28:I:484:LEU:O	28:I:485:LYS:C	2.43	0.57
1:A:542:ASN:O	1:A:546:LEU:HB2	2.04	0.57
4:E:119:THR:HG22	4:E:161:ARG:CB	2.31	0.57
6:J:658:ARG:CB	6:J:667:ILE:CB	2.82	0.57
7:L:261:LYS:HE2	7:L:261:LYS:HA	1.84	0.57
10:O:260:THR:HG21	10:O:273:GLN:OE1	2.04	0.57
16:G:147:C:OP1	18:U:659:LYS:CE	2.52	0.57
16:G:152:C:C2'	16:G:153:C:H6	2.09	0.57
4:E:61:LEU:HD12	4:E:351:LEU:O	2.04	0.57
5:F:42:C:H2'	5:F:43:A:H8	1.69	0.57
10:O:233:THR:HA	10:O:272:ILE:O	2.03	0.57
1:A:610:HIS:NE2	34:A:3000:IHP:O33	2.36	0.57
2:B:96:A:C2'	2:B:97:G:H5'	2.34	0.57
2:B:96:A:C5	2:B:97:G:N7	2.73	0.57
16:G:26:U:H2'	16:G:27:U:C5'	2.34	0.57
16:G:146:C:C1'	16:G:147:C:C5	2.87	0.57
17:H:179:C:HO2'	17:H:180:G:H5'	1.65	0.57
4:E:257:ASN:O	4:E:257:ASN:ND2	2.38	0.57
3:C:167:TYR:CD1	3:C:167:TYR:N	2.73	0.57
4:E:75:HIS:H	4:E:81:LEU:HD23	1.69	0.57
4:E:94:ASN:ND2	4:E:100:ASP:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:123:LEU:HD13	7:L:124:LYS:H	1.70	0.57
12:R:178:ARG:HB2	15:W:118:ALA:HB2	1.87	0.57
27:K:19:PHE:CD2	27:K:172:LEU:N	2.72	0.57
27:K:135:TRP:O	27:K:136:LYS:CB	2.52	0.57
1:A:1629:ILE:HG22	1:A:1662:ILE:HG12	1.86	0.57
4:E:102:TYR:N	4:E:102:TYR:CD1	2.73	0.57
5:F:44:G:N7	16:G:1:G:C2	2.72	0.57
7:L:759:GLU:HG3	27:K:171:GLN:HE22	1.70	0.57
8:M:165:ASN:HD22	12:R:95:LYS:HA	1.69	0.57
1:A:1639:VAL:HG12	1:A:1719:PHE:HB3	1.86	0.57
14:T:200:ILE:HB	14:T:486:ILE:HB	1.87	0.57
18:U:662:ILE:C	18:U:662:ILE:HD12	2.25	0.57
1:A:1813:ARG:HD3	1:A:1814:THR:HG23	1.86	0.57
5:F:36:A:H8	5:F:36:A:C4'	2.18	0.57
5:F:45:A:C2	18:U:625:PHE:CD1	2.93	0.57
16:G:148:U:C6	16:G:148:U:C5'	2.83	0.57
28:I:749:SER:O	28:I:753:THR:CB	2.53	0.57
1:A:1820:LYS:NZ	1:A:1844:GLU:OE1	2.38	0.57
4:E:136:TRP:CD1	4:E:136:TRP:N	2.73	0.57
4:E:307:ARG:HB3	4:E:326:HIS:O	2.05	0.57
13:S:26:GLU:OE1	13:S:131:ARG:NH1	2.38	0.57
4:E:257:ASN:OD1	15:W:149:SER:CA	2.53	0.56
10:O:288:PHE:HD1	10:O:289:ASN:OD1	1.87	0.56
16:G:155:U:O2	16:G:155:U:H2'	2.05	0.56
17:H:69:U:O2'	17:H:70:C:C5'	2.44	0.56
1:A:382:GLU:HA	3:C:354:ARG:HH12	1.69	0.56
3:C:154:HIS:CB	3:C:158:ARG:HG3	2.36	0.56
4:E:83:SER:O	4:E:90:ILE:HA	2.05	0.56
4:E:145:LYS:NZ	4:E:184:LYS:HG2	2.20	0.56
10:O:149:LYS:NZ	10:O:290:LYS:HZ3	2.03	0.56
10:O:261:ILE:O	10:O:261:ILE:HG22	2.05	0.56
27:K:120:ARG:O	27:K:124:LEU:N	2.30	0.56
1:A:388:LEU:HD11	3:C:399:LEU:HD11	1.87	0.56
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.38	0.56
1:A:532:THR:HB	16:G:3:A:C5'	2.34	0.56
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	1.86	0.56
1:A:1513:MET:CE	18:U:622:ALA:HB3	2.36	0.56
3:C:142:LYS:CG	3:C:228:PHE:HD2	2.12	0.56
4:E:93:TRP:N	4:E:93:TRP:CD1	2.73	0.56
5:F:44:G:O2'	16:G:1:G:N2	2.35	0.56
17:H:40:C:O2'	17:H:41:U:C6	2.59	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:678:CYS:SG	18:U:718:HIS:CD2	2.98	0.56
1:A:419:ARG:NH2	1:A:423:ASP:O	2.39	0.56
4:E:93:TRP:CZ2	4:E:351:LEU:HD12	2.41	0.56
4:E:298:SER:HA	4:E:314:THR:CB	2.36	0.56
1:A:888:GLN:HE21	1:A:888:GLN:CA	2.16	0.56
5:F:29:A:N6	16:G:17:U:OP2	2.38	0.56
16:G:147:C:H5'	18:U:659:LYS:HZ2	1.70	0.56
18:U:809:ASP:O	18:U:813:SER:OG	2.13	0.56
1:A:1313:PRO:HG2	1:A:1335:ILE:HG22	1.86	0.56
1:A:1946:ASN:OD1	1:A:1986:LEU:CG	2.54	0.56
2:B:96:A:C4	2:B:97:G:C8	2.93	0.56
5:F:38:G:C2	5:F:39:A:C4	2.93	0.56
10:O:155:PRO:HA	12:R:188:PHE:CE1	2.34	0.56
16:G:22:C:C1'	16:G:23:U:P	2.94	0.56
17:H:36:G:O2'	17:H:37:U:C6	2.59	0.56
17:H:55:U:H2'	17:H:56:A:H8	1.70	0.56
17:H:57:A:H2'	17:H:58:U:H6	1.70	0.56
18:U:741:VAL:HG11	18:U:827:LEU:HG	1.88	0.56
6:J:293:ASN:ND2	7:L:226:ASP:O	2.38	0.56
7:L:710:ALA:HB2	27:K:120:ARG:HD3	1.82	0.56
18:U:671:GLN:HG3	18:U:763:GLN:O	2.06	0.56
3:C:158:ARG:HD3	3:C:537:TYR:OH	2.05	0.56
5:F:34:G:C5	5:F:35:A:C8	2.94	0.56
7:L:178:GLU:OE2	7:L:181:ARG:NH2	2.39	0.56
10:O:174:LYS:HA	15:W:205:VAL:HG22	1.88	0.56
10:O:252:PHE:O	10:O:255:PHE:CD2	2.57	0.56
17:H:59:A:H2'	17:H:60:U:H6	1.70	0.56
1:A:1941:ARG:O	1:A:1945:VAL:CG2	2.54	0.56
2:B:35:U:C5'	2:B:35:U:C6	2.85	0.56
10:O:258:ILE:CG2	10:O:274:PHE:HD1	2.19	0.56
12:R:193:LYS:HB3	15:W:145:ASN:HD21	1.71	0.56
18:U:678:CYS:SG	18:U:718:HIS:HD2	2.29	0.56
27:K:120:ARG:O	27:K:124:LEU:HB2	2.06	0.56
1:A:83:HIS:NE2	16:G:16:G:N7	2.51	0.55
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.89	0.55
4:E:232:ARG:O	4:E:262:TRP:HH2	1.89	0.55
4:E:304:SER:OG	4:E:306:ASP:OD1	2.17	0.55
7:L:259:ASP:CG	8:M:199:ARG:NH2	2.59	0.55
16:G:140:A:O2'	16:G:141:C:C6	2.59	0.55
1:A:1335:ILE:HG23	1:A:1365:ILE:HD11	1.88	0.55
1:A:1946:ASN:CG	1:A:1986:LEU:CG	2.73	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:134:LEU:HD13	3:C:202:ILE:HG23	1.88	0.55
4:E:75:HIS:HD2	4:E:80:THR:HG22	1.69	0.55
10:O:34:ILE:HB	12:R:197:ILE:HG12	1.89	0.55
16:G:5:G:C4	16:G:6:A:C5	2.94	0.55
17:H:83:A:N3	17:H:84:C:C5	2.74	0.55
1:A:1018:ASN:HA	1:A:1022:MET:O	2.06	0.55
1:A:1928:SER:OG	1:A:1930:TYR:CE1	2.55	0.55
5:F:22:A:H2'	15:W:130:ARG:HH21	1.71	0.55
10:O:260:THR:CB	10:O:273:GLN:HB3	2.36	0.55
12:R:148:ARG:NH2	14:T:299:THR:O	2.40	0.55
17:H:42:G:O2'	17:H:43:U:C6	2.59	0.55
17:H:54:U:H2'	17:H:55:U:C5	2.32	0.55
17:H:106:G:N2	17:H:107:A:N1	2.54	0.55
27:K:19:PHE:H	27:K:171:GLN:HG2	1.70	0.55
5:F:42:C:C2'	5:F:43:A:H5'	2.34	0.55
7:L:745:ALA:HB1	27:K:156:LEU:CG	2.36	0.55
17:H:160:A:H2'	17:H:161:U:C6	2.41	0.55
18:U:662:ILE:HD12	18:U:662:ILE:O	2.07	0.55
4:E:257:ASN:HB2	15:W:149:SER:HB2	1.87	0.55
12:R:228:PRO:HB2	12:R:230:MET:HE3	1.87	0.55
18:U:658:ARG:HG3	18:U:659:LYS:N	2.21	0.55
3:C:742:PRO:HG3	3:C:785:ARG:HD2	1.88	0.55
4:E:62:LEU:CD1	4:E:93:TRP:CG	2.90	0.55
4:E:74:PHE:CD2	4:E:336:HIS:HA	2.41	0.55
10:O:284:ALA:O	10:O:288:PHE:N	2.26	0.55
16:G:136:U:O2'	16:G:137:C:C6	2.58	0.55
17:H:10:C:H2'	17:H:11:G:H8	1.72	0.55
3:C:148:CYS:SG	3:C:417:ARG:NH2	2.79	0.55
4:E:82:ALA:HA	4:E:91:LEU:O	2.07	0.55
7:L:258:ARG:O	7:L:261:LYS:HB3	2.06	0.55
10:O:232:THR:HG22	10:O:277:ARG:HA	1.89	0.55
14:T:393:ASP:OD1	14:T:393:ASP:N	2.39	0.55
17:H:39:U:O2'	17:H:40:C:C6	2.59	0.55
6:J:770:ASP:CB	6:J:791:ASP:CB	2.85	0.55
10:O:243:ILE:CG2	10:O:294:ASN:OD1	2.53	0.55
17:H:80:A:O2'	17:H:81:G:H5'	2.07	0.55
1:A:1214:TRP:NE1	1:A:1276:GLU:OE2	2.34	0.55
3:C:523:GLN:HE21	3:C:558:PRO:HG3	1.70	0.55
5:F:37:C:C3'	5:F:38:G:C5'	2.85	0.55
5:F:44:G:N2	16:G:3:A:H62	1.92	0.55
5:F:92:A:C2	5:F:93:G:N7	2.74	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:259:ARG:HB2	10:O:274:PHE:N	2.21	0.55
13:S:52:LYS:HA	13:S:158:LYS:HA	1.89	0.55
17:H:7:U:H2'	17:H:8:C:H5'	1.89	0.55
17:H:80:A:C2	17:H:81:G:N7	2.75	0.55
18:U:550:ARG:HB2	18:U:660:LYS:CD	2.35	0.55
1:A:686:ARG:HH21	1:A:710:LEU:HD13	1.72	0.54
3:C:514:TYR:HB3	3:C:576:ILE:HD11	1.89	0.54
4:E:134:ALA:HB3	4:E:136:TRP:CZ2	2.42	0.54
6:J:618:GLN:O	6:J:634:GLU:CB	2.55	0.54
7:L:721:LEU:HA	7:L:724:TYR:CG	2.41	0.54
10:O:229:LYS:HA	10:O:277:ARG:NH2	2.22	0.54
16:G:3:A:O2'	16:G:4:A:P	2.65	0.54
17:H:34:U:C5'	18:U:662:ILE:CD1	2.84	0.54
17:H:57:A:C4	17:H:58:U:C5	2.95	0.54
17:H:59:A:C4	17:H:60:U:C5	2.95	0.54
27:K:18:TYR:CD2	27:K:168:LYS:HA	2.42	0.54
27:K:130:HIS:O	27:K:134:ALA:CB	2.54	0.54
1:A:1833:LEU:HD11	18:U:718:HIS:HB2	1.89	0.54
1:A:1863:VAL:HG11	1:A:1868:MET:HB2	1.89	0.54
4:E:82:ALA:CB	4:E:92:LEU:HD21	2.27	0.54
10:O:131:THR:O	15:W:108:ARG:NH1	2.36	0.54
17:H:67:C:H2'	17:H:68:G:H8	1.73	0.54
4:E:74:PHE:CE2	4:E:343:ILE:HG12	2.42	0.54
4:E:323:LEU:HD22	15:W:83:PRO:HG2	1.89	0.54
14:T:349:SER:OG	14:T:351:ASP:OD1	2.25	0.54
1:A:1830:GLN:HG2	1:A:1831:LYS:H	1.71	0.54
2:B:100:C:H2'	2:B:101:U:C6	2.42	0.54
9:N:118:ILE:HD12	9:N:132:ILE:HD12	1.89	0.54
10:O:229:LYS:CD	10:O:277:ARG:NH1	2.50	0.54
16:G:138:A:O2'	16:G:139:U:C6	2.59	0.54
16:G:152:C:C3'	16:G:153:C:C6	2.89	0.54
17:H:150:U:C2	17:H:151:C:C5	2.95	0.54
1:A:668:VAL:HB	5:F:68:C:H5''	1.89	0.54
1:A:671:THR:O	1:A:676:ARG:NH2	2.41	0.54
2:B:85:C:OP1	2:B:85:C:H3'	2.07	0.54
3:C:538:HIS:CE1	3:C:551:LEU:HD12	2.42	0.54
5:F:92:A:N3	5:F:93:G:C8	2.76	0.54
9:N:28:LYS:HD2	15:W:189:ILE:HG23	1.88	0.54
10:O:234:LEU:HD12	10:O:274:PHE:CZ	2.42	0.54
1:A:1614:ILE:HD13	1:A:1626:CYS:HB2	1.90	0.54
4:E:263:ASP:HB3	4:E:274:VAL:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:272:ILE:HG21	10:O:274:PHE:CE1	2.43	0.54
16:G:146:C:H1'	16:G:147:C:C5	2.42	0.54
16:G:152:C:O2	16:G:153:C:C6	2.61	0.54
17:H:38:A:O2'	17:H:39:U:C6	2.59	0.54
1:A:1597:PHE:HB3	1:A:1609:VAL:HG11	1.90	0.54
4:E:325:GLY:O	4:E:352:TYR:CZ	2.61	0.54
5:F:90:G:N2	5:F:91:A:C2	2.76	0.54
17:H:80:A:H2'	17:H:81:G:H5'	1.88	0.54
10:O:236:VAL:O	10:O:269:CYS:HA	2.07	0.54
10:O:294:ASN:O	10:O:296:ARG:HG3	2.07	0.54
16:G:120:G:C1'	29:Q:1019:SER:HA	2.37	0.54
27:K:17:PRO:CG	27:K:167:ARG:NH1	2.71	0.54
27:K:123:ASN:O	27:K:127:MET:HB2	2.07	0.54
1:A:608:LEU:HD13	1:A:632:ALA:HB1	1.90	0.54
1:A:657:ALA:O	1:A:661:GLU:HB2	2.08	0.54
4:E:80:THR:O	4:E:81:LEU:HD23	2.07	0.54
5:F:34:G:C5	5:F:35:A:N7	2.76	0.54
6:J:290:ARG:NH1	8:M:180:ASP:OD1	2.40	0.54
6:J:362:ALA:HA	6:J:365:ILE:HD12	1.89	0.54
17:H:183:G:C4	17:H:184:C:C5	2.95	0.54
18:U:671:GLN:OE1	18:U:671:GLN:HA	2.06	0.54
1:A:881:ILE:HG23	1:A:918:THR:HG23	1.90	0.54
1:A:1757:GLU:HG2	18:U:808:LYS:HE3	1.89	0.54
28:I:797:PHE:O	28:I:801:ASP:CB	2.56	0.54
1:A:143:GLN:NE2	1:A:207:PHE:O	2.34	0.53
1:A:787:GLU:OE2	1:A:790:ARG:NH2	2.38	0.53
3:C:637:LEU:HA	3:C:640:VAL:HG12	1.90	0.53
4:E:314:THR:HG23	4:E:315:THR:HG23	1.89	0.53
10:O:259:ARG:CA	10:O:273:GLN:O	2.56	0.53
17:H:31:G:O2'	17:H:32:U:C6	2.59	0.53
28:I:176:SER:HA	28:I:196:ALA:HB2	1.91	0.53
10:O:232:THR:OG1	10:O:273:GLN:HG3	2.07	0.53
17:H:83:A:C5	17:H:84:C:C4	2.97	0.53
12:R:68:HIS:NE2	13:S:89:ASP:O	2.41	0.53
12:R:106:GLN:HG2	12:R:110:LYS:HG2	1.89	0.53
28:I:343:LEU:N	29:Q:527:ILE:CB	2.71	0.53
1:A:1333:VAL:HG13	1:A:1365:ILE:HD13	1.90	0.53
1:A:1609:VAL:HG12	1:A:1631:LEU:HG	1.90	0.53
2:B:74:U:H3	2:B:76:A:H62	1.55	0.53
8:M:198:ARG:NH2	17:H:11:G:N7	2.48	0.53
12:R:196:VAL:HG11	15:W:120:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:694:VAL:HG12	18:U:695:LYS:HG3	1.91	0.53
1:A:1392:LYS:HD3	1:A:1407:ASP:HB3	1.91	0.53
2:B:72:U:H6	2:B:72:U:P	2.32	0.53
4:E:284:PHE:O	15:W:124:MET:HE2	2.09	0.53
4:E:309:VAL:O	4:E:309:VAL:HG12	2.09	0.53
12:R:64:PHE:O	12:R:71:GLN:NE2	2.41	0.53
12:R:65:PRO:HG2	13:S:90:LEU:HD22	1.91	0.53
16:G:5:G:N9	16:G:6:A:C8	2.76	0.53
1:A:1194:CYS:HB3	1:A:1230:LEU:HD23	1.91	0.53
2:B:68:C:O2	2:B:68:C:H2'	2.09	0.53
10:O:239:LEU:HD12	10:O:243:ILE:HD12	1.90	0.53
13:S:18:THR:HA	13:S:159:ILE:HA	1.91	0.53
18:U:605:ASN:HA	18:U:608:MET:HG2	1.91	0.53
28:I:176:SER:CB	28:I:196:ALA:CB	2.80	0.53
1:A:1405:LEU:O	1:A:1409:GLU:HB2	2.09	0.53
4:E:178:LEU:CD1	4:E:222:LEU:HD22	2.39	0.53
4:E:266:PRO:HB2	7:L:788:TYR:HB3	1.91	0.53
18:U:576:ARG:HH22	18:U:647:ARG:HD3	1.73	0.53
2:B:79:C:O2	2:B:79:C:H2'	2.07	0.53
4:E:323:LEU:N	4:E:323:LEU:HD23	2.24	0.53
6:J:496:ASP:CB	6:J:536:LEU:CB	2.87	0.53
8:M:236:ASN:ND2	8:M:242:ALA:O	2.42	0.53
16:G:152:C:C6	16:G:153:C:N4	2.74	0.53
2:B:67:A:H4'	2:B:68:C:C5	2.43	0.53
4:E:250:LEU:CD2	4:E:262:TRP:HB2	2.38	0.53
6:J:774:VAL:CA	6:J:787:LYS:CB	2.87	0.53
8:M:237:LEU:HD11	12:R:264:LEU:HB2	1.91	0.53
17:H:33:G:H4'	18:U:662:ILE:HD11	1.91	0.53
17:H:108:G:O2'	17:H:109:C:H5'	2.08	0.53
1:A:136:ILE:HG12	1:A:418:THR:HG22	1.91	0.53
2:B:96:A:N6	2:B:97:G:O6	2.42	0.53
3:C:749:THR:HG23	3:C:753:GLU:HB3	1.91	0.53
3:C:814:ARG:NH1	3:C:818:SER:OG	2.42	0.53
14:T:392:PRO:HG3	14:T:415:ILE:HA	1.91	0.53
16:G:141:C:O2'	16:G:142:U:C6	2.61	0.53
17:H:113:G:H2'	17:H:114:A:H8	1.72	0.53
1:A:1513:MET:HE2	18:U:622:ALA:HB3	1.91	0.52
1:A:1835:GLN:HB2	18:U:557:VAL:HG11	1.91	0.52
3:C:592:VAL:HG22	3:C:655:VAL:HG22	1.91	0.52
5:F:44:G:H21	16:G:3:A:N6	2.01	0.52
10:O:223:LEU:H	10:O:223:LEU:HD22	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:93:A:HO2'	17:H:94:A:H5'	1.70	0.52
17:H:148:C:H2'	17:H:149:A:C8	2.44	0.52
2:B:44:A:H8	2:B:44:A:O5'	1.92	0.52
4:E:147:LEU:HD12	4:E:179:TRP:CG	2.44	0.52
4:E:326:HIS:HE1	4:E:352:TYR:HD2	1.57	0.52
12:R:151:LEU:HD22	14:T:323:VAL:HG11	1.91	0.52
18:U:550:ARG:HB3	18:U:660:LYS:CD	2.39	0.52
2:B:38:C:C5	2:B:39:C:C2	2.97	0.52
2:B:70:A:H2'	2:B:71:C:C6	2.44	0.52
3:C:166:CYS:O	3:C:170:ILE:HG22	2.10	0.52
3:C:173:THR:OG1	3:C:642:HIS:NE2	2.39	0.52
14:T:391:SER:OG	14:T:393:ASP:OD1	2.28	0.52
16:G:2:U:C2	18:U:625:PHE:HB3	2.45	0.52
17:H:114:A:H2'	17:H:115:G:C8	2.40	0.52
17:H:180:G:H2'	17:H:181:G:C8	2.44	0.52
27:K:119:VAL:O	27:K:123:ASN:HB2	2.08	0.52
3:C:167:TYR:CE2	3:C:536:ARG:HB2	2.45	0.52
4:E:56:GLN:HG3	4:E:56:GLN:O	2.09	0.52
4:E:161:ARG:NH1	4:E:203:ASP:OD1	2.42	0.52
5:F:92:A:H2'	5:F:93:G:H8	1.74	0.52
10:O:222:ARG:CZ	10:O:222:ARG:N	2.73	0.52
17:H:70:C:H2'	17:H:71:C:C6	2.44	0.52
18:U:548:LEU:HD21	18:U:661:ALA:HB1	1.91	0.52
1:A:641:MET:HA	1:A:644:ILE:HG22	1.91	0.52
3:C:166:CYS:SG	3:C:536:ARG:CZ	2.97	0.52
4:E:123:MET:HB3	4:E:125:PHE:CE1	2.37	0.52
4:E:162:ARG:CZ	4:E:203:ASP:O	2.57	0.52
4:E:251:LEU:CG	4:E:291:CYS:SG	2.98	0.52
10:O:155:PRO:CB	12:R:188:PHE:CE1	2.92	0.52
4:E:284:PHE:HZ	15:W:120:ILE:HD13	1.74	0.52
6:J:591:LEU:O	6:J:592:ALA:HB3	2.09	0.52
17:H:89:U:H2'	17:H:90:A:H8	1.75	0.52
17:H:179:C:O2	17:H:180:G:C8	2.63	0.52
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.42	0.52
10:O:223:LEU:H	10:O:223:LEU:CD1	1.98	0.52
16:G:22:C:O4'	16:G:23:U:OP1	2.28	0.52
17:H:71:C:H2'	17:H:72:U:C6	2.45	0.52
18:U:546:VAL:HG23	18:U:546:VAL:O	2.08	0.52
27:K:19:PHE:HB2	27:K:171:GLN:CG	2.39	0.52
3:C:139:HIS:HB2	35:C:1500:GTP:C5'	2.40	0.52
7:L:710:ALA:C	27:K:124:LEU:CD2	2.78	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:759:GLU:HB2	27:K:167:ARG:CD	2.40	0.52
16:G:7:G:N3	16:G:7:G:C2'	2.69	0.52
17:H:179:C:C2	17:H:180:G:C8	2.98	0.52
18:U:765:HIS:HD2	18:U:766:MET:O	1.93	0.52
1:A:1309:SER:OG	1:A:1310:ARG:N	2.42	0.52
17:H:89:U:H2'	17:H:90:A:C8	2.44	0.52
28:I:545:ILE:C	28:I:547:LEU:N	2.52	0.52
28:I:795:ILE:N	28:I:795:ILE:CD1	2.73	0.52
1:A:388:LEU:O	3:C:379:LYS:NZ	2.39	0.52
1:A:1179:SER:O	1:A:1201:ARG:NH2	2.40	0.52
1:A:1833:LEU:CD1	18:U:718:HIS:HB2	2.40	0.52
3:C:829:GLU:HB2	3:C:907:VAL:HG22	1.92	0.52
4:E:116:HIS:HE1	4:E:158:TYR:HE1	1.58	0.52
4:E:257:ASN:CG	15:W:149:SER:HB3	2.30	0.52
7:L:251:LEU:HB2	7:L:254:GLU:HB3	1.92	0.52
7:L:759:GLU:HG2	27:K:167:ARG:CD	2.39	0.52
16:G:152:C:C1'	16:G:153:C:C5	2.93	0.52
17:H:77:C:H2'	17:H:78:C:C6	2.45	0.52
17:H:83:A:C4	17:H:84:C:C4	2.98	0.52
18:U:662:ILE:HG13	18:U:663:ALA:N	2.24	0.52
18:U:666:ARG:NH2	18:U:666:ARG:CG	2.73	0.52
1:A:1946:ASN:OD1	1:A:1986:LEU:HB3	2.09	0.51
3:C:476:CYS:HB2	3:C:565:ILE:HB	1.92	0.51
4:E:101:ASN:HD22	4:E:101:ASN:N	2.06	0.51
10:O:257:GLU:HG2	10:O:257:GLU:O	2.09	0.51
12:R:193:LYS:HB2	15:W:145:ASN:HD21	1.73	0.51
17:H:34:U:H5'	18:U:662:ILE:CD1	2.41	0.51
17:H:83:A:C5	17:H:84:C:C5	2.98	0.51
33:V:370:LYS:N	33:V:372:GLU:O	2.44	0.51
2:B:99:C:H2'	2:B:100:C:C6	2.45	0.51
3:C:221:ILE:O	3:C:495:ARG:NH1	2.43	0.51
3:C:670:SER:HB2	3:C:689:ALA:H	1.74	0.51
4:E:65:HIS:NE2	4:E:91:LEU:HD12	2.26	0.51
4:E:300:ILE:O	4:E:311:VAL:HA	2.09	0.51
5:F:44:G:O6	16:G:2:U:C5	2.63	0.51
5:F:82:A:N6	12:R:258:LYS:NZ	2.57	0.51
10:O:250:ASN:HD21	13:S:91:LYS:HE3	1.74	0.51
17:H:67:C:H2'	17:H:68:G:C8	2.45	0.51
1:A:1699:THR:HA	1:A:1717:ASN:HD22	1.76	0.51
1:A:1782:ASP:HB3	1:A:1841:THR:HG21	1.92	0.51
3:C:158:ARG:HB3	3:C:158:ARG:CZ	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:277:PHE:HE2	4:E:300:ILE:HD12	1.75	0.51
4:E:277:PHE:CE2	4:E:300:ILE:CD1	2.88	0.51
4:E:277:PHE:CE2	4:E:300:ILE:HD13	2.41	0.51
10:O:258:ILE:CG2	10:O:274:PHE:CD1	2.91	0.51
16:G:134:U:C2'	16:G:135:G:H8	2.13	0.51
17:H:81:G:H2'	17:H:82:G:C8	2.45	0.51
17:H:111:G:O3'	17:H:112:G:O4'	2.28	0.51
28:I:729:SER:O	28:I:732:ALA:HB3	2.09	0.51
2:B:77:G:C6	2:B:80:U:C4	2.98	0.51
3:C:308:CYS:SG	3:C:309:PHE:N	2.84	0.51
4:E:265:ARG:H	4:E:272:ARG:HH21	1.57	0.51
5:F:34:G:H2'	5:F:35:A:H8	1.74	0.51
17:H:153:A:C3'	17:H:154:C:C5'	2.85	0.51
1:A:435:CYS:SG	1:A:439:GLN:NE2	2.67	0.51
3:C:832:TYR:HD1	3:C:900:VAL:O	1.93	0.51
4:E:93:TRP:CZ2	4:E:351:LEU:HD11	2.46	0.51
4:E:115:LEU:CD2	4:E:126:SER:HB2	2.41	0.51
16:G:6:A:N6	16:G:7:G:O6	2.43	0.51
1:A:1296:GLN:NE2	1:A:1317:TYR:OH	2.43	0.51
4:E:80:THR:HG23	4:E:81:LEU:N	2.24	0.51
7:L:259:ASP:CB	8:M:199:ARG:NH2	2.74	0.51
7:L:731:LEU:HD11	27:K:143:VAL:HG12	1.93	0.51
10:O:136:MET:O	10:O:140:ALA:HB2	2.11	0.51
10:O:235:TYR:CD1	10:O:271:PHE:HE1	2.29	0.51
16:G:5:G:N3	16:G:6:A:C5	2.77	0.51
17:H:71:C:O5'	17:H:71:C:H6	1.94	0.51
17:H:72:U:H2'	17:H:73:C:C6	2.45	0.51
17:H:88:A:H2'	17:H:89:U:C6	2.46	0.51
17:H:168:A:N3	17:H:168:A:H2'	2.25	0.51
4:E:209:ILE:HG21	4:E:250:LEU:HD13	1.92	0.51
6:J:228:ARG:NH2	6:J:257:GLU:OE1	2.43	0.51
16:G:6:A:H3'	16:G:7:G:C8	2.45	0.51
16:G:143:U:H6	16:G:143:U:C5'	2.23	0.51
1:A:1832:ARG:NH1	18:U:680:ASP:OD2	2.44	0.51
4:E:62:LEU:HB3	4:E:351:LEU:HD12	1.93	0.51
4:E:114:GLU:O	4:E:127:ALA:N	2.40	0.51
4:E:355:GLU:N	15:W:82:ASN:OD1	2.33	0.51
17:H:7:U:C2'	17:H:8:C:H5'	2.41	0.51
1:A:947:PRO:HA	1:A:1437:ARG:HH22	1.76	0.51
12:R:262:ILE:HB	12:R:267:ARG:HH21	1.75	0.51
16:G:134:U:C3'	16:G:135:G:H8	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:106:G:N2	17:H:107:A:C6	2.79	0.51
1:A:1017:ILE:HD11	1:A:1031:ILE:HD11	1.93	0.51
3:C:529:ARG:H	3:C:553:GLU:HB3	1.74	0.51
5:F:38:G:N3	5:F:39:A:N7	2.58	0.51
17:H:83:A:N1	17:H:84:C:C4	2.79	0.51
17:H:90:A:H2'	17:H:91:U:C6	2.45	0.51
18:U:621:MET:HA	18:U:626:MET:SD	2.51	0.51
18:U:753:PHE:HB2	18:U:824:ASP:HB2	1.91	0.51
27:K:196:GLU:O	27:K:199:ILE:CG1	2.59	0.51
4:E:54:SER:HB3	4:E:355:GLU:OE1	2.11	0.50
7:L:696:LEU:HA	27:K:110:SER:CB	2.40	0.50
8:M:178:GLU:OE1	8:M:181:ARG:NH1	2.41	0.50
10:O:234:LEU:HD12	10:O:274:PHE:HZ	1.75	0.50
11:P:17:GLY:N	11:P:20:GLU:OE1	2.41	0.50
16:G:152:C:O2	16:G:153:C:C5	2.63	0.50
17:H:182:U:O2'	17:H:183:G:C5'	2.44	0.50
28:I:238:LEU:O	28:I:242:ALA:N	2.42	0.50
28:I:795:ILE:N	28:I:795:ILE:HD12	2.27	0.50
1:A:163:ARG:HE	1:A:625:PRO:HB3	1.74	0.50
1:A:381:PRO:O	3:C:354:ARG:NH2	2.43	0.50
4:E:322:LYS:HG2	15:W:89:PHE:HE2	1.75	0.50
13:S:63:GLN:NE2	13:S:111:GLN:OE1	2.44	0.50
14:T:343:PRO:HG2	14:T:356:LEU:HD23	1.92	0.50
27:K:134:ALA:O	27:K:136:LYS:N	2.44	0.50
7:L:259:ASP:HB3	8:M:199:ARG:NH2	2.27	0.50
10:O:222:ARG:H	10:O:222:ARG:NE	2.08	0.50
16:G:133:A:O2'	16:G:135:G:OP1	2.20	0.50
1:A:309:ARG:HE	1:A:310:THR:H	1.58	0.50
3:C:157:ILE:CG2	3:C:158:ARG:HG2	2.16	0.50
3:C:938:ARG:HH21	3:C:942:GLY:HA3	1.76	0.50
4:E:178:LEU:N	4:E:178:LEU:HD23	2.26	0.50
17:H:47:U:H5'	17:H:47:U:O2	2.12	0.50
17:H:84:C:H2'	17:H:85:A:C8	2.46	0.50
28:I:264:ASP:O	28:I:268:ARG:CB	2.59	0.50
2:B:69:A:H3'	2:B:70:A:N3	2.26	0.50
4:E:178:LEU:CD2	4:E:208:ILE:CD1	2.90	0.50
5:F:38:G:C2	5:F:39:A:N7	2.79	0.50
5:F:44:G:O6	16:G:2:U:H5	1.95	0.50
12:R:252:SER:OG	12:R:255:LYS:O	2.30	0.50
3:C:259:LYS:HG2	35:C:1500:GTP:C6	2.47	0.50
4:E:243:LEU:CD1	4:E:247:GLY:CA	2.88	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:615:LEU:CB	6:J:638:GLU:CB	2.89	0.50
10:O:229:LYS:HA	10:O:277:ARG:HH22	1.77	0.50
17:H:56:A:C6	17:H:92:U:N3	2.78	0.50
1:A:1946:ASN:OD1	1:A:1986:LEU:CB	2.60	0.50
3:C:137:HIS:O	3:C:207:GLY:O	2.30	0.50
4:E:57:ALA:O	4:E:355:GLU:CG	2.59	0.50
4:E:260:ARG:NH1	4:E:276:ILE:HD11	2.26	0.50
4:E:284:PHE:O	15:W:124:MET:CE	2.59	0.50
5:F:38:G:O6	16:G:9:C:N3	2.45	0.50
16:G:146:C:O2'	16:G:147:C:H6	1.87	0.50
16:G:152:C:H2'	16:G:152:C:O2	2.10	0.50
17:H:83:A:HO2'	17:H:84:C:H5'	1.72	0.50
28:I:337:LEU:O	28:I:340:ARG:N	2.45	0.50
1:A:1275:ARG:NH1	1:A:1373:GLN:O	2.42	0.50
2:B:8:G:C2'	2:B:8:G:N3	2.74	0.50
2:B:75:G:O6	2:B:76:A:C5	2.65	0.50
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.93	0.50
3:C:531:TRP:HB2	3:C:551:LEU:HB2	1.94	0.50
5:F:78:A:H4'	6:J:237:LYS:HE2	1.94	0.50
6:J:311:GLN:HG3	8:M:131:GLN:HG2	1.93	0.50
7:L:209:ASP:HB2	10:O:113:ASN:HD21	1.76	0.50
16:G:146:C:OP2	16:G:146:C:H2'	2.12	0.50
18:U:662:ILE:O	18:U:666:ARG:HG3	2.12	0.50
1:A:888:GLN:CA	1:A:888:GLN:NE2	2.74	0.50
1:A:1836:LEU:HD21	18:U:547:ILE:HG21	1.94	0.50
3:C:500:THR:HG22	3:C:545:PRO:HA	1.93	0.50
4:E:101:ASN:N	4:E:101:ASN:ND2	2.60	0.50
14:T:250:ARG:NH1	14:T:266:GLU:OE2	2.44	0.50
18:U:546:VAL:HG11	18:U:665:HIS:NE2	2.26	0.50
4:E:62:LEU:O	4:E:351:LEU:N	2.38	0.49
4:E:134:ALA:HB1	4:E:143:ARG:CD	2.40	0.49
16:G:21:A:H3'	16:G:21:A:P	2.52	0.49
17:H:57:A:N6	17:H:91:U:C2	2.80	0.49
2:B:79:C:C5'	2:B:79:C:C6	2.95	0.49
3:C:849:VAL:HG22	3:C:852:ARG:HH21	1.77	0.49
12:R:178:ARG:NH1	15:W:141:PRO:O	2.45	0.49
15:W:103:GLN:NE2	15:W:111:LEU:O	2.45	0.49
17:H:34:U:H5'	18:U:662:ILE:CG1	2.35	0.49
1:A:254:TYR:OH	1:A:434:HIS:O	2.30	0.49
6:J:322:MET:O	8:M:181:ARG:NH1	2.45	0.49
14:T:213:GLU:HG3	14:T:218:TRP:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:134:U:C3'	16:G:135:G:C8	2.95	0.49
17:H:54:U:C6	17:H:55:U:C5	3.00	0.49
28:I:545:ILE:HG12	28:I:546:SER:H	1.77	0.49
28:I:585:ASP:O	28:I:586:GLY:C	2.50	0.49
1:A:1104:ASP:OD1	1:A:1107:ARG:NH2	2.46	0.49
1:A:1491:LYS:O	1:A:1710:ASN:ND2	2.46	0.49
3:C:147:ASP:OD2	3:C:164:ASP:CB	2.57	0.49
4:E:57:ALA:O	4:E:355:GLU:HB2	2.09	0.49
4:E:336:HIS:CD2	4:E:339:GLU:OE1	2.66	0.49
6:J:260:ARG:HD3	7:L:214:ILE:HG12	1.95	0.49
17:H:92:U:O2'	17:H:93:A:H5'	2.13	0.49
2:B:67:A:H4'	2:B:68:C:N4	2.27	0.49
3:C:561:LYS:NZ	3:C:611:ASN:OD1	2.42	0.49
4:E:55:LEU:CD1	4:E:96:TYR:CZ	2.96	0.49
4:E:62:LEU:HB2	4:E:351:LEU:CB	2.19	0.49
4:E:117:TYR:HE1	4:E:121:GLY:O	1.96	0.49
4:E:229:TYR:CE2	4:E:272:ARG:NH1	2.79	0.49
5:F:14:C:H2'	5:F:15:A:H8	1.77	0.49
6:J:238:ASN:HD22	6:J:244:ASN:HD21	1.61	0.49
12:R:241:GLU:HA	12:R:244:GLU:HG2	1.94	0.49
1:A:1320:LYS:HG2	18:U:798:MET:HG2	1.93	0.49
1:A:1606:ILE:O	1:A:1634:SER:OG	2.30	0.49
3:C:219:LEU:HD13	3:C:245:HIS:HD2	1.77	0.49
3:C:699:ASP:OD2	3:C:722:TYR:OH	2.30	0.49
10:O:260:THR:CG2	10:O:273:GLN:CD	2.81	0.49
13:S:98:LEU:H	13:S:131:ARG:HA	1.77	0.49
14:T:380:LEU:HG	14:T:400:PHE:HZ	1.76	0.49
17:H:180:G:H2'	17:H:181:G:H8	1.76	0.49
28:I:405:TYR:O	28:I:409:GLY:HA3	2.13	0.49
3:C:154:HIS:HB3	3:C:158:ARG:HG3	1.93	0.49
1:A:256:TYR:HE1	1:A:332:TYR:HB2	1.77	0.49
3:C:140:HIS:N	35:C:1500:GTP:O2B	2.46	0.49
4:E:58:PRO:O	15:W:82:ASN:OD1	2.30	0.49
7:L:699:ASN:CG	27:K:114:LEU:CB	2.80	0.49
1:A:546:LEU:HD22	1:A:648:LEU:HD11	1.95	0.49
3:C:154:HIS:HB2	3:C:158:ARG:HG3	1.95	0.49
3:C:277:LYS:NZ	3:C:864:PRO:O	2.41	0.49
6:J:354:LEU:HD22	6:J:389:HIS:HE1	1.78	0.49
12:R:192:ALA:HB2	15:W:153:ILE:HD13	1.95	0.49
13:S:41:GLU:OE2	13:S:44:ARG:NH2	2.45	0.49
18:U:539:GLU:HG2	18:U:546:VAL:CG2	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:174:GLU:HG3	3:C:181:ILE:H	1.77	0.49
7:L:252:ARG:HH11	7:L:252:ARG:CG	2.19	0.49
16:G:7:G:N2	16:G:8:C:H1'	2.28	0.49
27:K:19:PHE:HB2	27:K:171:GLN:HG2	1.95	0.49
1:A:888:GLN:HE21	1:A:888:GLN:H	1.56	0.48
1:A:995:ARG:HH12	12:R:295:ASP:HB2	1.77	0.48
4:E:257:ASN:OD1	15:W:149:SER:HB3	2.13	0.48
6:J:466:ARG:O	28:I:606:TRP:CB	2.61	0.48
8:M:235:GLN:HB3	8:M:239:ARG:HH21	1.76	0.48
9:N:101:CYS:SG	9:N:139:CYS:HB2	2.53	0.48
12:R:228:PRO:HB2	12:R:230:MET:CE	2.43	0.48
16:G:152:C:C1'	16:G:153:C:H5	2.25	0.48
17:H:54:U:N3	17:H:94:A:N6	2.61	0.48
1:A:1947:ASN:O	1:A:1950:ALA:N	2.46	0.48
5:F:41:A:N6	16:G:6:A:H61	2.08	0.48
5:F:92:A:H2'	5:F:93:G:C8	2.47	0.48
10:O:222:ARG:N	10:O:222:ARG:NE	2.60	0.48
2:B:78:U:H6	2:B:78:U:H3'	1.79	0.48
3:C:205:THR:HB	3:C:215:VAL:HG22	1.94	0.48
3:C:779:LEU:O	3:C:938:ARG:NH1	2.46	0.48
12:R:184:GLN:NE2	12:R:184:GLN:CA	2.73	0.48
12:R:281:ASN:ND2	12:R:282:GLU:OE1	2.47	0.48
18:U:691:ALA:HB3	18:U:698:LEU:H	1.77	0.48
3:C:258:ASN:OD1	3:C:259:LYS:N	2.46	0.48
4:E:131:LYS:CB	4:E:152:SER:O	2.62	0.48
7:L:252:ARG:NH1	7:L:252:ARG:CG	2.77	0.48
7:L:714:GLU:N	27:K:124:LEU:HD21	2.28	0.48
1:A:1201:ARG:HG3	1:A:1202:THR:H	1.78	0.48
2:B:69:A:H3'	2:B:70:A:C2	2.48	0.48
2:B:89:U:O2'	2:B:90:U:O5'	2.30	0.48
3:C:663:CYS:HB2	3:C:828:MET:HB2	1.94	0.48
13:S:84:ASP:OD1	13:S:108:ASN:ND2	2.46	0.48
17:H:78:C:H2'	17:H:79:G:H8	1.78	0.48
1:A:27:GLU:OE2	4:E:194:TYR:OH	2.32	0.48
2:B:96:A:C2	2:B:97:G:C4	3.02	0.48
4:E:314:THR:CG2	4:E:315:THR:HG23	2.44	0.48
17:H:172:C:C2	17:H:173:C:C5	3.01	0.48
3:C:157:ILE:HG13	3:C:158:ARG:H	1.79	0.48
3:C:191:PRO:HA	3:C:197:SER:HA	1.95	0.48
3:C:342:ARG:NH2	3:C:356:PHE:O	2.46	0.48
4:E:78:GLY:C	4:E:336:HIS:HE1	2.08	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:145:LYS:HZ1	4:E:184:LYS:HG2	1.79	0.48
9:N:18:ILE:HG21	9:N:70:ILE:HD11	1.96	0.48
17:H:166:G:N3	17:H:166:G:H2'	2.29	0.48
28:I:327:LEU:O	28:I:330:ARG:N	2.46	0.48
1:A:56:ALA:O	9:N:109:ARG:NH1	2.38	0.48
1:A:529:THR:OG1	18:U:581:THR:OG1	2.23	0.48
1:A:825:ILE:HA	1:A:933:ARG:HH12	1.78	0.48
1:A:941:LYS:HB3	1:A:951:LEU:HD11	1.95	0.48
2:B:77:G:C6	2:B:80:U:C5	3.01	0.48
3:C:492:ALA:O	3:C:551:LEU:HA	2.14	0.48
3:C:619:THR:HG22	3:C:629:ILE:HG13	1.95	0.48
4:E:74:PHE:CD1	4:E:81:LEU:HD21	2.47	0.48
4:E:231:MET:SD	4:E:262:TRP:CE3	3.07	0.48
7:L:222:LEU:HD12	12:R:84:ASN:HB2	1.96	0.48
17:H:168:A:H3'	17:H:169:C:C6	2.49	0.48
27:K:19:PHE:HE2	27:K:172:LEU:O	1.96	0.48
3:C:104:LEU:HD21	3:C:166:CYS:SG	2.53	0.48
3:C:924:GLN:OE1	3:C:928:HIS:NE2	2.41	0.48
4:E:115:LEU:HD23	4:E:126:SER:CB	2.43	0.48
5:F:35:A:H2'	5:F:35:A:N3	2.29	0.48
13:S:15:TYR:HB2	13:S:163:TYR:HB2	1.94	0.48
28:I:348:VAL:CB	28:I:357:VAL:HA	2.44	0.48
1:A:1946:ASN:HB2	1:A:1986:LEU:HD23	1.85	0.48
2:B:20:G:O6	2:B:58:U:O2	2.32	0.48
8:M:230:THR:HB	12:R:265:ASP:HB2	1.95	0.48
14:T:347:THR:HG22	14:T:357:TRP:HE1	1.78	0.48
17:H:56:A:N6	17:H:92:U:H3	2.07	0.48
17:H:57:A:N1	17:H:91:U:O2	2.47	0.48
28:I:748:VAL:O	28:I:752:ALA:N	2.40	0.48
1:A:1306:LYS:HD2	1:A:1306:LYS:HA	1.73	0.47
3:C:139:HIS:HB2	35:C:1500:GTP:O3A	2.14	0.47
4:E:162:ARG:HH22	4:E:204:THR:HA	1.76	0.47
5:F:34:G:C2'	5:F:35:A:O5'	2.61	0.47
13:S:25:LEU:HD22	13:S:98:LEU:HD22	1.96	0.47
14:T:373:LYS:HD2	14:T:392:PRO:HB2	1.96	0.47
16:G:148:U:C6	16:G:148:U:C4'	2.97	0.47
17:H:80:A:H2'	17:H:81:G:C8	2.39	0.47
17:H:83:A:C4	17:H:84:C:C6	3.01	0.47
1:A:209:ASP:HB2	1:A:212:PRO:HA	1.95	0.47
3:C:700:ILE:O	3:C:740:THR:OG1	2.31	0.47
3:C:832:TYR:HD1	3:C:901:PHE:HA	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:44:G:C6	16:G:2:U:H5	2.28	0.47
13:S:55:ARG:HB3	13:S:63:GLN:HB3	1.96	0.47
14:T:418:THR:HG21	14:T:467:ALA:HA	1.95	0.47
27:K:18:TYR:CD2	27:K:168:LYS:CA	2.97	0.47
28:I:545:ILE:HG13	28:I:581:GLU:HA	1.94	0.47
1:A:255:PHE:HB3	1:A:259:ASP:HB3	1.95	0.47
7:L:731:LEU:CD1	27:K:143:VAL:HG12	2.45	0.47
8:M:221:LYS:NZ	17:H:18:U:OP2	2.47	0.47
12:R:193:LYS:HD2	15:W:145:ASN:ND2	2.30	0.47
13:S:57:ILE:HD13	15:W:97:ASN:HB3	1.96	0.47
14:T:336:VAL:HG23	14:T:347:THR:HB	1.95	0.47
16:G:152:C:N1	16:G:153:C:H5	2.05	0.47
17:H:27:U:HO2'	17:H:28:C:H5'	1.72	0.47
4:E:147:LEU:HD23	4:E:147:LEU:H	1.80	0.47
10:O:235:TYR:HD1	10:O:271:PHE:CE1	2.30	0.47
27:K:195:ILE:CG1	27:K:196:GLU:N	2.78	0.47
1:A:51:PHE:CE2	4:E:66:GLU:HG2	2.49	0.47
1:A:1946:ASN:OD1	1:A:1986:LEU:HD23	2.06	0.47
4:E:76:PRO:CG	4:E:121:GLY:CA	2.59	0.47
7:L:731:LEU:C	27:K:142:LEU:HD21	2.34	0.47
16:G:143:U:H2'	16:G:145:U:O4	2.14	0.47
16:G:146:C:N1	16:G:147:C:C5	2.82	0.47
28:I:337:LEU:O	28:I:338:ILE:C	2.53	0.47
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.97	0.47
1:A:1832:ARG:NE	1:A:1832:ARG:CA	2.73	0.47
3:C:167:TYR:O	3:C:535:ALA:HB1	2.15	0.47
10:O:240:GLY:HA3	10:O:296:ARG:NH1	2.29	0.47
16:G:21:A:H8	16:G:21:A:O5'	1.97	0.47
28:I:197:ALA:HB1	28:I:211:SER:CB	2.44	0.47
1:A:1306:LYS:HB3	1:A:1308:PRO:HD2	1.96	0.47
1:A:1802:PRO:CG	1:A:1824:THR:CG2	2.91	0.47
1:A:1946:ASN:ND2	1:A:1986:LEU:HG	2.30	0.47
2:B:93:U:H4'	2:B:94:U:H5''	1.97	0.47
4:E:266:PRO:CD	7:L:785:GLN:HB2	2.44	0.47
10:O:64:ARG:HH11	10:O:66:LYS:HG2	1.80	0.47
13:S:122:LEU:HA	13:S:126:HIS:HD2	1.80	0.47
14:T:390:GLY:HA3	14:T:416:ILE:HD11	1.95	0.47
16:G:22:C:C4'	16:G:23:U:OP1	2.63	0.47
17:H:89:U:H6	17:H:89:U:O5'	1.98	0.47
18:U:811:ARG:HH11	18:U:811:ARG:CG	2.14	0.47
28:I:238:LEU:O	28:I:241:ASP:CB	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:I:338:ILE:O	28:I:342:PRO:N	2.47	0.47
28:I:520:ILE:O	28:I:524:TYR:CA	2.61	0.47
28:I:521:VAL:O	28:I:527:PHE:N	2.48	0.47
4:E:250:LEU:HD22	4:E:262:TRP:HB2	1.97	0.47
5:F:37:C:H2'	5:F:38:G:C4'	2.44	0.47
12:R:106:GLN:NE2	12:R:225:PRO:HD2	2.29	0.47
14:T:379:VAL:HG21	14:T:420:THR:HA	1.97	0.47
15:W:216:LEU:HA	15:W:219:ILE:HG22	1.97	0.47
16:G:2:U:C6	16:G:2:U:P	3.08	0.47
16:G:2:U:C6	16:G:2:U:O5'	2.68	0.47
1:A:1517:LYS:HD2	1:A:1522:GLN:HG2	0.86	0.47
2:B:75:G:O6	2:B:76:A:N7	2.47	0.47
3:C:589:LYS:HG3	3:C:628:VAL:HG13	1.96	0.47
4:E:117:TYR:CE1	4:E:121:GLY:O	2.68	0.47
4:E:243:LEU:HD11	4:E:247:GLY:CA	2.42	0.47
4:E:263:ASP:OD1	4:E:272:ARG:HB3	2.15	0.47
3:C:136:GLY:HA3	3:C:142:LYS:HZ3	1.80	0.47
3:C:224:GLY:HA3	3:C:438:ILE:HD12	1.95	0.47
4:E:116:HIS:CE1	4:E:158:TYR:HD1	2.29	0.47
4:E:297:GLY:O	4:E:314:THR:OG1	2.19	0.47
5:F:20:A:H4'	9:N:97:TYR:HE1	1.80	0.47
7:L:751:THR:O	7:L:755:LEU:N	2.38	0.47
14:T:254:VAL:HG22	14:T:261:LEU:HD23	1.97	0.47
27:K:19:PHE:CE2	27:K:175:GLY:CA	2.88	0.47
1:A:1430:LEU:HD21	1:A:1459:ARG:HE	1.80	0.46
1:A:1836:LEU:HD21	18:U:547:ILE:CG2	2.45	0.46
1:A:1836:LEU:HD23	18:U:547:ILE:HG21	1.97	0.46
2:B:8:G:N3	2:B:8:G:H2'	2.30	0.46
10:O:272:ILE:CG2	10:O:274:PHE:CZ	2.99	0.46
1:A:332:TYR:O	3:C:888:ARG:NH2	2.39	0.46
1:A:1802:PRO:HG2	1:A:1824:THR:HG23	1.98	0.46
3:C:832:TYR:CD1	3:C:901:PHE:HA	2.51	0.46
10:O:36:MET:HB3	10:O:57:TRP:HB3	1.97	0.46
10:O:260:THR:HG22	10:O:273:GLN:CG	2.40	0.46
18:U:551:THR:HG22	18:U:664:GLU:OE2	2.15	0.46
18:U:752:ILE:HD12	18:U:773:LEU:HD21	1.97	0.46
18:U:805:LEU:HD11	18:U:832:ALA:HB2	1.95	0.46
33:V:299:LYS:O	33:V:301:GLN:N	2.48	0.46
3:C:173:THR:HG1	3:C:642:HIS:HE2	1.61	0.46
3:C:259:LYS:HE3	35:C:1500:GTP:C4	2.50	0.46
3:C:440:SER:O	3:C:442:LYS:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:59:ILE:HD13	15:W:82:ASN:ND2	2.29	0.46
4:E:232:ARG:O	4:E:262:TRP:CH2	2.67	0.46
6:J:774:VAL:HA	6:J:787:LYS:CB	2.45	0.46
16:G:148:U:C2	17:H:30:A:C2	2.87	0.46
3:C:135:CYS:HB2	3:C:242:LEU:HD13	1.98	0.46
3:C:692:LEU:HD12	3:C:696:LEU:HB3	1.97	0.46
6:J:261:ALA:HA	6:J:264:ILE:HD12	1.98	0.46
10:O:155:PRO:HD3	12:R:188:PHE:CE1	2.45	0.46
1:A:1237:MET:HG2	1:A:1284:LEU:HD23	1.97	0.46
7:L:759:GLU:CD	27:K:171:GLN:HE22	2.18	0.46
1:A:378:PHE:HB3	3:C:342:ARG:HH11	1.81	0.46
1:A:1337:GLN:O	1:A:1341:ARG:NH2	2.49	0.46
4:E:55:LEU:HG	4:E:96:TYR:HH	1.76	0.46
6:J:224:LYS:NZ	6:J:257:GLU:OE2	2.39	0.46
7:L:264:LYS:HE3	7:L:264:LYS:HB2	1.60	0.46
7:L:731:LEU:N	7:L:731:LEU:CD2	2.79	0.46
11:P:19:GLY:HA2	11:P:23:LEU:HD12	1.96	0.46
17:H:59:A:H2'	17:H:60:U:C6	2.50	0.46
33:V:219:TYR:HA	33:V:235:TYR:O	2.16	0.46
1:A:372:PRO:HG2	3:C:342:ARG:HG2	1.98	0.46
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.97	0.46
1:A:1513:MET:CE	18:U:622:ALA:CB	2.94	0.46
1:A:1830:GLN:HG3	1:A:1834:GLY:HA2	1.98	0.46
4:E:125:PHE:N	4:E:125:PHE:CD1	2.82	0.46
10:O:230:THR:H	10:O:277:ARG:CZ	2.28	0.46
13:S:38:ASN:HD21	13:S:76:SER:HB2	1.81	0.46
13:S:148:ASN:HD21	13:S:152:ARG:HB2	1.81	0.46
17:H:113:G:O2'	17:H:114:A:H5'	2.15	0.46
18:U:537:GLY:HA3	18:U:548:LEU:HD12	1.97	0.46
18:U:626:MET:SD	18:U:643:LYS:HE3	2.56	0.46
18:U:771:ILE:HG21	18:U:850:ILE:HG21	1.97	0.46
1:A:76:MET:O	1:A:85:LYS:NZ	2.38	0.46
1:A:678:GLU:HG2	1:A:749:TRP:HH2	1.81	0.46
1:A:1517:LYS:NZ	1:A:1517:LYS:CB	2.73	0.46
7:L:21:ALA:HB1	7:L:159:LEU:HD21	1.97	0.46
27:K:188:LEU:C	27:K:188:LEU:HD13	2.36	0.46
28:I:464:ALA:O	28:I:465:ARG:C	2.53	0.46
1:A:402:ILE:HG21	3:C:268:LYS:HD3	1.98	0.46
1:A:1312:PRO:HB2	1:A:1314:VAL:HG12	1.97	0.46
1:A:1833:LEU:HD11	18:U:718:HIS:O	2.16	0.46
2:B:87:A:H2'	2:B:87:A:N3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:69:VAL:HG11	4:E:345:ALA:HB1	1.92	0.46
4:E:326:HIS:CD2	4:E:346:SER:HB3	2.50	0.46
1:A:1889:LEU:HG	1:A:2013:GLY:HA3	1.96	0.46
3:C:534:VAL:O	3:C:534:VAL:HG12	2.16	0.46
4:E:321:TYR:CZ	4:E:356:ILE:CG2	2.96	0.46
16:G:2:U:O2	18:U:625:PHE:HB3	2.16	0.46
17:H:73:C:O5'	17:H:73:C:H6	1.99	0.46
17:H:164:C:HO2'	17:H:165:A:P	2.39	0.46
18:U:546:VAL:HB	18:U:665:HIS:CE1	2.50	0.46
28:I:238:LEU:O	28:I:241:ASP:N	2.49	0.46
3:C:166:CYS:SG	3:C:536:ARG:NH2	2.89	0.45
4:E:55:LEU:CD1	4:E:96:TYR:OH	2.64	0.45
4:E:63:SER:O	4:E:93:TRP:CZ3	2.62	0.45
4:E:260:ARG:CD	4:E:276:ILE:HG12	2.46	0.45
5:F:36:A:N6	16:G:10:U:H3	2.14	0.45
7:L:789:ALA:O	7:L:792:LEU:CG	2.64	0.45
14:T:390:GLY:HA2	14:T:395:ILE:HG12	1.98	0.45
17:H:33:G:P	18:U:666:ARG:HE	2.37	0.45
28:I:315:SER:O	28:I:316:GLU:C	2.54	0.45
1:A:1244:VAL:HG11	1:A:1291:CYS:HB3	1.98	0.45
2:B:36:C:C2'	2:B:37:G:H5'	2.45	0.45
4:E:277:PHE:CE2	4:E:300:ILE:HD12	2.52	0.45
14:T:214:PRO:HG3	14:T:256:THR:HG22	1.98	0.45
14:T:395:ILE:HD13	14:T:419:LEU:HD21	1.96	0.45
16:G:23:U:C6	16:G:23:U:H5''	2.51	0.45
16:G:27:U:HO2'	16:G:28:A:C4'	2.29	0.45
17:H:41:U:O2'	17:H:42:G:C8	2.66	0.45
17:H:57:A:H2'	17:H:58:U:C6	2.50	0.45
17:H:172:C:O5'	17:H:172:C:H6	1.98	0.45
1:A:1946:ASN:ND2	1:A:1986:LEU:HD21	2.30	0.45
4:E:339:GLU:HB3	4:E:340:PRO:HD2	1.99	0.45
14:T:387:PHE:HB3	14:T:400:PHE:CZ	2.51	0.45
17:H:33:G:H3'	18:U:666:ARG:CD	2.46	0.45
1:A:466:ALA:CA	2:B:20:G:N2	2.46	0.45
1:A:516:LEU:HD11	1:A:538:SER:HB2	1.99	0.45
3:C:136:GLY:HA3	3:C:142:LYS:NZ	2.32	0.45
7:L:759:GLU:OE1	27:K:171:GLN:CD	2.55	0.45
10:O:260:THR:HG22	10:O:273:GLN:HG2	1.97	0.45
14:T:270:VAL:HB	14:T:284:TYR:HB2	1.98	0.45
28:I:405:TYR:O	28:I:409:GLY:CA	2.65	0.45
28:I:712:VAL:O	28:I:715:GLY:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:10:U:O2	2:B:69:A:N1	2.50	0.45
2:B:77:G:N7	2:B:80:U:O4	2.49	0.45
4:E:73:LYS:O	4:E:81:LEU:CD2	2.65	0.45
4:E:75:HIS:O	4:E:76:PRO:C	2.51	0.45
5:F:36:A:H2'	5:F:37:C:C6	2.52	0.45
7:L:74:LEU:HA	7:L:77:LEU:HB3	1.97	0.45
10:O:223:LEU:CD1	10:O:285:GLU:HA	2.44	0.45
15:W:148:VAL:HG21	15:W:151:LYS:HD3	1.98	0.45
16:G:146:C:C6	16:G:147:C:C5	3.05	0.45
17:H:56:A:H2'	17:H:57:A:H8	1.82	0.45
4:E:95:VAL:HA	4:E:99:CYS:SG	2.56	0.45
4:E:147:LEU:HD12	4:E:179:TRP:CD2	2.51	0.45
5:F:9:U:O2	5:F:10:U:N3	2.49	0.45
5:F:90:G:C6	5:F:91:A:C6	3.04	0.45
6:J:224:LYS:HE2	6:J:255:LEU:HD13	1.98	0.45
10:O:59:PRO:HB2	10:O:63:MET:HG3	1.99	0.45
12:R:229:VAL:O	12:R:230:MET:HB2	2.15	0.45
16:G:27:U:HO2'	16:G:28:A:C5'	2.27	0.45
16:G:145:U:C6	16:G:145:U:OP2	2.70	0.45
2:B:96:A:N1	2:B:97:G:C5	2.84	0.45
3:C:134:LEU:O	3:C:205:THR:OG1	2.31	0.45
4:E:74:PHE:CD1	4:E:81:LEU:CD2	2.99	0.45
4:E:135:VAL:HB	4:E:145:LYS:O	2.17	0.45
4:E:153:PHE:HD1	4:E:153:PHE:H	1.64	0.45
4:E:164:PRO:O	4:E:166:LEU:HG	2.17	0.45
4:E:228:THR:HG22	4:E:229:TYR:HD1	1.81	0.45
5:F:21:U:H5'	9:N:120:ARG:O	2.16	0.45
10:O:234:LEU:HB2	10:O:272:ILE:HB	1.99	0.45
16:G:139:U:O2'	16:G:140:A:C8	2.67	0.45
17:H:91:U:O5'	17:H:91:U:H6	2.00	0.45
1:A:136:ILE:HG22	1:A:138:PRO:HD2	1.98	0.45
1:A:246:LEU:HD22	1:A:408:PRO:HG2	1.97	0.45
1:A:266:SER:OG	1:A:271:MET:O	2.31	0.45
3:C:166:CYS:O	3:C:170:ILE:CG2	2.65	0.45
4:E:55:LEU:C	4:E:57:ALA:H	2.20	0.45
4:E:157:CYS:HA	4:E:168:CYS:O	2.17	0.45
10:O:162:PRO:O	10:O:182:ARG:NE	2.46	0.45
10:O:224:ASP:O	10:O:302:TRP:CE2	2.69	0.45
17:H:33:G:H3'	18:U:666:ARG:HD2	1.98	0.45
1:A:1544:ARG:HB2	1:A:1547:VAL:HG12	1.98	0.45
1:A:1835:GLN:CB	18:U:557:VAL:HG11	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:677:GLU:HB3	3:C:684:LYS:HG2	1.98	0.45
4:E:153:PHE:N	4:E:153:PHE:CD1	2.85	0.45
8:M:210:TYR:HB2	8:M:215:ASN:HB3	1.99	0.45
9:N:70:ILE:HG12	9:N:74:LEU:HD23	1.98	0.45
10:O:253:TYR:OH	13:S:123:ASP:OD2	2.26	0.45
16:G:5:G:C2	16:G:6:A:C6	3.05	0.45
16:G:120:G:C2'	29:Q:1019:SER:H	2.27	0.45
1:A:1110:ILE:HD11	1:A:1149:LEU:HB2	1.98	0.45
1:A:1128:TYR:OH	1:A:1175:VAL:O	2.34	0.45
2:B:78:U:O2'	2:B:79:C:OP1	2.28	0.45
11:P:23:LEU:HD23	11:P:26:LEU:HD13	1.98	0.45
16:G:2:U:OP1	16:G:2:U:C6	2.70	0.45
18:U:867:GLU:HB3	18:U:872:GLN:HB3	1.99	0.45
27:K:156:LEU:O	27:K:160:ILE:CG1	2.65	0.45
3:C:108:THR:HG21	3:C:538:HIS:O	2.17	0.44
4:E:74:PHE:CD2	4:E:335:PHE:C	2.91	0.44
5:F:29:A:H62	16:G:16:G:H1'	1.82	0.44
5:F:40:U:O4	5:F:41:A:N6	2.50	0.44
10:O:256:GLY:CA	12:R:70:ALA:HB2	2.43	0.44
17:H:58:U:H2'	17:H:59:A:H8	1.82	0.44
18:U:713:ILE:HB	18:U:768:TYR:HB3	1.97	0.44
1:A:758:ARG:HA	1:A:758:ARG:HD2	1.76	0.44
4:E:276:ILE:C	4:E:277:PHE:CD1	2.91	0.44
4:E:323:LEU:HD21	15:W:83:PRO:O	2.17	0.44
5:F:38:G:C4	5:F:39:A:N7	2.85	0.44
7:L:706:GLU:O	27:K:121:ILE:CG1	2.65	0.44
14:T:329:HIS:HD1	14:T:349:SER:HG	1.61	0.44
1:A:711:GLN:HE22	17:H:18:U:H3'	1.82	0.44
3:C:853:ARG:NH2	3:C:886:ASP:OD2	2.50	0.44
4:E:57:ALA:HA	4:E:58:PRO:HD3	1.82	0.44
4:E:116:HIS:O	4:E:124:LEU:CD1	2.57	0.44
14:T:355:ARG:HH11	14:T:364:THR:HG21	1.81	0.44
1:A:888:GLN:OE1	7:L:130:PRO:HG2	2.15	0.44
3:C:507:VAL:HG13	3:C:565:ILE:HG23	2.00	0.44
4:E:115:LEU:HD23	4:E:126:SER:HB2	1.99	0.44
4:E:131:LYS:HD3	4:E:152:SER:N	2.32	0.44
5:F:44:G:C2'	16:G:1:G:H22	2.31	0.44
17:H:83:A:H2'	17:H:84:C:C5	2.44	0.44
27:K:17:PRO:HD2	27:K:171:GLN:OE1	2.16	0.44
27:K:18:TYR:HB2	27:K:171:GLN:OE1	2.17	0.44
27:K:120:ARG:O	27:K:124:LEU:CB	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:I:176:SER:HA	28:I:196:ALA:CB	2.47	0.44
1:A:759:GLU:OE2	1:A:762:ARG:NH1	2.43	0.44
1:A:1011:ALA:HB2	7:L:80:THR:HB	1.98	0.44
1:A:1947:ASN:O	1:A:1949:ARG:N	2.50	0.44
2:B:74:U:H6	2:B:74:U:H5''	1.83	0.44
3:C:92:PRO:HA	14:T:278:ASN:HD21	1.83	0.44
5:F:82:A:H62	12:R:258:LYS:HZ2	1.64	0.44
10:O:78:LYS:HD3	10:O:94:ILE:HG21	2.00	0.44
16:G:21:A:O5'	16:G:21:A:C8	2.70	0.44
1:A:1392:LYS:NZ	1:A:1407:ASP:O	2.45	0.44
2:B:75:G:C6	2:B:76:A:C8	3.03	0.44
4:E:58:PRO:CD	4:E:59:ILE:N	2.79	0.44
4:E:321:TYR:CZ	4:E:356:ILE:HG23	2.40	0.44
5:F:58:G:H2'	5:F:59:G:C8	2.53	0.44
10:O:154:THR:C	12:R:188:PHE:CE1	2.88	0.44
10:O:250:ASN:O	10:O:253:TYR:CD2	2.71	0.44
15:W:159:ALA:O	15:W:164:GLY:N	2.51	0.44
16:G:154:U:C6	16:G:154:U:O5'	2.70	0.44
17:H:81:G:H2'	17:H:82:G:H8	1.83	0.44
1:A:103:LEU:HD11	1:A:554:THR:HG22	2.00	0.44
1:A:828:PRO:HA	1:A:829:PRO:HD3	1.81	0.44
5:F:38:G:C4	5:F:39:A:C8	3.06	0.44
5:F:81:C:C6	5:F:81:C:C4'	3.01	0.44
10:O:251:HIS:O	10:O:251:HIS:CD2	2.70	0.44
1:A:1354:ARG:NE	1:A:1357:MET:SD	2.91	0.44
2:B:90:U:OP2	2:B:90:U:H4'	2.17	0.44
4:E:119:THR:HG21	4:E:161:ARG:CB	2.32	0.44
7:L:267:LEU:C	7:L:267:LEU:CD2	2.85	0.44
7:L:759:GLU:HG2	27:K:167:ARG:CG	2.48	0.44
16:G:5:G:C5	16:G:6:A:C4	3.06	0.44
17:H:54:U:C6	17:H:55:U:H5	2.36	0.44
17:H:80:A:N3	17:H:81:G:N7	2.66	0.44
17:H:84:C:H2'	17:H:85:A:H8	1.83	0.44
33:V:369:ILE:C	33:V:372:GLU:O	2.56	0.44
1:A:1340:LEU:HD12	1:A:1355:SER:HB2	1.99	0.44
3:C:250:ARG:HG3	3:C:451:HIS:CD2	2.53	0.44
3:C:631:GLY:HA3	3:C:637:LEU:HD21	2.00	0.44
4:E:145:LYS:HE2	4:E:145:LYS:HA	2.00	0.44
7:L:703:MET:O	7:L:707:ALA:HB3	2.18	0.44
10:O:272:ILE:HG22	10:O:274:PHE:CE1	2.52	0.44
17:H:155:C:H6	17:H:155:C:O5'	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:694:VAL:N	18:U:732:GLU:OE2	2.50	0.44
28:I:545:ILE:O	28:I:548:PHE:N	2.51	0.44
1:A:163:ARG:HH21	1:A:625:PRO:HB3	1.83	0.43
1:A:680:HIS:NE2	14:T:266:GLU:O	2.37	0.43
1:A:1836:LEU:CD2	18:U:547:ILE:CG2	2.96	0.43
3:C:163:GLN:HE21	3:C:163:GLN:HB2	1.55	0.43
3:C:538:HIS:CE1	3:C:551:LEU:HD11	2.46	0.43
3:C:853:ARG:NH1	3:C:879:ASP:O	2.48	0.43
10:O:272:ILE:HG22	10:O:274:PHE:CZ	2.53	0.43
18:U:655:GLU:O	18:U:658:ARG:CG	2.65	0.43
18:U:670:ALA:O	18:U:674:LYS:HG2	2.18	0.43
18:U:819:PRO:HB2	18:U:835:ILE:HB	2.00	0.43
3:C:101:LYS:HA	3:C:485:ASP:HB2	1.99	0.43
4:E:101:ASN:ND2	4:E:101:ASN:H	2.16	0.43
2:B:68:C:C6	2:B:68:C:OP1	2.70	0.43
2:B:72:U:OP2	2:B:72:U:C6	2.72	0.43
3:C:115:GLU:CD	3:C:189:VAL:HG23	2.38	0.43
4:E:58:PRO:O	4:E:59:ILE:HB	2.16	0.43
14:T:416:ILE:HA	14:T:431:ALA:HA	1.98	0.43
16:G:154:U:H3'	16:G:154:U:H6	1.84	0.43
28:I:477:GLN:O	28:I:480:VAL:O	2.37	0.43
1:A:533:LYS:HD2	16:G:3:A:O2'	2.17	0.43
1:A:1946:ASN:OD1	1:A:1986:LEU:HG	2.19	0.43
2:B:9:G:N3	2:B:9:G:C2'	2.79	0.43
3:C:230:ASP:OD2	3:C:262:ARG:NH1	2.52	0.43
18:U:805:LEU:HD13	18:U:810:ILE:HG12	1.99	0.43
4:E:75:HIS:H	4:E:81:LEU:CD2	2.30	0.43
5:F:42:C:C2'	5:F:43:A:C5'	2.95	0.43
5:F:43:A:H8	5:F:43:A:O5'	2.02	0.43
10:O:193:LEU:O	10:O:196:GLN:NE2	2.52	0.43
14:T:382:PRO:HB2	14:T:383:ARG:HD2	1.99	0.43
17:H:82:G:C2'	17:H:83:A:H5'	2.49	0.43
4:E:260:ARG:HD2	4:E:276:ILE:HG12	2.00	0.43
7:L:166:LYS:HA	7:L:169:ARG:HG2	2.00	0.43
10:O:223:LEU:HA	10:O:288:PHE:CD2	2.53	0.43
10:O:239:LEU:CD1	10:O:243:ILE:HD12	2.49	0.43
3:C:371:GLU:O	3:C:375:GLU:HB3	2.18	0.43
4:E:131:LYS:HD3	4:E:152:SER:CA	2.48	0.43
4:E:147:LEU:N	4:E:147:LEU:CD2	2.73	0.43
13:S:90:LEU:HB3	13:S:128:ILE:HD12	2.00	0.43
13:S:160:ILE:HG22	13:S:161:LYS:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:T:439:TRP:HD1	14:T:446:ASN:HA	1.83	0.43
18:U:685:PRO:O	18:U:687:HIS:ND1	2.48	0.43
27:K:131:GLY:O	27:K:135:TRP:N	2.46	0.43
2:B:35:U:C6	2:B:35:U:C4'	3.02	0.43
4:E:165:GLN:HG3	4:E:181:ILE:HD11	2.01	0.43
4:E:277:PHE:CD1	4:E:277:PHE:N	2.85	0.43
17:H:80:A:N1	17:H:81:G:C5	2.87	0.43
28:I:712:VAL:O	28:I:713:ARG:C	2.56	0.43
3:C:263:LEU:HD23	3:C:267:LEU:HD12	2.00	0.43
3:C:624:SER:HB3	3:C:941:LYS:HA	2.01	0.43
4:E:127:ALA:HB2	4:E:157:CYS:HB3	2.00	0.43
4:E:313:ASP:CB	4:E:320:LEU:HD21	2.48	0.43
10:O:25:GLN:NE2	12:R:181:PRO:HB3	2.34	0.43
10:O:92:LEU:HD11	10:O:151:ALA:HA	2.01	0.43
12:R:52:PRO:HG3	12:R:67:ILE:HG21	2.00	0.43
13:S:102:ASN:ND2	13:S:104:GLY:O	2.51	0.43
14:T:399:LYS:HD2	14:T:406:ILE:HD11	2.01	0.43
15:W:150:ALA:C	15:W:151:LYS:HD2	2.21	0.43
16:G:141:C:O2'	16:G:142:U:OP2	2.36	0.43
16:G:145:U:H6	16:G:145:U:H2'	1.61	0.43
17:H:8:C:C2	17:H:9:U:C5	3.07	0.43
17:H:175:G:C6	17:H:176:G:C5	3.07	0.43
1:A:1510:GLU:CD	1:A:1510:GLU:N	2.73	0.43
3:C:300:LEU:HA	3:C:306:ASN:HD21	1.84	0.43
10:O:182:ARG:NH1	10:O:184:GLU:OE2	2.45	0.43
13:S:93:THR:HG23	13:S:118:PRO:HB3	2.01	0.43
17:H:112:G:H2'	17:H:113:G:C8	2.50	0.43
27:K:112:ALA:O	27:K:116:HIS:CG	2.70	0.43
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.52	0.42
3:C:118:PHE:HE2	3:C:122:LEU:HD11	1.84	0.42
10:O:259:ARG:HB2	10:O:273:GLN:O	2.19	0.42
17:H:33:G:H2'	17:H:33:G:OP2	2.19	0.42
17:H:83:A:C5	17:H:84:C:N4	2.85	0.42
17:H:98:G:OP1	17:H:98:G:C8	2.72	0.42
1:A:224:THR:HG23	2:B:12:U:H5''	2.01	0.42
4:E:109:SER:CA	4:E:130:ASP:OD2	2.67	0.42
4:E:326:HIS:HD1	4:E:352:TYR:HE2	1.66	0.42
7:L:250:GLU:CD	7:L:250:GLU:N	2.73	0.42
8:M:207:ASP:OD1	8:M:207:ASP:N	2.52	0.42
10:O:149:LYS:NZ	10:O:290:LYS:HG2	2.34	0.42
17:H:108:G:C5	17:H:109:C:N4	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:751:CYS:HB2	18:U:826:GLY:HA2	2.00	0.42
1:A:442:LYS:NZ	34:A:3000:IHP:O45	2.48	0.42
1:A:1515:TRP:CE3	1:A:1515:TRP:CA	3.02	0.42
2:B:77:G:C5	2:B:80:U:O4	2.72	0.42
3:C:214:GLU:OE1	3:C:480:LYS:NZ	2.40	0.42
5:F:45:A:C4	18:U:625:PHE:CE1	3.07	0.42
9:N:128:VAL:HG13	9:N:130:ARG:H	1.84	0.42
10:O:221:PRO:HA	10:O:222:ARG:CZ	2.48	0.42
17:H:30:A:O2'	17:H:31:G:H8	1.98	0.42
17:H:80:A:C2	17:H:81:G:C8	3.07	0.42
1:A:686:ARG:HE	1:A:710:LEU:HD22	1.83	0.42
2:B:89:U:HO2'	2:B:90:U:P	2.43	0.42
3:C:160:ARG:CD	3:C:164:ASP:HB2	2.49	0.42
4:E:119:THR:HG23	4:E:161:ARG:CB	2.37	0.42
5:F:35:A:C2'	5:F:36:A:OP1	2.68	0.42
5:F:38:G:C2	5:F:39:A:C6	3.06	0.42
10:O:155:PRO:CG	12:R:188:PHE:HA	2.49	0.42
10:O:230:THR:H	10:O:277:ARG:NH1	2.17	0.42
10:O:236:VAL:HB	10:O:270:ALA:O	2.19	0.42
14:T:198:ARG:HB3	14:T:488:VAL:HB	2.01	0.42
17:H:114:A:N3	17:H:115:G:C8	2.88	0.42
1:A:833:LYS:HG3	1:A:834:HIS:CD2	2.54	0.42
4:E:178:LEU:HG	4:E:188:GLN:HB2	2.01	0.42
8:M:190:ILE:HG12	8:M:193:ARG:HH22	1.84	0.42
17:H:32:U:O2'	17:H:33:G:OP2	2.37	0.42
17:H:32:U:O2'	17:H:33:G:C8	2.66	0.42
1:A:380:LEU:HD12	1:A:384:VAL:HG21	2.00	0.42
1:A:1518:LEU:C	1:A:1519:THR:OG1	2.53	0.42
1:A:1628:ASP:OD2	1:A:1664:ILE:N	2.45	0.42
3:C:664:GLU:HB3	3:C:820:PHE:HZ	1.83	0.42
12:R:60:ASP:HB2	13:S:134:GLN:HA	2.02	0.42
17:H:169:C:O5'	17:H:169:C:H6	2.03	0.42
18:U:844:TYR:OH	18:U:862:ARG:NH1	2.53	0.42
28:I:577:ARG:O	28:I:580:PHE:O	2.37	0.42
1:A:97:HIS:HE1	2:B:56:C:H5''	1.85	0.42
1:A:533:LYS:N	16:G:3:A:H5'	2.34	0.42
2:B:43:U:H3'	2:B:44:A:C8	2.54	0.42
2:B:75:G:C6	2:B:76:A:C5	3.06	0.42
4:E:75:HIS:N	4:E:81:LEU:CD2	2.82	0.42
4:E:108:HIS:CD2	4:E:136:TRP:CZ2	3.07	0.42
4:E:257:ASN:CG	15:W:149:SER:CB	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:265:ARG:H	4:E:272:ARG:HH22	1.66	0.42
4:E:276:ILE:O	4:E:277:PHE:HD1	2.01	0.42
4:E:307:ARG:NH1	15:W:143:LEU:CG	2.79	0.42
5:F:49:G:H2'	5:F:50:A:H8	1.84	0.42
5:F:91:A:C2	17:H:8:C:O2	2.73	0.42
10:O:251:HIS:CE1	10:O:291:LEU:CD1	3.02	0.42
17:H:80:A:C4	17:H:81:G:C8	3.08	0.42
1:A:135:VAL:HG11	1:A:421:ALA:HB2	2.00	0.42
1:A:1211:ASP:OD1	1:A:1211:ASP:N	2.52	0.42
1:A:1802:PRO:CG	1:A:1824:THR:HG23	2.50	0.42
1:A:1836:LEU:HD12	1:A:1836:LEU:HA	1.84	0.42
1:A:1946:ASN:CG	1:A:1986:LEU:HG	2.40	0.42
3:C:87:GLN:HE21	14:T:239:LYS:HG2	1.85	0.42
3:C:136:GLY:N	3:C:142:LYS:HD3	2.35	0.42
4:E:74:PHE:CD2	4:E:336:HIS:CA	3.02	0.42
4:E:234:HIS:ND1	4:E:256:ASP:OD2	2.50	0.42
10:O:50:ARG:HA	10:O:51:PRO:HD3	1.89	0.42
10:O:259:ARG:C	10:O:273:GLN:O	2.58	0.42
17:H:108:G:C5	17:H:109:C:C4	3.08	0.42
17:H:178:A:N3	17:H:178:A:H2'	2.33	0.42
1:A:357:ASN:ND2	3:C:866:SER:O	2.52	0.42
3:C:814:ARG:HA	3:C:817:TYR:HD2	1.84	0.42
5:F:20:A:O2'	9:N:120:ARG:NH2	2.53	0.42
6:J:377:LYS:HE2	6:J:377:LYS:HB3	1.85	0.42
10:O:215:LYS:O	10:O:219:THR:HG23	2.20	0.42
10:O:220:MET:HE3	10:O:220:MET:HB3	1.69	0.42
13:S:92:PHE:CD2	13:S:122:LEU:HB3	2.55	0.42
14:T:353:THR:HG22	14:T:369:THR:HG22	2.01	0.42
15:W:140:ASP:OD2	15:W:145:ASN:OD1	2.38	0.42
16:G:3:A:H1'	16:G:4:A:P	2.60	0.42
16:G:146:C:P	16:G:146:C:C3'	3.07	0.42
16:G:152:C:C2	16:G:153:C:C6	2.96	0.42
17:H:33:G:O3'	18:U:662:ILE:HD11	2.16	0.42
27:K:19:PHE:CZ	27:K:176:SER:N	2.87	0.42
1:A:490:VAL:HG21	1:A:565:ARG:HG3	2.01	0.42
1:A:1069:ASN:ND2	1:A:1073:SER:O	2.53	0.42
1:A:1501:LEU:HD13	1:A:1753:LEU:HD11	2.01	0.42
3:C:104:LEU:HD13	3:C:172:PHE:HE1	1.85	0.42
5:F:91:A:N1	17:H:8:C:C2	2.88	0.42
9:N:70:ILE:HG23	9:N:74:LEU:HB3	2.02	0.42
16:G:146:C:H2'	16:G:146:C:H6	1.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:7:U:H3'	17:H:8:C:C5	2.55	0.42
28:I:790:ARG:CB	28:I:801:ASP:HA	2.48	0.42
3:C:171:LEU:HD22	3:C:181:ILE:HD11	2.02	0.41
3:C:514:TYR:HB2	3:C:521:ASP:HB3	2.02	0.41
4:E:83:SER:O	4:E:90:ILE:CA	2.67	0.41
4:E:289:LEU:HD12	4:E:303:GLY:O	2.21	0.41
4:E:323:LEU:HD22	15:W:83:PRO:HD2	2.01	0.41
13:S:72:ARG:NH2	15:W:88:MET:O	2.52	0.41
16:G:120:G:H2'	29:Q:1019:SER:H	1.85	0.41
18:U:810:ILE:H	18:U:810:ILE:HG13	1.49	0.41
4:E:178:LEU:CD2	4:E:208:ILE:HD13	2.47	0.41
14:T:220:VAL:HG11	14:T:261:LEU:HD21	2.01	0.41
16:G:5:G:C8	16:G:6:A:C8	3.07	0.41
16:G:143:U:H6	16:G:143:U:H5''	1.84	0.41
17:H:108:G:H2'	17:H:109:C:C5	2.47	0.41
28:I:526:MET:O	28:I:526:MET:SD	2.79	0.41
1:A:237:THR:HA	1:A:240:ARG:HD3	2.01	0.41
2:B:81:U:HO2'	2:B:82:A:P	2.40	0.41
5:F:92:A:C2	5:F:93:G:C8	3.08	0.41
7:L:759:GLU:HG2	27:K:167:ARG:HG2	2.02	0.41
15:W:77:LYS:HD3	15:W:77:LYS:HA	1.93	0.41
16:G:145:U:OP2	16:G:145:U:C5	2.73	0.41
16:G:153:C:O2	16:G:153:C:H2'	2.19	0.41
17:H:8:C:C2'	17:H:9:U:C6	2.95	0.41
1:A:941:LYS:HA	1:A:941:LYS:HD2	1.74	0.41
3:C:160:ARG:HD2	3:C:164:ASP:HB2	2.03	0.41
4:E:74:PHE:CD2	4:E:336:HIS:N	2.88	0.41
4:E:243:LEU:HD22	4:E:243:LEU:HA	1.86	0.41
6:J:188:GLN:NE2	7:L:140:ASP:OD1	2.54	0.41
1:A:534:GLU:OE2	5:F:38:G:C5'	2.69	0.41
1:A:946:GLU:O	1:A:1437:ARG:NH2	2.54	0.41
1:A:1321:GLU:HG3	1:A:1322:LEU:HD22	2.02	0.41
1:A:1899:VAL:HB	1:A:1902:PHE:HD2	1.85	0.41
3:C:412:ILE:O	3:C:416:LEU:HB2	2.20	0.41
4:E:75:HIS:O	4:E:78:GLY:N	2.53	0.41
4:E:276:ILE:C	4:E:277:PHE:HD1	2.23	0.41
5:F:82:A:N6	12:R:258:LYS:HZ2	2.17	0.41
9:N:57:THR:HG23	9:N:85:ASP:H	1.85	0.41
12:R:234:SER:O	12:R:235:ARG:O	2.38	0.41
14:T:297:HIS:NE2	14:T:339:GLN:O	2.54	0.41
16:G:145:U:O3'	18:U:658:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:103:U:C3'	17:H:104:U:H5'	2.51	0.41
17:H:149:A:N6	17:H:183:G:O6	2.53	0.41
1:A:995:ARG:NH1	12:R:291:LEU:O	2.53	0.41
1:A:1260:VAL:HG21	1:A:1325:LEU:HD13	2.03	0.41
2:B:87:A:H5'	2:B:88:A:OP1	2.20	0.41
5:F:79:C:N4	7:L:166:LYS:HD2	2.36	0.41
12:R:183:GLN:CG	12:R:183:GLN:O	2.69	0.41
16:G:126:C:H4'	16:G:127:U:C1'	2.50	0.41
16:G:141:C:O2'	16:G:142:U:C5	2.72	0.41
16:G:147:C:OP2	18:U:659:LYS:CB	2.68	0.41
18:U:548:LEU:HD22	18:U:661:ALA:CA	2.47	0.41
1:A:858:GLN:OE1	1:A:861:ARG:NH1	2.54	0.41
1:A:1663:ASP:HB3	1:A:1702:LEU:HB2	2.02	0.41
1:A:1971:LEU:HB2	1:A:1976:TRP:CE2	2.55	0.41
3:C:369:PHE:O	3:C:373:ILE:HB	2.21	0.41
3:C:590:ILE:HG22	3:C:592:VAL:HG23	2.02	0.41
3:C:831:TYR:HB2	3:C:903:HIS:HB3	2.02	0.41
4:E:284:PHE:HB3	15:W:139:LEU:HD22	2.01	0.41
7:L:710:ALA:O	27:K:124:LEU:HD22	2.16	0.41
14:T:354:ILE:HD12	14:T:398:TRP:HZ3	1.86	0.41
17:H:147:G:N3	17:H:148:C:C6	2.88	0.41
27:K:19:PHE:CD2	27:K:171:GLN:O	2.73	0.41
1:A:447:TYR:HE1	1:A:611:LEU:HA	1.86	0.41
1:A:549:GLU:HB3	1:A:591:MET:HG2	2.03	0.41
1:A:1426:ASP:OD1	1:A:1426:ASP:N	2.53	0.41
2:B:77:G:C5	2:B:80:U:C4	3.08	0.41
3:C:115:GLU:OE1	3:C:189:VAL:CG2	2.64	0.41
4:E:115:LEU:HD13	4:E:116:HIS:N	2.36	0.41
4:E:128:SER:O	4:E:154:VAL:HB	2.21	0.41
4:E:265:ARG:N	4:E:272:ARG:HH21	2.18	0.41
6:J:206:LEU:HD21	7:L:171:ALA:HB1	2.02	0.41
7:L:741:GLN:O	7:L:744:GLN:CG	2.69	0.41
16:G:146:C:HO2'	16:G:147:C:C5'	2.23	0.41
16:G:150:U:C6	16:G:150:U:C4'	3.04	0.41
18:U:591:PHE:N	18:U:594:ASP:OD2	2.54	0.41
1:A:103:LEU:HB2	1:A:638:LEU:HD21	2.03	0.41
1:A:1631:LEU:HD13	1:A:1660:TYR:HD2	1.86	0.41
1:A:1946:ASN:ND2	1:A:1986:LEU:CG	2.84	0.41
3:C:142:LYS:O	3:C:145:PHE:HB3	2.21	0.41
3:C:277:LYS:HD2	3:C:865:GLY:HA3	2.03	0.41
3:C:685:ILE:HD11	3:C:808:ILE:HG23	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:81:LEU:HD22	4:E:81:LEU:HA	1.86	0.41
4:E:88:ARG:HD2	4:E:110:GLY:N	2.36	0.41
4:E:161:ARG:HG2	4:E:161:ARG:HH11	1.86	0.41
4:E:284:PHE:CE2	15:W:120:ILE:HG23	2.56	0.41
4:E:319:ILE:H	4:E:319:ILE:HG12	1.66	0.41
10:O:136:MET:O	10:O:140:ALA:CB	2.69	0.41
12:R:58:PHE:HZ	12:R:71:GLN:HG3	1.86	0.41
12:R:72:TYR:HA	12:R:73:PRO:HD3	1.95	0.41
17:H:7:U:N3	17:H:8:C:C5	2.89	0.41
17:H:78:C:H2'	17:H:79:G:C8	2.56	0.41
17:H:112:G:O5'	17:H:112:G:H8	2.04	0.41
27:K:18:TYR:CB	27:K:168:LYS:HA	2.51	0.41
1:A:1132:LYS:HA	1:A:1139:ARG:HH12	1.85	0.41
1:A:1217:GLN:HA	1:A:1224:ARG:HA	2.02	0.41
4:E:219:VAL:HB	4:E:229:TYR:HB2	2.02	0.41
15:W:144:ASP:OD1	15:W:144:ASP:N	2.51	0.41
17:H:59:A:C6	17:H:60:U:C4	3.09	0.41
1:A:552:ARG:NH1	1:A:589:THR:O	2.54	0.40
1:A:1519:THR:O	1:A:1522:GLN:HB2	2.21	0.40
1:A:1876:LEU:HD12	1:A:1884:ILE:HD11	2.02	0.40
3:C:230:ASP:HB3	3:C:233:GLU:HB2	2.03	0.40
3:C:705:VAL:HG22	3:C:717:PHE:HE2	1.87	0.40
4:E:74:PHE:HE1	4:E:95:VAL:HG21	1.86	0.40
4:E:137:ASP:OD1	4:E:137:ASP:N	2.53	0.40
6:J:201:ARG:HB3	6:J:203:LEU:HD23	2.03	0.40
7:L:250:GLU:CD	7:L:250:GLU:H	2.24	0.40
10:O:169:VAL:HA	15:W:216:LEU:HD13	2.03	0.40
10:O:221:PRO:CB	10:O:289:ASN:ND2	2.82	0.40
14:T:190:TRP:HE1	14:T:498:GLU:HB3	1.86	0.40
16:G:146:C:OP2	16:G:146:C:C3'	2.68	0.40
17:H:55:U:H2'	17:H:56:A:C8	2.53	0.40
17:H:168:A:H5'	17:H:169:C:H5	1.87	0.40
27:K:19:PHE:HB2	27:K:171:GLN:HB3	2.03	0.40
27:K:134:ALA:O	27:K:137:VAL:N	2.40	0.40
28:I:616:TYR:O	28:I:618:ARG:N	2.54	0.40
1:A:1838:LYS:HG3	1:A:1868:MET:SD	2.62	0.40
1:A:1954:LEU:HD21	1:A:1983:LEU:HD11	2.02	0.40
3:C:101:LYS:NZ	3:C:106:GLU:OE1	2.39	0.40
3:C:216:THR:HG22	3:C:220:ARG:HH12	1.86	0.40
3:C:778:PRO:HB3	3:C:817:TYR:HD1	1.85	0.40
4:E:66:GLU:HB2	4:E:87:ASP:CG	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:266:PRO:HG2	7:L:785:GLN:C	2.41	0.40
5:F:49:G:H2'	5:F:50:A:C8	2.56	0.40
6:J:223:TYR:OH	7:L:248:ASP:OD1	2.39	0.40
16:G:5:G:C2	16:G:6:A:N6	2.89	0.40
16:G:146:C:C2'	16:G:147:C:C6	3.03	0.40
17:H:37:U:O2'	17:H:38:A:C8	2.67	0.40
28:I:606:TRP:O	28:I:609:ALA:HB3	2.21	0.40
1:A:170:ASP:HB3	1:A:173:GLU:HG3	2.03	0.40
1:A:963:GLN:HG3	1:A:1077:ILE:HG23	2.03	0.40
1:A:1248:LEU:O	1:A:1298:ARG:NH1	2.45	0.40
1:A:1556:ASP:OD1	1:A:1557:LEU:N	2.48	0.40
1:A:1781:ASP:HB3	1:A:1808:PHE:HB3	2.03	0.40
3:C:595:VAL:HG22	3:C:654:LYS:HG3	2.03	0.40
4:E:57:ALA:O	4:E:355:GLU:HG3	2.20	0.40
6:J:493:ALA:CB	6:J:499:ARG:CB	2.96	0.40
7:L:699:ASN:CB	27:K:114:LEU:HB2	2.51	0.40
9:N:37:HIS:HA	9:N:40:LYS:HE2	2.03	0.40
10:O:278:GLN:O	10:O:282:VAL:HG23	2.22	0.40
12:R:106:GLN:OE1	12:R:225:PRO:HG2	2.22	0.40
16:G:146:C:O2'	16:G:147:C:C5'	2.69	0.40
17:H:149:A:C2'	17:H:150:U:H5'	2.51	0.40
28:I:559:THR:CB	28:I:570:GLY:HA3	2.51	0.40
33:V:191:THR:HA	33:V:236:MET:O	2.21	0.40
1:A:165:ARG:NH2	1:A:168:PRO:O	2.55	0.40
1:A:312:TYR:OH	3:C:886:ASP:OD2	2.36	0.40
1:A:668:VAL:O	14:T:285:HIS:NE2	2.47	0.40
1:A:1615:HIS:HA	1:A:1616:PRO:HD3	1.97	0.40
1:A:1862:ILE:HG12	1:A:1885:LYS:HB3	2.02	0.40
2:B:67:A:O5'	2:B:68:C:N4	2.55	0.40
3:C:227:LEU:HD21	3:C:239:THR:HG23	2.03	0.40
4:E:68:GLU:HG2	4:E:347:SER:HB2	2.03	0.40
4:E:118:ASN:ND2	4:E:119:THR:N	2.53	0.40
4:E:162:ARG:HH21	4:E:204:THR:HA	1.82	0.40
4:E:177:LYS:C	4:E:178:LEU:HD23	2.41	0.40
5:F:34:G:C6	5:F:35:A:C5	3.10	0.40
7:L:11:TRP:HE1	7:L:133:GLU:HG3	1.85	0.40
10:O:175:ARG:HB2	10:O:179:CYS:HB2	2.04	0.40
16:G:9:C:C2'	16:G:10:U:C6	3.00	0.40
17:H:57:A:C6	17:H:58:U:C4	3.10	0.40
17:H:91:U:C2'	17:H:92:U:H5'	2.51	0.40
18:U:680:ASP:OD1	18:U:680:ASP:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.90	0.40
4:E:90:ILE:HD13	4:E:112:VAL:HG11	1.86	0.40
4:E:248:SER:HB2	4:E:249:TYR:HD1	1.78	0.40
4:E:260:ARG:CZ	4:E:276:ILE:HD11	2.51	0.40
5:F:44:G:C6	16:G:2:U:O4	2.75	0.40
5:F:44:G:N7	16:G:1:G:N1	2.69	0.40
5:F:57:U:H2'	5:F:58:G:C8	2.55	0.40
6:J:196:ARG:HA	8:M:208:ILE:HD11	2.04	0.40
7:L:696:LEU:HA	27:K:110:SER:HB2	2.02	0.40
7:L:696:LEU:CA	27:K:110:SER:OG	2.67	0.40
10:O:44:GLU:HA	10:O:51:PRO:HA	2.04	0.40
10:O:56:ARG:HD2	10:O:67:LYS:HE2	2.04	0.40
10:O:107:MET:HA	10:O:108:PRO:HD3	1.98	0.40
10:O:223:LEU:HB3	10:O:288:PHE:HB2	2.02	0.40
17:H:153:A:H3'	17:H:154:C:H5'	1.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1977/2335 (85%)	1799 (91%)	160 (8%)	18 (1%)	14	29
3	C	886/972 (91%)	799 (90%)	84 (10%)	3 (0%)	37	55
4	E	301/357 (84%)	268 (89%)	22 (7%)	11 (4%)	2	5
6	J	536/848 (63%)	495 (92%)	37 (7%)	4 (1%)	19	36
7	L	459/802 (57%)	421 (92%)	33 (7%)	5 (1%)	12	25
8	M	128/243 (53%)	115 (90%)	13 (10%)	0	100	100
9	N	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
10	O	288/420 (69%)	262 (91%)	24 (8%)	2 (1%)	19	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	P	114/229 (50%)	96 (84%)	17 (15%)	1 (1%)	14	29
12	R	268/536 (50%)	234 (87%)	30 (11%)	4 (2%)	8	19
13	S	157/166 (95%)	141 (90%)	16 (10%)	0	100	100
14	T	315/514 (61%)	297 (94%)	16 (5%)	2 (1%)	22	40
15	W	156/579 (27%)	134 (86%)	18 (12%)	4 (3%)	4	10
18	U	343/894 (38%)	289 (84%)	49 (14%)	5 (2%)	8	19
19	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
19	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
20	b	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
20	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
21	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
21	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
22	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
22	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
23	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
23	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
24	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
24	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
25	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
25	n	63/76 (83%)	61 (97%)	2 (3%)	0	100	100
26	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	3	8
26	r	129/504 (26%)	119 (92%)	8 (6%)	2 (2%)	8	18
26	s	65/504 (13%)	62 (95%)	2 (3%)	1 (2%)	8	19
26	t	65/504 (13%)	64 (98%)	0	1 (2%)	8	19
27	K	144/225 (64%)	130 (90%)	7 (5%)	7 (5%)	2	3
28	I	538/855 (63%)	501 (93%)	25 (5%)	12 (2%)	5	12
29	Q	1304/1485 (88%)	1278 (98%)	25 (2%)	1 (0%)	48	69
30	y	77/301 (26%)	74 (96%)	3 (4%)	0	100	100
31	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	10	22
32	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
33	V	661/795 (83%)	614 (93%)	40 (6%)	7 (1%)	12	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	10524/16892 (62%)	9733 (92%)	695 (7%)	96 (1%)	17	29

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1306	LYS
1	A	1519	THR
1	A	1639	VAL
1	A	1653	ASP
1	A	1948	ASP
4	E	56	GLN
4	E	58	PRO
4	E	59	ILE
4	E	112	VAL
4	E	193	THR
7	L	118	ASP
10	O	259	ARG
12	R	190	SER
18	U	613	ASN
18	U	793	ASP
26	q	59	HIS
26	q	60	PRO
26	s	71	ILE
26	t	69	THR
27	K	78	PRO
27	K	90	PRO
27	K	136	LYS
28	I	239	ASN
28	I	404	PHE
28	I	424	VAL
28	I	464	ALA
28	I	721	LYS
33	V	376	LEU
1	A	136	ILE
1	A	626	GLY
1	A	803	ALA
1	A	1305	SER
1	A	1367	ASN
1	A	1654	SER
6	J	592	ALA
6	J	709	VAL
7	L	765	ARG

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Mol	Chain	Res	Type
12	R	52	PRO
14	T	406	ILE
18	U	579	VAL
26	q	9	ASN
26	r	9	ASN
27	K	135	TRP
27	K	172	LEU
28	I	546	SER
28	I	618	ARG
28	I	634	ILE
29	Q	346	PRO
31	o	160	LYS
33	V	422	ASN
33	V	490	TYR
1	A	625	PRO
1	A	1366	PRO
3	C	94	ILE
11	P	205	LYS
12	R	53	ARG
12	R	235	ARG
26	q	19	PRO
28	I	601	GLN
33	V	300	PHE
33	V	395	GLN
1	A	187	PRO
1	A	1251	SER
1	A	1419	ILE
3	C	138	LEU
3	C	163	GLN
4	E	61	LEU
4	E	143	ARG
4	E	159	PRO
4	E	162	ARG
4	E	324	PRO
7	L	585	TYR
15	W	148	VAL
18	U	845	PHE
27	K	65	ILE
28	I	617	GLU
31	o	32	PRO
1	A	1365	ILE
6	J	241	VAL

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Mol	Chain	Res	Type
6	J	341	PRO
10	O	20	PHE
15	W	77	LYS
15	W	205	VAL
15	W	208	PRO
18	U	792	SER
28	I	796	LEU
1	A	108	MET
7	L	763	ILE
7	L	764	PRO
14	T	343	PRO
27	K	17	PRO
28	I	321	GLU
33	V	184	PRO
4	E	319	ILE
33	V	369	ILE
26	r	60	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1792/2108 (85%)	1754 (98%)	38 (2%)	48	72
3	C	787/866 (91%)	762 (97%)	25 (3%)	34	60
4	E	259/300 (86%)	203 (78%)	56 (22%)	1	0
6	J	242/751 (32%)	241 (100%)	1 (0%)	89	95
7	L	248/709 (35%)	233 (94%)	15 (6%)	16	32
8	M	117/209 (56%)	114 (97%)	3 (3%)	41	67
9	N	130/130 (100%)	130 (100%)	0	100	100
10	O	259/361 (72%)	237 (92%)	22 (8%)	8	18
11	P	104/203 (51%)	102 (98%)	2 (2%)	52	74
12	R	227/457 (50%)	217 (96%)	10 (4%)	24	46
13	S	129/134 (96%)	127 (98%)	2 (2%)	58	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	T	273/441 (62%)	272 (100%)	1 (0%)	89	95
15	W	135/502 (27%)	131 (97%)	4 (3%)	36	62
18	U	313/806 (39%)	292 (93%)	21 (7%)	13	27
27	K	54/196 (28%)	44 (82%)	10 (18%)	1	1
28	I	12/749 (2%)	6 (50%)	6 (50%)	0	0
All	All	5081/8922 (57%)	4865 (96%)	216 (4%)	27	47

All (216) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	ARG
1	A	409	ARG
1	A	470	ARG
1	A	642	ARG
1	A	668	VAL
1	A	676	ARG
1	A	888	GLN
1	A	994	ASN
1	A	1109	LEU
1	A	1195	ARG
1	A	1216	LEU
1	A	1505	LYS
1	A	1510	GLU
1	A	1512	SER
1	A	1513	MET
1	A	1515	TRP
1	A	1516	LYS
1	A	1517	LYS
1	A	1518	LEU
1	A	1522	GLN
1	A	1527	ASN
1	A	1532	ARG
1	A	1593	LEU
1	A	1622	MET
1	A	1636	LYS
1	A	1649	LYS
1	A	1813	ARG
1	A	1825	SER
1	A	1826	VAL
1	A	1831	LYS

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Mol	Chain	Res	Type
1	A	1832	ARG
1	A	1833	LEU
1	A	1835	GLN
1	A	1836	LEU
1	A	1838	LYS
1	A	1927	ILE
1	A	1945	VAL
1	A	1946	ASN
3	C	114	TYR
3	C	115	GLU
3	C	116	MET
3	C	117	ASP
3	C	128	LEU
3	C	135	CYS
3	C	138	LEU
3	C	139	HIS
3	C	158	ARG
3	C	160	ARG
3	C	161	TYR
3	C	163	GLN
3	C	175	GLN
3	C	238	ASN
3	C	313	GLN
3	C	394	ARG
3	C	495	ARG
3	C	513	ASN
3	C	536	ARG
3	C	537	TYR
3	C	673	LYS
3	C	775	ARG
3	C	786	ASN
3	C	814	ARG
3	C	832	TYR
4	E	55	LEU
4	E	59	ILE
4	E	60	MET
4	E	62	LEU
4	E	65	HIS
4	E	66	GLU
4	E	72	CYS
4	E	74	PHE
4	E	79	SER

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Mol	Chain	Res	Type
4	E	80	THR
4	E	81	LEU
4	E	87	ASP
4	E	90	ILE
4	E	93	TRP
4	E	99	CYS
4	E	101	ASN
4	E	102	TYR
4	E	104	THR
4	E	106	LYS
4	E	108	HIS
4	E	109	SER
4	E	113	MET
4	E	114	GLU
4	E	117	TYR
4	E	118	ASN
4	E	124	LEU
4	E	125	PHE
4	E	129	THR
4	E	130	ASP
4	E	132	THR
4	E	136	TRP
4	E	138	SER
4	E	142	GLU
4	E	143	ARG
4	E	145	LYS
4	E	147	LEU
4	E	148	LYS
4	E	153	PHE
4	E	161	ARG
4	E	229	TYR
4	E	243	LEU
4	E	248	SER
4	E	250	LEU
4	E	258	THR
4	E	265	ARG
4	E	270	LYS
4	E	271	GLU
4	E	273	CYS
4	E	289	LEU
4	E	290	ARG
4	E	307	ARG

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Mol	Chain	Res	Type
4	E	317	ARG
4	E	318	ARG
4	E	319	ILE
4	E	326	HIS
4	E	336	HIS
6	J	591	LEU
7	L	13	ASN
7	L	202	ARG
7	L	250	GLU
7	L	251	LEU
7	L	252	ARG
7	L	255	LYS
7	L	260	ARG
7	L	261	LYS
7	L	262	LYS
7	L	264	LYS
7	L	731	LEU
7	L	755	LEU
7	L	761	SER
7	L	766	ARG
7	L	781	GLU
8	M	134	GLN
8	M	212	ASN
8	M	215	ASN
10	O	78	LYS
10	O	79	ASN
10	O	146	MET
10	O	216	ARG
10	O	218	SER
10	O	220	MET
10	O	222	ARG
10	O	223	LEU
10	O	227	GLU
10	O	229	LYS
10	O	242	THR
10	O	243	ILE
10	O	244	THR
10	O	246	THR
10	O	247	ASP
10	O	248	LEU
10	O	258	ILE
10	O	259	ARG

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Mol	Chain	Res	Type
10	O	260	THR
10	O	287	SER
10	O	288	PHE
10	O	294	ASN
11	P	75	ASN
11	P	212	ASN
12	R	95	LYS
12	R	163	MET
12	R	166	ARG
12	R	183	GLN
12	R	184	GLN
12	R	189	ASN
12	R	190	SER
12	R	276	GLN
12	R	281	ASN
12	R	305	ARG
13	S	61	MET
13	S	102	ASN
14	T	308	ARG
15	W	145	ASN
15	W	148	VAL
15	W	149	SER
15	W	193	LEU
18	U	539	GLU
18	U	550	ARG
18	U	589	ARG
18	U	624	LYS
18	U	626	MET
18	U	652	GLU
18	U	655	GLU
18	U	657	GLN
18	U	658	ARG
18	U	662	ILE
18	U	664	GLU
18	U	667	SER
18	U	668	LEU
18	U	671	GLN
18	U	672	MET
18	U	702	ASN
18	U	737	ARG
18	U	806	SER
18	U	808	LYS

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Mol	Chain	Res	Type
18	U	809	ASP
18	U	810	ILE
27	K	38	GLU
27	K	90	PRO
27	K	115	GLU
27	K	117	GLN
27	K	119	VAL
27	K	120	ARG
27	K	126	LEU
27	K	130	HIS
27	K	161	GLN
27	K	171	GLN
28	I	384	THR
28	I	399	VAL
28	I	486	VAL
28	I	526	MET
28	I	545	ILE
28	I	795	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	73	HIS
1	A	97	HIS
1	A	328	HIS
1	A	357	ASN
1	A	361	HIS
1	A	723	ASN
1	A	775	ASN
1	A	792	HIS
1	A	793	ASN
1	A	860	GLN
1	A	884	HIS
1	A	888	GLN
1	A	1042	GLN
1	A	1124	ASN
1	A	1148	ASN
1	A	1296	GLN
1	A	1363	GLN
1	A	1373	GLN
1	A	1487	HIS

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Mol	Chain	Res	Type
1	A	1522	GLN
1	A	1527	ASN
1	A	1531	ASN
1	A	1580	HIS
1	A	1784	ASN
1	A	1811	ASN
1	A	1816	GLN
1	A	1835	GLN
1	A	1894	GLN
1	A	1946	ASN
3	C	82	GLN
3	C	163	GLN
3	C	238	ASN
3	C	245	HIS
3	C	451	HIS
3	C	513	ASN
3	C	523	GLN
3	C	538	HIS
3	C	548	ASN
3	C	786	ASN
4	E	101	ASN
4	E	108	HIS
4	E	116	HIS
4	E	118	ASN
4	E	165	GLN
6	J	244	ASN
6	J	344	GLN
6	J	347	HIS
6	J	389	HIS
6	J	410	HIS
7	L	13	ASN
8	M	136	HIS
8	M	212	ASN
9	N	99	ASN
9	N	116	ASN
10	O	79	ASN
10	O	251	HIS
10	O	254	GLN
10	O	268	GLN
11	P	75	ASN
11	P	212	ASN
12	R	184	GLN

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Mol	Chain	Res	Type
12	R	189	ASN
12	R	276	GLN
12	R	279	HIS
12	R	281	ASN
13	S	102	ASN
14	T	216	ASN
14	T	370	ASN
15	W	82	ASN
15	W	145	ASN
15	W	184	ASN
18	U	702	ASN
18	U	718	HIS
18	U	765	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	G	67/272 (24%)	55 (82%)	14 (20%)
17	H	129/188 (68%)	53 (41%)	2 (1%)
2	B	97/117 (82%)	57 (58%)	4 (4%)
5	F	96/107 (89%)	42 (43%)	7 (7%)
All	All	389/684 (56%)	207 (53%)	27 (6%)

All (207) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	8	G
2	B	9	G
2	B	10	U
2	B	11	U
2	B	12	U
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G
2	B	25	C
2	B	26	A
2	B	27	U
2	B	28	A

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Mol	Chain	Res	Type
2	B	33	U
2	B	34	U
2	B	35	U
2	B	36	C
2	B	37	G
2	B	38	C
2	B	39	C
2	B	40	U
2	B	45	C
2	B	47	A
2	B	48	A
2	B	52	U
2	B	53	U
2	B	67	A
2	B	68	C
2	B	69	A
2	B	70	A
2	B	71	C
2	B	72	U
2	B	73	C
2	B	74	U
2	B	75	G
2	B	76	A
2	B	77	G
2	B	78	U
2	B	79	C
2	B	80	U
2	B	81	U
2	B	82	A
2	B	83	A
2	B	84	C
2	B	85	C
2	B	86	C
2	B	87	A
2	B	88	A
2	B	89	U
2	B	90	U
2	B	91	U
2	B	92	U
2	B	94	U
2	B	95	G
2	B	96	A

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Mol	Chain	Res	Type
5	F	5	U
5	F	6	C
5	F	7	G
5	F	9	U
5	F	10	U
5	F	12	G
5	F	22	A
5	F	25	C
5	F	26	U
5	F	27	A
5	F	28	A
5	F	29	A
5	F	33	G
5	F	34	G
5	F	35	A
5	F	36	A
5	F	37	C
5	F	41	A
5	F	42	C
5	F	43	A
5	F	44	G
5	F	45	A
5	F	46	G
5	F	48	A
5	F	51	U
5	F	53	A
5	F	54	G
5	F	56	A
5	F	59	G
5	F	60	C
5	F	61	C
5	F	66	C
5	F	68	C
5	F	69	A
5	F	74	U
5	F	78	A
5	F	79	C
5	F	81	C
5	F	82	A
5	F	84	A
5	F	87	C
5	F	91	A

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Mol	Chain	Res	Type
16	G	2	U
16	G	3	A
16	G	4	A
16	G	6	A
16	G	7	G
16	G	8	C
16	G	9	C
16	G	11	A
16	G	12	G
16	G	17	U
16	G	20	A
16	G	21	A
16	G	22	C
16	G	23	U
16	G	24	G
16	G	25	G
16	G	26	U
16	G	27	U
16	G	28	A
16	G	29	C
16	G	30	C
16	G	119	G
16	G	120	G
16	G	121	G
16	G	122	U
16	G	123	U
16	G	125	C
16	G	127	U
16	G	128	U
16	G	129	G
16	G	130	A
16	G	131	U
16	G	132	G
16	G	133	A
16	G	134	U
16	G	135	G
16	G	136	U
16	G	137	C
16	G	138	A
16	G	139	U
16	G	140	A
16	G	141	C

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Mol	Chain	Res	Type
16	G	142	U
16	G	143	U
16	G	144	A
16	G	145	U
16	G	146	C
16	G	147	C
16	G	148	U
16	G	149	G
16	G	150	U
16	G	151	C
16	G	152	C
16	G	154	U
16	G	155	U
17	H	8	C
17	H	14	C
17	H	15	U
17	H	16	U
17	H	19	G
17	H	20	G
17	H	24	A
17	H	28	C
17	H	29	A
17	H	30	A
17	H	31	G
17	H	32	U
17	H	33	G
17	H	34	U
17	H	35	A
17	H	36	G
17	H	37	U
17	H	38	A
17	H	39	U
17	H	40	C
17	H	41	U
17	H	42	G
17	H	43	U
17	H	44	U
17	H	45	C
17	H	46	U
17	H	47	U
17	H	69	U
17	H	74	U

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Mol	Chain	Res	Type
17	H	79	G
17	H	81	G
17	H	83	A
17	H	92	U
17	H	94	A
17	H	98	G
17	H	106	G
17	H	107	A
17	H	109	C
17	H	112	G
17	H	114	A
17	H	150	U
17	H	154	C
17	H	157	G
17	H	164	C
17	H	165	A
17	H	166	G
17	H	167	U
17	H	168	A
17	H	169	C
17	H	177	A
17	H	178	A
17	H	179	C
17	H	182	U

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	78	U
2	B	79	C
2	B	92	U
2	B	95	G
5	F	5	U
5	F	33	G
5	F	35	A
5	F	50	A
5	F	58	G
5	F	81	C
5	F	82	A
16	G	1	G
16	G	2	U
16	G	3	A

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Mol	Chain	Res	Type
16	G	7	G
16	G	8	C
16	G	16	G
16	G	21	A
16	G	22	C
16	G	134	U
16	G	142	U
16	G	143	U
16	G	144	A
16	G	145	U
16	G	150	U
17	H	7	U
17	H	28	C

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

2 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	$\# Z > 2$
12	SEP	R	224	12	8,9,10	0.83	0	8,12,14	1.08	0
12	SEP	R	232	12	8,9,10	0.98	0	8,12,14	2.08	2 (25%)

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
12	SEP	R	224	12	-	0/5/8/10	-
12	SEP	R	232	12	-	1/5/8/10	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	R	232	SEP	OG-CB-CA	4.44	112.47	108.14
12	R	232	SEP	P-OG-CB	-2.36	111.81	118.30

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	R	232	SEP	N-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	R	232	SEP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 14 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
35	GTP	C	1500	36	26,34,34	0.98	1 (3%)	32,54,54	1.49	5 (15%)
34	IHP	A	3000	-	36,36,36	0.71	0	54,60,60	0.96	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
35	GTP	C	1500	36	-	4/18/38/38	0/3/3/3
34	IHP	A	3000	-	-	5/30/54/54	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	C	1500	GTP	C6-N1	-2.98	1.33	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	C	1500	GTP	PA-O3A-PB	-3.99	119.15	132.83
35	C	1500	GTP	PB-O3B-PG	-3.76	119.91	132.83
35	C	1500	GTP	C5-C6-N1	2.66	118.65	113.95
35	C	1500	GTP	O6-C6-C5	-2.35	119.78	124.37
35	C	1500	GTP	C8-N7-C5	2.27	107.32	102.99

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	C	1500	GTP	C5'-O5'-PA-O3A
35	C	1500	GTP	C5'-O5'-PA-O1A
35	C	1500	GTP	C5'-O5'-PA-O2A
34	A	3000	IHP	C1-O11-P1-O21
34	A	3000	IHP	C3-O13-P3-O23
34	A	3000	IHP	C4-O14-P4-O24
34	A	3000	IHP	C1-O11-P1-O31
34	A	3000	IHP	C3-O13-P3-O43
35	C	1500	GTP	PB-O3A-PA-O2A

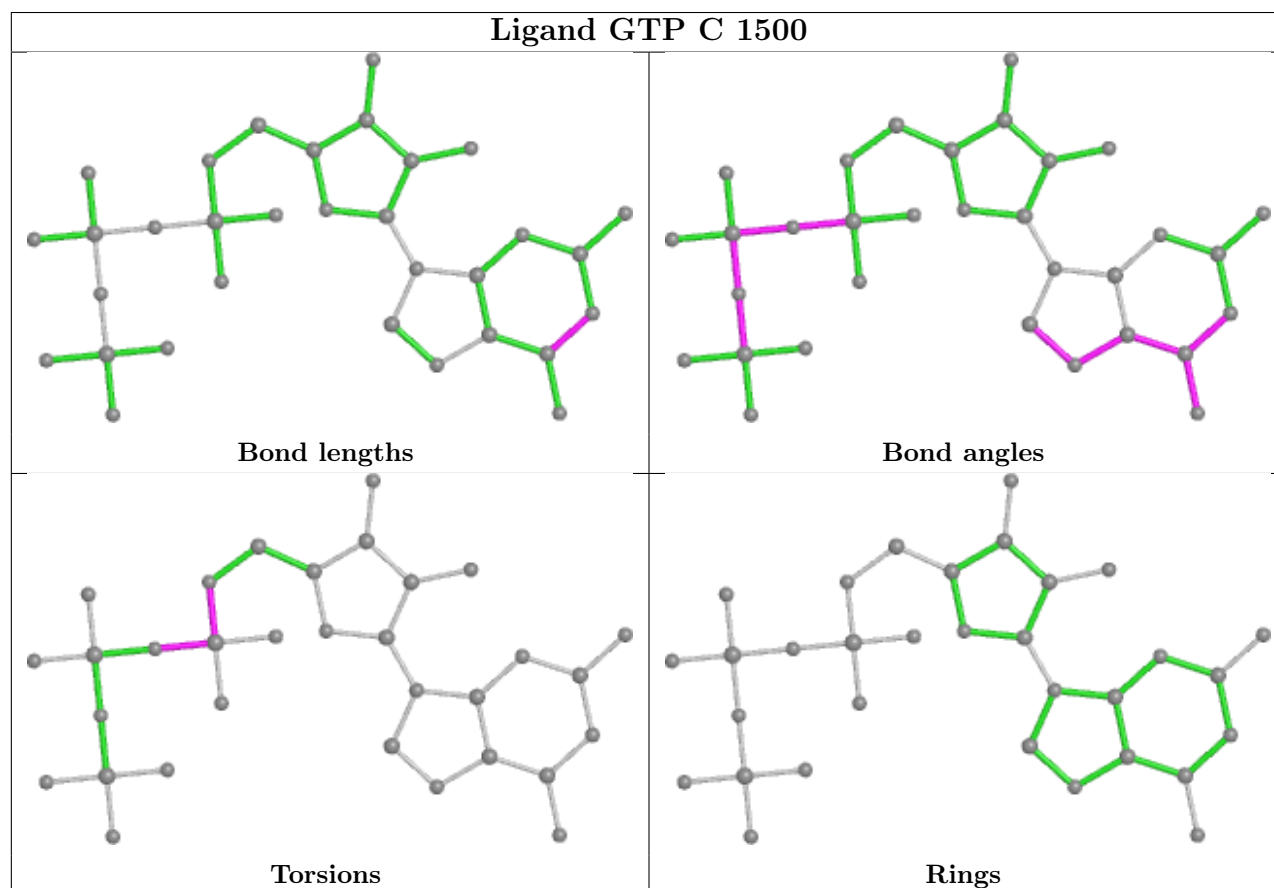
There are no ring outliers.

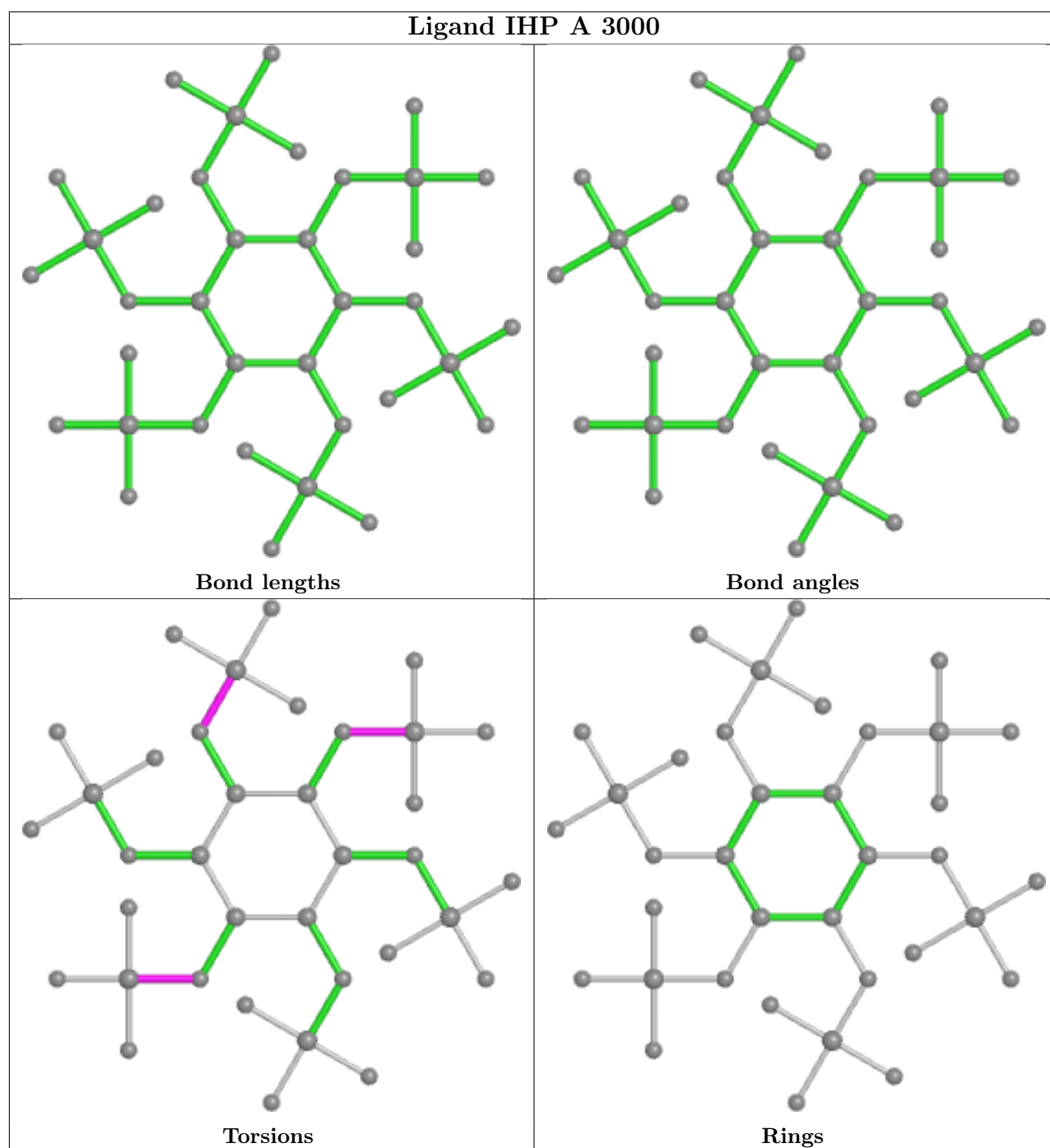
2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	C	1500	GTP	9	0
34	A	3000	IHP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

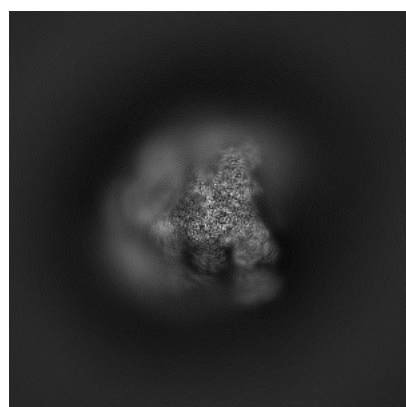
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9647. These allow visual inspection of the internal detail of the map and identification of artifacts.

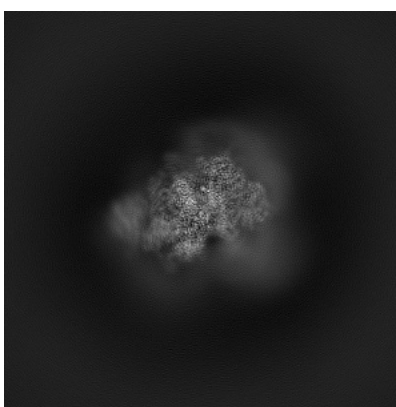
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

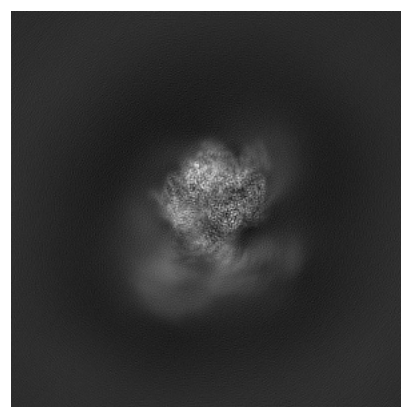
6.1.1 Primary map



X



Y

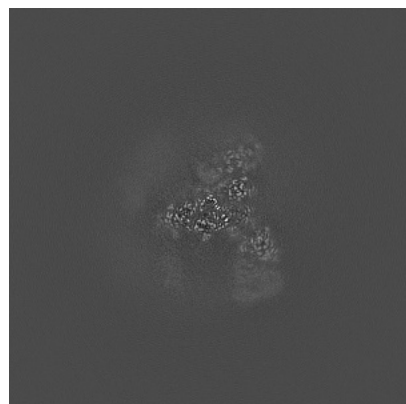


Z

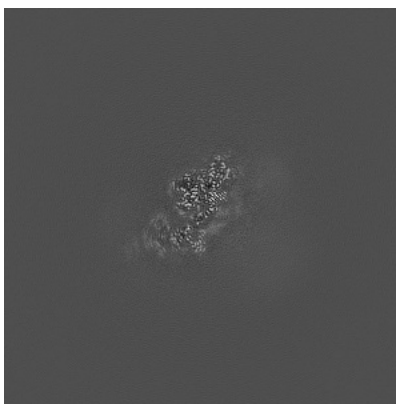
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

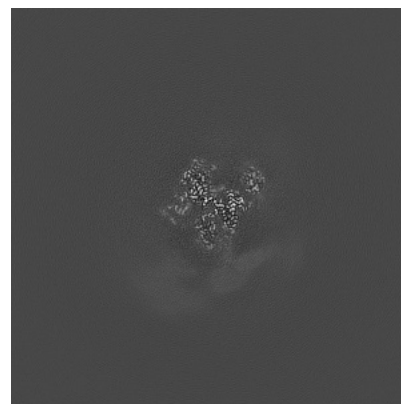
6.2.1 Primary map



X Index: 200



Y Index: 200

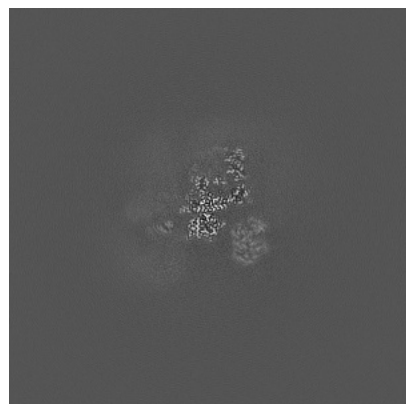


Z Index: 200

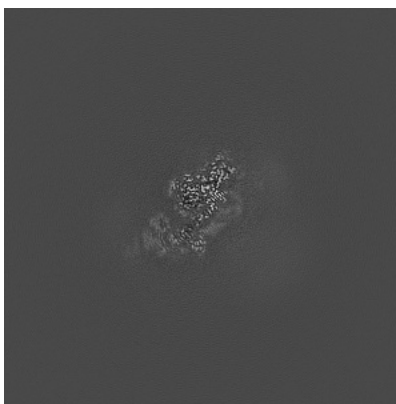
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

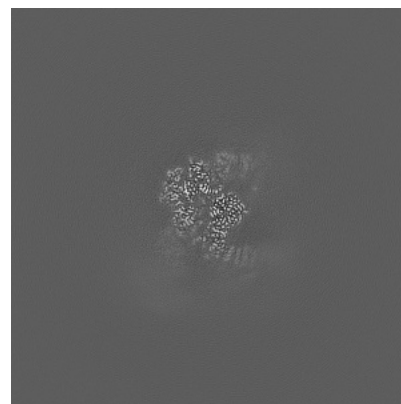
6.3.1 Primary map



X Index: 221



Y Index: 201

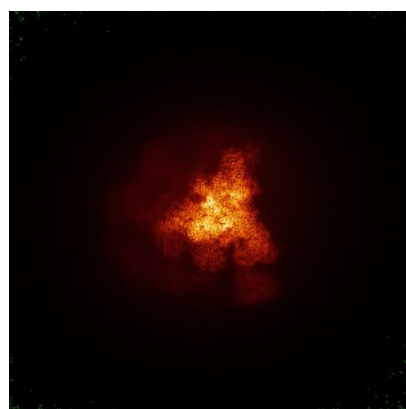


Z Index: 185

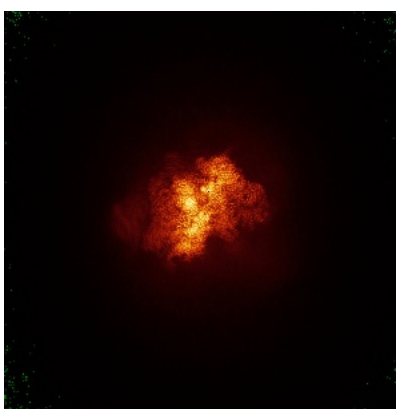
The images above show the largest variance slices of the map in three orthogonal directions.

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

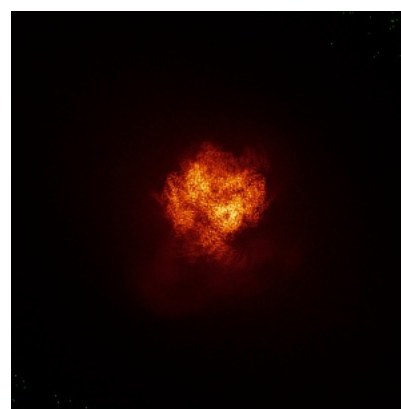
6.4.1 Primary map



X



Y

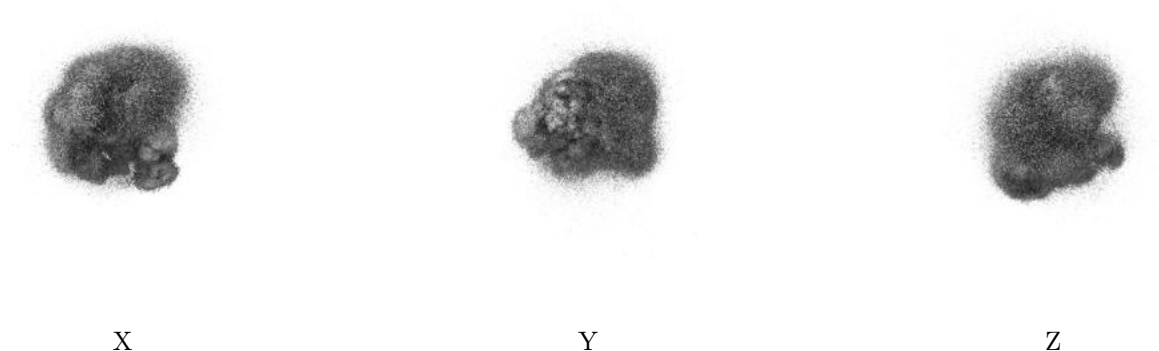


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

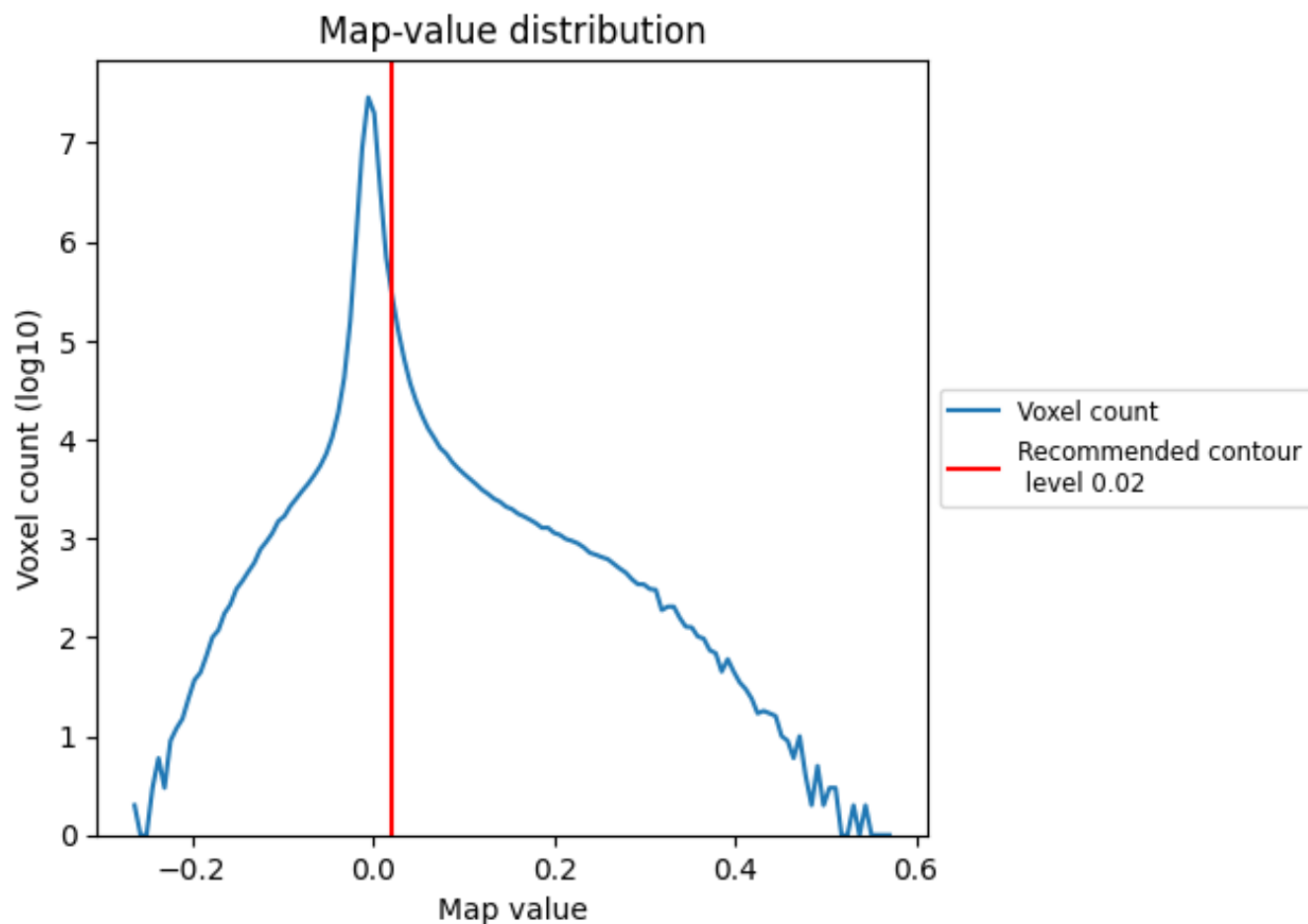
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

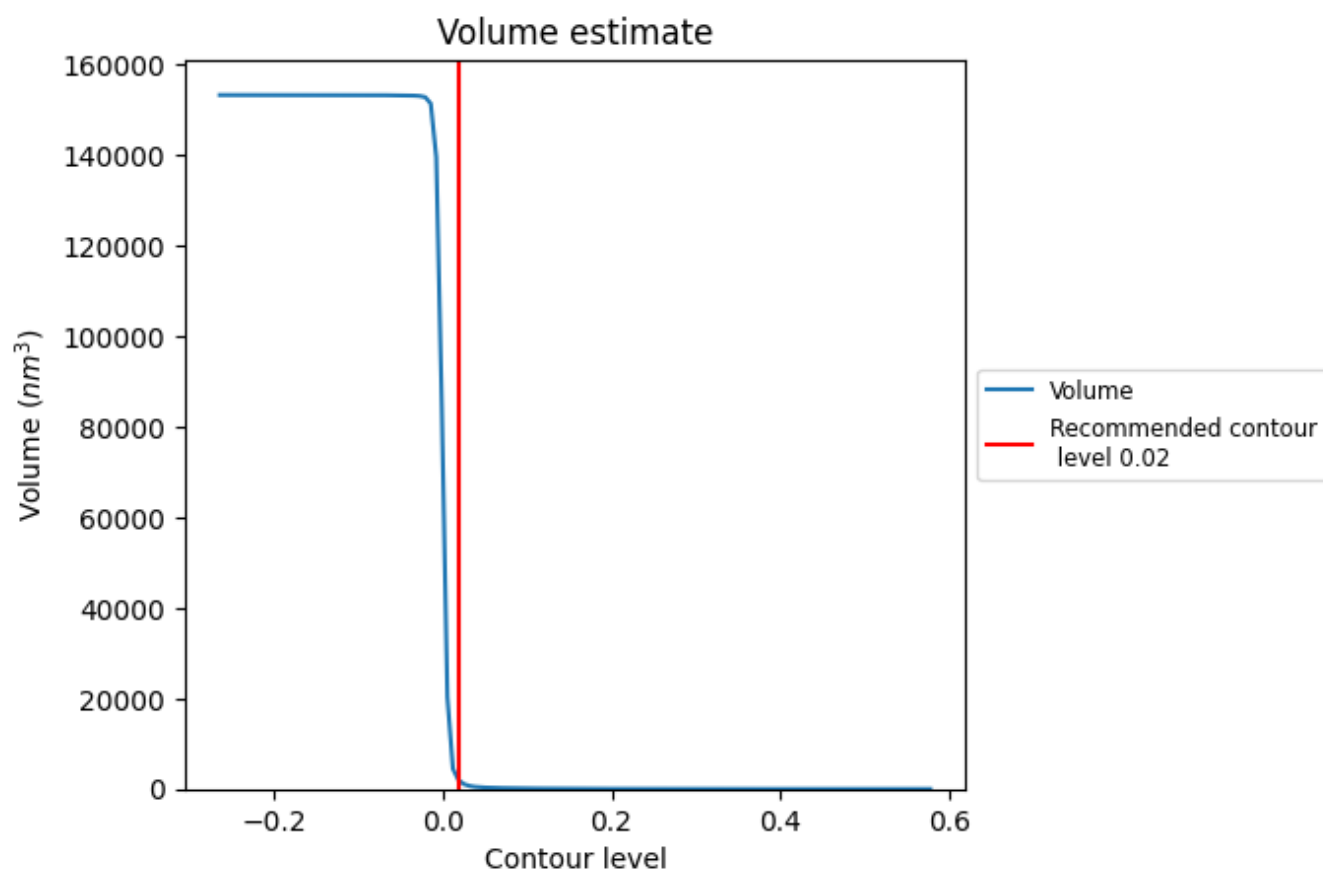
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

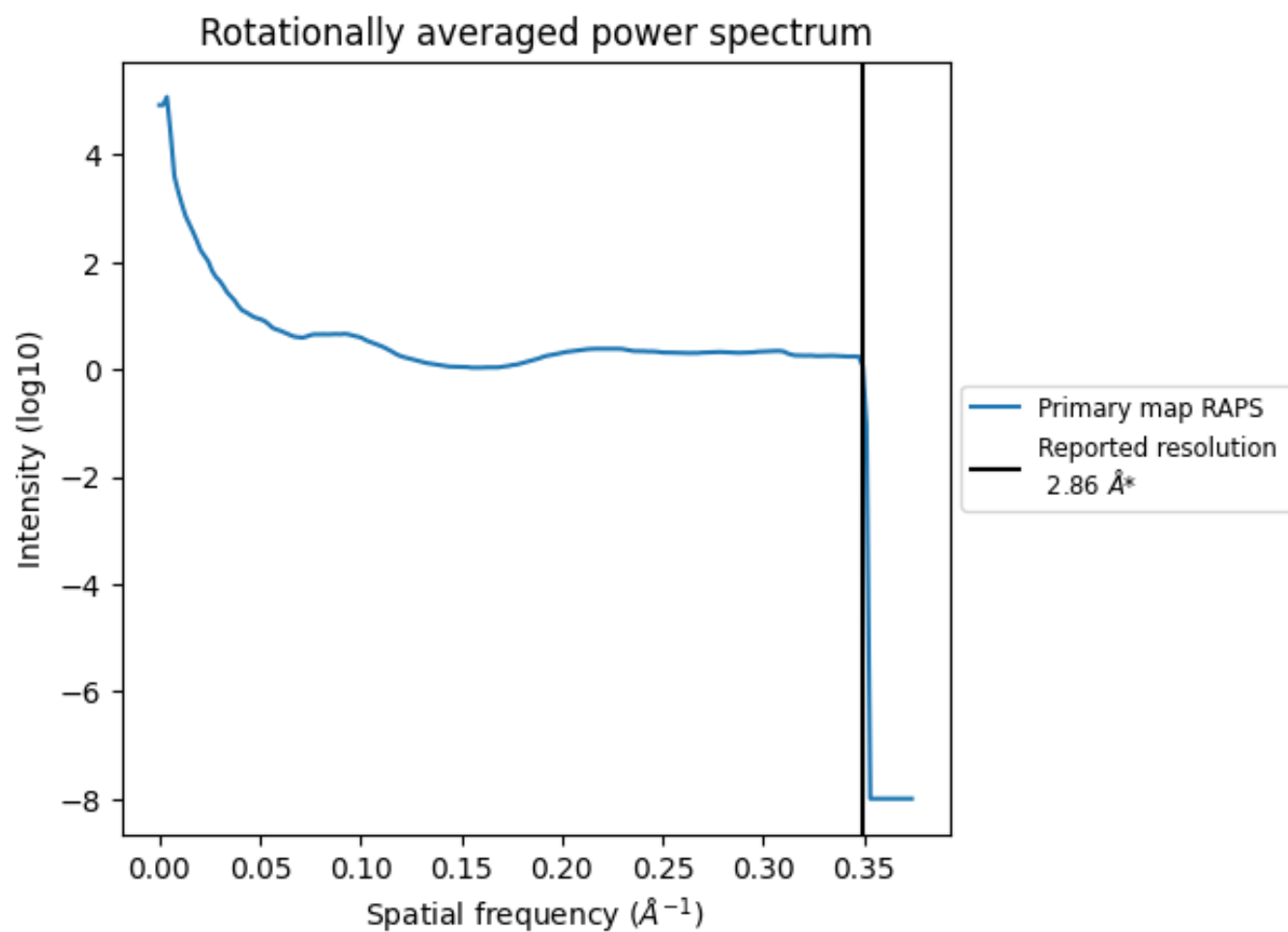
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1797 nm^3 ; this corresponds to an approximate mass of 1623 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.350 Å⁻¹

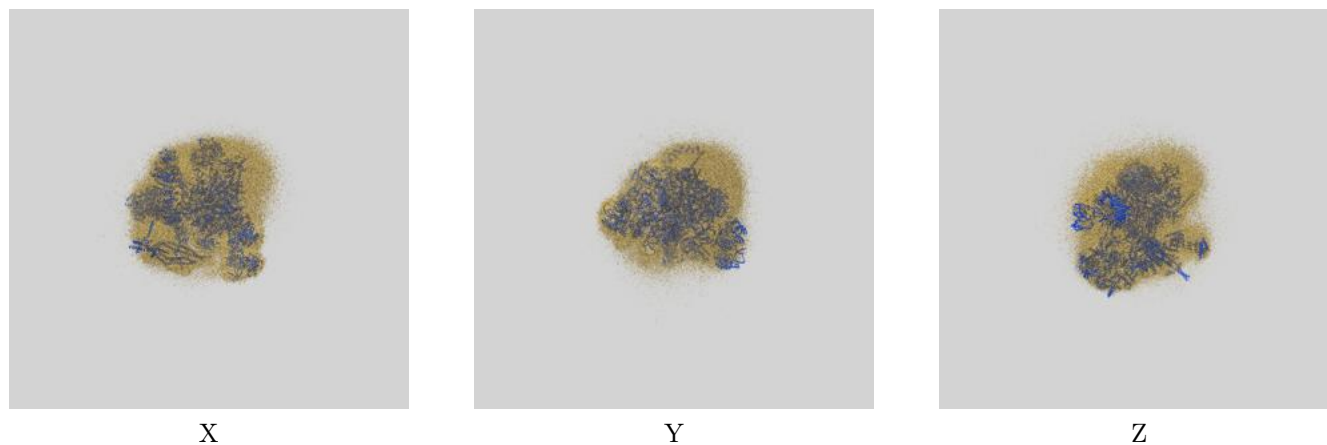
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

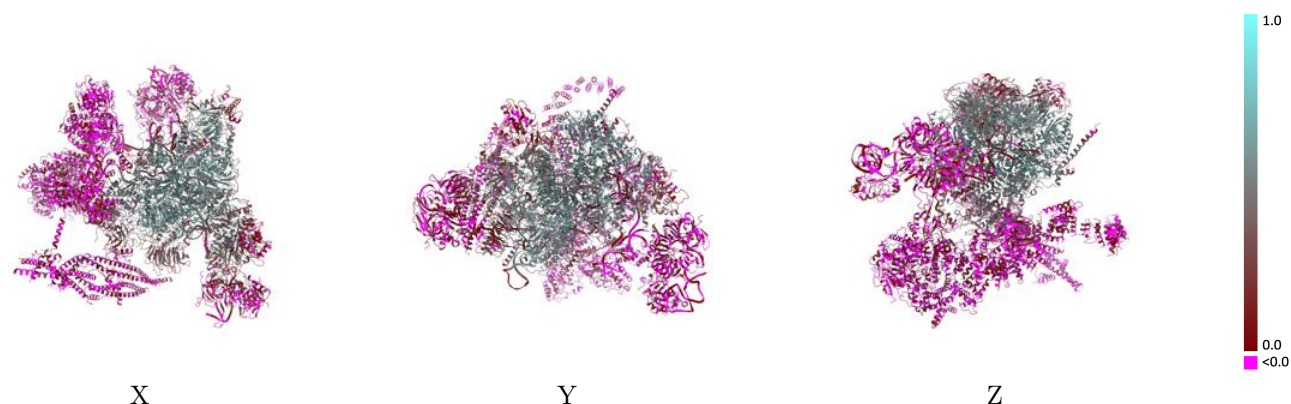
This section contains information regarding the fit between EMDB map EMD-9647 and PDB model 6ID1. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



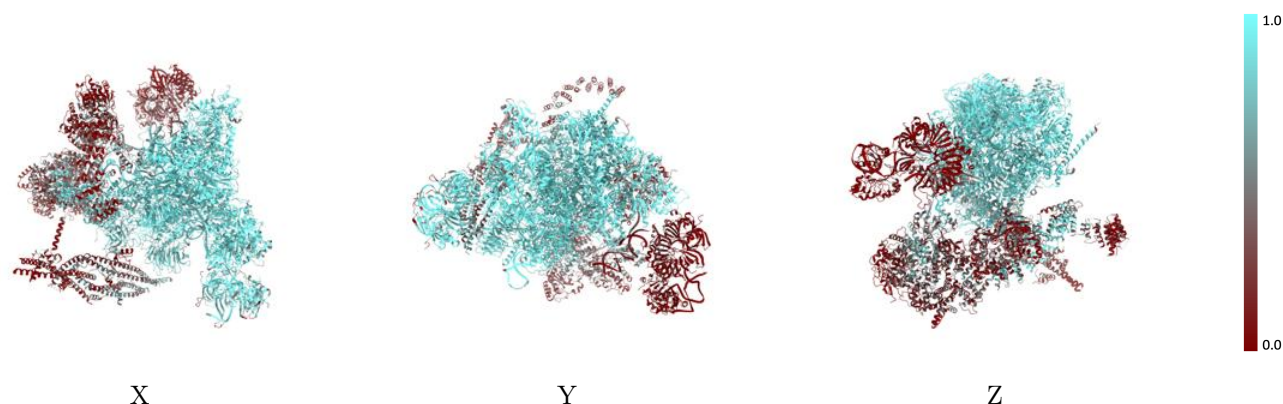
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



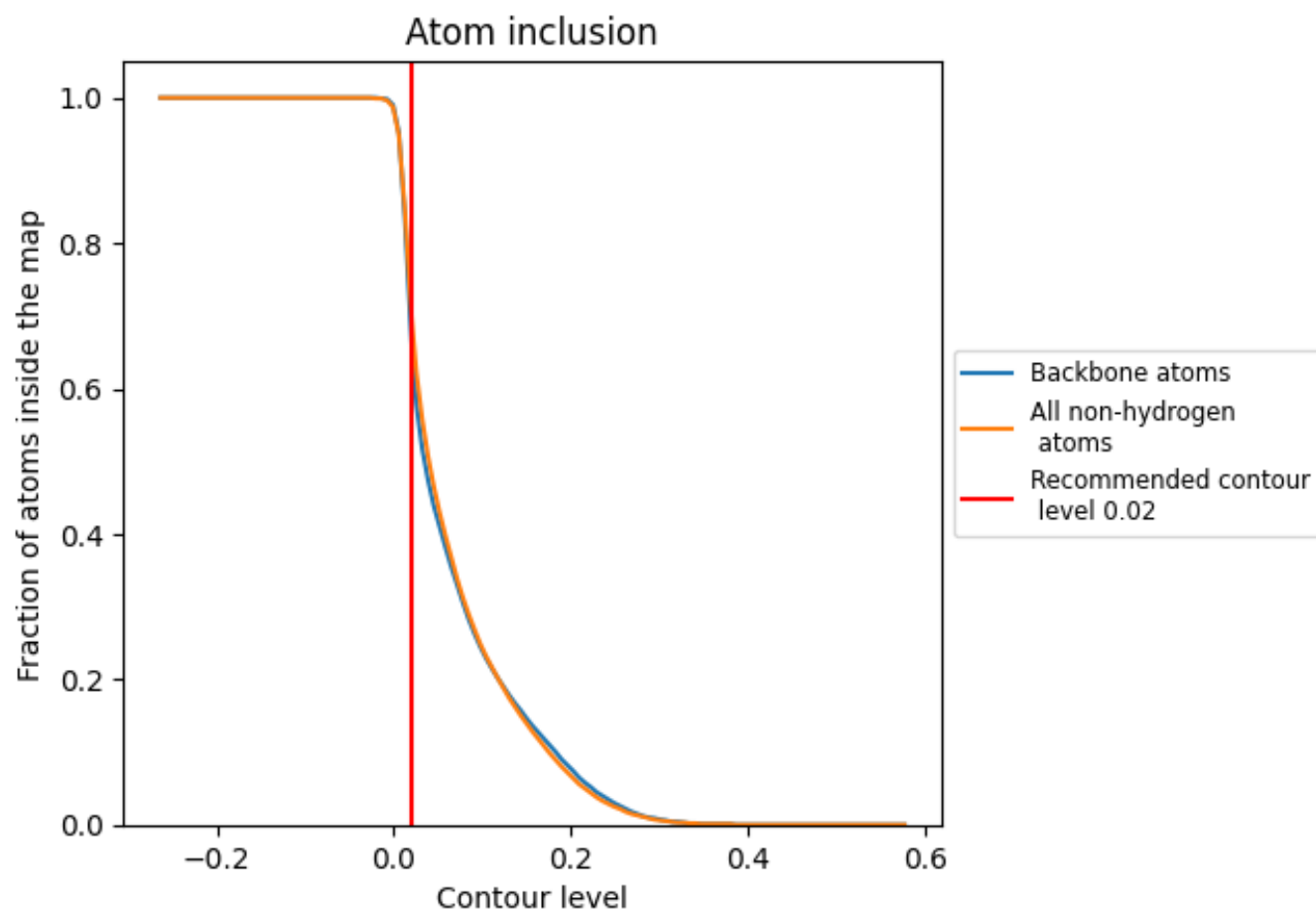
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ



















The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7010	 0.2910
A	 0.9460	 0.5070
B	 0.9160	 0.3290
C	 0.9180	 0.3560
E	 0.9000	 0.2990
F	 0.9430	 0.4390
G	 0.7810	 0.1720
H	 0.3200	 0.0900
I	 0.6000	 0.0420
J	 0.6430	 0.2780
K	 0.3970	 0.0550
L	 0.6340	 0.2560
M	 0.8280	 0.4070
N	 0.9670	 0.5630
O	 0.8550	 0.3890
P	 0.8590	 0.4360
Q	 0.2360	 0.0140
R	 0.8910	 0.4260
S	 0.8480	 0.2520
T	 0.9800	 0.5940
U	 0.9240	 0.4780
V	 0.1900	 0.0130
W	 0.8400	 0.3760
a	 0.8900	 0.2050
b	 0.7920	 0.1000
c	 0.9060	 0.1090
d	 0.8460	 0.0450
e	 0.7800	 0.0620
f	 0.7950	 -0.0090
g	 0.7580	 0.0680
h	 0.1090	 0.0110
i	 0.1180	 0.0280
j	 0.0890	 0.0510
k	 0.0170	 -0.0070
l	 0.0280	 0.0100



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Chain	Atom inclusion	Q-score
m	 0.0170	 -0.0010
n	 0.0940	 0.0070
o	 0.0590	 0.0290
p	 0.0600	 0.0360
q	 0.1210	 -0.0070
r	 0.3720	 0.0170
s	 0.4000	 -0.0250
t	 0.1640	 0.0090
y	 0.4690	 0.0440