



Full wwPDB EM Validation Report ⓘ

Jun 24, 2026 – 12:09 AM EDT

PDB ID : 7SFR / pdb_00007sfr
EMDB ID : EMD-25100
Title : Unmethylated Mtb Ribosome 50S with SEQ-9
Authors : Xing, Z.; Cui, Z.; Zhang, J.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2021-10-04
Resolution : 2.60 Å (reported)
Based on initial model : 7KGB

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

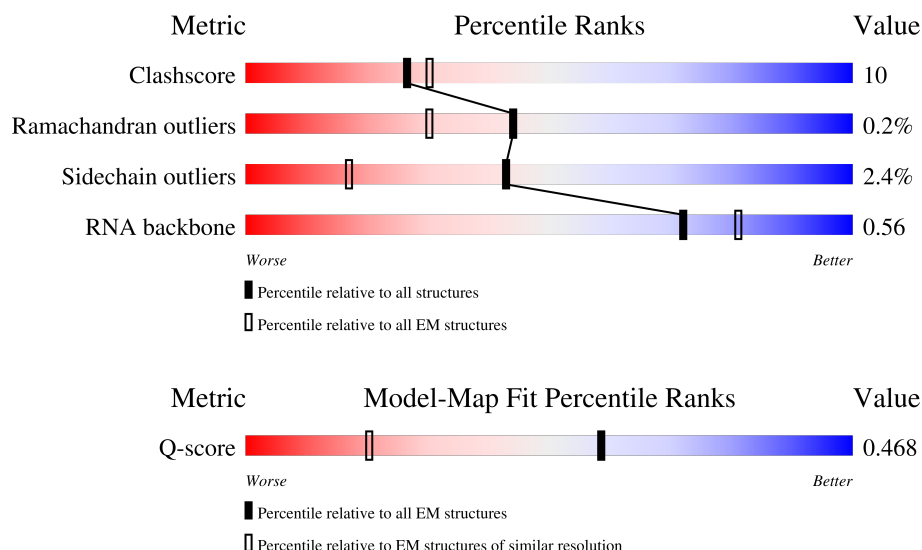
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	0	57	42% 77% 18% 5%
2	1	55	13% 69% 16% 13%
3	2	47	79% 11% 11%

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Mol	Chain	Length	Quality of chain
4	3	64	
5	4	37	
6	6	80	
7	A	3138	
8	B	115	
9	C	279	
10	D	213	
11	E	207	
12	F	178	
13	G	177	
14	H	152	
15	J	195	
16	K	122	
17	L	146	
18	M	138	
19	N	180	
20	O	122	
21	P	113	
22	Q	129	
23	R	104	
24	S	197	
25	T	100	
26	U	105	
27	V	215	
28	W	86	

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Mol	Chain	Length	Quality of chain
29	X	64	
30	Y	77	
31	Z	65	
32	a	1537	
33	c	274	
34	d	201	
35	e	220	
36	f	96	
37	g	156	
38	h	132	
39	i	151	
40	j	101	
41	k	139	
42	l	124	
43	m	124	
44	n	61	
45	o	89	
46	p	162	
47	q	135	
48	r	84	
49	s	93	
50	t	86	
51	v	22	

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
53	WDP	A	3201	-	-	X	-

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 143665 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	54	Total	C	N	O	0	0
			429	266	94	69		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	48	Total	C	N	O	S	0	0
			400	245	84	67	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	42	Total	C	N	O	S	0	0
			358	212	94	51	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	3	62	Total	C	N	O	0	0
			494	298	112	84		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	37	Total	C	N	O	S	0	0
			299	182	66	47	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	1	VAL	MET	conflict	UNP A0A3E0V5U0

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	57	Total	C	N	O	S	0	0
			446	277	82	82	5		

- Molecule 7 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	3118	Total	C	N	O	P	0	0
			66961	29850	12340	21653	3118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	115	Total	C	N	O	P	0	0
			2458	1097	456	790	115		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	272	Total	C	N	O	S	0	0
			2088	1277	437	369	5		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	213	Total	C	N	O	S	0	0
			1590	985	307	292	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	207	Total	C	N	O	S	0	0
			1552	958	303	289	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	178	Total	C	N	O	S	0	0
			1408	885	267	251	5		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	174	Total	C	N	O	S	0	0
			1330	836	249	244	1		

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	47	Total	C	N	O	S	0	0
			350	220	64	65	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	146	Total	C	N	O	S	0	0
			1143	724	217	199	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	121	Total	C	N	O	S	0	0
			934	585	179	168	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	1	VAL	MET	conflict	UNP A0A045HTP7

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	143	Total	C	N	O	S	0	0
			1068	662	216	188	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	134	Total	C	N	O	S	0	0
			1072	679	215	177	1		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	116	Total	C	N	O	S	0	0
			908	574	175	158	1		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	116	Total	C	N	O		0	0
			886	541	188	157			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	112	Total	C	N	O	S	0	0
			907	573	174	159	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	122	Total	C	N	O		0	0
			980	608	205	167			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	100	Total	C	N	O		0	0
			757	482	138	137			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	113	Total	C	N	O		0	0
			860	533	178	149			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	98	Total	C	N	O		0	0
			759	480	141	138			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	90	Total	C	N	O	S	0	0
			699	430	138	129	2		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	95	Total	C	N	O		0	0
			735	456	152	127			

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	71	Total	C	N	O		0	0
			526	325	108	93			

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	63	Total	C	N	O	S	0	0
			476	289	101	81	5		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	65	Total	C	N	O	S	0	0
			541	331	106	103	1		

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	59	Total	C	N	O		0	0
			476	293	101	82			

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1519	Total	C	N	O	P	0	0
			32621	14536	5961	10605	1519		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	207	Total	C	N	O	S	0	0
			1654	1030	322	298	4		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	200	Total	C	N	O	S	0	0
			1650	1036	316	296	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	160	Total	C	N	O	S	0	0
			1149	726	214	206	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	95	Total	C	N	O	S	0	0
			757	480	133	141	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	152	Total	C	N	O	S	0	0
			1193	742	234	215	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	130	Total	C	N	O	S	0	0
			999	627	187	184	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	127	Total	C	N	O		0	0
			993	628	195	170			

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	99	Total	C	N	O	S	0	0
			789	496	146	144	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	117	Total	C	N	O		0	0
			873	540	175	158			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	122	Total	C	N	O	S	0	0
			959	594	197	166	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	116	Total	C	N	O	S	0	0
			945	578	196	168	3		

- Molecule 44 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	60	Total	C	N	O	S	0	0
			468	294	96	73	5		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	87	Total	C	N	O		0	0
			718	449	144	125			

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	91	Total	C	N	O		0	0
			728	462	140	126			

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	93	Total	C	N	O	S	0	0
			754	471	149	131	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	63	Total	C	N	O	S	0	0
			497	309	96	89	3		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	83	Total	C	N	O	S	0	0
			672	432	125	114	1		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	82	Total	C	N	O		0	0
			631	381	137	113			

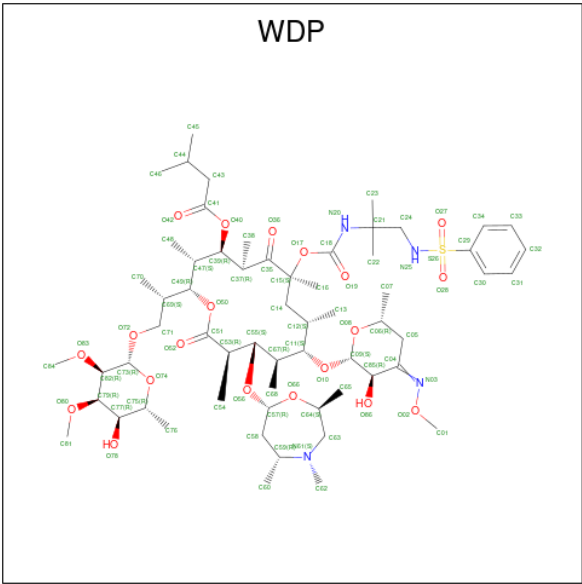
- Molecule 51 is a protein called peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	22	Total	C	N	O		0	0
			186	111	47	28			

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	1	1	Total	Zn	0
			1	1	
52	4	1	Total	Zn	0
			1	1	
52	6	1	Total	Zn	0
			1	1	
52	X	1	Total	Zn	0
			1	1	
52	n	1	Total	Zn	0
			1	1	
52	r	1	Total	Zn	0
			1	1	

- Molecule 53 is Sequanamycin 9 (CCD ID: WDP) (formula: C₆₁H₁₀₂N₄O₂₀S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
53	A	1	Total	C	N	O	S	0
			86	61	4	20	1	

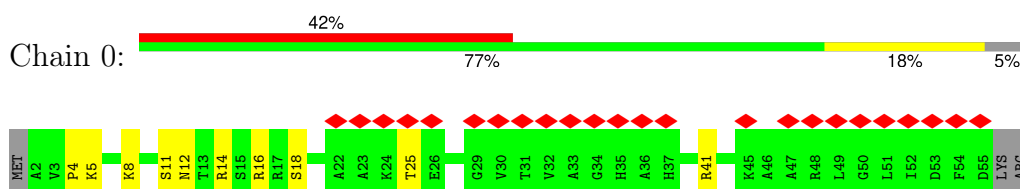
- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	307	Total	Mg	0
			307	307	
54	B	7	Total	Mg	0
			7	7	
54	C	3	Total	Mg	0
			3	3	
54	D	1	Total	Mg	0
			1	1	
54	L	1	Total	Mg	0
			1	1	
54	M	1	Total	Mg	0
			1	1	
54	a	125	Total	Mg	0
			125	125	
54	e	1	Total	Mg	0
			1	1	
54	t	1	Total	Mg	0
			1	1	

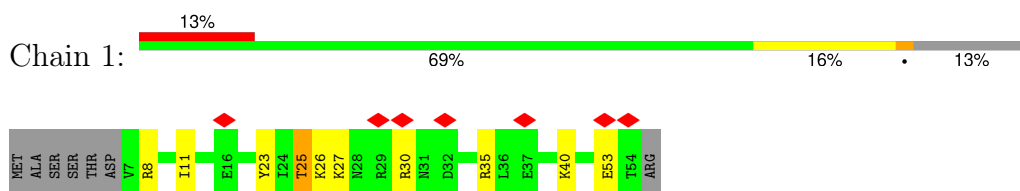
3 Residue-property plots [i](#)

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

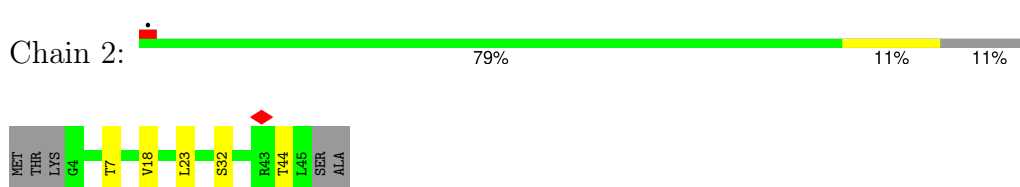
- Molecule 1: 50S ribosomal protein L32



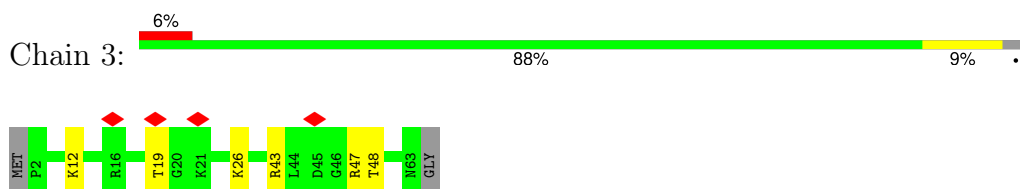
- Molecule 2: 50S ribosomal protein L33



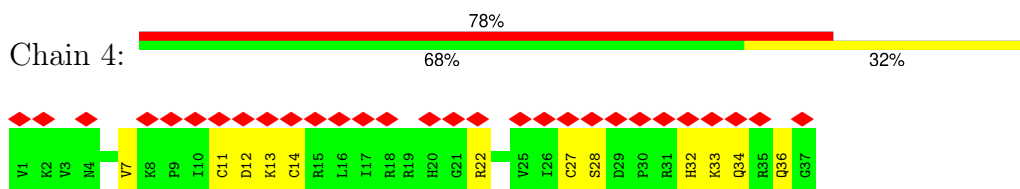
- Molecule 3: 50S ribosomal protein L34



- Molecule 4: 50S ribosomal protein L35

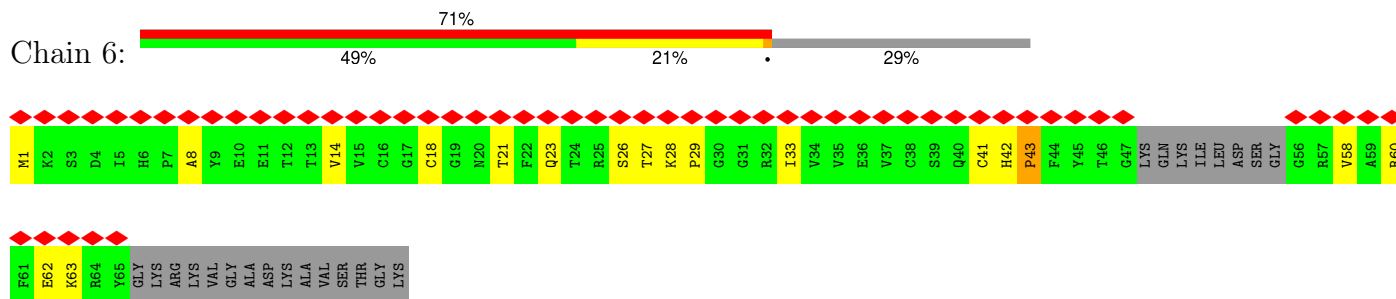


- Molecule 5: 50S ribosomal protein L36



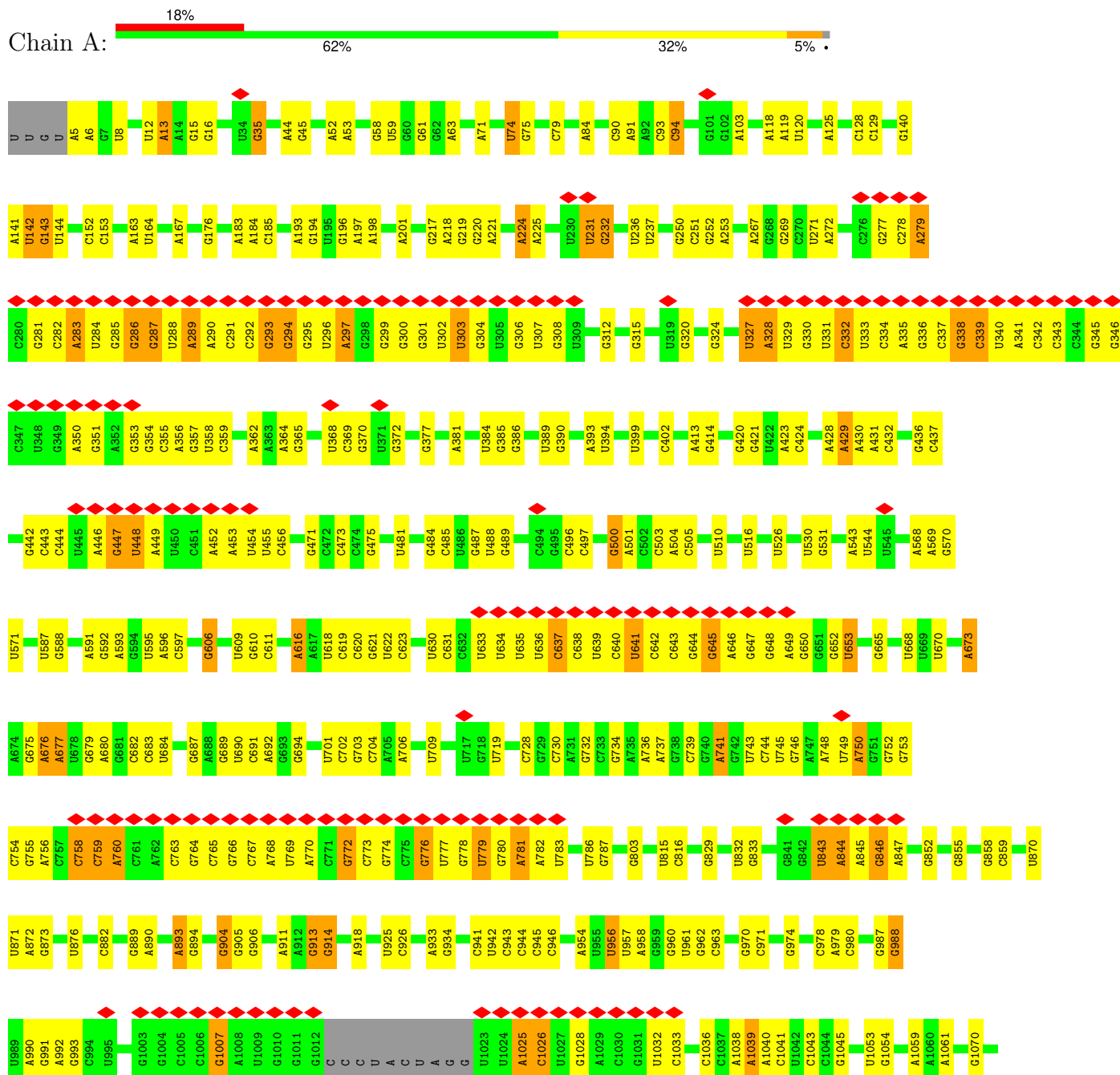
- Molecule 6: 50S ribosomal protein L31

Chain 6:

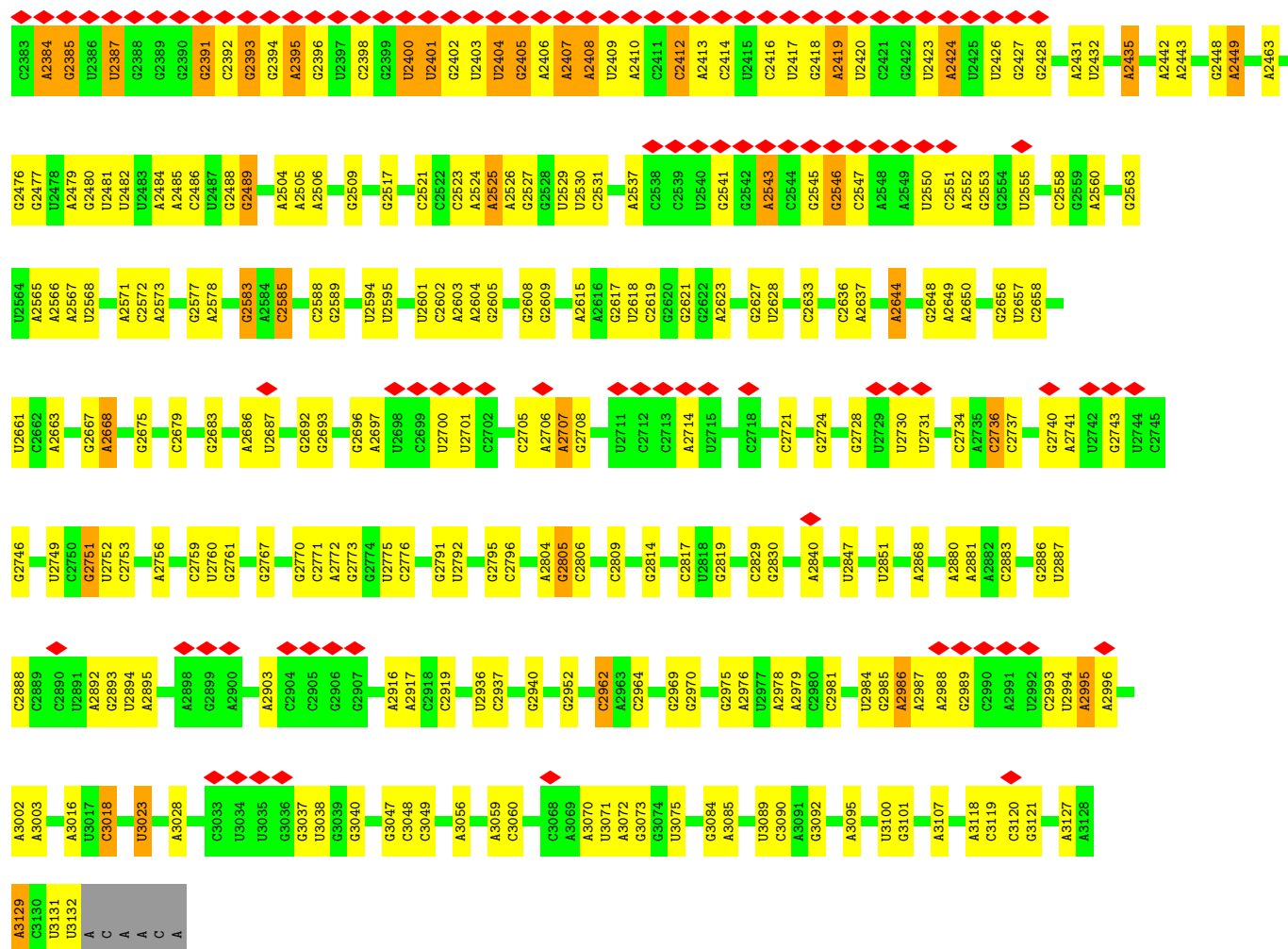


- Molecule 7: 23S rRNA

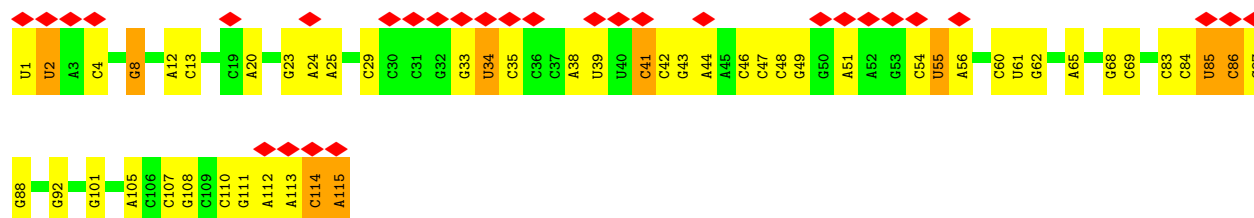
Chain A:



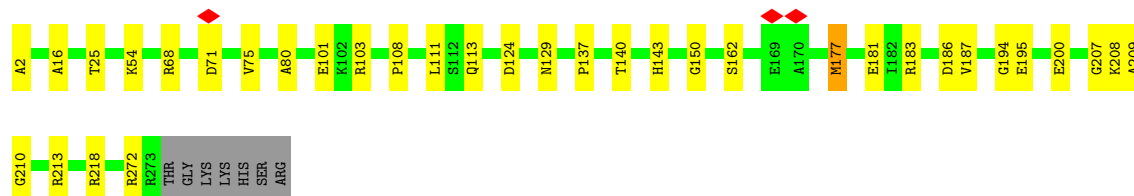
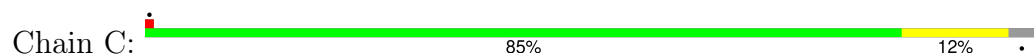




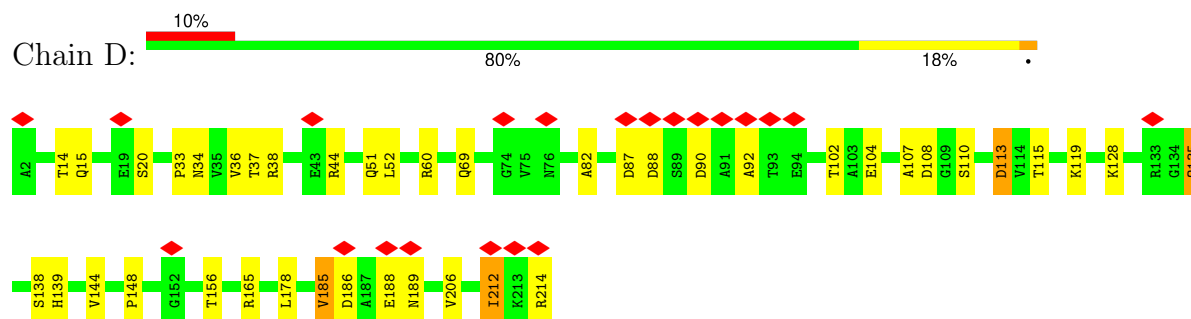
• Molecule 8: 5S rRNA



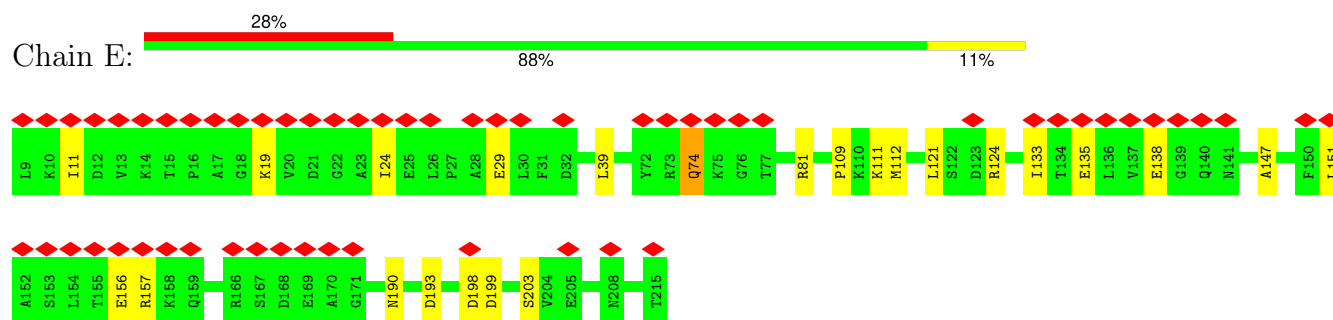
• Molecule 9: 50S ribosomal protein L2



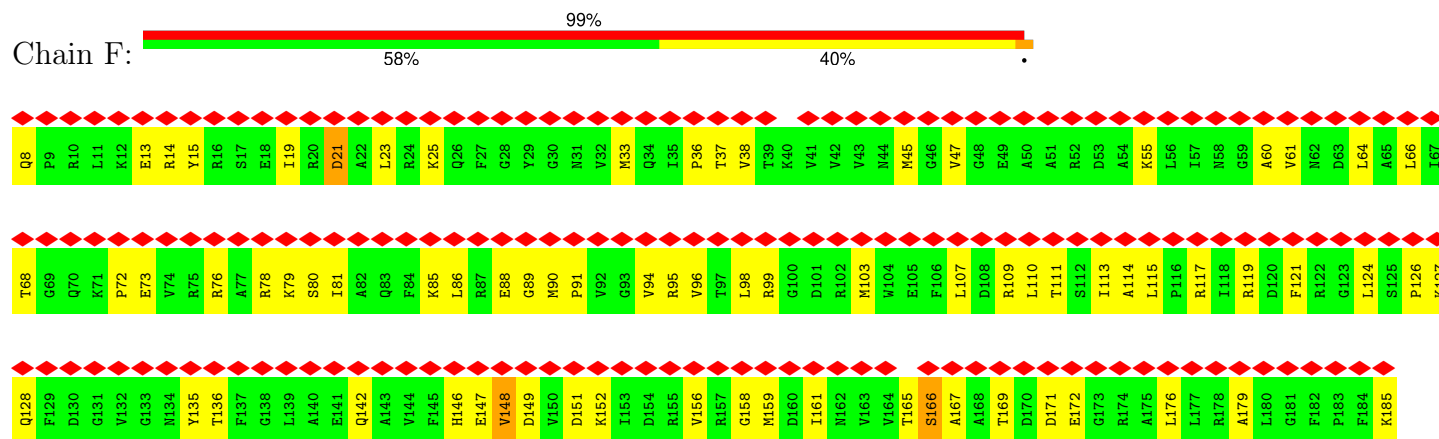
- Molecule 10: 50S ribosomal protein L3



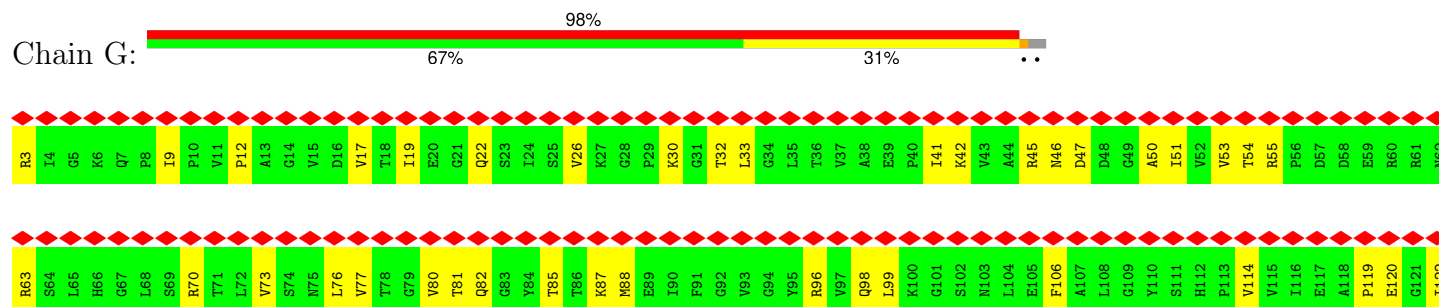
- Molecule 11: 50S ribosomal protein L4



- Molecule 12: 50S ribosomal protein L5

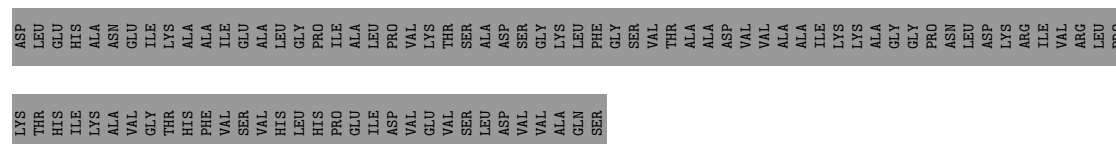
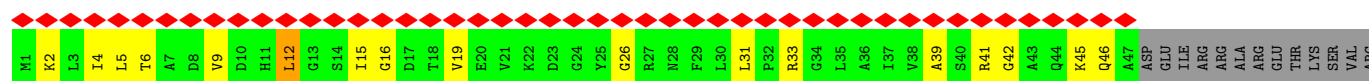


- Molecule 13: 50S ribosomal protein L6

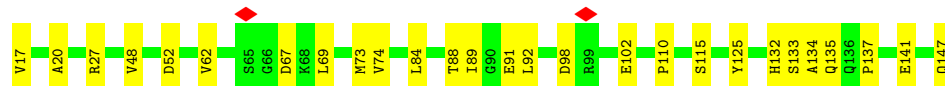
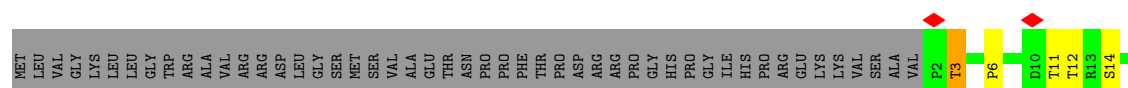




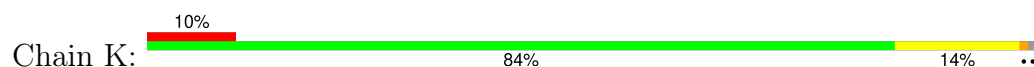
• Molecule 14: 50S ribosomal protein L9



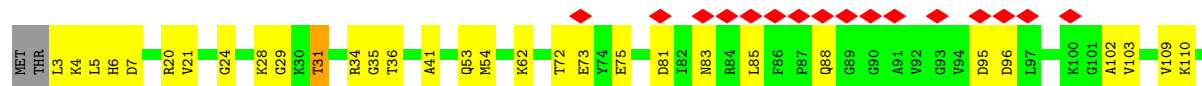
• Molecule 15: 50S ribosomal protein L13



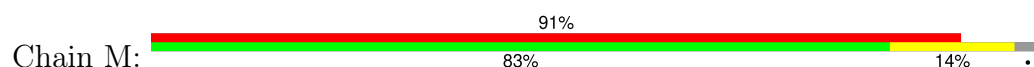
• Molecule 16: 50S ribosomal protein L14

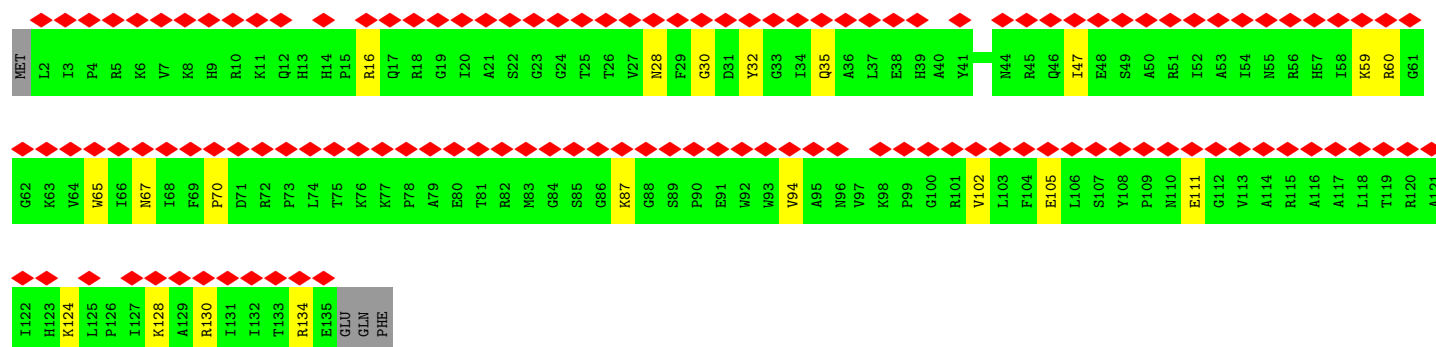


• Molecule 17: 50S ribosomal protein L15

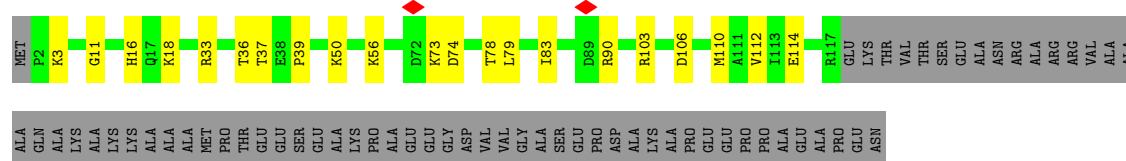


• Molecule 18: 50S ribosomal protein L16





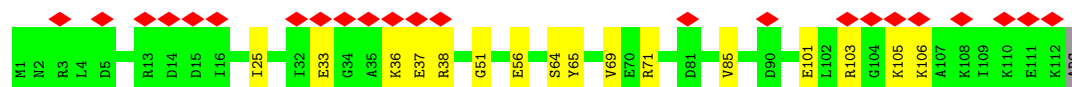
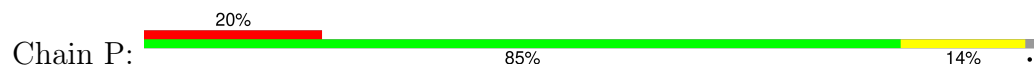
- Molecule 19: 50S ribosomal protein L17



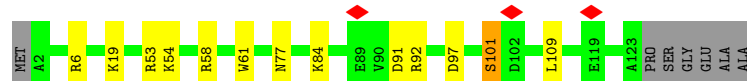
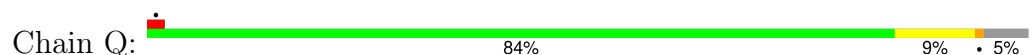
- Molecule 20: 50S ribosomal protein L18



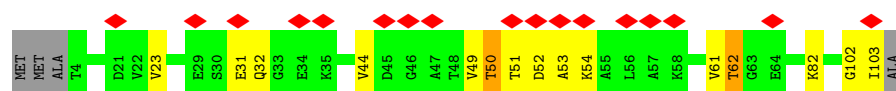
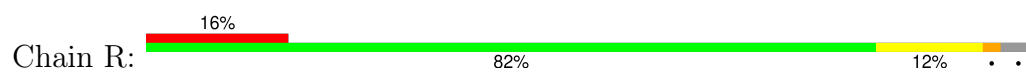
- Molecule 21: 50S ribosomal protein L19



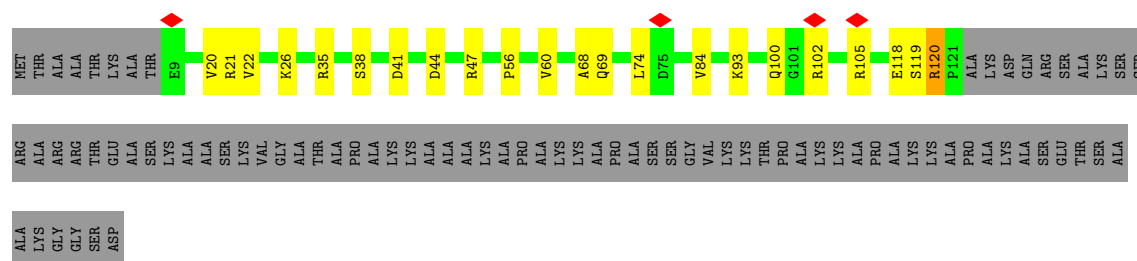
- Molecule 22: 50S ribosomal protein L20



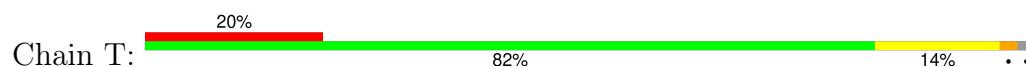
- Molecule 23: 50S ribosomal protein L21



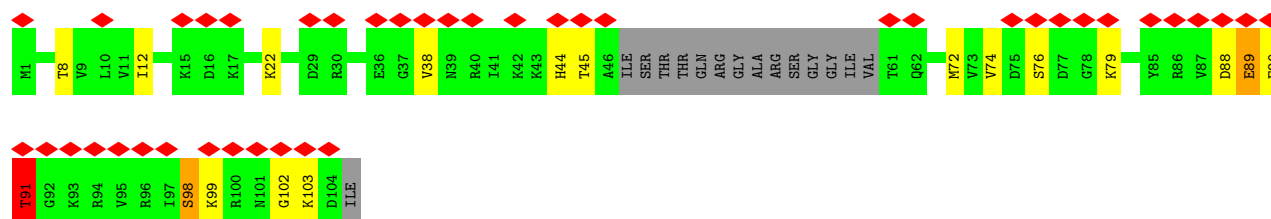
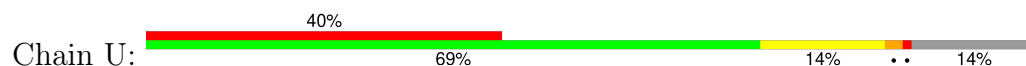
• Molecule 24: 50S ribosomal protein L22



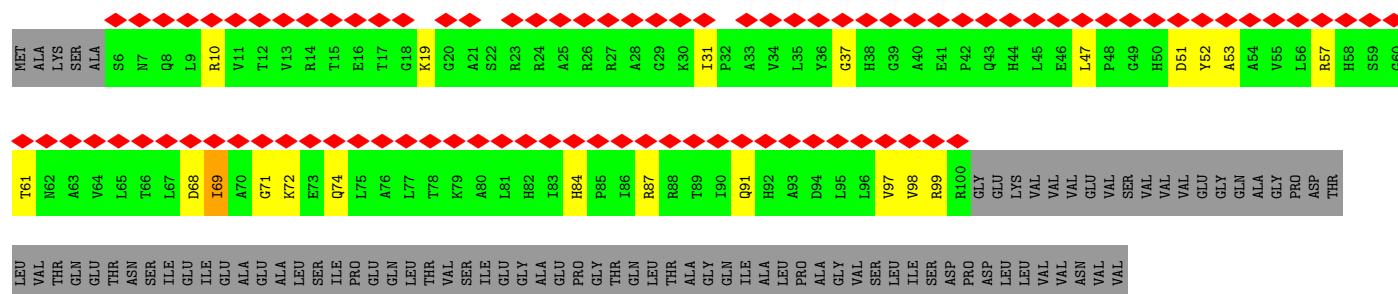
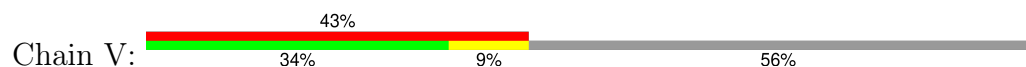
• Molecule 25: 50S ribosomal protein L23



• Molecule 26: 50S ribosomal protein L24



• Molecule 27: 50S ribosomal protein L25



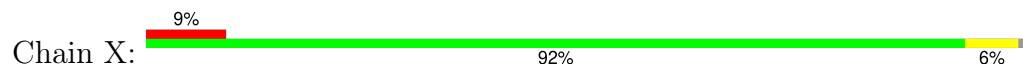
LYS
ALA
PRO
THR
GLU
GLU
LEU
SER
GLY
GLY
VAL
ALA
GLY
ALA
GLU
GLU
ALA
GLU
GLU
GLY
GLU
GLU
SER
GLU

• Molecule 28: 50S ribosomal protein L27



MET
ALA
HIS
LYS
LYS
GLY
ALA
SER
SER
SER
ARG
N12
A18
V38
R39
Q40
V49
N50
G55
D56
D57
T58
K72
R73
G74
R75
I80
V81
G82
SER
THR
THR
ALA

• Molecule 29: 50S ribosomal protein L28



M1
V18
R24
R41
P42
G43
V51
G59
K60
I61
T62
R63
GLY

• Molecule 30: 50S ribosomal protein L29



MET
ALA
VAL
G4
V5
S6
P7
G8
E9
L10
R11
E12
L13
T14
D15
E16
E17
R21
L22
R23
E24
E28
F34
Q35
M36
A37
T38
G39
Q40
L41
N42
R45
L46
L47
R48
T49
V50
E53
R56
L61
R64
E65
L68
ALA
THR
GLY
PRO
ASP
GLY
LYS
GLU
SER

• Molecule 31: 50S ribosomal protein L30



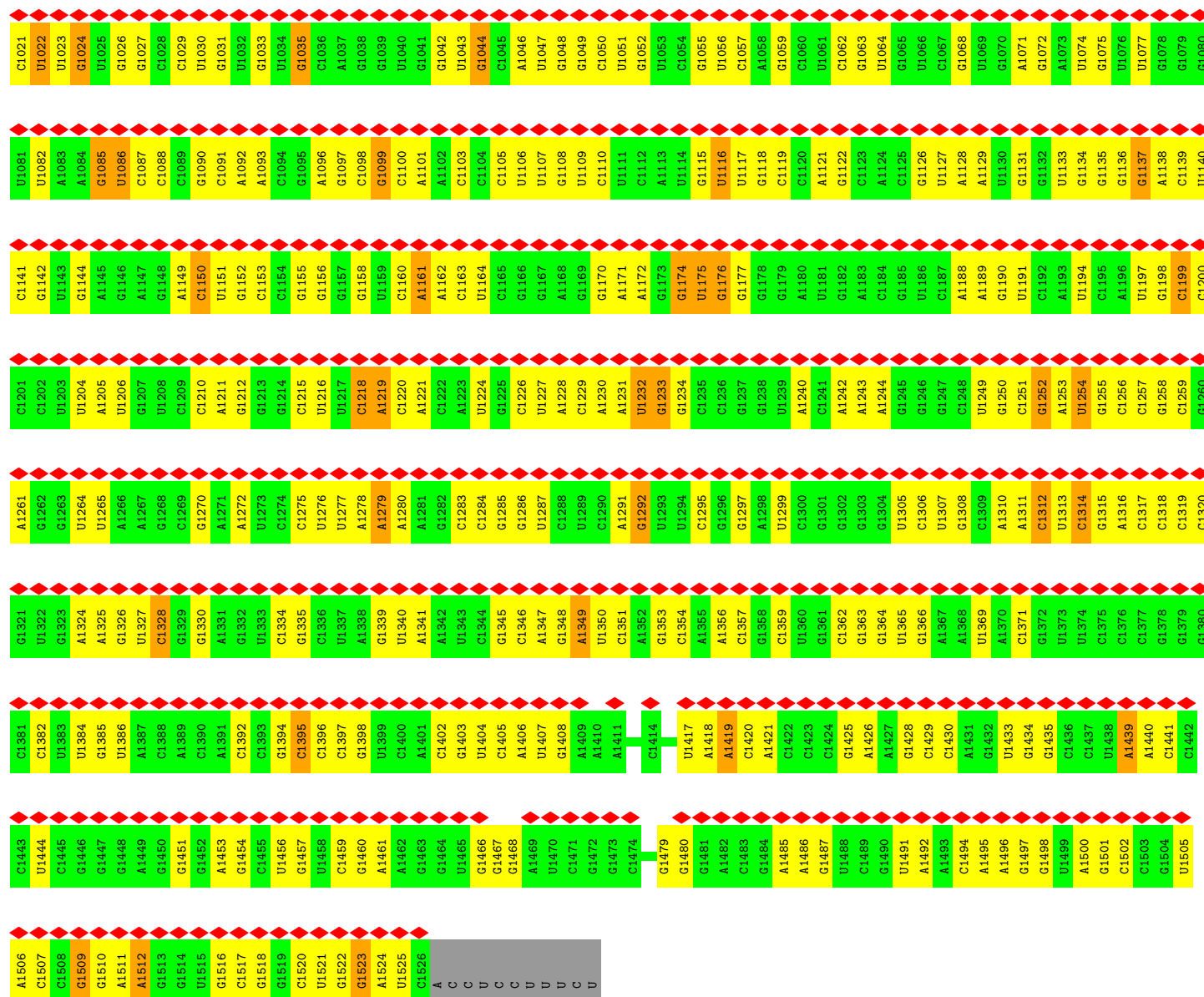
MET
S2
Q3
L4
V9
R10
S11
A15
K18
Q19
R20
E21
S22
R29
H33
E38
D39
N40
R44
G45
L46
V50
E55
V56
E57
P58
A59
Q60
THR
GLY
LYS
THR

• Molecule 32: 16S rRNA

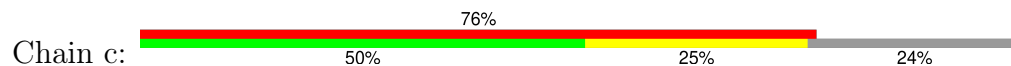


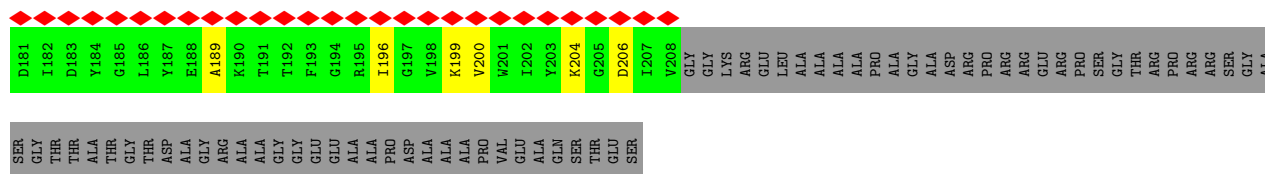
U
U
U
U
G
U
U8
G9
G10
A11
G12
A13
G14
U15
U16
U17
G18
A19
U20
C21
C22
U23
G24
G25
C26
U27
C28
A29
G30
G31
U30
A32
C33
G34
A35
A36
C37
G38
C39
U40
G41
G42
C43
G44
G45
C46
G47
U48
G49
C50
U51
U52
A53
A54
C55
A56
C57
A58
U59
G60
C61
A62
A63
G64
U65
C66
G67
A68
A69
C70
G71
G72
A73
A74
A75
G76
G77
U78
C79
U80
C81
U82
U83
C84
G85
G86
A87
G88
A89
U90
C91
A92
C93
G94
C95
A96
G97
U98
G99
U100
C101
G102
A103
A104
C105
G106
G107
U108
A109
U110
A111
G112
U113
G114
A115
C116
A117
U118
G119
U120
G121
G122
G123
U124
G125
A126
U127
C128
U129
G130
C131
C132
C133
U134
G135
C136
A137
C138
U139
U140
C141
G142
G143
G144
A145
U146
A147
A148
G149
C150
C151
U152
G153
G154
C155
A156
G157
A158
C159
U160
G161
G162
G163
U164
C165
U166
A167
A168
U169
A170
C171
C172
G173
G174
A175
U176
A177
U178
G179
A180

A961	A962	C963	G964	C965	G966	A967	A968	G969	A970	A971	C972	C973	U974	U975	A976	C977	C978	U979	G980	G981	G982	U983	U984	U985	A986	A987	C988	A989	U990	G991	C992	A993	C994	A995	G996	G997	A998	C999	G1000	C1001	G1002	U1003	G1004	U1005	A1006	G1007	A1008	G1009	U1010	U1011	A1012	G1013	G1014	C1015	G1016	U1017	U1018	C1019	C1020		
A901	A902	C903	U904	C905	A906	A907	A908	G909	G910	A911	A912	U913	U914	G915	A916	C917	G918	G919	G920	G921	C922	C923	C924	C925	C926	C927	A928	C929	A930	A931	C932	C933	C934	G935	C936	G937	G938	A939	G940	C941	A942	U943	U944	U945	G946	G947	A948	U949	U950	A951	A952	C953	U954	C955	G956	C957	U958	G959	C960		
G941	A942	U943	C944	C945	G946	U947	G948	C949	C950	G951	U952	A953	G954	C955	U956	A957	A958	C959	G960	C961	A962	U963	U964	A965	A966	A967	U968	A969	C970	C971	C972	C973	G974	C975	C976	U977	U978	A979	G980	C981	G982	U983	U984	U985	C986	G987	C988	U989	C990	G991	C992	U993	A994	C995	G996	C997	U998	A999	U1000		
A781	G782	A783	U784	A785	C786	C787	G788	U789	G790	G791	U792	A793	G794	U795	C796	C797	A798	C799	G800	C801	C802	G803	U804	A805	A806	A807	C808	G809	U810	U811	G812	G813	A814	U815	A816	C817	U818	A819	C820	G821	U822	G823	U824	G825	U826	C827	U828	U829	U830	C831	C832	U833	U834	C835	C836	U837	U838	G839	G840		
G721	G722	C723	G724	G725	G726	U727	C728	U729	C730	U731	G732	G733	G734	C735	A736	G737	U738	A739	A740	C741	U742	G743	A744	C745	G746	C747	U748	G749	A750	G751	G752	A753	G754	C755	G756	A757	U758	C759	A760	G761	G762	U763	G764	G765	G766	G767	A768	G769	C770	G771	A772	A773	C774	A775	G776	G777	A778	U779	U780		
A661	C662	U663	G664	G665	A666	A667	U668	U669	C670	C671	U672	G673	G674	U675	G676	U677	A678	G679	C680	G681	C682	U683	G684	G685	A686	A687	U688	G689	C690	G691	C692	A693	G694	A695	U696	A697	U698	C699	A700	G701	G702	U703	G704	A705	A706	A707	C708	A709	C710	U711	G712	G713	U714	G715	G716	C717	U718	A719	A720		
U601	C602	U603	C604	A605	C606	G607	G608	C609	U610	U611	A612	G613	C614	U615	G616	U617	G618	A619	G620	C621	C622	U623	A624	C625	G626	G627	G628	C629	G630	A631	U632	A633	C634	G635	G636	G637	C638	A639	G640	A641	C642	U643	A644	G645	A646	G647	U648	A649	C650	U651	G652	C653	A654	G655	G656	G657	U658	A659	G660		
G541	U542	U543	G544	U545	C546	C547	G548	G549	A550	A551	U552	U553	A554	C555	U556	U557	G558	G559	C560	G561	C562	U563	A564	A565	G566	A567	G568	C569	U570	C571	G572	U573	A574	G575	G576	U577	G578	C579	U580	U581	U582	G583	U584	C585	G586	C587	G588	U589	U590	U591	U592	U593	C594	G595	U596	G597	A598	A599	A600		
U481	G482	G422	G423	A484	G485	A486	A487	G488	A489	A490	G491	C492	A493	C494	C495	G496	G497	C498	C499	A500	A501	C502	C442	U444	C445	G446	U507	G508	C509	C510	A511	G451	G452	U454	C455	C456	G457	C517	G518	C519	G520	U521	U522	A523	A524	U525	A526	C527	G528	U529	A530	U471	G472	A473	C474	G475	G476	U477	A478	A479	G480
G361	A362	A363	U364	A365	U366	U367	G368	C369	A370	C371	A372	A373	U374	G375	G376	G377	C378	G379	C380	A381	A382	G383	C384	C385	U386	A447	A387	A388	U389	G390	C391	A392	G393	C394	A395	A396	C397	G398	C399	C400	G401	C402	G403	U404	G405	G406	G407	A408	G409	A410	U411	G412	A413	C414	G415	G416	C417	C418	U419	U420	
G301	G302	A303	G304	U305	C306	C307	G308	G309	C310	C311	A312	A313	C314	C315	U316	G317	G318	G319	A320	C321	U322	A323	A324	G325	U326	A327	A328	C329	G330	C331	C332	C333	C334	A335	G336	C337	C338	U339	C340	C341	U342	G343	G344	G345	G346	C347	A348	G349	C350	C351	A352	C353	C354	A355	G356	U357	G358	U359	G360		
U241	A242	A243	C244	A245	G246	C247	U248	U249	C250	U251	U252	A253	G254	U255	G256	G257	G258	G259	U260	G261	A262	C263	G264	G265	C266	C267	U268	A269	C270	C271	A272	C273	G274	G275	C276	C277	A278	C279	G280	C281	G282	G283	G284	G285	U286	A287	G288	C289	C290	G291	C292	C293	C294	U295	G296	U297	G298	A299	G300		
C181	C182	A183	C184	G185	G186	G187	A188	U189	G190	C191	A192	C193	G194	U195	C196	U197	U198	G199	U200	G201	G202	C203	G204	G205	A206	A207	A208	G209	C210	C211	C212	U213	U214	U215	A216	C217	C218	G219	G220	G221	G222	U223	G224	G225	G226	A227	U228	G229	A230	C231	C232	C233	C234	C235	G236	G237	G238	A239	C240		

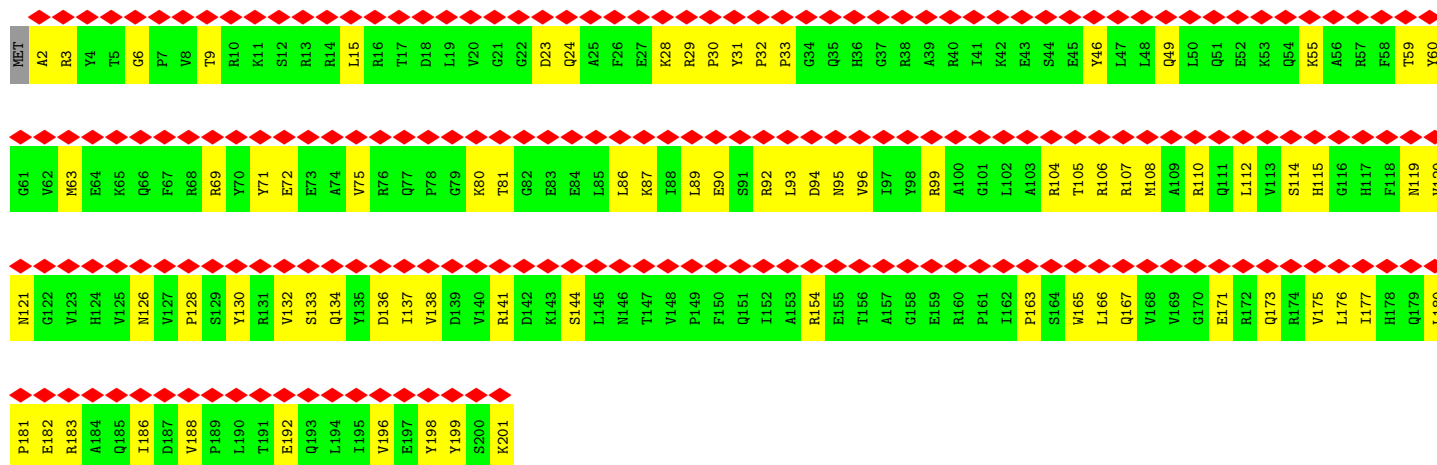


• Molecule 33: 30S ribosomal protein S3

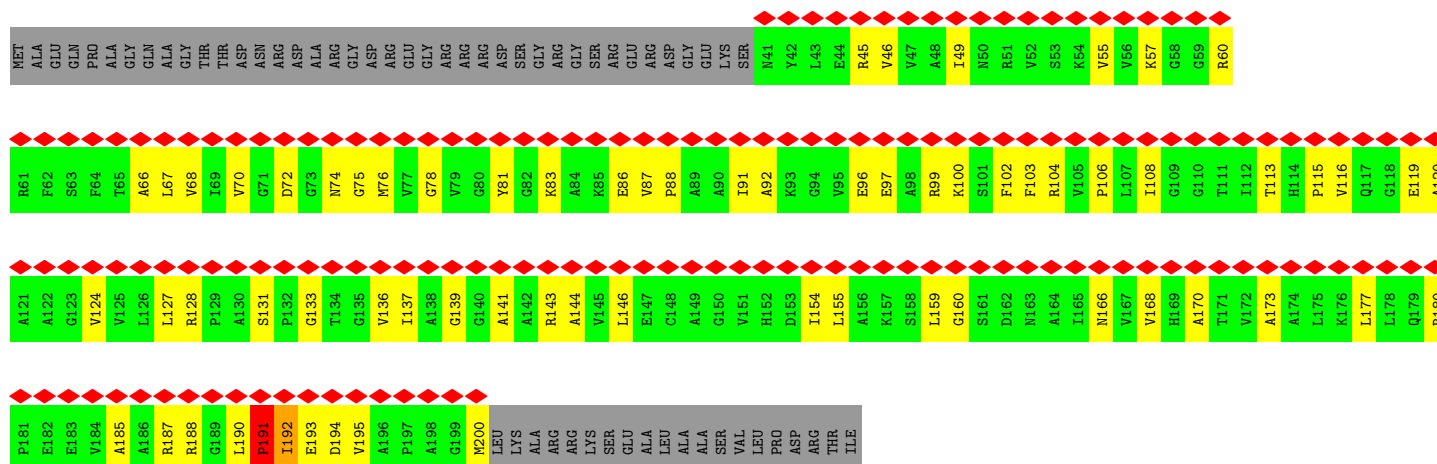
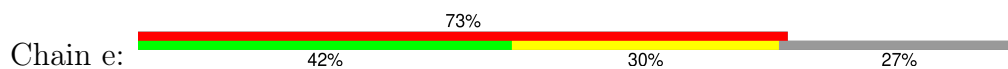




• Molecule 34: 30S ribosomal protein S4

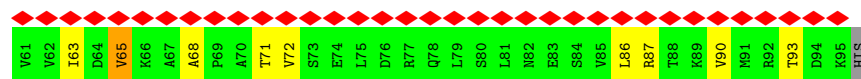


• Molecule 35: 30S ribosomal protein S5



• Molecule 36: 30S ribosomal protein S6





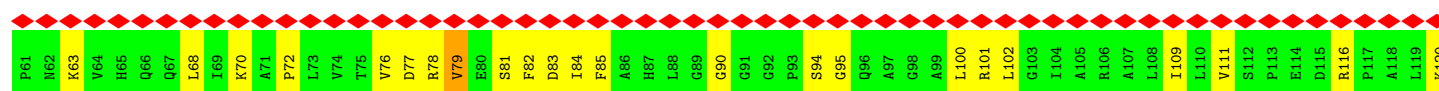
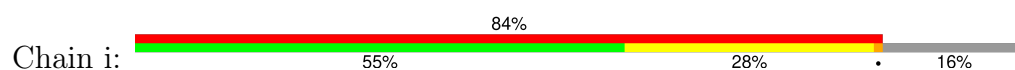
• Molecule 37: 30S ribosomal protein S7



• Molecule 38: 30S ribosomal protein S8

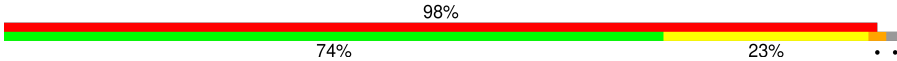


• Molecule 39: 30S ribosomal protein S9



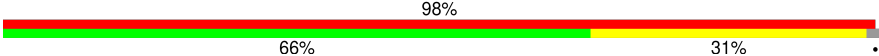
• Molecule 40: 30S ribosomal protein S10

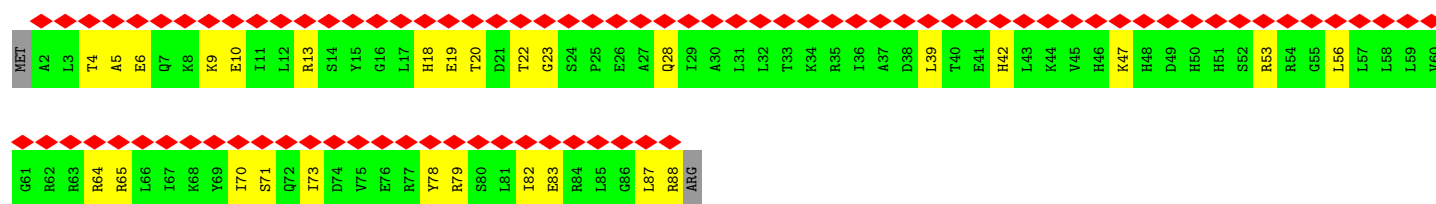


Chain n: 



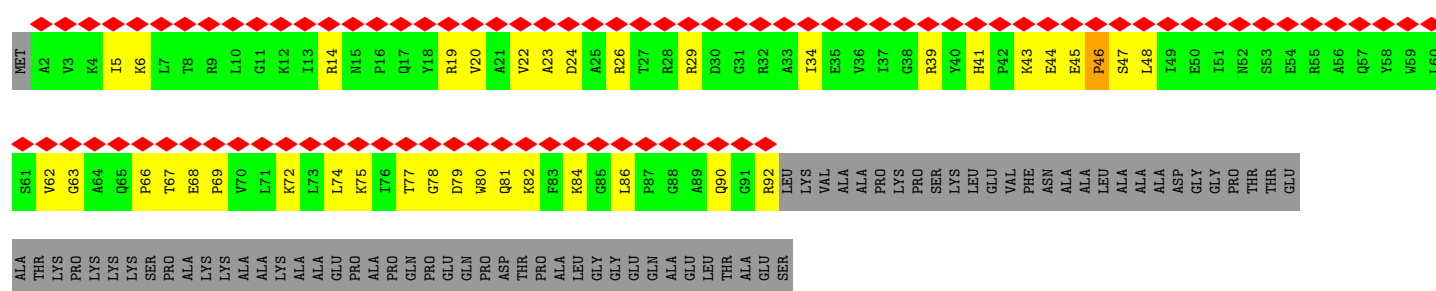
- Molecule 45: 30S ribosomal protein S15

Chain o: 



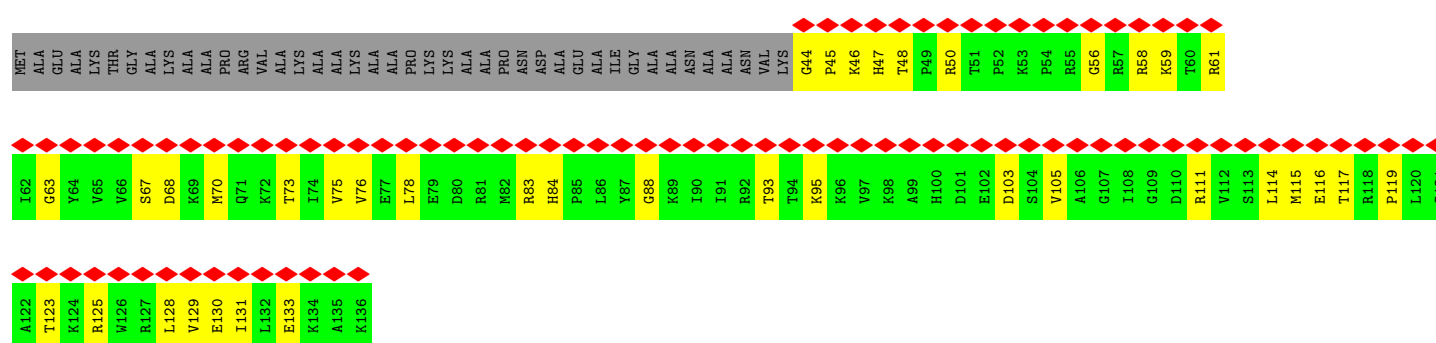
- Molecule 46: 30S ribosomal protein S16

Chain p: 

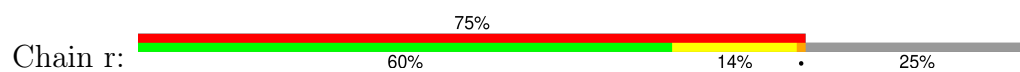


- Molecule 47: 30S ribosomal protein S17

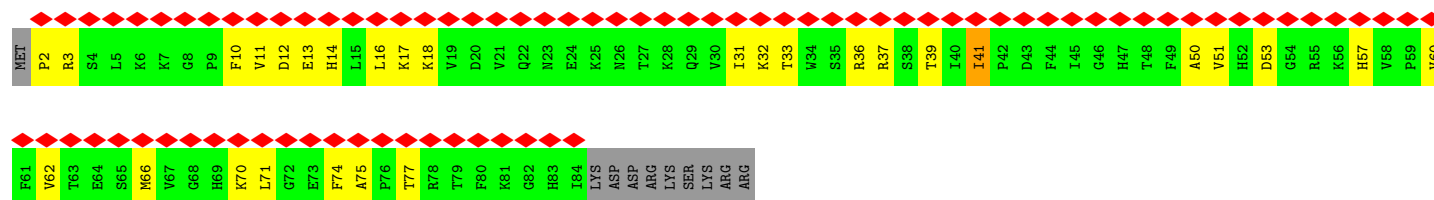
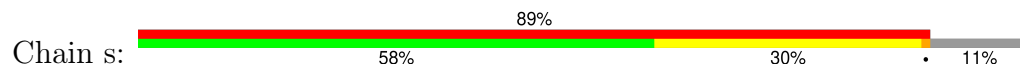
Chain q: 



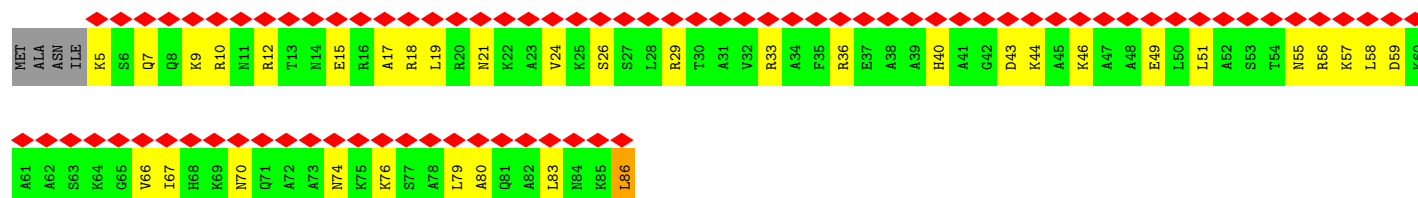
- Molecule 48: 30S ribosomal protein S18



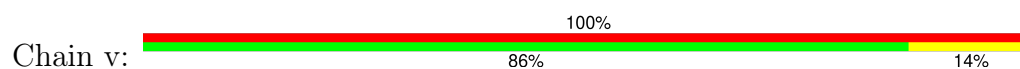
• Molecule 49: 30S ribosomal protein S19



• Molecule 50: 30S ribosomal protein S20



• Molecule 51: peptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	719250	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 ($e^-/\text{\AA}^2$)	42	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	1.618	Depositor
Minimum map value	-0.335	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.4	Depositor
Map size ($\text{\AA}$)	348.6, 348.6, 348.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83000004, 0.83000004, 0.83000004	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, 6MZ, ZN, MG, WDP, OMG, OMC, MA6, 5MU, 5MC, 4OC, 2MG, G7M

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.20	0/435	0.28	0/581
2	1	0.21	0/407	0.29	0/543
3	2	0.35	0/361	0.39	0/473
4	3	0.21	0/499	0.30	0/664
5	4	0.18	0/303	0.29	0/402
6	6	0.48	1/455 (0.2%)	0.73	3/611 (0.5%)
7	A	0.31	1/74851 (0.0%)	0.29	0/116786
8	B	0.17	0/2749	0.23	0/4284
9	C	0.30	0/2129	0.39	0/2861
10	D	0.29	0/1613	0.41	0/2174
11	E	0.28	0/1575	0.39	0/2129
12	F	0.15	0/1429	0.41	0/1921
13	G	0.16	0/1351	0.35	0/1824
14	H	0.14	0/353	0.36	0/474
15	J	0.32	0/1170	0.36	0/1584
16	K	0.28	0/944	0.37	0/1268
17	L	0.26	0/1081	0.39	0/1443
18	M	0.17	0/1098	0.31	0/1481
19	N	0.33	0/925	0.36	0/1242
20	O	0.16	0/895	0.36	0/1202
21	P	0.29	0/922	0.39	0/1236
22	Q	0.35	0/992	0.41	0/1329
23	R	0.31	0/766	0.45	0/1030
24	S	0.30	0/874	0.35	0/1186
25	T	0.27	0/770	0.37	0/1038
26	U	0.26	0/705	0.64	2/941 (0.2%)
27	V	0.15	0/747	0.37	0/1010
28	W	0.25	0/531	0.39	0/707
29	X	0.32	0/484	0.38	0/648
30	Y	0.24	0/544	0.35	0/727
31	Z	0.28	0/480	0.42	0/645
32	a	0.11	1/36305 (0.0%)	0.22	0/56645

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.12	0/1678	0.32	0/2254
34	d	0.12	0/1683	0.31	0/2269
35	e	0.45	2/1165 (0.2%)	0.68	3/1578 (0.2%)
36	f	0.13	0/767	0.33	0/1036
37	g	0.13	0/1210	0.34	0/1631
38	h	0.18	0/1014	0.49	1/1369 (0.1%)
39	i	0.13	0/1011	0.41	0/1356
40	j	0.12	0/803	0.38	0/1086
41	k	0.13	0/891	0.33	0/1204
42	l	0.14	0/970	0.44	0/1295
43	m	0.13	0/953	0.38	0/1274
44	n	0.11	0/477	0.28	0/634
45	o	0.12	0/727	0.32	0/973
46	p	0.13	0/742	0.34	0/1000
47	q	0.13	0/766	0.36	0/1024
48	r	0.12	0/502	0.30	0/674
49	s	0.14	0/690	0.38	0/928
50	t	0.17	0/633	0.43	0/838
51	v	0.12	0/188	0.32	0/243
All	All	0.25	5/155613 (0.0%)	0.30	9/233755 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
17	L	0	2
23	R	0	1
26	U	0	2
42	l	0	1
All	All	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	e	191	PRO	CG-CD	-13.31	1.05	1.50
6	6	43	PRO	CG-CD	-8.39	1.22	1.50
7	A	2296	A	C6-N6	6.21	1.46	1.33
35	e	191	PRO	N-CD	5.45	1.55	1.47
32	a	1491	UR3	O3'-P	5.03	1.61	1.56

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	e	191	PRO	N-CD-CG	-15.42	80.07	103.20
6	6	43	PRO	N-CD-CG	-10.72	87.12	103.20
35	e	191	PRO	CA-N-CD	-10.64	97.11	112.00
38	h	68	PRO	CA-N-CD	-9.60	98.56	112.00
35	e	191	PRO	CA-CB-CG	-8.72	87.93	104.50
6	6	43	PRO	CA-N-CD	-7.81	101.07	112.00
26	U	89	GLU	CA-C-N	7.81	135.75	121.70
26	U	89	GLU	C-N-CA	7.81	135.75	121.70
6	6	43	PRO	CA-CB-CG	-5.30	94.42	104.50

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	L	20	ARG	Peptide
17	L	28	LYS	Peptide
23	R	50	THR	Peptide
26	U	90	GLU	Peptide
26	U	91	THR	Peptide
42	l	113	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	429	0	465	8	0
2	1	400	0	409	8	0
3	2	358	0	390	2	0
4	3	494	0	533	5	0
5	4	299	0	323	13	0
6	6	446	0	431	11	0
7	A	66961	0	33727	760	0
8	B	2458	0	1252	40	0
9	C	2088	0	2123	21	0
10	D	1590	0	1632	30	0
11	E	1552	0	1593	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	F	1408	0	1449	72	0
13	G	1330	0	1390	35	0
14	H	350	0	367	15	0
15	J	1143	0	1173	23	0
16	K	934	0	993	12	0
17	L	1068	0	1129	27	0
18	M	1072	0	1115	13	0
19	N	908	0	956	15	0
20	O	886	0	924	27	0
21	P	907	0	947	12	0
22	Q	980	0	1028	14	0
23	R	757	0	817	9	0
24	S	860	0	903	13	0
25	T	759	0	809	13	0
26	U	699	0	738	12	0
27	V	735	0	767	18	0
28	W	526	0	548	9	0
29	X	476	0	492	2	0
30	Y	541	0	551	19	0
31	Z	476	0	509	7	0
32	a	32621	0	16427	706	0
33	c	1654	0	1694	48	0
34	d	1650	0	1671	66	0
35	e	1149	0	1207	49	0
36	f	757	0	796	23	0
37	g	1193	0	1256	34	0
38	h	999	0	1034	33	0
39	i	993	0	1052	40	0
40	j	789	0	821	40	0
41	k	873	0	887	34	0
42	l	959	0	1045	40	0
43	m	945	0	992	47	0
44	n	468	0	492	16	0
45	o	718	0	760	19	0
46	p	728	0	764	32	0
47	q	754	0	811	31	0
48	r	497	0	514	9	0
49	s	672	0	690	21	0
50	t	631	0	681	28	0
51	v	186	0	202	3	0
52	1	1	0	0	0	0
52	4	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	6	1	0	0	0	0
52	X	1	0	0	0	0
52	n	1	0	0	0	0
52	r	1	0	0	0	0
53	A	86	0	0	21	0
54	A	307	0	0	0	0
54	B	7	0	0	0	0
54	C	3	0	0	0	0
54	D	1	0	0	0	0
54	L	1	0	0	0	0
54	M	1	0	0	0	0
54	a	125	0	0	0	0
54	e	1	0	0	0	0
54	t	1	0	0	0	0
All	All	143665	0	94279	2338	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 10.

All (2338) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1959:A:C2	7:A:1970:G:N1	2.02	1.25
7:A:1959:A:H2	7:A:1970:G:N1	1.35	1.24
7:A:2741:A:H62	53:A:3201:WDP:C07	1.67	1.06
32:a:990:U:H3	32:a:1035:G:H1	1.05	1.01
7:A:1592:U:H3	7:A:1613:G:H1	1.01	0.98
7:A:2741:A:N6	53:A:3201:WDP:C07	2.26	0.97
32:a:1107:U:H3	32:a:1176:G:H1	1.05	0.97
32:a:152:U:H3	32:a:161:G:H1	1.04	0.95
7:A:2297:A:H1'	53:A:3201:WDP:O19	1.69	0.93
32:a:1106:U:H3	32:a:1177:G:H1	1.00	0.93
32:a:140:U:H3	32:a:174:G:H1	1.10	0.91
19:N:37:THR:HG22	19:N:39:PRO:HD2	1.54	0.90
15:J:73:MET:HE1	15:J:88:THR:HG22	1.52	0.89
7:A:2335:U:H3	7:A:2428:G:H1	0.91	0.88
7:A:2006:G:H1	7:A:2217:C:H5	1.23	0.87
7:A:2741:A:C8	53:A:3201:WDP:N03	2.45	0.85
7:A:2751:G:OP1	10:D:165:ARG:NH1	2.10	0.85
32:a:1118:G:H22	32:a:1137:G:H1	1.25	0.84
32:a:436:U:HO2'	34:d:115:HIS:HD1	1.17	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2309:C:H5	7:A:2675:G:H1	1.26	0.83
7:A:687:G:N7	22:Q:6:ARG:NH2	2.28	0.82
20:O:42:ILE:HD11	20:O:79:VAL:HG11	1.60	0.82
7:A:873:G:H1	7:A:882:C:H5	1.24	0.82
33:c:94:THR:HG23	33:c:96:LYS:H	1.45	0.82
32:a:1255:G:H1	32:a:1264:U:H3	1.27	0.81
7:A:1959:A:N1	7:A:1970:G:O6	2.12	0.81
34:d:138:VAL:HB	34:d:175:VAL:HB	1.60	0.81
32:a:995:A:H61	32:a:1029:C:H42	1.29	0.80
25:T:70:ARG:HH11	25:T:71:THR:H	1.30	0.80
6:6:27:THR:HG23	6:6:29:PRO:HD2	1.64	0.79
7:A:281:G:H1	7:A:307:U:H3	1.32	0.78
7:A:1517:C:H5	7:A:1532:G:H1	1.29	0.78
32:a:655:G:H22	32:a:732:G:H1	1.32	0.78
34:d:167:GLN:HE22	34:d:176:LEU:HB2	1.49	0.77
7:A:2400:U:H5'	7:A:2401:U:H5''	1.66	0.77
38:h:68:PRO:HD2	38:h:69:SER:N	1.98	0.76
7:A:1959:A:H2	7:A:1970:G:C2	2.03	0.76
35:e:200:MET:H	35:e:200:MET:HE2	1.50	0.76
7:A:2741:A:N7	53:A:3201:WDP:N03	2.33	0.76
32:a:74:A:N6	32:a:94:C:O2	2.19	0.76
18:M:65:TRP:HB2	18:M:105:GLU:HB2	1.67	0.76
50:t:15:GLU:HA	50:t:18:ARG:HD3	1.67	0.76
8:B:39:U:O2	8:B:44:A:N6	2.17	0.76
38:h:68:PRO:HD2	38:h:69:SER:H	1.51	0.76
7:A:8:U:H3	7:A:3129:A:H62	1.33	0.75
7:A:1559:A:N6	7:A:1645:A:OP1	2.19	0.75
7:A:193:A:H2'	7:A:194:G:C8	2.21	0.75
12:F:45:MET:HA	12:F:45:MET:HE3	1.69	0.75
32:a:550:A:H4'	32:a:551:A:H3'	1.68	0.75
32:a:593:U:H3	32:a:627:G:H1	1.31	0.75
32:a:631:A:N3	38:h:109:SER:OG	2.20	0.75
11:E:156:GLU:OE1	11:E:156:GLU:N	2.20	0.75
7:A:763:C:N4	7:A:764:G:O6	2.18	0.75
7:A:1959:A:N1	7:A:1970:G:C6	2.54	0.75
32:a:1425:G:O2'	32:a:1461:A:N6	2.20	0.74
7:A:946:C:H5	7:A:1322:G:H1	1.35	0.74
7:A:787:G:H21	11:E:112:MET:HE1	1.51	0.74
7:A:1212:G:N2	7:A:1215:A:OP2	2.18	0.74
32:a:1440:A:OP1	32:a:1441:C:N4	2.14	0.74
7:A:2297:A:C1'	53:A:3201:WDP:O19	2.36	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2297:A:N1	53:A:3201:WDP:C85	2.50	0.74
12:F:21:ASP:OD1	12:F:21:ASP:N	2.13	0.74
13:G:33:LEU:HB2	13:G:76:LEU:HD11	1.69	0.74
7:A:1824:C:H2'	7:A:1825:A:H8	1.52	0.73
7:A:1111:C:O2	51:v:21:ARG:NH2	2.21	0.73
27:V:10:ARG:NH1	27:V:10:ARG:HA	2.03	0.73
33:c:52:ALA:HB2	33:c:114:LEU:HG	1.71	0.73
7:A:2940:G:OP1	19:N:73:LYS:NZ	2.21	0.73
20:O:65:VAL:HG13	20:O:66:ARG:HE	1.53	0.73
7:A:1960:C:N3	7:A:1969:U:O4	2.21	0.73
7:A:2894:U:O2	7:A:2903:A:N7	2.22	0.73
32:a:452:G:N1	32:a:471:U:N3	2.37	0.72
2:l:8:ARG:NH1	7:A:2523:C:OP2	2.23	0.72
7:A:2566:A:H2'	7:A:2567:A:C8	2.23	0.72
11:E:138:GLU:N	11:E:138:GLU:OE2	2.22	0.72
39:i:48:LYS:H	39:i:83:ASP:HB3	1.55	0.71
35:e:127:LEU:HB3	35:e:154:ILE:HD11	1.72	0.71
7:A:140:G:H21	7:A:1540:G:H1'	1.54	0.71
42:l:113:ALA:O	42:l:115:SER:N	2.23	0.71
7:A:2174:A:H2	7:A:2181:U:H3	1.38	0.71
32:a:408:G:H5''	34:d:24:GLN:HE21	1.55	0.71
7:A:2363:A:O2'	7:A:2410:A:N6	2.24	0.71
25:T:69:THR:HG23	25:T:70:ARG:HD3	1.73	0.71
32:a:452:G:N2	32:a:471:U:O2	2.24	0.71
7:A:1658:A:H61	7:A:1815:U:H3	1.38	0.70
43:m:91:ARG:HH21	43:m:96:MET:HG2	1.57	0.70
7:A:1600:C:H42	7:A:1605:G:H1	1.38	0.70
32:a:1001:C:H2'	32:a:1002:G:C8	2.27	0.70
35:e:45:ARG:HH21	35:e:144:ALA:HB2	1.57	0.70
36:f:1:MET:HA	36:f:1:MET:HE2	1.72	0.70
7:A:635:U:O2	7:A:648:G:N2	2.18	0.70
40:j:50:CYS:SG	40:j:62:ARG:NH1	2.64	0.70
47:q:83:ARG:NH1	47:q:84:HIS:O	2.24	0.70
34:d:86:LEU:HD13	34:d:183:ARG:HD3	1.73	0.70
39:i:25:ARG:HE	39:i:26:PRO:HD2	1.56	0.70
32:a:1051:U:H2'	32:a:1052:G:H8	1.57	0.69
42:l:33:VAL:HG12	42:l:56:LYS:H	1.55	0.69
32:a:1072:G:N7	35:e:83:LYS:NZ	2.41	0.69
7:A:1842:C:N4	7:A:1857:G:OP2	2.26	0.69
10:D:87:ASP:OD2	10:D:88:ASP:N	2.22	0.69
34:d:105:THR:OG1	34:d:108:MET:SD	2.47	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:30:ARG:HE	2:1:30:ARG:HA	1.56	0.69
7:A:2106:C:N4	7:A:2109:G:N3	2.40	0.69
32:a:704:G:H2'	32:a:705:G:C8	2.27	0.69
32:a:874:G:OP2	42:l:9:ARG:NH2	2.26	0.69
33:c:133:MET:HE3	33:c:168:TYR:HD1	1.58	0.69
7:A:1176:G:O2'	7:A:1239:A:N1	2.25	0.69
32:a:1308:G:N1	32:a:1311:A:OP2	2.27	0.69
12:F:159:MET:HE1	12:F:161:ILE:HD11	1.75	0.68
32:a:412:G:O2'	32:a:427:G:N2	2.27	0.68
33:c:46:LEU:HA	33:c:48:ARG:HH12	1.58	0.68
7:A:1638:C:H2'	7:A:1639:G:C8	2.29	0.68
32:a:1395:4OC:H2'	32:a:1396:C:O4'	1.92	0.68
32:a:705:G:H2'	32:a:706:A:H8	1.59	0.68
12:F:90:MET:N	12:F:90:MET:SD	2.67	0.68
26:U:89:GLU:HA	26:U:91:THR:H	1.59	0.68
32:a:990:U:O2	32:a:1035:G:N2	2.23	0.68
12:F:73:GLU:OE1	12:F:95:ARG:NH2	2.27	0.68
20:O:72:LYS:HB3	20:O:107:ARG:HD3	1.76	0.68
32:a:705:G:H2'	32:a:706:A:C8	2.28	0.68
7:A:709:U:OP2	11:E:111:LYS:NZ	2.27	0.67
7:A:2770:G:O2'	7:A:2895:A:N1	2.26	0.67
10:D:212:ILE:O	10:D:214:ARG:NH1	2.27	0.67
25:T:51:ALA:O	25:T:91:ARG:NH2	2.26	0.67
32:a:668:U:H1'	41:k:131:VAL:HG21	1.76	0.67
32:a:1340:U:H4'	39:i:143:ARG:HG3	1.74	0.67
26:U:89:GLU:HA	26:U:91:THR:N	2.09	0.67
32:a:268:U:H2'	32:a:269:A:C8	2.29	0.67
32:a:1107:U:O2	32:a:1176:G:N2	2.23	0.67
7:A:843:U:OP2	45:o:88:ARG:NH1	2.27	0.67
7:A:974:G:OP2	7:A:974:G:N2	2.24	0.67
32:a:271:C:H2'	32:a:272:A:H8	1.60	0.67
32:a:1194:U:O2'	44:n:27:CYS:SG	2.52	0.67
7:A:272:A:OP2	7:A:315:G:N1	2.24	0.67
31:Z:15:ALA:O	31:Z:20:ARG:NH1	2.28	0.67
40:j:31:ARG:H	40:j:31:ARG:HD2	1.60	0.67
7:A:1171:G:N2	7:A:1242:U:O2	2.27	0.67
37:g:129:ASN:HB3	37:g:131:LEU:HD22	1.77	0.67
37:g:138:ARG:NH2	37:g:139:GLU:OE2	2.28	0.67
32:a:99:G:N7	50:t:9:LYS:NZ	2.35	0.67
39:i:134:ARG:NH1	44:n:61:TRP:OXT	2.26	0.67
7:A:285:G:N2	7:A:303:U:O2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2426:U:H2'	7:A:2427:G:C8	2.30	0.67
34:d:120:VAL:HA	34:d:138:VAL:HA	1.75	0.67
40:j:52:ILE:HG13	44:n:41:ARG:HE	1.60	0.67
2:1:40:LYS:NZ	7:A:2585:C:OP1	2.28	0.67
15:J:6:PRO:HG2	15:J:48:VAL:HG21	1.77	0.67
4:3:43:ARG:NH2	7:A:2601:U:OP2	2.28	0.66
7:A:746:G:N2	7:A:749:U:OP2	2.24	0.66
37:g:113:GLU:HB2	37:g:119:ARG:HG2	1.78	0.66
5:4:22:ARG:HA	5:4:22:ARG:NE	2.09	0.66
32:a:389:U:H4'	46:p:29:ARG:HH21	1.61	0.66
37:g:22:LEU:O	37:g:26:LEU:HD12	1.95	0.66
7:A:2566:A:H2'	7:A:2567:A:H8	1.58	0.66
33:c:36:VAL:HG21	44:n:26:LYS:HG2	1.78	0.66
46:p:45:GLU:HB2	46:p:46:PRO:HD3	1.77	0.66
32:a:357:U:H2'	32:a:358:G:H8	1.60	0.66
37:g:68:ASN:O	37:g:138:ARG:NH1	2.29	0.66
44:n:24:CYS:HB2	44:n:40:CYS:HB3	1.77	0.66
12:F:61:VAL:HG13	12:F:72:PRO:HD2	1.76	0.66
32:a:709:A:O5'	41:k:129:ASN:ND2	2.28	0.66
12:F:76:ARG:HA	12:F:91:PRO:HA	1.78	0.66
32:a:997:G:H22	32:a:1027:G:H22	1.42	0.66
40:j:47:ASN:HB2	40:j:67:MET:HB3	1.78	0.66
7:A:2409:U:H4'	7:A:2410:A:H5'	1.77	0.65
30:Y:14:THR:O	30:Y:64:ARG:NH1	2.29	0.65
32:a:477:U:H2'	32:a:478:A:H8	1.59	0.65
34:d:92:ARG:NH2	34:d:94:ASP:OD1	2.28	0.65
7:A:1656:G:O2'	7:A:1816:A:N6	2.29	0.65
24:S:35:ARG:NH1	24:S:84:VAL:O	2.29	0.65
32:a:29:A:H61	32:a:549:G:H1'	1.62	0.65
32:a:39:C:O2'	42:l:114:ARG:NH2	2.29	0.65
30:Y:13:LEU:HB3	30:Y:17:GLU:HB2	1.76	0.65
39:i:116:ARG:O	39:i:120:LYS:HB2	1.97	0.65
7:A:2380:C:H1'	7:A:2385:G:H22	1.60	0.65
25:T:4:LEU:HD23	25:T:4:LEU:H	1.61	0.65
32:a:1087:C:O2	32:a:1162:A:O2'	2.14	0.65
39:i:109:ILE:HD12	39:i:116:ARG:HD2	1.78	0.65
7:A:1084:G:OP2	18:M:87:LYS:NZ	2.26	0.65
9:C:143:HIS:ND1	9:C:194:GLY:O	2.28	0.65
25:T:96:PHE:O	30:Y:40:GLN:NE2	2.29	0.65
32:a:617:U:H2'	32:a:618:G:H8	1.61	0.65
7:A:1081:G:OP1	18:M:16:ARG:NH1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1471:U:OP1	25:T:19:LYS:NZ	2.30	0.65
25:T:53:LYS:HD2	25:T:87:ALA:HB2	1.78	0.65
32:a:256:G:H1	32:a:268:U:H3	1.44	0.65
35:e:185:ALA:HB1	35:e:191:PRO:HD3	1.78	0.65
7:A:2418:G:OP2	7:A:2419:A:N6	2.29	0.65
7:A:2488:G:O2'	7:A:2734:C:OP1	2.13	0.65
14:H:9:VAL:HG21	14:H:12:LEU:HB2	1.78	0.65
32:a:517:C:O2'	32:a:518:G7M:O4'	2.14	0.65
32:a:127:U:H1'	32:a:261:G:H21	1.61	0.65
7:A:2408:A:OP2	7:A:2410:A:N6	2.29	0.65
23:R:44:VAL:HG22	23:R:49:VAL:HG12	1.77	0.65
32:a:400:C:O2'	32:a:612:A:N3	2.29	0.65
32:a:1119:C:O2'	39:i:39:ARG:NH1	2.30	0.65
32:a:1224:U:OP1	39:i:147:GLN:NE2	2.30	0.65
37:g:75:VAL:HG21	37:g:144:MET:SD	2.37	0.65
43:m:14:ARG:HD2	43:m:42:ASP:HA	1.78	0.65
7:A:442:G:H2'	7:A:443:C:C6	2.32	0.64
7:A:1647:U:H2'	7:A:1648:A:H8	1.62	0.64
7:A:1772:G:HO2'	7:A:1775:G:H1	1.44	0.64
32:a:1141:C:OP1	39:i:32:ARG:NH2	2.30	0.64
7:A:307:U:H2'	7:A:308:G:H8	1.62	0.64
14:H:2:LYS:HA	14:H:19:VAL:HG11	1.77	0.64
32:a:111:A:N6	32:a:312:A:N3	2.44	0.64
32:a:221:U:H2'	32:a:222:G:H8	1.61	0.64
40:j:66:GLU:OE2	40:j:68:ARG:NH1	2.29	0.64
7:A:2087:A:H2'	7:A:2088:A:C8	2.32	0.64
7:A:1566:G:O6	7:A:1637:U:O4	2.14	0.64
32:a:24:G:H2'	32:a:25:G:H8	1.63	0.64
32:a:617:U:H2'	32:a:618:G:C8	2.31	0.64
32:a:735:C:H2'	32:a:736:A:H8	1.62	0.64
34:d:138:VAL:N	34:d:175:VAL:O	2.31	0.64
7:A:324:G:H1	7:A:452:A:H2	1.45	0.64
7:A:1707:A:H2'	7:A:1708:A:C8	2.33	0.64
12:F:45:MET:HE1	12:F:159:MET:HB3	1.80	0.64
32:a:1359:C:O2'	40:j:62:ARG:NH2	2.29	0.64
41:k:62:PHE:HE2	41:k:75:LEU:HD21	1.63	0.64
7:A:676:A:N6	7:A:2272:U:OP1	2.30	0.64
7:A:872:A:O2'	7:A:1894:U:OP1	2.16	0.64
32:a:1258:G:N2	32:a:1261:A:OP2	2.21	0.64
40:j:80:THR:HB	40:j:83:THR:HG22	1.79	0.64
7:A:1007:G:N1	7:A:1028:G:N3	2.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:402:C:H5''	34:d:128:PRO:HD2	1.78	0.64
42:l:50:ARG:HB3	42:l:66:TYR:HE1	1.63	0.64
5:4:33:LYS:NZ	7:A:2981:C:OP1	2.31	0.64
47:q:83:ARG:HH11	47:q:88:GLY:HA2	1.63	0.64
33:c:4:LYS:HE2	33:c:150:ARG:HH12	1.62	0.63
7:A:3073:G:OP1	19:N:3:LYS:NZ	2.30	0.63
32:a:413:A:H8	32:a:430:A:H2	1.46	0.63
34:d:49:GLN:HB3	34:d:198:TYR:HB2	1.80	0.63
50:t:66:VAL:HG23	50:t:67:ILE:HG23	1.78	0.63
7:A:1171:G:H1	7:A:1242:U:H3	1.45	0.63
7:A:1959:A:C2	7:A:1970:G:C6	2.86	0.63
13:G:45:ARG:HH21	13:G:51:ILE:HA	1.63	0.63
34:d:80:LYS:HG3	35:e:133:GLY:HA2	1.79	0.63
32:a:463:U:OP1	46:p:75:LYS:NZ	2.31	0.63
32:a:1347:A:H2'	32:a:1348:G:C8	2.33	0.63
32:a:1466:G:H2'	32:a:1467:G:C8	2.33	0.63
32:a:615:U:H2'	32:a:616:G:H8	1.62	0.63
6:6:14:VAL:HG22	6:6:33:ILE:HD11	1.81	0.63
20:O:34:VAL:HA	20:O:98:ASP:HB3	1.81	0.63
32:a:643:U:O4	32:a:743:G:O2'	2.17	0.63
32:a:668:U:H3	32:a:704:G:H22	1.45	0.63
45:o:47:LYS:O	45:o:53:ARG:NH2	2.32	0.63
7:A:1953:G:H1	7:A:1976:G:H1	1.45	0.63
27:V:99:ARG:H	27:V:99:ARG:HD2	1.64	0.63
32:a:607:G:H1	32:a:615:U:H3	1.46	0.63
35:e:74:ASN:OD1	35:e:75:GLY:N	2.32	0.63
49:s:62:VAL:HG13	49:s:66:MET:HB2	1.80	0.63
7:A:285:G:N2	7:A:302:U:O2	2.32	0.63
21:P:33:GLU:HG3	21:P:38:ARG:HH21	1.64	0.63
32:a:68:A:N7	32:a:216:A:N6	2.47	0.63
32:a:1299:U:OP1	43:m:101:GLN:NE2	2.32	0.63
7:A:1124:C:OP2	22:Q:54:LYS:NZ	2.30	0.62
30:Y:28:GLU:OE2	30:Y:46:ARG:NH2	2.31	0.62
7:A:871:U:H2'	7:A:872:A:C8	2.33	0.62
32:a:971:A:N6	32:a:1308:G:O2'	2.28	0.62
32:a:1158:G:N1	32:a:1161:A:OP2	2.31	0.62
9:C:162:SER:HB3	9:C:195:GLU:HG3	1.82	0.62
32:a:134:U:O2	32:a:224:G:O6	2.17	0.62
32:a:1108:G:N2	32:a:1172:A:N3	2.48	0.62
8:B:112:A:H2'	8:B:113:A:C8	2.34	0.62
32:a:1363:G:H2'	32:a:1364:G:H8	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:844:A:OP1	45:o:64:ARG:NH1	2.33	0.62
7:A:2156:A:O2'	7:A:2157:A:N7	2.33	0.62
9:C:2:ALA:HB1	9:C:200:GLU:HG3	1.82	0.62
21:P:51:GLY:HA2	21:P:56:GLU:HG3	1.80	0.62
32:a:665:G:H2'	32:a:666:A:H8	1.64	0.62
7:A:638:C:N3	7:A:640:C:N4	2.47	0.62
32:a:1210:C:H2'	32:a:1211:A:H8	1.63	0.62
32:a:1347:A:H2'	32:a:1348:G:H8	1.64	0.62
17:L:145:GLU:OE1	17:L:145:GLU:N	2.33	0.62
32:a:1098:C:OP2	33:c:172:ARG:NH1	2.33	0.62
48:r:20:CYS:HB3	48:r:23:CYS:HB2	1.80	0.62
32:a:48:U:OP1	32:a:306:C:O2'	2.17	0.61
32:a:185:G:H1	32:a:198:U:H3	1.47	0.61
32:a:664:G:H2'	32:a:665:G:C8	2.35	0.61
13:G:85:THR:HG23	13:G:135:SER:HB2	1.80	0.61
49:s:11:VAL:HG23	49:s:16:LEU:HD11	1.82	0.61
49:s:12:ASP:HB3	49:s:14:HIS:CD2	2.35	0.61
32:a:492:C:H2'	32:a:493:A:C8	2.35	0.61
7:A:359:C:N4	7:A:362:A:N7	2.48	0.61
39:i:72:PRO:HD3	39:i:101:ARG:HG3	1.81	0.61
5:4:22:ARG:NH2	7:A:1253:C:H4'	2.14	0.61
7:A:471:G:H22	7:A:481:U:H3	1.48	0.61
12:F:81:ILE:O	12:F:86:LEU:N	2.31	0.61
20:O:33:LEU:HB3	20:O:97:PHE:HA	1.81	0.61
32:a:135:G:O2'	47:q:44:GLY:O	2.18	0.61
7:A:308:G:H5'	14:H:41:ARG:HD2	1.82	0.61
32:a:1068:G:N2	32:a:1071:A:OP2	2.21	0.61
34:d:120:VAL:HG12	34:d:138:VAL:HG22	1.83	0.61
7:A:503:C:H2'	7:A:504:A:C8	2.36	0.61
7:A:3023:U:O2	10:D:69:GLN:NE2	2.34	0.61
13:G:88:MET:HE1	13:G:134:VAL:HG23	1.83	0.61
7:A:2335:U:O2	7:A:2428:G:N2	2.26	0.61
12:F:23:LEU:HD11	12:F:176:LEU:HD13	1.83	0.61
14:H:6:THR:HA	14:H:15:ILE:HG23	1.82	0.61
32:a:1109:U:OP1	39:i:32:ARG:NH1	2.33	0.61
33:c:87:ARG:NH2	33:c:98:VAL:O	2.34	0.61
39:i:78:ARG:HB2	39:i:79:VAL:HG22	1.82	0.61
4:3:12:LYS:NZ	7:A:251:C:O2	2.28	0.61
7:A:3018:C:N4	15:J:102:GLU:OE1	2.33	0.61
7:A:3023:U:OP1	10:D:44:ARG:NH1	2.33	0.61
32:a:179:G:OP1	32:a:205:G:N2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:65:VAL:HG21	33:c:90:LEU:HD21	1.81	0.61
10:D:38:ARG:HB3	10:D:51:GLN:HB2	1.82	0.60
32:a:1086:U:OP1	32:a:1099:G:N2	2.34	0.60
7:A:337:C:H2'	7:A:338:G:C4	2.36	0.60
10:D:186:ASP:OD2	10:D:189:ASN:ND2	2.24	0.60
32:a:462:C:H5''	32:a:463:U:H5	1.66	0.60
32:a:496:G:H2'	32:a:497:G:C8	2.36	0.60
33:c:121:GLU:O	33:c:125:ASN:ND2	2.34	0.60
38:h:110:SER:HB2	38:h:113:LEU:HD11	1.82	0.60
7:A:220:G:H22	7:A:237:U:H4'	1.65	0.60
27:V:10:ARG:HA	27:V:10:ARG:CZ	2.31	0.60
32:a:49:G:O2'	32:a:364:U:O2	2.20	0.60
32:a:174:G:H2'	32:a:175:A:H8	1.67	0.60
34:d:99:ARG:HB3	34:d:163:PRO:HG2	1.83	0.60
39:i:81:SER:OG	39:i:82:PHE:N	2.30	0.60
7:A:1159:G:OP2	18:M:128:LYS:NZ	2.34	0.60
7:A:1193:C:N4	7:A:1198:A:O2'	2.33	0.60
7:A:2636:C:H2'	7:A:2637:A:H8	1.66	0.60
32:a:224:G:O2'	47:q:48:THR:O	2.18	0.60
7:A:2034:C:OP2	9:C:183:ARG:NH2	2.34	0.60
24:S:38:SER:OG	24:S:41:ASP:OD2	2.19	0.60
32:a:1030:U:H2'	32:a:1031:G:H8	1.67	0.60
35:e:49:ILE:HD13	35:e:66:ALA:HB2	1.81	0.60
38:h:36:ILE:HA	38:h:39:ILE:HD12	1.82	0.60
7:A:530:U:H2'	7:A:531:G:C8	2.36	0.60
19:N:11:GLY:O	19:N:16:HIS:ND1	2.34	0.60
22:Q:97:ASP:O	22:Q:101:SER:OG	2.18	0.60
32:a:413:A:OP2	32:a:427:G:N1	2.34	0.60
32:a:572:G:OP1	45:o:65:ARG:NH2	2.34	0.60
32:a:1044:G:N2	32:a:1049:G:O6	2.34	0.60
34:d:104:ARG:HB3	34:d:108:MET:HG2	1.83	0.60
42:l:114:ARG:HD2	42:l:121:LYS:HA	1.84	0.60
38:h:118:ALA:HA	38:h:121:GLN:HE21	1.67	0.60
7:A:1544:G:H2'	7:A:1545:G:C8	2.37	0.60
32:a:323:G:N1	32:a:326:A:OP2	2.33	0.60
32:a:413:A:C8	32:a:430:A:H2	2.19	0.60
32:a:1339:G:O6	39:i:33:ARG:NH2	2.34	0.60
37:g:74:GLU:HG2	37:g:91:VAL:HG22	1.84	0.60
6:6:8:ALA:H	6:6:28:LYS:HZ3	1.50	0.60
7:A:284:U:OP2	7:A:286:G:N1	2.34	0.60
7:A:334:C:H2'	7:A:335:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1824:C:H2'	7:A:1825:A:C8	2.36	0.60
32:a:537:G:H4'	32:a:539:G:H4'	1.82	0.60
7:A:732:G:H1	7:A:739:C:H5	1.48	0.60
35:e:86:GLU:HB3	35:e:88:PRO:HD2	1.84	0.60
7:A:2529:U:OP1	7:A:2618:U:O2'	2.20	0.59
10:D:107:ALA:O	10:D:110:SER:OG	2.17	0.59
11:E:157:ARG:NH2	11:E:199:ASP:OD2	2.34	0.59
32:a:1059:G:N1	32:a:1099:G:H1'	2.17	0.59
32:a:1402:C:H2'	32:a:1403:G:H8	1.67	0.59
50:t:29:ARG:O	50:t:33:ARG:HG2	2.01	0.59
32:a:891:G:N2	32:a:894:A:OP2	2.32	0.59
32:a:1348:G:H2'	32:a:1349:A:C8	2.36	0.59
7:A:1775:G:H2'	7:A:1776:A:O4'	2.01	0.59
13:G:55:ARG:NH1	13:G:63:ARG:HG2	2.16	0.59
32:a:48:U:H2'	32:a:49:G:H8	1.66	0.59
8:B:42:C:O2	12:F:99:ARG:NH1	2.34	0.59
41:k:33:ILE:HB	41:k:96:VAL:HG12	1.84	0.59
17:L:95:ASP:OD1	17:L:96:ASP:N	2.35	0.59
23:R:31:GLU:CD	23:R:32:GLN:H	2.10	0.59
32:a:334:C:H2'	32:a:335:A:H8	1.66	0.59
32:a:207:A:C8	32:a:221:U:H1'	2.37	0.59
32:a:268:U:H2'	32:a:269:A:H8	1.67	0.59
35:e:115:PRO:HB3	35:e:128:ARG:HG2	1.84	0.59
47:q:128:LEU:HD21	47:q:131:ILE:HD11	1.85	0.59
1:O:11:SER:OG	7:A:16:G:O2'	2.21	0.59
7:A:287:G:H8	7:A:302:U:H2'	1.66	0.59
7:A:1980:U:H2'	7:A:1981:C:C6	2.37	0.59
7:A:2297:A:C2	53:A:3201:WDP:C85	2.86	0.59
7:A:3071:U:H2'	7:A:3072:A:C8	2.37	0.59
32:a:782:G:O6	32:a:783:A:N6	2.36	0.59
32:a:942:A:OP2	43:m:106:ASN:ND2	2.25	0.59
48:r:22:PHE:HB2	48:r:60:HIS:ND1	2.18	0.59
7:A:1969:U:H2'	7:A:1970:G:C8	2.37	0.59
34:d:90:GLU:OE2	34:d:99:ARG:NH2	2.35	0.59
34:d:120:VAL:HG23	34:d:121:ASN:H	1.68	0.59
32:a:986:G:H2'	32:a:988:C:H41	1.68	0.59
32:a:999:C:N4	32:a:1000:G:O6	2.35	0.59
32:a:1351:C:H1'	32:a:1354:C:H41	1.68	0.59
7:A:622:U:H2'	7:A:623:C:C6	2.38	0.58
7:A:2036:A:H2'	7:A:2037:A:C8	2.38	0.58
7:A:2360:G:N2	7:A:2363:A:N3	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:2:ALA:N	34:d:63:MET:SD	2.76	0.58
7:A:1157:A:H2'	7:A:1158:A:C8	2.38	0.58
32:a:292:G:N2	32:a:305:U:O4	2.37	0.58
7:A:776:G:H2'	7:A:777:U:C6	2.38	0.58
7:A:1638:C:H2'	7:A:1639:G:H8	1.68	0.58
7:A:1672:A:H2'	7:A:1673:A:C8	2.38	0.58
7:A:2013:U:H5	7:A:2018:A:N7	2.02	0.58
12:F:111:THR:HA	12:F:115:LEU:HD12	1.86	0.58
25:T:70:ARG:HD3	25:T:70:ARG:H	1.68	0.58
32:a:1103:C:H1'	33:c:179:ARG:HH21	1.68	0.58
34:d:192:GLU:N	34:d:192:GLU:OE1	2.35	0.58
8:B:8:G:OP1	20:O:32:ARG:NH2	2.36	0.58
12:F:72:PRO:HB3	12:F:96:VAL:HB	1.84	0.58
7:A:430:A:H2'	7:A:431:A:C8	2.39	0.58
7:A:503:C:H2'	7:A:504:A:H8	1.68	0.58
7:A:2159:C:H2'	7:A:2160:A:H8	1.67	0.58
25:T:70:ARG:HG2	25:T:71:THR:HG23	1.85	0.58
32:a:953:U:H4'	32:a:954:U:H5''	1.85	0.58
42:l:56:LYS:HD3	42:l:62:GLU:HG2	1.85	0.58
44:n:32:ALA:HB1	44:n:41:ARG:HB2	1.85	0.58
53:A:3201:WDP:O36	53:A:3201:WDP:N20	2.36	0.58
32:a:123:G:O3'	47:q:58:ARG:NH1	2.36	0.58
32:a:573:U:OP2	32:a:749:G:N1	2.28	0.58
32:a:817:C:O2	38:h:16:ASN:ND2	2.37	0.58
42:l:83:ARG:NH1	42:l:84:GLY:O	2.37	0.58
7:A:1007:G:N1	7:A:1028:G:O2'	2.35	0.58
7:A:1567:U:H4'	7:A:1568:A:H8	1.68	0.58
7:A:2352:G:H22	7:A:2385:G:H5''	1.69	0.58
7:A:2636:C:H2'	7:A:2637:A:C8	2.39	0.58
28:W:39:ARG:HD3	28:W:58:THR:HG23	1.84	0.58
32:a:1210:C:H2'	32:a:1211:A:C8	2.38	0.58
35:e:200:MET:HE2	35:e:200:MET:N	2.18	0.58
46:p:74:LEU:HB3	46:p:80:TRP:HB2	1.85	0.58
7:A:1381:G:H5''	22:Q:6:ARG:HD3	1.86	0.58
7:A:2819:G:N2	7:A:2819:G:OP2	2.37	0.58
12:F:117:ARG:HE	43:m:3:ARG:NH2	2.01	0.58
32:a:682:G:H3'	41:k:38:ASN:HD21	1.69	0.58
32:a:1327:U:H5''	32:a:1328:C:H5'	1.84	0.58
34:d:119:ASN:HD21	34:d:141:ARG:HH21	1.52	0.58
35:e:136:VAL:HG12	35:e:154:ILE:HG22	1.85	0.58
7:A:1281:G:N3	22:Q:77:ASN:ND2	2.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:119:ARG:HH22	43:m:3:ARG:CZ	2.17	0.58
13:G:158:TYR:O	13:G:172:ARG:NH2	2.36	0.58
26:U:98:SER:O	26:U:102:GLY:HA3	2.04	0.58
32:a:971:A:O2'	32:a:1314:C:N3	2.35	0.58
32:a:1175:U:O2'	32:a:1177:G:OP2	2.22	0.58
32:a:1366:G:H5''	37:g:36:LYS:HD2	1.84	0.58
7:A:2204:A:N3	7:A:2830:G:O2'	2.36	0.58
8:B:35:C:N3	8:B:48:C:O2'	2.35	0.58
12:F:8:GLN:NE2	12:F:13:GLU:OE1	2.36	0.58
32:a:48:U:H2'	32:a:49:G:C8	2.39	0.58
32:a:178:G:O2'	32:a:180:A:N1	2.33	0.58
34:d:165:TRP:CE2	34:d:181:PRO:HB3	2.39	0.58
42:l:25:LYS:HD2	42:l:59:SER:HB2	1.85	0.58
5:4:12:ASP:OD1	5:4:13:LYS:NZ	2.37	0.57
7:A:630:U:H2'	7:A:631:C:C6	2.39	0.57
7:A:1807:A:H2'	7:A:1808:A:C8	2.39	0.57
7:A:2572:C:H1'	20:O:22:LYS:HD2	1.86	0.57
32:a:1420:C:H2'	32:a:1421:A:H8	1.69	0.57
43:m:96:MET:HG3	43:m:97:PRO:HD2	1.86	0.57
7:A:645:G:N2	7:A:646:A:H62	2.01	0.57
7:A:1774:U:O4'	7:A:1775:G:N2	2.37	0.57
32:a:1155:G:H2'	32:a:1156:G:C8	2.38	0.57
7:A:760:A:N6	7:A:781:A:O4'	2.37	0.57
32:a:1284:C:H2'	32:a:1285:G:H8	1.70	0.57
7:A:390:G:N1	7:A:393:A:OP2	2.35	0.57
7:A:988:G:O2'	7:A:1045:G:O6	2.20	0.57
32:a:130:G:O6	46:p:26:ARG:NH1	2.38	0.57
32:a:336:G:H2'	32:a:337:A:H8	1.69	0.57
32:a:549:G:OP2	32:a:550:A:O2'	2.21	0.57
32:a:915:G:H5''	35:e:57:LYS:NZ	2.19	0.57
32:a:1152:G:O6	32:a:1174:G:O6	2.23	0.57
7:A:786:U:H2'	7:A:787:G:C8	2.39	0.57
8:B:47:C:OP1	20:O:37:ARG:NH2	2.38	0.57
12:F:117:ARG:O	43:m:3:ARG:NH2	2.37	0.57
14:H:5:LEU:HG	14:H:16:GLY:H	1.68	0.57
24:S:56:PRO:O	24:S:60:VAL:HG23	2.04	0.57
32:a:185:G:O6	32:a:198:U:O4	2.22	0.57
32:a:336:G:H2'	32:a:337:A:C8	2.40	0.57
32:a:395:G:O2'	32:a:397:C:OP1	2.19	0.57
33:c:11:ARG:NH2	33:c:177:THR:O	2.37	0.57
7:A:2985:G:H21	7:A:2995:A:H62	1.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:64:LEU:HB3	12:F:72:PRO:HG3	1.86	0.57
20:O:77:VAL:O	20:O:81:GLN:HG3	2.04	0.57
32:a:543:U:H2'	32:a:544:G:H8	1.69	0.57
32:a:644:A:OP1	38:h:55:ARG:NH2	2.38	0.57
32:a:802:C:O2'	32:a:894:A:N1	2.37	0.57
34:d:59:THR:HG22	34:d:106:ARG:HH12	1.70	0.57
7:A:787:G:H21	11:E:112:MET:CE	2.15	0.57
7:A:1141:C:O2	15:J:27:ARG:NH1	2.37	0.57
7:A:1558:A:H3'	7:A:1645:A:H61	1.69	0.57
32:a:24:G:H2'	32:a:25:G:C8	2.39	0.57
32:a:895:G:H2'	32:a:896:G:H8	1.68	0.57
8:B:12:A:N1	8:B:68:G:O2'	2.31	0.57
32:a:35:A:H2'	32:a:36:A:C8	2.40	0.57
32:a:727:U:H2'	32:a:728:C:C6	2.40	0.57
32:a:786:C:O2'	41:k:138:ARG:O	2.20	0.57
32:a:1115:G:N2	32:a:1116:U:O4	2.37	0.57
46:p:14:ARG:O	46:p:43:LYS:NZ	2.37	0.57
32:a:1405:C:H2'	32:a:1406:A:C8	2.40	0.57
46:p:5:ILE:HB	46:p:66:PRO:HB3	1.86	0.57
7:A:278:C:H2'	7:A:279:A:H8	1.70	0.57
7:A:743:U:H2'	7:A:744:C:C6	2.39	0.57
7:A:1592:U:O4	7:A:1613:G:O6	2.22	0.57
32:a:70:C:H2'	32:a:71:G:C8	2.40	0.57
32:a:74:A:H61	32:a:94:C:H1'	1.70	0.57
32:a:271:C:H2'	32:a:272:A:C8	2.40	0.57
32:a:706:A:H2'	32:a:707:A:C8	2.40	0.57
49:s:51:VAL:HG11	49:s:71:LEU:HB3	1.87	0.57
7:A:961:U:H2'	7:A:962:G:H8	1.70	0.56
7:A:1140:G:N2	15:J:147:GLN:OE1	2.31	0.56
7:A:1658:A:H3'	7:A:1659:G:H8	1.70	0.56
7:A:1714:U:H2'	7:A:1715:A:H8	1.70	0.56
7:A:3028:A:H62	7:A:3127:A:H2	1.53	0.56
32:a:198:U:OP1	47:q:47:HIS:NE2	2.33	0.56
32:a:615:U:H2'	32:a:616:G:C8	2.40	0.56
32:a:1077:U:H3	32:a:1090:G:H22	1.53	0.56
7:A:1650:U:H2'	7:A:1651:C:C6	2.40	0.56
7:A:2583:G:N3	7:A:2619:C:H2'	2.19	0.56
32:a:435:C:H2'	32:a:436:U:C6	2.40	0.56
33:c:169:ARG:HH22	33:c:173:VAL:H	1.53	0.56
37:g:116:MET:HA	37:g:119:ARG:HB2	1.87	0.56
38:h:85:LEU:HD13	42:l:4:ILE:HG13	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:640:C:H3'	7:A:641:U:H5'	1.87	0.56
7:A:2151:A:N6	32:a:1487:G:OP2	2.39	0.56
9:C:68:ARG:NH1	9:C:150:GLY:O	2.38	0.56
9:C:80:ALA:O	9:C:113:GLN:NE2	2.38	0.56
12:F:36:PRO:HB3	12:F:167:ALA:HB2	1.87	0.56
20:O:93:ASP:O	20:O:121:SER:OG	2.19	0.56
32:a:228:U:O2'	46:p:24:ASP:OD2	2.20	0.56
32:a:736:A:OP1	32:a:844:C:O2'	2.22	0.56
32:a:797:C:H2'	32:a:798:A:H8	1.69	0.56
37:g:51:ARG:HD3	37:g:58:PRO:HD3	1.87	0.56
45:o:23:GLY:O	45:o:28:GLN:NE2	2.39	0.56
50:t:56:ARG:HH11	50:t:57:LYS:HZ3	1.52	0.56
7:A:942:U:H2'	7:A:943:C:C6	2.41	0.56
7:A:1039:A:H2'	7:A:1040:A:C8	2.41	0.56
7:A:1672:A:H2'	7:A:1673:A:H8	1.71	0.56
7:A:2936:U:H2'	7:A:2937:C:C6	2.40	0.56
16:K:106:LEU:HB2	16:K:115:ILE:HD11	1.86	0.56
30:Y:61:LEU:O	30:Y:65:GLU:HG3	2.05	0.56
32:a:913:U:H2'	32:a:914:U:C6	2.40	0.56
50:t:51:LEU:HD11	50:t:80:ALA:HA	1.88	0.56
7:A:307:U:H2'	7:A:308:G:C8	2.40	0.56
7:A:829:G:O2'	7:A:1867:A:N3	2.36	0.56
7:A:2309:C:H5	7:A:2675:G:N1	2.01	0.56
17:L:31:THR:HB	17:L:35:GLY:H	1.70	0.56
27:V:74:GLN:HE22	27:V:97:VAL:HB	1.71	0.56
32:a:405:G:O2'	34:d:3:ARG:NH2	2.38	0.56
7:A:616:A:C2	7:A:2280:A:H2'	2.41	0.56
32:a:702:G:OP1	36:f:54:LYS:NZ	2.38	0.56
32:a:727:U:H2'	32:a:728:C:H6	1.70	0.56
7:A:2354:A:O2'	7:A:2356:A:N6	2.39	0.56
7:A:3131:U:H2'	7:A:3132:U:C6	2.40	0.56
12:F:68:THR:HB	12:F:98:LEU:HD21	1.87	0.56
12:F:115:LEU:HD22	12:F:124:LEU:HD21	1.88	0.56
46:p:41:HIS:HB2	46:p:48:LEU:HB3	1.87	0.56
8:B:29:C:OP1	20:O:9:ARG:NH1	2.38	0.56
14:H:42:GLY:HA2	14:H:45:LYS:HB2	1.87	0.56
32:a:9:G:O6	35:e:131:SER:N	2.38	0.56
32:a:494:C:OP1	42:l:116:ARG:NH1	2.38	0.56
32:a:1149:A:N7	32:a:1172:A:N6	2.54	0.56
7:A:297:A:N1	7:A:341:A:N6	2.53	0.56
7:A:1952:C:H2'	7:A:1953:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:4:C:O2'	8:B:25:A:N1	2.33	0.56
15:J:110:PRO:O	15:J:115:SER:OG	2.14	0.56
32:a:463:U:H4'	46:p:81:GLN:HE21	1.71	0.56
32:a:575:G:H1	32:a:748:U:H3	1.53	0.56
32:a:757:A:OP2	32:a:803:G:N2	2.38	0.56
32:a:968:A:H4'	32:a:969:G:H5''	1.86	0.56
1:O:14:ARG:NH2	7:A:606:G:OP2	2.39	0.56
5:4:22:ARG:HH22	7:A:1253:C:H4'	1.71	0.56
7:A:293:G:H2'	7:A:294:G:C8	2.40	0.56
7:A:350:A:H2'	7:A:351:G:C8	2.41	0.56
7:A:640:C:H41	7:A:641:U:H5	1.53	0.56
7:A:1561:C:H2'	7:A:1562:A:C8	2.40	0.56
7:A:1561:C:H2'	7:A:1562:A:H8	1.69	0.56
7:A:2484:A:H2'	7:A:2485:A:H8	1.70	0.56
7:A:2543:A:N6	12:F:158:GLY:O	2.39	0.56
32:a:764:G:O6	32:a:798:A:N6	2.39	0.56
39:i:42:LEU:HD11	39:i:82:PHE:HE2	1.70	0.56
42:l:78:SER:OG	42:l:103:ASP:OD2	2.23	0.56
43:m:18:ALA:HA	43:m:21:TYR:HD1	1.70	0.56
2:l:25:THR:OG1	2:l:26:LYS:N	2.38	0.55
32:a:703:A:H2'	32:a:704:G:C8	2.42	0.55
35:e:188:ARG:NH1	35:e:193:GLU:OE2	2.39	0.55
35:e:194:ASP:OD2	35:e:195:VAL:N	2.39	0.55
46:p:44:GLU:HG3	46:p:48:LEU:HB2	1.87	0.55
7:A:2341:C:H2'	7:A:2342:G:C8	2.40	0.55
7:A:2481:U:H2'	7:A:2482:U:C6	2.41	0.55
32:a:582:U:H2'	32:a:583:G:H8	1.71	0.55
32:a:1007:G:H21	32:a:1211:A:H1'	1.70	0.55
41:k:74:GLN:O	41:k:78:GLU:HG2	2.06	0.55
7:A:1644:U:H3'	7:A:1645:A:H8	1.71	0.55
7:A:2571:A:OP1	28:W:75:ARG:NH2	2.39	0.55
32:a:22:C:OP1	35:e:166:ASN:ND2	2.28	0.55
32:a:62:A:H3'	32:a:330:G:H22	1.70	0.55
32:a:643:U:H1'	32:a:644:A:H8	1.71	0.55
46:p:81:GLN:HG3	46:p:86:LEU:HD12	1.88	0.55
50:t:44:LYS:NZ	50:t:83:LEU:O	2.40	0.55
7:A:2303:C:H1'	7:A:2687:U:H3	1.70	0.55
32:a:275:G:H5'	47:q:70:MET:HE2	1.87	0.55
32:a:829:U:H2'	32:a:830:U:C6	2.41	0.55
32:a:1133:U:H2'	32:a:1134:G:H8	1.72	0.55
32:a:1240:A:N6	32:a:1280:A:OP2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:9:ILE:HB	13:G:51:ILE:HB	1.89	0.55
33:c:162:MET:N	33:c:162:MET:SD	2.79	0.55
7:A:193:A:H2'	7:A:194:G:H8	1.71	0.55
25:T:70:ARG:HD3	25:T:70:ARG:N	2.22	0.55
32:a:108:G:N3	32:a:352:A:O2'	2.38	0.55
32:a:143:G:H2'	32:a:144:G:C8	2.42	0.55
32:a:408:G:OP1	34:d:104:ARG:NH2	2.40	0.55
41:k:62:PHE:CE2	41:k:75:LEU:HD21	2.40	0.55
43:m:13:LYS:NZ	43:m:14:ARG:H	2.05	0.55
50:t:51:LEU:HD13	50:t:83:LEU:HD22	1.88	0.55
32:a:1231:A:N6	32:a:1291:A:C2	2.75	0.55
7:A:2721:C:N3	18:M:124:LYS:NZ	2.55	0.55
8:B:112:A:H2'	8:B:113:A:H8	1.72	0.55
32:a:478:A:H3'	32:a:479:G:H8	1.72	0.55
32:a:1242:A:H2'	32:a:1243:A:C8	2.41	0.55
32:a:1346:C:H2'	32:a:1347:A:H8	1.71	0.55
7:A:307:U:O2'	14:H:41:ARG:NH1	2.30	0.55
32:a:505:C:H2'	32:a:506:G:C8	2.42	0.55
32:a:988:C:H2'	32:a:989:A:H8	1.70	0.55
49:s:18:LYS:HD2	49:s:31:ILE:HD11	1.88	0.55
7:A:332:C:H2'	7:A:333:U:C6	2.41	0.55
12:F:149:ASP:H	12:F:152:LYS:NZ	2.05	0.55
18:M:67:ASN:ND2	18:M:102:VAL:O	2.37	0.55
32:a:44:G:H2'	32:a:45:G:H8	1.72	0.55
13:G:55:ARG:HH12	13:G:63:ARG:HG2	1.73	0.54
20:O:95:VAL:HG22	20:O:120:LEU:HD12	1.89	0.54
32:a:591:G:H2'	32:a:592:U:C6	2.42	0.54
32:a:753:A:H2'	32:a:754:G:C8	2.42	0.54
32:a:943:U:OP2	43:m:102:ARG:NE	2.40	0.54
32:a:1047:U:H2'	32:a:1048:G:H8	1.72	0.54
40:j:35:SER:OG	40:j:78:ASP:OD1	2.25	0.54
7:A:430:A:H2'	7:A:431:A:H8	1.71	0.54
7:A:1545:G:H22	7:A:1823:A:H2	1.55	0.54
7:A:1969:U:H2'	7:A:1970:G:H8	1.72	0.54
31:Z:18:LYS:O	31:Z:22:SER:OG	2.25	0.54
32:a:472:G:O2'	32:a:474:C:N4	2.41	0.54
32:a:815:U:H2'	32:a:816:A:H8	1.72	0.54
32:a:915:G:H2'	32:a:916:A:C8	2.41	0.54
35:e:75:GLY:HA3	35:e:104:ARG:HH22	1.72	0.54
43:m:18:ALA:HA	43:m:21:TYR:CD1	2.42	0.54
7:A:79:C:HO2'	7:A:429:A:H8	1.50	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1431:A:H4'	7:A:1432:A:H5''	1.89	0.54
7:A:1552:G:H2'	7:A:1553:U:C6	2.43	0.54
7:A:1808:A:H2'	7:A:1809:A:C8	2.42	0.54
7:A:2323:U:H2'	7:A:2324:G:C8	2.42	0.54
7:A:2484:A:H2'	7:A:2485:A:C8	2.42	0.54
32:a:860:G:O2'	32:a:866:A:N1	2.39	0.54
7:A:925:U:H2'	7:A:926:C:C6	2.42	0.54
7:A:1566:G:H1	7:A:1637:U:H3	0.74	0.54
7:A:2984:U:N3	7:A:2994:U:O4	2.31	0.54
13:G:99:LEU:HD12	13:G:126:VAL:HG23	1.89	0.54
32:a:570:U:H5'	32:a:719:A:H1'	1.90	0.54
53:A:3201:WDP:C49	53:A:3201:WDP:C41	2.86	0.54
12:F:72:PRO:HB2	12:F:94:VAL:HG12	1.90	0.54
32:a:1520:C:H2'	32:a:1521:U:C6	2.42	0.54
34:d:182:GLU:O	34:d:186:ILE:HD12	2.08	0.54
7:A:1741:C:H2'	7:A:1742:U:C6	2.42	0.54
32:a:447:A:O5'	32:a:476:G:N2	2.35	0.54
32:a:1284:C:H2'	32:a:1285:G:C8	2.42	0.54
32:a:1523:G:H2'	32:a:1524:A:C8	2.43	0.54
7:A:1007:G:H22	7:A:1028:G:H1'	1.72	0.54
7:A:2524:A:H4'	7:A:2525:A:O4'	2.07	0.54
32:a:434:U:H2'	32:a:435:C:C6	2.43	0.54
32:a:609:C:N4	32:a:612:A:OP2	2.38	0.54
32:a:672:U:H2'	32:a:673:G:C8	2.42	0.54
33:c:151:VAL:HG13	33:c:200:VAL:HG22	1.90	0.54
34:d:60:TYR:OH	34:d:183:ARG:NE	2.41	0.54
12:F:14:ARG:NH2	12:F:179:ALA:O	2.40	0.54
32:a:291:G:C5	32:a:292:G:H1'	2.42	0.54
32:a:951:A:N6	49:s:77:THR:O	2.39	0.54
35:e:190:LEU:O	35:e:192:ILE:N	2.38	0.54
38:h:5:ASP:OD1	38:h:79:ARG:NH1	2.41	0.54
7:A:93:C:H2'	7:A:94:C:O4'	2.08	0.54
7:A:2683:G:OP1	11:E:81:ARG:NH2	2.40	0.54
40:j:4:GLN:HB3	40:j:76:ILE:HB	1.90	0.54
7:A:1208:C:H2'	7:A:1209:C:C6	2.43	0.54
7:A:1492:G:H2'	7:A:1493:C:C6	2.42	0.54
7:A:1623:G:O2'	7:A:1625:U:O4	2.18	0.54
53:A:3201:WDP:C60	53:A:3201:WDP:C64	2.85	0.54
32:a:678:A:H5''	41:k:59:HIS:CE1	2.43	0.54
32:a:947:G:H2'	32:a:948:A:C8	2.42	0.54
36:f:43:TRP:HB2	36:f:60:TYR:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l:35:THR:HG22	42:l:77:HIS:HB3	1.90	0.54
53:A:3201:WDP:C14	53:A:3201:WDP:C38	2.86	0.53
12:F:113:ILE:HD13	12:F:146:HIS:CE1	2.43	0.53
32:a:43:C:H2'	32:a:44:G:H8	1.73	0.53
32:a:610:U:N3	34:d:126:ASN:OD1	2.41	0.53
32:a:692:C:OP1	32:a:693:A:O2'	2.14	0.53
32:a:925:C:O3'	37:g:4:LYS:NZ	2.40	0.53
38:h:93:ASN:OD1	38:h:93:ASN:N	2.41	0.53
7:A:588:G:N1	7:A:591:A:OP2	2.38	0.53
7:A:1087:A:H2'	7:A:1088:A:C8	2.43	0.53
7:A:1567:U:H4'	7:A:1568:A:C8	2.43	0.53
32:a:140:U:O2	32:a:174:G:N2	2.36	0.53
32:a:1144:G:P	40:j:72:ARG:HH12	2.32	0.53
32:a:1310:A:H5''	49:s:2:PRO:HB3	1.90	0.53
41:k:85:GLN:NE2	41:k:113:ALA:O	2.39	0.53
7:A:291:C:H2'	7:A:292:C:C6	2.43	0.53
7:A:1127:C:OP1	22:Q:84:LYS:NZ	2.41	0.53
7:A:2098:U:OP1	7:A:2648:G:O2'	2.20	0.53
7:A:2894:U:C2	7:A:2903:A:N7	2.77	0.53
7:A:2969:G:H2'	7:A:2970:G:C8	2.42	0.53
11:E:39:LEU:HD11	11:E:112:MET:HB3	1.90	0.53
14:H:2:LYS:HB3	14:H:39:ALA:HB3	1.89	0.53
30:Y:14:THR:H	30:Y:17:GLU:CD	2.16	0.53
33:c:57:GLU:HB2	33:c:64:ARG:HB3	1.90	0.53
36:f:23:LEU:HA	36:f:26:PHE:HD2	1.72	0.53
46:p:5:ILE:HG12	46:p:22:VAL:HG22	1.91	0.53
7:A:1884:G:O2'	19:N:106:ASP:OD2	2.19	0.53
7:A:1954:U:H2'	7:A:1955:G:C8	2.43	0.53
7:A:2180:C:OP2	7:A:2181:U:O2'	2.18	0.53
7:A:2335:U:H2'	7:A:2336:C:C6	2.43	0.53
12:F:110:LEU:HD12	12:F:114:ALA:HB3	1.90	0.53
37:g:71:PRO:HD2	37:g:96:SER:HB2	1.90	0.53
43:m:15:MET:HE1	43:m:34:LEU:HD11	1.89	0.53
43:m:25:ILE:HG12	43:m:29:ARG:HB3	1.91	0.53
7:A:1617:U:H2'	7:A:1618:C:C6	2.43	0.53
7:A:1707:A:H2'	7:A:1708:A:H8	1.73	0.53
9:C:124:ASP:O	9:C:129:ASN:ND2	2.30	0.53
16:K:80:ASP:OD2	21:P:103:ARG:NH2	2.41	0.53
32:a:505:C:H2'	32:a:506:G:H8	1.74	0.53
50:t:70:ASN:O	50:t:74:ASN:ND2	2.41	0.53
7:A:1641:U:H2'	7:A:1642:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1842:C:H4'	7:A:1843:A:H5''	1.91	0.53
7:A:2749:U:O2'	10:D:148:PRO:O	2.25	0.53
32:a:411:U:H3'	32:a:412:G:H4'	1.91	0.53
32:a:725:G:N2	48:r:73:GLU:OE2	2.42	0.53
40:j:52:ILE:HG13	44:n:41:ARG:NE	2.23	0.53
43:m:51:GLU:O	43:m:54:ILE:HG13	2.08	0.53
7:A:1559:A:OP2	7:A:1645:A:N6	2.41	0.53
7:A:1743:C:H2'	7:A:1744:A:H8	1.73	0.53
12:F:119:ARG:HA	12:F:119:ARG:HE	1.73	0.53
12:F:171:ASP:OD1	12:F:172:GLU:N	2.41	0.53
30:Y:36:MET:HE3	30:Y:41:LEU:HB3	1.91	0.53
32:a:102:G:N7	50:t:10:ARG:NH2	2.52	0.53
7:A:1683:A:OP1	7:A:1698:C:N4	2.35	0.53
7:A:1980:U:H2'	7:A:1981:C:H6	1.74	0.53
35:e:91:ILE:HD12	35:e:92:ALA:N	2.24	0.53
7:A:2127:A:H2'	7:A:2128:A:C8	2.44	0.53
32:a:139:U:H5''	32:a:140:U:H5'	1.91	0.53
32:a:918:G:H1	32:a:1384:U:H3	1.55	0.53
32:a:1218:C:H3'	43:m:96:MET:HE1	1.90	0.53
39:i:68:LEU:HG	39:i:101:ARG:HD3	1.91	0.53
50:t:17:ALA:O	50:t:21:ASN:ND2	2.39	0.53
7:A:777:U:H2'	7:A:778:G:C8	2.44	0.53
7:A:1125:G:H4'	22:Q:91:ASP:OD2	2.09	0.53
7:A:1567:U:O2'	7:A:1568:A:N7	2.38	0.53
7:A:3089:U:H2'	7:A:3090:C:C6	2.44	0.53
13:G:119:PRO:HG2	13:G:122:ILE:HG13	1.91	0.53
32:a:43:C:H2'	32:a:44:G:C8	2.44	0.53
32:a:122:G:O2'	47:q:59:LYS:NZ	2.41	0.53
32:a:451:A:N7	46:p:47:SER:OG	2.37	0.53
32:a:1100:C:H2'	32:a:1101:A:H8	1.74	0.53
39:i:78:ARG:O	39:i:78:ARG:HD3	2.09	0.53
7:A:278:C:H2'	7:A:279:A:C8	2.43	0.52
53:A:3201:WDP:C38	53:A:3201:WDP:C48	2.86	0.52
17:L:3:LEU:HD13	17:L:4:LYS:HG2	1.90	0.52
32:a:145:A:H2'	32:a:146:U:C6	2.44	0.52
32:a:321:C:H2'	32:a:322:U:C6	2.43	0.52
32:a:653:C:H2'	32:a:654:A:C8	2.44	0.52
32:a:1082:U:N3	32:a:1085:G:OP2	2.37	0.52
32:a:1310:A:O2'	49:s:37:ARG:HB2	2.10	0.52
32:a:1479:G:H2'	32:a:1480:G:C8	2.44	0.52
41:k:29:GLY:HA2	41:k:47:PRO:HD3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:447:G:HO2'	7:A:448:U:H6	1.54	0.52
7:A:2391:G:H3'	7:A:2392:C:H6	1.73	0.52
7:A:2962:C:OP1	10:D:128:LYS:NZ	2.42	0.52
11:E:29:GLU:OE1	11:E:29:GLU:N	2.24	0.52
32:a:1135:G:H2'	32:a:1136:G:H8	1.73	0.52
34:d:96:VAL:HG13	34:d:166:LEU:HD11	1.92	0.52
42:l:27:SER:OG	42:l:29:GLN:O	2.26	0.52
47:q:103:ASP:OD1	47:q:103:ASP:N	2.42	0.52
7:A:324:G:H22	7:A:452:A:H2	1.56	0.52
7:A:334:C:H2'	7:A:335:A:H8	1.73	0.52
7:A:2309:C:H2'	7:A:2310:C:H6	1.75	0.52
33:c:59:THR:HG22	40:j:94:ALA:HB2	1.91	0.52
7:A:635:U:H3	7:A:648:G:H1	0.72	0.52
32:a:249:U:O2	32:a:251:U:N3	2.41	0.52
32:a:1088:C:O2'	32:a:1161:A:N3	2.36	0.52
41:k:75:LEU:HD12	41:k:76:ALA:N	2.24	0.52
48:r:46:GLY:O	48:r:72:ARG:NH2	2.43	0.52
7:A:1484:A:H2'	7:A:1485:A:C8	2.45	0.52
7:A:1957:A:H61	7:A:1972:G:H1'	1.74	0.52
7:A:2775:U:H2'	7:A:2776:C:C6	2.44	0.52
7:A:3028:A:N6	7:A:3127:A:OP2	2.42	0.52
10:D:52:LEU:N	10:D:82:ALA:O	2.42	0.52
32:a:237:G:H2'	32:a:238:G:C8	2.45	0.52
32:a:824:U:H3	32:a:846:G:H1	1.57	0.52
32:a:1242:A:H4'	39:i:90:GLY:HA2	1.91	0.52
7:A:2252:A:H2'	7:A:2253:A:C8	2.45	0.52
7:A:2342:G:H2'	7:A:2343:G:H5''	1.92	0.52
13:G:32:THR:O	13:G:33:LEU:HD13	2.10	0.52
18:M:28:ASN:N	18:M:105:GLU:OE2	2.38	0.52
30:Y:12:GLU:N	30:Y:12:GLU:OE2	2.43	0.52
32:a:320:A:H61	32:a:331:G:H1	1.55	0.52
32:a:518:G7M:O2'	32:a:526:A:N1	2.37	0.52
32:a:990:U:O4	32:a:1035:G:O6	2.28	0.52
32:a:1139:C:H2'	32:a:1140:U:H6	1.73	0.52
32:a:1317:C:H2'	32:a:1318:C:H6	1.74	0.52
35:e:81:TYR:N	35:e:97:GLU:OE1	2.43	0.52
45:o:39:LEU:HD13	45:o:56:LEU:HB2	1.91	0.52
7:A:8:U:H3	7:A:3129:A:N6	2.06	0.52
7:A:342:C:H2'	7:A:343:C:C6	2.44	0.52
7:A:1577:C:H1'	36:f:17:ARG:HE	1.74	0.52
7:A:2545:G:H5'	7:A:2546:G:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:133:ILE:HD12	11:E:203:SER:HA	1.91	0.52
32:a:48:U:H3	32:a:395:G:H1	1.58	0.52
32:a:139:U:H1'	32:a:220:G:N2	2.25	0.52
32:a:871:C:H5'	38:h:83:PRO:HG2	1.92	0.52
35:e:187:ARG:NH2	38:h:73:SER:O	2.40	0.52
41:k:43:THR:HA	41:k:54:TRP:HA	1.91	0.52
41:k:79:ASN:O	41:k:82:ARG:HG3	2.09	0.52
7:A:1138:A:N3	7:A:1283:C:O2'	2.43	0.52
7:A:2275:U:H2'	7:A:2276:C:C6	2.44	0.52
32:a:730:C:O2'	45:o:42:HIS:ND1	2.41	0.52
32:a:1261:A:HO2'	32:a:1317:C:HO2'	1.57	0.52
36:f:24:GLU:HA	36:f:27:LEU:HD12	1.92	0.52
7:A:648:G:H2'	7:A:649:A:H8	1.75	0.52
7:A:1955:G:N2	7:A:1974:G:H1	2.07	0.52
7:A:1957:A:N6	7:A:1972:G:H1'	2.24	0.52
7:A:2752:U:H2'	7:A:2753:C:C6	2.45	0.52
8:B:54:C:H1'	12:F:33:MET:HE1	1.92	0.52
16:K:122:LEU:HD13	21:P:69:VAL:HG11	1.92	0.52
17:L:88:GLN:CD	17:L:88:GLN:H	2.17	0.52
27:V:87:ARG:HH21	27:V:91:GLN:HE21	1.57	0.52
32:a:408:G:O6	32:a:433:C:N4	2.43	0.52
46:p:23:ALA:HA	46:p:34:ILE:HG13	1.91	0.52
7:A:2485:A:H2'	7:A:2486:C:H6	1.75	0.52
32:a:1279:A:H2'	32:a:1280:A:C8	2.45	0.52
37:g:15:ASP:OD2	37:g:44:TYR:OH	2.26	0.52
46:p:77:THR:HG23	46:p:79:ASP:H	1.74	0.52
7:A:2989:G:C4	13:G:3:ARG:HD3	2.44	0.51
8:B:38:A:H2'	8:B:39:U:C6	2.45	0.51
30:Y:50:VAL:HA	30:Y:53:GLU:HG2	1.91	0.51
32:a:15:U:O2	32:a:25:G:O6	2.28	0.51
32:a:954:U:OP2	32:a:1215:C:O2'	2.21	0.51
34:d:137:ILE:HG22	34:d:176:LEU:HG	1.92	0.51
47:q:115:MET:HE1	47:q:117:THR:HG22	1.92	0.51
7:A:680:A:OP1	7:A:1386:U:O2'	2.25	0.51
7:A:690:U:H2'	7:A:691:C:C6	2.45	0.51
7:A:871:U:H2'	7:A:872:A:H8	1.74	0.51
7:A:2354:A:C2	7:A:2407:A:H5''	2.45	0.51
7:A:2485:A:H2'	7:A:2486:C:C6	2.45	0.51
7:A:2916:A:H2'	7:A:2917:A:C8	2.46	0.51
20:O:27:THR:HG23	20:O:30:ARG:H	1.74	0.51
32:a:492:C:H5''	42:l:114:ARG:HH22	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:578:G:OP1	38:h:86:ARG:NH2	2.43	0.51
32:a:947:G:H2'	32:a:948:A:H8	1.76	0.51
32:a:1013:G:N2	32:a:1014:G:N7	2.58	0.51
32:a:1097:G:H2'	32:a:1098:C:C6	2.45	0.51
7:A:803:G:H2'	7:A:933:A:H61	1.75	0.51
7:A:1157:A:N3	7:A:2724:G:O2'	2.37	0.51
7:A:1192:G:N1	7:A:1205:C:O2	2.44	0.51
7:A:1618:C:H2'	7:A:1619:U:O4'	2.11	0.51
20:O:41:HIS:ND1	20:O:60:SER:OG	2.38	0.51
24:S:93:LYS:HB3	24:S:105:ARG:HD3	1.92	0.51
26:U:74:VAL:HG12	26:U:76:SER:H	1.75	0.51
32:a:408:G:OP2	34:d:24:GLN:NE2	2.43	0.51
32:a:901:A:H2'	32:a:902:A:H8	1.74	0.51
32:a:1346:C:H2'	32:a:1347:A:C8	2.45	0.51
7:A:682:C:H2'	7:A:683:C:C6	2.45	0.51
7:A:2741:A:O2'	53:A:3201:WDP:C01	2.58	0.51
13:G:26:VAL:HG23	13:G:80:VAL:HG21	1.91	0.51
43:m:63:ASN:OD1	43:m:63:ASN:N	2.41	0.51
7:A:484:G:H2'	7:A:485:C:C6	2.46	0.51
7:A:609:U:H2'	7:A:610:G:C8	2.44	0.51
7:A:1902:G:O2'	7:A:2229:U:O4	2.20	0.51
13:G:19:ILE:HD11	13:G:45:ARG:NH1	2.26	0.51
13:G:138:ASP:OD1	13:G:141:LYS:N	2.27	0.51
26:U:98:SER:OG	26:U:99:LYS:O	2.27	0.51
32:a:1313:U:H3'	32:a:1314:C:H2'	1.92	0.51
38:h:108:THR:HB	38:h:123:VAL:HG12	1.93	0.51
39:i:32:ARG:H	39:i:102:LEU:HD23	1.76	0.51
7:A:1953:G:N2	7:A:1976:G:H22	2.09	0.51
32:a:127:U:H2'	32:a:128:C:C6	2.45	0.51
32:a:972:C:O2	44:n:19:ARG:NE	2.44	0.51
32:a:1339:G:C8	39:i:130:ARG:HB3	2.46	0.51
32:a:1397:C:H2'	32:a:1398:G:C8	2.45	0.51
46:p:78:GLY:O	46:p:82:LYS:HG3	2.11	0.51
7:A:306:G:H21	14:H:45:LYS:NZ	2.09	0.51
7:A:2372:A:C8	7:A:2373:A:C8	2.99	0.51
13:G:106:PHE:HB2	13:G:114:VAL:HB	1.92	0.51
32:a:44:G:H2'	32:a:45:G:C8	2.44	0.51
32:a:945:U:H2'	32:a:946:G:H8	1.75	0.51
40:j:44:THR:HG21	40:j:68:ARG:HD3	1.93	0.51
40:j:84:VAL:HG22	40:j:88:MET:HE3	1.91	0.51
7:A:728:C:O2'	7:A:786:U:OP1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1714:U:H2'	7:A:1715:A:C8	2.45	0.51
7:A:2341:C:H2'	7:A:2342:G:H8	1.76	0.51
28:W:73:ARG:HG3	28:W:73:ARG:O	2.11	0.51
30:Y:34:PHE:O	30:Y:38:THR:HG23	2.11	0.51
32:a:459:G:N7	32:a:460:U:O2'	2.44	0.51
32:a:946:G:H2'	32:a:947:G:H8	1.76	0.51
32:a:1020:C:O2	32:a:1026:G:N1	2.37	0.51
35:e:137:ILE:HD13	35:e:155:LEU:HD23	1.91	0.51
50:t:44:LYS:HZ3	50:t:86:LEU:HB2	1.75	0.51
7:A:691:C:H2'	7:A:692:A:H8	1.75	0.51
7:A:1247:G:H2'	7:A:1248:U:O4'	2.11	0.51
7:A:2381:G:OP1	7:A:2382:C:N4	2.44	0.51
7:A:2435:A:H5'	14:H:33:ARG:NH2	2.25	0.51
28:W:56:ASP:OD1	28:W:58:THR:OG1	2.29	0.51
32:a:997:G:H2'	32:a:998:A:C8	2.46	0.51
32:a:1251:C:O2'	32:a:1275:C:O2	2.16	0.51
32:a:1278:A:H2'	32:a:1279:A:H4'	1.92	0.51
35:e:55:VAL:HG22	35:e:60:ARG:NH1	2.26	0.51
7:A:5:A:H2'	7:A:6:A:C8	2.46	0.51
7:A:287:G:C8	7:A:302:U:H2'	2.44	0.51
7:A:293:G:H8	7:A:338:G:H2'	1.75	0.51
7:A:332:C:H2'	7:A:333:U:H6	1.75	0.51
7:A:956:U:HO2'	7:A:2668:A:H2	1.58	0.51
7:A:2338:G:H2'	7:A:2339:U:C6	2.46	0.51
7:A:2423:U:H3'	7:A:2424:A:H5''	1.93	0.51
7:A:2567:A:H2'	7:A:2568:U:C6	2.46	0.51
7:A:2987:A:OP2	7:A:2988:A:O2'	2.28	0.51
12:F:147:GLU:OE1	12:F:147:GLU:N	2.41	0.51
32:a:698:U:OP1	41:k:97:LYS:NZ	2.29	0.51
32:a:913:U:H2'	32:a:914:U:H6	1.75	0.51
42:l:79:MET:HE3	42:l:102:LEU:HD13	1.93	0.51
49:s:39:THR:HG23	49:s:70:LYS:HE2	1.93	0.51
50:t:7:GLN:HG2	50:t:10:ARG:HB2	1.92	0.51
7:A:844:A:H2'	7:A:845:A:C8	2.46	0.50
7:A:1176:G:N2	7:A:1239:A:O2'	2.35	0.50
7:A:1647:U:H2'	7:A:1648:A:C8	2.43	0.50
7:A:1667:G:H2'	7:A:1668:C:C6	2.46	0.50
7:A:2375:C:N4	7:A:2391:G:O6	2.44	0.50
32:a:938:G:H21	32:a:1326:G:H4'	1.76	0.50
32:a:1348:G:O2'	32:a:1349:A:H5'	2.10	0.50
33:c:38:ILE:HD11	33:c:56:ILE:HD13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1209:C:H2'	7:A:1210:U:C6	2.46	0.50
7:A:2435:A:H5'	14:H:33:ARG:HH21	1.75	0.50
18:M:47:ILE:HD12	18:M:70:PRO:HG3	1.92	0.50
32:a:591:G:H2'	32:a:592:U:H6	1.75	0.50
33:c:129:PHE:CE2	33:c:130:ARG:HG3	2.45	0.50
37:g:90:GLU:H	37:g:90:GLU:CD	2.19	0.50
37:g:103:TRP:CD2	37:g:137:ARG:HG2	2.46	0.50
49:s:53:ASP:HB3	49:s:75:ALA:HB1	1.92	0.50
7:A:1733:A:H2'	7:A:1735:C:C5	2.46	0.50
32:a:670:C:H2'	32:a:671:C:H6	1.76	0.50
33:c:87:ARG:HH21	33:c:99:GLN:HA	1.75	0.50
35:e:106:PRO:HB3	35:e:180:ARG:HG2	1.93	0.50
7:A:355:C:H2'	7:A:356:A:C8	2.47	0.50
7:A:362:A:H2	7:A:442:G:HO2'	1.58	0.50
7:A:683:C:H2'	7:A:684:U:C6	2.46	0.50
7:A:752:G:O2'	7:A:2589:G:OP1	2.27	0.50
7:A:1297:A:H2'	7:A:1298:U:C6	2.46	0.50
32:a:410:A:O2'	32:a:412:G:N3	2.38	0.50
32:a:575:G:H2'	32:a:576:G:C8	2.47	0.50
32:a:792:U:H2'	32:a:793:A:C8	2.47	0.50
32:a:1234:G:H1	32:a:1287:U:H3	1.59	0.50
33:c:46:LEU:HD12	33:c:48:ARG:HH12	1.76	0.50
38:h:11:LEU:HD22	38:h:77:LEU:HD22	1.92	0.50
44:n:47:MET:HE1	44:n:52:GLU:HB2	1.92	0.50
7:A:640:C:H3'	7:A:641:U:C5'	2.42	0.50
7:A:1516:A:O2'	7:A:1527:U:O2	2.29	0.50
7:A:2100:A:N6	7:A:2113:G:O2'	2.44	0.50
7:A:2106:C:H2'	7:A:2107:A:O3'	2.12	0.50
10:D:36:VAL:HG23	10:D:37:THR:H	1.76	0.50
13:G:165:TYR:HB2	13:G:168:GLU:HG2	1.93	0.50
27:V:69:ILE:HG22	27:V:71:GLY:H	1.75	0.50
32:a:709:A:H2	48:r:47:LYS:HE2	1.76	0.50
32:a:1334:C:H2'	32:a:1335:G:C8	2.47	0.50
36:f:20:ALA:O	36:f:24:GLU:HG2	2.11	0.50
37:g:57:ASP:OD1	37:g:59:VAL:HG22	2.11	0.50
7:A:2603:A:OP1	28:W:55:GLY:N	2.44	0.50
7:A:2730:U:H2'	7:A:2731:U:C6	2.47	0.50
9:C:137:PRO:O	9:C:140:THR:OG1	2.25	0.50
12:F:109:ARG:HG2	12:F:113:ILE:HD11	1.92	0.50
15:J:14:SER:OG	15:J:52:ASP:OD1	2.28	0.50
27:V:87:ARG:NH2	27:V:91:GLN:HE21	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:648:U:O2'	45:o:22:THR:O	2.29	0.50
42:l:33:VAL:HG13	42:l:35:THR:HG23	1.92	0.50
7:A:743:U:H2'	7:A:744:C:H6	1.77	0.50
7:A:1600:C:N4	7:A:1605:G:H1	2.06	0.50
7:A:1742:U:H2'	7:A:1743:C:C6	2.46	0.50
7:A:1772:G:O2'	7:A:1775:G:N1	2.37	0.50
7:A:2541:G:H21	12:F:136:THR:HG21	1.77	0.50
7:A:2700:U:H2'	7:A:2701:U:C6	2.46	0.50
8:B:41:C:C6	12:F:73:GLU:HB2	2.47	0.50
17:L:85:LEU:HD11	17:L:102:ALA:HB2	1.94	0.50
19:N:103:ARG:HD3	19:N:110:MET:SD	2.51	0.50
32:a:943:U:H2'	32:a:944:G:C8	2.46	0.50
32:a:1253:A:H5'	32:a:1275:C:H4'	1.93	0.50
32:a:1418:A:H2'	32:a:1419:A:O4'	2.11	0.50
32:a:1420:C:H2'	32:a:1421:A:C8	2.46	0.50
33:c:53:ASP:HB2	33:c:68:HIS:HB2	1.93	0.50
43:m:88:GLN:HG2	43:m:98:VAL:HB	1.93	0.50
7:A:1903:A:O2'	7:A:1909:G:N7	2.43	0.50
31:Z:4:LEU:HG	31:Z:39:ASP:HB2	1.92	0.50
32:a:417:C:H2'	32:a:418:C:C6	2.47	0.50
32:a:545:U:H2'	32:a:546:C:C6	2.47	0.50
5:4:22:ARG:NH1	5:4:36:GLN:HB3	2.27	0.50
7:A:758:C:O2'	7:A:759:C:O4'	2.30	0.50
7:A:3047:G:H2'	7:A:3048:C:H6	1.77	0.50
32:a:191:C:N4	47:q:56:GLY:O	2.43	0.50
32:a:901:A:H2'	32:a:902:A:C8	2.47	0.50
32:a:1133:U:H2'	32:a:1134:G:C8	2.47	0.50
7:A:961:U:H2'	7:A:962:G:C8	2.47	0.49
7:A:2343:G:O6	7:A:2420:U:O2	2.30	0.49
7:A:2381:G:OP1	7:A:2384:A:N6	2.41	0.49
8:B:1:U:H2'	8:B:2:U:C6	2.47	0.49
14:H:4:ILE:HD13	14:H:46:GLN:HE22	1.77	0.49
15:J:67:ASP:OD1	15:J:67:ASP:N	2.41	0.49
16:K:45:ASP:OD2	16:K:46:ALA:N	2.45	0.49
17:L:103:VAL:HG21	17:L:109:VAL:HG22	1.94	0.49
32:a:406:G:OP1	34:d:107:ARG:NH1	2.44	0.49
32:a:504:A:H2'	32:a:505:C:H6	1.77	0.49
32:a:1012:A:O2'	32:a:1013:G:O4'	2.18	0.49
32:a:1135:G:H2'	32:a:1136:G:C8	2.46	0.49
7:A:308:G:O4'	14:H:41:ARG:NH1	2.45	0.49
7:A:442:G:H2'	7:A:443:C:H6	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2024:C:H2'	7:A:2025:A:C5	2.47	0.49
32:a:256:G:O6	32:a:269:A:N6	2.46	0.49
33:c:141:MET:HE1	33:c:149:ILE:HG22	1.94	0.49
41:k:122:ASP:OD1	41:k:124:THR:OG1	2.26	0.49
7:A:74:U:H3'	30:Y:48:ARG:HH22	1.77	0.49
32:a:485:G:H2'	32:a:487:A:H8	1.77	0.49
32:a:748:U:H2'	32:a:749:G:O4'	2.12	0.49
32:a:827:G:H1	32:a:843:U:H3	1.59	0.49
32:a:1100:C:H2'	32:a:1101:A:C8	2.47	0.49
35:e:87:VAL:HG23	35:e:88:PRO:HD3	1.94	0.49
37:g:42:ILE:HD13	37:g:116:MET:HB2	1.94	0.49
42:l:75:GLN:OE1	42:l:75:GLN:N	2.45	0.49
2:1:30:ARG:HA	2:1:30:ARG:NE	2.26	0.49
7:A:1627:C:N4	7:A:1628:G:O6	2.44	0.49
7:A:2371:A:H5''	7:A:2395:A:H4'	1.95	0.49
7:A:2740:G:H5''	7:A:2741:A:H5''	1.93	0.49
10:D:90:ASP:OD2	10:D:90:ASP:N	2.42	0.49
32:a:603:U:H2'	32:a:604:C:C6	2.47	0.49
32:a:655:G:N2	32:a:732:G:H1	2.05	0.49
7:A:778:G:O2'	7:A:779:U:H5'	2.13	0.49
7:A:957:U:H4'	7:A:960:G:N1	2.28	0.49
7:A:1713:G:O2'	7:A:1753:G:O6	2.22	0.49
32:a:225:G:H5''	47:q:50:ARG:HD3	1.94	0.49
32:a:674:G:H1	32:a:698:U:H3	1.59	0.49
32:a:818:U:H5''	38:h:22:HIS:CE1	2.47	0.49
33:c:42:LEU:O	33:c:46:LEU:HB3	2.12	0.49
35:e:70:VAL:O	35:e:78:GLY:N	2.44	0.49
39:i:141:LYS:HB2	39:i:144:LYS:HB3	1.94	0.49
43:m:81:LYS:HZ3	43:m:88:GLN:HB3	1.77	0.49
45:o:10:GLU:OE2	45:o:13:ARG:NH1	2.46	0.49
7:A:196:G:H2'	7:A:197:A:O4'	2.12	0.49
7:A:333:U:H2'	7:A:334:C:H6	1.78	0.49
7:A:1629:U:H2'	7:A:1630:G:H8	1.76	0.49
7:A:2809:C:O2'	10:D:156:THR:O	2.29	0.49
15:J:20:ALA:HB1	15:J:62:VAL:HG12	1.94	0.49
32:a:35:A:H2'	32:a:36:A:H8	1.76	0.49
32:a:36:A:N3	42:l:29:GLN:NE2	2.59	0.49
32:a:70:C:H2'	32:a:71:G:H8	1.76	0.49
32:a:699:C:H2'	32:a:700:A:H8	1.78	0.49
32:a:916:A:H2'	32:a:917:C:C6	2.48	0.49
37:g:130:GLY:HA2	37:g:135:VAL:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:736:A:H2'	7:A:737:A:C8	2.48	0.49
7:A:1231:C:H2'	7:A:1232:A:H8	1.77	0.49
23:R:52:ASP:OD1	23:R:54:LYS:N	2.44	0.49
24:S:21:ARG:HG2	24:S:21:ARG:HH11	1.78	0.49
32:a:1279:A:H2	32:a:1345:G:H1'	1.78	0.49
36:f:45:LYS:HD2	36:f:59:ILE:HG12	1.95	0.49
45:o:71:SER:HA	45:o:78:TYR:HB2	1.94	0.49
50:t:56:ARG:HH11	50:t:57:LYS:NZ	2.09	0.49
7:A:350:A:H2'	7:A:351:G:H8	1.75	0.49
7:A:2751:G:H2'	7:A:2752:U:C6	2.47	0.49
12:F:37:THR:O	12:F:166:SER:N	2.41	0.49
12:F:76:ARG:HD3	12:F:89:GLY:HA2	1.95	0.49
32:a:554:A:O2'	32:a:557:G:O3'	2.31	0.49
32:a:1011:U:N3	32:a:1012:A:N1	2.60	0.49
32:a:1232:U:H4'	37:g:38:LEU:HD11	1.94	0.49
40:j:7:ARG:HB3	40:j:101:GLN:HB2	1.95	0.49
7:A:385:G:H2'	7:A:386:G:H8	1.76	0.49
7:A:1215:A:H4'	7:A:1232:A:C2	2.48	0.49
7:A:2985:G:O6	7:A:2993:C:H5''	2.13	0.49
32:a:204:G:H2'	32:a:205:G:C8	2.47	0.49
32:a:230:A:H2'	32:a:231:G:H8	1.78	0.49
32:a:551:A:C4	35:e:159:LEU:HD22	2.47	0.49
32:a:569:C:O2'	32:a:719:A:N3	2.36	0.49
32:a:673:G:H2'	32:a:674:G:H8	1.77	0.49
32:a:1394:G:H2'	32:a:1395:4OC:O4'	2.13	0.49
33:c:119:VAL:O	33:c:123:LEU:HG	2.12	0.49
46:p:90:GLN:HE22	46:p:92:ARG:HB2	1.76	0.49
49:s:14:HIS:HA	49:s:17:LYS:HD3	1.93	0.49
7:A:1446:C:O2'	7:A:1523:G:N3	2.46	0.49
7:A:2338:G:O2'	7:A:2339:U:O4'	2.18	0.49
21:P:64:SER:OG	21:P:65:TYR:N	2.44	0.49
30:Y:36:MET:HE3	30:Y:36:MET:HA	1.95	0.49
32:a:104:A:H5'	32:a:105:C:H5	1.78	0.49
32:a:1008:A:H2'	32:a:1009:G:C8	2.47	0.49
32:a:1456:U:H2'	32:a:1457:G:H8	1.78	0.49
34:d:141:ARG:HB2	34:d:144:SER:HB3	1.95	0.49
48:r:22:PHE:HB2	48:r:60:HIS:HD1	1.78	0.49
7:A:224:A:H3'	7:A:510:U:H5'	1.95	0.48
7:A:832:U:H2'	7:A:833:G:O4'	2.11	0.48
7:A:1947:A:H3'	7:A:1948:A:H2'	1.95	0.48
7:A:2166:A:H2'	7:A:2167:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2627:G:H5'	7:A:2628:U:O4'	2.13	0.48
7:A:2775:U:H2'	7:A:2776:C:H6	1.77	0.48
32:a:428:U:H5'	34:d:9:THR:OG1	2.12	0.48
32:a:572:G:N1	32:a:750:A:OP2	2.42	0.48
32:a:748:U:OP1	32:a:813:G:O2'	2.31	0.48
32:a:1199:C:H2'	32:a:1200:C:H6	1.78	0.48
32:a:1242:A:H2'	32:a:1243:A:H8	1.78	0.48
43:m:91:ARG:HE	43:m:96:MET:HG2	1.78	0.48
7:A:2551:C:OP2	12:F:78:ARG:NH1	2.42	0.48
32:a:603:U:H2'	32:a:604:C:H6	1.78	0.48
32:a:753:A:H2'	32:a:754:G:H8	1.77	0.48
32:a:972:C:OP1	32:a:1215:C:N4	2.47	0.48
32:a:1211:A:H2'	32:a:1212:G:H8	1.77	0.48
33:c:112:ALA:C	33:c:114:LEU:H	2.21	0.48
7:A:1216:G:O2'	7:A:1218:G:H5'	2.13	0.48
7:A:1446:C:H2'	7:A:1447:U:C6	2.49	0.48
7:A:2231:U:H4'	10:D:138:SER:HB3	1.96	0.48
13:G:46:ASN:ND2	13:G:47:ASP:OD1	2.45	0.48
31:Z:46:LEU:O	31:Z:50:VAL:HG22	2.13	0.48
32:a:65:U:H3	32:a:100:G:H1	1.61	0.48
32:a:404:U:OP1	34:d:3:ARG:NH2	2.46	0.48
32:a:456:C:H2'	32:a:457:G:H8	1.78	0.48
32:a:582:U:H2'	32:a:583:G:C8	2.49	0.48
32:a:672:U:H2'	32:a:673:G:H8	1.78	0.48
32:a:728:C:H2'	32:a:729:U:H6	1.78	0.48
32:a:1405:C:H2'	32:a:1406:A:H8	1.79	0.48
7:A:2392:C:H2'	7:A:2393:G:C4	2.48	0.48
8:B:38:A:C2	8:B:43:G:C2	3.02	0.48
12:F:15:TYR:HA	12:F:19:ILE:HG13	1.95	0.48
13:G:17:VAL:HG22	13:G:26:VAL:HG12	1.95	0.48
13:G:128:ALA:HB3	13:G:131:LYS:HB2	1.94	0.48
32:a:145:A:H1'	32:a:1439:A:C2	2.47	0.48
32:a:492:C:H2'	32:a:493:A:H8	1.79	0.48
32:a:874:G:P	42:l:9:ARG:HH22	2.35	0.48
42:l:24:LEU:HA	42:l:30:ARG:HG3	1.96	0.48
50:t:55:ASN:OD1	50:t:79:LEU:HD11	2.13	0.48
7:A:858:G:C5	9:C:208:LYS:HB2	2.48	0.48
7:A:1053:U:H2'	7:A:1054:G:C8	2.48	0.48
7:A:1905:C:O2	10:D:139:HIS:NE2	2.43	0.48
27:V:53:ALA:O	27:V:57:ARG:HG2	2.13	0.48
32:a:728:C:H2'	32:a:729:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:h:10:PHE:HD1	38:h:27:LEU:HD11	1.78	0.48
40:j:57:LYS:HG2	40:j:57:LYS:O	2.13	0.48
7:A:231:U:H2'	7:A:232:G:O4'	2.14	0.48
7:A:454:U:H2'	7:A:455:U:H6	1.78	0.48
7:A:652:G:H2'	7:A:653:U:H5''	1.95	0.48
32:a:1047:U:H2'	32:a:1048:G:C8	2.49	0.48
32:a:1218:C:OP2	43:m:91:ARG:NH2	2.46	0.48
35:e:173:ALA:O	35:e:177:LEU:HD22	2.13	0.48
37:g:75:VAL:HG22	37:g:86:GLN:HB3	1.94	0.48
43:m:12:ASP:HB2	43:m:46:ARG:NH2	2.28	0.48
46:p:74:LEU:HD13	46:p:79:ASP:HB3	1.94	0.48
7:A:677:A:OP2	7:A:2737:C:O2'	2.32	0.48
7:A:1825:A:H2'	7:A:1826:C:C6	2.48	0.48
7:A:2297:A:N1	53:A:3201:WDP:O86	2.47	0.48
7:A:2363:A:H5'	7:A:2364:G:H5'	1.95	0.48
7:A:2552:A:H2'	7:A:2553:G:H8	1.79	0.48
8:B:110:C:H2'	8:B:111:G:H8	1.78	0.48
9:C:186:ASP:OD1	9:C:187:VAL:N	2.47	0.48
32:a:413:A:H8	32:a:430:A:C2	2.30	0.48
32:a:444:U:H2'	32:a:445:C:C6	2.49	0.48
32:a:544:G:H2'	32:a:545:U:C6	2.49	0.48
33:c:180:ALA:HA	33:c:206:ASP:HA	1.96	0.48
43:m:20:THR:HG21	43:m:27:ARG:HD2	1.95	0.48
7:A:488:U:H2'	7:A:489:G:O4'	2.14	0.48
7:A:691:C:H2'	7:A:692:A:C8	2.48	0.48
7:A:1548:G:O2'	7:A:1820:A:N1	2.36	0.48
7:A:1917:C:H2'	7:A:1918:C:C6	2.49	0.48
7:A:2111:G:H2'	7:A:2112:U:C6	2.49	0.48
7:A:2537:A:H61	7:A:2555:U:H3	1.62	0.48
7:A:2741:A:C8	53:A:3201:WDP:O02	2.67	0.48
32:a:41:G:H4'	32:a:538:A:C6	2.48	0.48
32:a:426:U:H3'	32:a:427:G:H8	1.79	0.48
32:a:504:A:H2'	32:a:505:C:C6	2.49	0.48
32:a:829:U:H3	32:a:841:G:H1	1.62	0.48
45:o:82:ILE:HD12	45:o:87:LEU:HB2	1.95	0.48
47:q:68:ASP:N	47:q:68:ASP:OD1	2.46	0.48
7:A:143:G:H5'	7:A:144:U:OP2	2.14	0.48
7:A:285:G:C2	7:A:303:U:O2	2.66	0.48
7:A:1263:G:C2	51:v:7:LYS:HG3	2.49	0.48
7:A:2032:U:OP2	9:C:272:ARG:NH2	2.43	0.48
7:A:2880:A:H2'	7:A:2881:A:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:71:ASP:OD1	9:C:71:ASP:N	2.39	0.48
13:G:76:LEU:O	13:G:80:VAL:HG23	2.14	0.48
32:a:83:U:H1'	32:a:86:G:H1'	1.95	0.48
32:a:172:C:H2'	32:a:173:G:H8	1.79	0.48
32:a:269:A:H2'	32:a:270:C:H6	1.78	0.48
32:a:462:C:H5''	32:a:463:U:C5	2.46	0.48
32:a:1050:C:OP2	33:c:199:LYS:NZ	2.36	0.48
32:a:1211:A:H2'	32:a:1212:G:C8	2.49	0.48
32:a:1365:U:OP1	39:i:95:GLY:N	2.45	0.48
32:a:1505:U:H2'	32:a:1506:A:H8	1.77	0.48
1:O:41:ARG:NH1	7:A:3121:G:O4'	2.47	0.48
7:A:2529:U:H2'	7:A:2530:U:C6	2.49	0.48
7:A:3100:U:OP2	7:A:3101:G:O2'	2.26	0.48
19:N:79:LEU:HA	19:N:83:ILE:HD12	1.95	0.48
32:a:11:A:N6	34:d:201:LYS:HB2	2.29	0.48
7:A:362:A:N1	7:A:442:G:H1'	2.29	0.47
7:A:1641:U:H2'	7:A:1642:G:H8	1.77	0.47
7:A:2225:C:H2'	7:A:2226:A:H8	1.79	0.47
10:D:104:GLU:OE2	10:D:104:GLU:N	2.45	0.47
26:U:89:GLU:CA	26:U:91:THR:H	2.25	0.47
27:V:99:ARG:H	27:V:99:ARG:CD	2.27	0.47
32:a:359:G:H2'	32:a:360:G:C8	2.48	0.47
32:a:719:A:H2'	32:a:720:A:C8	2.49	0.47
32:a:1467:G:H2'	32:a:1468:G:O4'	2.14	0.47
33:c:156:ARG:HH21	33:c:161:GLU:HA	1.79	0.47
41:k:65:SER:OG	41:k:66:ARG:NH1	2.46	0.47
7:A:1509:A:O2'	7:A:1511:G:N7	2.47	0.47
7:A:1720:G:H2'	7:A:1721:A:H8	1.78	0.47
7:A:3047:G:H2'	7:A:3048:C:C6	2.49	0.47
53:A:3201:WDP:C38	53:A:3201:WDP:C16	2.91	0.47
11:E:19:LYS:HD3	11:E:19:LYS:N	2.28	0.47
11:E:198:ASP:OD2	17:L:4:LYS:NZ	2.31	0.47
13:G:53:VAL:HG21	13:G:70:ARG:HB2	1.96	0.47
17:L:24:GLY:O	17:L:29:GLY:HA2	2.13	0.47
22:Q:19:LYS:HE2	22:Q:19:LYS:HB2	1.66	0.47
23:R:50:THR:O	23:R:52:ASP:N	2.46	0.47
32:a:683:U:OP2	41:k:38:ASN:ND2	2.37	0.47
32:a:806:A:N7	32:a:1502:C:O2'	2.41	0.47
32:a:876:C:H2'	32:a:877:U:C6	2.49	0.47
32:a:1305:U:H2'	32:a:1306:C:H6	1.79	0.47
32:a:1339:G:H8	39:i:130:ARG:HB3	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:42:LEU:HD22	39:i:111:VAL:HG21	1.96	0.47
43:m:13:LYS:HZ2	43:m:14:ARG:H	1.60	0.47
49:s:32:LYS:HD3	49:s:32:LYS:HA	1.72	0.47
7:A:289:A:H1'	7:A:304:G:H1'	1.97	0.47
7:A:340:U:H3	7:A:341:A:H62	1.61	0.47
7:A:2270:G:OP1	7:A:2692:G:O2'	2.25	0.47
32:a:20:U:H2'	32:a:21:C:C6	2.50	0.47
32:a:29:A:N6	32:a:549:G:H1'	2.29	0.47
32:a:492:C:H5''	42:l:114:ARG:NH2	2.29	0.47
32:a:1144:G:OP1	40:j:72:ARG:NH1	2.38	0.47
32:a:1163:C:H2'	32:a:1164:U:C6	2.49	0.47
34:d:69:ARG:HA	34:d:72:GLU:HG2	1.96	0.47
43:m:15:MET:HA	43:m:18:ALA:HB3	1.96	0.47
5:4:12:ASP:OD1	5:4:12:ASP:N	2.47	0.47
6:6:1:MET:SD	6:6:1:MET:N	2.75	0.47
7:A:368:U:H2'	7:A:369:C:C6	2.49	0.47
11:E:11:ILE:HD11	11:E:24:ILE:HB	1.96	0.47
12:F:21:ASP:O	12:F:25:LYS:HG2	2.14	0.47
32:a:423:G:H2'	32:a:424:G:C8	2.49	0.47
32:a:452:G:O6	32:a:471:U:O4	2.32	0.47
32:a:469:A:H2'	32:a:470:U:C6	2.50	0.47
32:a:775:A:H2'	32:a:776:G:C8	2.50	0.47
32:a:1155:G:H2'	32:a:1156:G:H8	1.80	0.47
32:a:1243:A:N3	32:a:1362:C:O2'	2.35	0.47
41:k:56:SER:H	41:k:59:HIS:HB3	1.78	0.47
41:k:63:LYS:HA	41:k:63:LYS:HD2	1.66	0.47
7:A:1129:A:H2'	7:A:1130:A:C8	2.49	0.47
7:A:2303:C:H1'	7:A:2687:U:N3	2.29	0.47
11:E:109:PRO:HG2	11:E:112:MET:HE3	1.97	0.47
16:K:63:VAL:HG12	16:K:106:LEU:HD11	1.96	0.47
20:O:114:ALA:O	20:O:118:ASN:HB2	2.14	0.47
32:a:108:G:H2'	32:a:109:U:C6	2.49	0.47
32:a:132:C:O2'	46:p:63:GLY:O	2.29	0.47
32:a:177:A:C4	32:a:206:A:N6	2.82	0.47
32:a:207:A:H8	32:a:221:U:H1'	1.79	0.47
32:a:970:A:N6	32:a:1216:U:O4'	2.48	0.47
32:a:1311:A:H3'	49:s:3:ARG:NE	2.29	0.47
32:a:1500:A:H2'	32:a:1501:G:C8	2.49	0.47
34:d:75:VAL:HA	34:d:81:THR:HG22	1.96	0.47
40:j:52:ILE:H	44:n:41:ARG:HE	1.62	0.47
44:n:47:MET:HE3	44:n:47:MET:HB3	1.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:11:ILE:HD13	2:1:27:LYS:HG2	1.97	0.47
8:B:13:C:OP2	8:B:69:C:O2'	2.32	0.47
20:O:82:LEU:HG	20:O:86:ARG:HH22	1.80	0.47
27:V:51:ASP:OD1	27:V:52:TYR:N	2.48	0.47
32:a:275:G:H5'	47:q:70:MET:CE	2.45	0.47
32:a:775:A:H2'	32:a:776:G:H8	1.79	0.47
32:a:1498:G:N3	32:a:1498:G:H2'	2.30	0.47
32:a:1509:2MG:N2	32:a:1512:MA6:OP2	2.48	0.47
33:c:46:LEU:HA	33:c:48:ARG:NH1	2.27	0.47
7:A:683:C:H2'	7:A:684:U:H6	1.80	0.47
7:A:1110:A:OP2	7:A:1111:C:N4	2.40	0.47
7:A:1212:G:O2'	7:A:1215:A:N6	2.48	0.47
7:A:1304:U:O2'	7:A:1305:U:O5'	2.30	0.47
13:G:22:GLN:NE2	13:G:41:ILE:O	2.47	0.47
15:J:74:VAL:HG21	15:J:92:LEU:HD12	1.97	0.47
17:L:83:ASN:HB2	17:L:117:LEU:HD12	1.95	0.47
26:U:88:ASP:O	26:U:89:GLU:HG2	2.15	0.47
27:V:69:ILE:N	27:V:72:LYS:O	2.47	0.47
32:a:23:U:H2'	32:a:24:G:O4'	2.15	0.47
32:a:235:G:H5''	47:q:95:LYS:NZ	2.30	0.47
32:a:409:G:H4'	32:a:410:A:H5'	1.97	0.47
32:a:470:U:H2'	32:a:471:U:C6	2.50	0.47
32:a:699:C:H2'	32:a:700:A:C8	2.49	0.47
32:a:1116:U:O2'	32:a:1117:U:O5'	2.26	0.47
32:a:1242:A:C2	32:a:1363:G:H1'	2.50	0.47
39:i:32:ARG:HG2	39:i:37:VAL:HG22	1.97	0.47
39:i:54:ARG:HD2	39:i:59:TYR:HD1	1.80	0.47
42:l:82:VAL:HG22	42:l:97:ILE:HD13	1.96	0.47
45:o:18:HIS:O	45:o:20:THR:N	2.47	0.47
7:A:455:U:H2'	7:A:456:C:H6	1.80	0.47
7:A:1682:U:H2'	7:A:1683:A:H8	1.79	0.47
7:A:1958:C:H5	7:A:1971:G:H21	1.63	0.47
7:A:2746:G:O2'	7:A:2792:U:O2'	2.20	0.47
16:K:17:LYS:NZ	16:K:47:ILE:HG22	2.29	0.47
24:S:44:ASP:HA	24:S:47:ARG:HB3	1.96	0.47
32:a:1062:C:H2'	32:a:1063:G:H8	1.80	0.47
32:a:1253:A:C2	32:a:1254:U:H1'	2.50	0.47
46:p:67:THR:OG1	46:p:69:PRO:HD2	2.15	0.47
7:A:992:A:H2'	7:A:993:G:C8	2.50	0.47
7:A:2577:G:H2'	7:A:2578:A:C8	2.50	0.47
17:L:73:GLU:OE2	17:L:73:GLU:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:L:81:ASP:O	17:L:85:LEU:HG	2.15	0.47
19:N:110:MET:HE3	19:N:110:MET:HB3	1.77	0.47
24:S:118:GLU:OE2	24:S:120:ARG:NH1	2.47	0.47
32:a:369:C:H2'	32:a:370:A:C8	2.50	0.47
32:a:444:U:H3	32:a:480:G:H1	1.63	0.47
32:a:700:A:H2'	32:a:701:G:H8	1.80	0.47
32:a:1007:G:H2'	32:a:1008:A:C4	2.50	0.47
32:a:1365:U:H5''	39:i:94:SER:HB3	1.97	0.47
39:i:70:LYS:HB3	39:i:70:LYS:HE2	1.66	0.47
43:m:13:LYS:HE3	43:m:17:VAL:HB	1.95	0.47
7:A:979:A:H2'	7:A:980:C:C6	2.50	0.47
7:A:2093:A:OP2	7:A:2121:G:N2	2.48	0.47
7:A:2771:C:OP1	7:A:2903:A:O2'	2.32	0.47
7:A:3071:U:H2'	7:A:3072:A:H8	1.78	0.47
15:J:135:GLN:O	15:J:137:PRO:HD3	2.15	0.47
22:Q:58:ARG:HA	22:Q:61:TRP:CE3	2.50	0.47
32:a:74:A:N1	32:a:94:C:O2'	2.42	0.47
32:a:946:G:H2'	32:a:947:G:C8	2.49	0.47
33:c:118:GLY:O	33:c:122:GLN:HG2	2.14	0.47
43:m:51:GLU:OE1	43:m:55:HIS:HE1	1.98	0.47
7:A:635:U:O4	7:A:648:G:O6	2.33	0.46
7:A:843:U:O2	7:A:846:G:H8	1.98	0.46
7:A:943:C:H1'	7:A:1356:G:N2	2.30	0.46
7:A:1629:U:H2'	7:A:1630:G:C8	2.50	0.46
7:A:2761:G:O2'	7:A:3002:A:O2'	2.32	0.46
13:G:87:LYS:NZ	13:G:133:THR:HG23	2.30	0.46
27:V:37:GLY:HA3	27:V:97:VAL:HG22	1.97	0.46
32:a:12:G:H5'	35:e:139:GLY:HA3	1.96	0.46
32:a:180:A:H8	50:t:76:LYS:HZ1	1.60	0.46
32:a:269:A:H2'	32:a:270:C:C6	2.50	0.46
32:a:630:G:O6	32:a:631:A:N6	2.48	0.46
40:j:66:GLU:O	44:n:57:GLN:NE2	2.48	0.46
46:p:68:GLU:HG2	46:p:69:PRO:HD3	1.96	0.46
7:A:448:U:H2'	7:A:449:A:C8	2.50	0.46
7:A:1546:G:H2'	7:A:1547:C:H6	1.79	0.46
7:A:2302:C:H2'	7:A:2303:C:H6	1.80	0.46
18:M:32:TYR:OH	18:M:111:GLU:HG3	2.16	0.46
32:a:206:A:H8	32:a:221:U:O2'	1.97	0.46
32:a:1141:C:H2'	32:a:1142:G:C8	2.50	0.46
32:a:1199:C:H2'	32:a:1200:C:C6	2.50	0.46
32:a:1392:C:O2	32:a:1495:A:N6	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:63:VAL:HB	33:c:98:VAL:HG22	1.97	0.46
40:j:54:SER:HB3	40:j:58:TYR:HB2	1.97	0.46
49:s:12:ASP:HB3	49:s:14:HIS:HD2	1.76	0.46
7:A:636:U:O2'	7:A:637:C:H6	1.99	0.46
7:A:748:A:H2'	7:A:750:A:C8	2.50	0.46
7:A:978:C:H2'	7:A:979:A:H8	1.79	0.46
7:A:1720:G:H2'	7:A:1721:A:C8	2.50	0.46
7:A:2311:U:H2'	7:A:2312:U:C6	2.50	0.46
7:A:2371:A:H8	7:A:2395:A:H5'	1.80	0.46
7:A:2372:A:N1	7:A:2393:G:O2'	2.47	0.46
7:A:2975:G:H2'	7:A:2976:A:C8	2.50	0.46
32:a:18:G:H1'	35:e:60:ARG:NH1	2.30	0.46
32:a:516:C:O2'	32:a:517:C:H5'	2.15	0.46
32:a:633:A:N3	38:h:107:SER:OG	2.46	0.46
32:a:1505:U:H2'	32:a:1506:A:C8	2.50	0.46
35:e:96:GLU:O	35:e:100:LYS:HD2	2.16	0.46
37:g:26:LEU:O	37:g:30:VAL:HG22	2.15	0.46
42:l:88:LYS:HA	42:l:88:LYS:HD2	1.72	0.46
7:A:219:G:H2'	7:A:220:G:C8	2.51	0.46
7:A:1588:U:H2'	7:A:1589:C:C6	2.50	0.46
7:A:2087:A:H2'	7:A:2088:A:H8	1.77	0.46
7:A:2442:A:H2'	7:A:2443:A:H8	1.81	0.46
12:F:64:LEU:O	12:F:68:THR:OG1	2.31	0.46
12:F:85:LYS:HA	12:F:85:LYS:HD2	1.73	0.46
16:K:98:ILE:HB	16:K:118:ALA:HA	1.98	0.46
32:a:625:C:H2'	32:a:626:G:C8	2.50	0.46
32:a:948:A:H2'	32:a:949:U:C6	2.51	0.46
32:a:969:G:OP2	32:a:1350:U:O2'	2.33	0.46
32:a:1055:G:H5'	32:a:1057:C:H5'	1.98	0.46
32:a:1139:C:H2'	32:a:1140:U:C6	2.50	0.46
32:a:1524:A:H2'	32:a:1525:U:C6	2.51	0.46
33:c:150:ARG:HB2	33:c:173:VAL:HG21	1.98	0.46
36:f:47:ARG:C	36:f:47:ARG:HD2	2.41	0.46
45:o:70:ILE:HA	45:o:73:ILE:HG22	1.97	0.46
5:4:11:CYS:HB3	5:4:32:HIS:HE1	1.81	0.46
7:A:753:G:H2'	7:A:754:C:C6	2.51	0.46
7:A:954:A:O2'	17:L:53:GLN:OE1	2.27	0.46
7:A:1192:G:H2'	7:A:1193:C:C6	2.50	0.46
7:A:1648:A:H3'	7:A:1649:G:H8	1.80	0.46
7:A:2479:A:H2'	7:A:2480:G:C8	2.50	0.46
7:A:2883:C:H4'	7:A:2970:G:O2'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:204:G:O2'	50:t:59:ASP:OD2	2.22	0.46
32:a:217:G:H2'	32:a:218:C:O4'	2.16	0.46
32:a:375:G:OP1	46:p:67:THR:OG1	2.17	0.46
32:a:706:A:H2'	32:a:707:A:H8	1.78	0.46
36:f:12:PRO:HA	36:f:45:LYS:HZ3	1.80	0.46
7:A:1635:C:H3'	7:A:1636:U:C5	2.51	0.46
7:A:2886:G:H2'	7:A:2887:U:C6	2.51	0.46
8:B:111:G:H2'	8:B:112:A:H8	1.79	0.46
20:O:65:VAL:HG22	20:O:66:ARG:HH21	1.81	0.46
32:a:20:U:H2'	32:a:21:C:H6	1.80	0.46
32:a:915:G:H5''	35:e:57:LYS:HZ1	1.80	0.46
32:a:971:A:C8	32:a:972:C:H5	2.33	0.46
32:a:1307:U:H2'	32:a:1308:G:C8	2.51	0.46
32:a:1385:G:H2'	32:a:1386:U:C6	2.50	0.46
7:A:744:C:H2'	7:A:745:U:C6	2.50	0.46
7:A:1825:A:H2'	7:A:1826:C:H6	1.80	0.46
18:M:35:GLN:OE1	18:M:130:ARG:NH2	2.40	0.46
32:a:229:G:H2'	32:a:230:A:O4'	2.16	0.46
32:a:1315:G:N2	32:a:1353:G:O2'	2.47	0.46
7:A:368:U:H2'	7:A:369:C:H6	1.81	0.46
7:A:987:G:N3	7:A:2506:A:H2'	2.31	0.46
7:A:1958:C:H3'	7:A:1959:A:H8	1.80	0.46
9:C:101:GLU:OE2	9:C:103:ARG:NE	2.49	0.46
10:D:36:VAL:HG23	10:D:37:THR:N	2.31	0.46
12:F:38:VAL:HA	12:F:165:THR:HA	1.97	0.46
12:F:127:LYS:HA	12:F:127:LYS:HD3	1.74	0.46
15:J:3:THR:HG21	22:Q:61:TRP:HE1	1.81	0.46
21:P:25:ILE:HD13	21:P:85:VAL:HA	1.97	0.46
32:a:566:G:O2'	32:a:812:G:OP2	2.31	0.46
32:a:1516:G:OP1	41:k:138:ARG:NH1	2.49	0.46
47:q:58:ARG:HD3	47:q:115:MET:SD	2.56	0.46
50:t:36:ARG:HG3	50:t:40:HIS:CE1	2.51	0.46
6:6:42:HIS:ND1	6:6:43:PRO:O	2.49	0.46
7:A:61:G:OP1	30:Y:45:ARG:NH2	2.48	0.46
7:A:1098:G:H2'	7:A:1099:U:C6	2.51	0.46
7:A:1198:A:N6	7:A:1202:A:OP1	2.48	0.46
7:A:2102:C:H2'	7:A:2103:C:C6	2.50	0.46
7:A:2250:G:N7	24:S:26:LYS:NZ	2.63	0.46
12:F:79:LYS:HE3	12:F:80:SER:H	1.81	0.46
32:a:584:U:H3	32:a:637:G:H1	1.64	0.46
32:a:770:C:H2'	32:a:771:G:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:978:C:H2'	32:a:979:U:C6	2.51	0.46
32:a:1008:A:N3	32:a:1210:C:O2'	2.41	0.46
32:a:1334:C:H2'	32:a:1335:G:H8	1.80	0.46
32:a:1459:C:H2'	32:a:1460:G:O4'	2.15	0.46
32:a:1523:G:C6	32:a:1524:A:C6	3.04	0.46
34:d:31:TYR:O	34:d:33:PRO:HD3	2.16	0.46
34:d:93:LEU:HG	34:d:130:TYR:HB3	1.97	0.46
35:e:139:GLY:O	35:e:143:ARG:HB3	2.16	0.46
42:l:6:GLN:HG2	42:l:9:ARG:HH21	1.81	0.46
45:o:10:GLU:O	45:o:13:ARG:HG3	2.16	0.46
7:A:291:C:O2'	7:A:304:G:H4'	2.15	0.46
7:A:1178:C:C2	7:A:1179:A:C8	3.03	0.46
7:A:1525:U:H2'	7:A:1526:A:O4'	2.16	0.46
8:B:41:C:N4	12:F:95:ARG:HH12	2.14	0.46
13:G:131:LYS:NZ	13:G:166:GLU:OE1	2.48	0.46
15:J:92:LEU:HD23	15:J:92:LEU:HA	1.77	0.46
21:P:105:LYS:HZ3	21:P:106:LYS:HD3	1.81	0.46
32:a:679:G:O5'	41:k:59:HIS:HA	2.16	0.46
32:a:1077:U:H3	32:a:1090:G:H1	1.63	0.46
32:a:1127:U:H2'	32:a:1128:A:C8	2.51	0.46
32:a:1292:G:H1'	32:a:1295:C:N4	2.31	0.46
34:d:87:LYS:HD2	34:d:180:LEU:HD13	1.97	0.46
34:d:108:MET:SD	34:d:108:MET:N	2.88	0.46
7:A:2365:A:OP2	7:A:2366:C:N4	2.49	0.45
7:A:2431:A:H2'	7:A:2432:U:C6	2.51	0.45
8:B:61:U:H2'	8:B:62:G:H8	1.81	0.45
11:E:147:ALA:O	11:E:151:LEU:HD23	2.16	0.45
23:R:52:ASP:OD1	23:R:52:ASP:C	2.59	0.45
23:R:62:THR:H	23:R:102:GLY:HA3	1.80	0.45
32:a:137:A:H2'	32:a:138:C:C6	2.51	0.45
37:g:16:PRO:HG2	39:i:63:LYS:HB3	1.98	0.45
43:m:65:LYS:HG2	43:m:69:ASP:OD1	2.16	0.45
46:p:19:ARG:HA	46:p:39:ARG:HA	1.98	0.45
6:6:26:SER:OG	6:6:27:THR:N	2.49	0.45
7:A:335:A:H2'	7:A:336:G:C8	2.51	0.45
7:A:1739:C:H2'	7:A:1740:G:H8	1.82	0.45
7:A:1981:C:H2'	7:A:1982:C:C6	2.51	0.45
7:A:2170:A:H2'	7:A:2171:G:O4'	2.16	0.45
7:A:2297:A:H1'	53:A:3201:WDP:C18	2.43	0.45
7:A:2384:A:H3'	7:A:2385:G:C8	2.52	0.45
12:F:128:GLN:HB2	12:F:135:TYR:CE1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:120:GLU:H	13:G:120:GLU:CD	2.24	0.45
32:a:490:A:H4'	32:a:491:G:H5'	1.98	0.45
32:a:570:U:H2'	32:a:571:C:C6	2.50	0.45
32:a:1500:A:C6	32:a:1523:G:C6	3.04	0.45
36:f:54:LYS:HE2	36:f:54:LYS:HB2	1.88	0.45
43:m:34:LEU:HD22	43:m:39:ILE:HG23	1.97	0.45
7:A:58:G:H2'	7:A:59:U:C6	2.52	0.45
7:A:328:A:H1'	7:A:449:A:N1	2.31	0.45
7:A:1281:G:N2	22:Q:77:ASN:HD21	2.13	0.45
7:A:2509:G:OP1	28:W:18:ALA:HB1	2.16	0.45
7:A:2887:U:H2'	7:A:2888:C:H6	1.80	0.45
12:F:66:LEU:HD11	12:F:148:VAL:HB	1.98	0.45
19:N:36:THR:OG1	19:N:37:THR:N	2.49	0.45
32:a:76:G:H2'	32:a:77:G:C8	2.51	0.45
32:a:134:U:H2'	32:a:135:G:H8	1.80	0.45
32:a:334:C:O2'	32:a:1426:A:N3	2.47	0.45
32:a:503:U:H2'	32:a:504:A:C8	2.52	0.45
32:a:870:C:OP1	38:h:82:LYS:NZ	2.41	0.45
32:a:1149:A:H5'	32:a:1150:C:C6	2.51	0.45
32:a:1226:C:H2'	32:a:1227:U:C6	2.52	0.45
32:a:1506:A:H2'	32:a:1507:C:C6	2.50	0.45
34:d:154:ARG:HD2	34:d:173:GLN:HE22	1.81	0.45
36:f:10:LEU:HB2	36:f:59:ILE:HB	1.97	0.45
39:i:140:LYS:HA	39:i:140:LYS:HD3	1.62	0.45
42:l:69:GLY:HA3	42:l:107:VAL:HG21	1.97	0.45
7:A:431:A:H2'	7:A:432:C:C6	2.51	0.45
7:A:1131:G:H5''	51:v:15:LYS:HG2	1.98	0.45
7:A:2795:G:H2'	7:A:2796:C:C6	2.51	0.45
7:A:2969:G:H4'	10:D:178:LEU:HD12	1.98	0.45
13:G:12:PRO:HG2	13:G:81:THR:HG21	1.99	0.45
21:P:36:LYS:HE2	21:P:36:LYS:HA	1.98	0.45
32:a:379:G:N2	32:a:382:A:OP2	2.49	0.45
32:a:585:C:H2'	32:a:586:G:O4'	2.16	0.45
32:a:742:U:H2'	32:a:743:G:O4'	2.16	0.45
33:c:120:ALA:HA	33:c:189:ALA:HB2	1.98	0.45
33:c:145:ASN:OD1	33:c:145:ASN:N	2.49	0.45
1:0:8:LYS:HE3	1:0:12:ASN:HB3	1.98	0.45
7:A:1295:A:H2'	7:A:1296:C:C6	2.52	0.45
7:A:1750:C:H2'	7:A:1751:C:C6	2.51	0.45
7:A:3092:G:N2	7:A:3095:A:OP2	2.32	0.45
7:A:3132:U:O2	15:J:134:ALA:HB1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:113:ASP:OD2	10:D:178:LEU:HA	2.17	0.45
20:O:21:ARG:NH2	20:O:49:ASP:OD1	2.49	0.45
32:a:59:U:H2'	32:a:60:G:C8	2.52	0.45
32:a:206:A:H2'	32:a:207:A:N3	2.32	0.45
32:a:410:A:N6	34:d:29:ARG:HD2	2.31	0.45
32:a:501:A:N3	32:a:534:U:H1'	2.31	0.45
32:a:592:U:H2'	32:a:593:U:C6	2.51	0.45
36:f:4:TYR:CD2	36:f:72:VAL:HG21	2.50	0.45
43:m:96:MET:HE2	43:m:96:MET:HB2	1.74	0.45
47:q:119:PRO:HA	47:q:125:ARG:HD3	1.99	0.45
7:A:252:G:H2'	7:A:253:A:C8	2.52	0.45
7:A:1245:U:H2'	7:A:1246:U:H6	1.81	0.45
27:V:84:HIS:HD2	27:V:87:ARG:HH21	1.64	0.45
32:a:74:A:C6	32:a:95:G:C8	3.05	0.45
32:a:787:C:O3'	41:k:137:ARG:NH2	2.46	0.45
35:e:141:ALA:HB1	35:e:168:VAL:HG23	1.98	0.45
37:g:66:LEU:HD12	37:g:67:ASP:N	2.32	0.45
7:A:1025:A:H5''	7:A:1026:C:H5	1.82	0.45
7:A:2594:U:H2'	7:A:2595:U:O4'	2.17	0.45
7:A:2893:G:H1'	7:A:2894:U:H5	1.81	0.45
7:A:3089:U:H2'	7:A:3090:C:H6	1.81	0.45
12:F:80:SER:OG	12:F:88:GLU:N	2.50	0.45
25:T:68:ARG:HB3	25:T:73:TYR:CE1	2.51	0.45
32:a:340:C:H2'	32:a:341:C:H6	1.81	0.45
32:a:499:C:H1'	32:a:500:A:N7	2.32	0.45
32:a:530:A:H2'	32:a:531:G:C8	2.52	0.45
32:a:1516:G:H2'	32:a:1517:C:C6	2.52	0.45
46:p:20:VAL:H	46:p:39:ARG:HA	1.82	0.45
47:q:70:MET:HB3	47:q:73:THR:HB	1.98	0.45
7:A:1221:C:H3'	7:A:1222:G:H8	1.82	0.45
7:A:1560:U:H5''	7:A:1561:C:H5	1.81	0.45
7:A:2602:C:H2'	7:A:2603:A:O4'	2.16	0.45
15:J:125:TYR:OH	15:J:132:HIS:NE2	2.41	0.45
32:a:462:C:H5'	32:a:463:U:OP2	2.17	0.45
32:a:496:G:H2'	32:a:497:G:H8	1.82	0.45
32:a:583:G:H2'	32:a:584:U:H6	1.81	0.45
32:a:682:G:H2'	32:a:683:U:C6	2.51	0.45
32:a:1397:C:H2'	32:a:1398:G:H8	1.82	0.45
32:a:1451:G:H5''	50:t:26:SER:OG	2.17	0.45
33:c:108:PRO:HB3	33:c:114:LEU:HD13	1.98	0.45
34:d:71:TYR:CZ	34:d:199:TYR:HB3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:134:ARG:H	39:i:134:ARG:HD2	1.82	0.45
7:A:84:A:C2	7:A:103:A:C5	3.05	0.45
7:A:381:A:N3	7:A:402:C:O2'	2.47	0.45
8:B:92:G:O6	27:V:19:LYS:NZ	2.50	0.45
32:a:161:G:H2'	32:a:162:G:C8	2.52	0.45
32:a:686:A:H2'	32:a:687:A:C8	2.51	0.45
32:a:792:U:H2'	32:a:793:A:H8	1.82	0.45
32:a:1257:C:H2'	32:a:1258:G:C8	2.52	0.45
34:d:15:LEU:HD13	34:d:55:LYS:HG2	1.99	0.45
34:d:192:GLU:O	34:d:196:VAL:HG13	2.17	0.45
35:e:46:VAL:HG12	35:e:68:VAL:HG22	1.98	0.45
40:j:52:ILE:N	44:n:41:ARG:HE	2.15	0.45
45:o:79:ARG:O	45:o:83:GLU:HG2	2.17	0.45
1:0:5:LYS:NZ	7:A:2294:G:O3'	2.48	0.45
3:2:7:THR:HG22	7:A:816:C:H1'	1.99	0.45
7:A:44:A:H2'	7:A:45:G:O4'	2.17	0.45
7:A:1076:C:H1'	7:A:1113:G:C8	2.52	0.45
7:A:1211:U:H3'	7:A:1212:G:H4'	1.98	0.45
12:F:113:ILE:HD12	12:F:114:ALA:N	2.32	0.45
32:a:199:G:H2'	32:a:200:U:C6	2.52	0.45
32:a:433:C:H2'	32:a:434:U:O4'	2.16	0.45
32:a:451:A:N7	46:p:46:PRO:HB2	2.32	0.45
32:a:871:C:H2'	32:a:872:C:C6	2.52	0.45
34:d:121:ASN:ND2	34:d:136:ASP:OD1	2.50	0.45
40:j:88:MET:HE2	40:j:88:MET:HB3	1.91	0.45
42:l:24:LEU:O	42:l:30:ARG:NE	2.48	0.45
46:p:72:LYS:HD3	46:p:72:LYS:HA	1.70	0.45
47:q:129:VAL:HG12	47:q:130:GLU:HG3	1.99	0.45
7:A:224:A:H5''	7:A:510:U:OP1	2.17	0.44
7:A:267:A:N1	7:A:516:U:O2'	2.48	0.44
7:A:289:A:H2	7:A:303:U:H4'	1.82	0.44
7:A:644:G:H2'	7:A:645:G:O4'	2.17	0.44
7:A:1075:A:H2'	7:A:1076:C:C6	2.53	0.44
7:A:1408:G:H2'	7:A:1409:C:C6	2.53	0.44
7:A:1556:C:H2'	7:A:1557:G:O4'	2.17	0.44
7:A:1670:G:H2'	7:A:1671:G:O4'	2.16	0.44
7:A:2431:A:H2'	7:A:2432:U:H6	1.82	0.44
15:J:73:MET:HA	15:J:73:MET:HE2	1.98	0.44
32:a:385:C:H2'	32:a:386:U:C6	2.52	0.44
32:a:507:U:H3'	32:a:508:G:C8	2.52	0.44
33:c:138:GLN:O	33:c:142:ARG:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:87:LYS:HD2	34:d:180:LEU:HD22	1.98	0.44
37:g:23:VAL:O	37:g:27:VAL:HG23	2.16	0.44
42:l:49:LEU:HD23	42:l:49:LEU:HA	1.83	0.44
49:s:50:ALA:HB1	49:s:57:HIS:HB3	1.99	0.44
49:s:60:VAL:HG21	49:s:74:PHE:HB2	1.98	0.44
1:0:18:SER:OG	7:A:15:G:H4'	2.17	0.44
7:A:327:U:H3'	7:A:328:A:C8	2.53	0.44
30:Y:38:THR:OG1	30:Y:40:GLN:OE1	2.29	0.44
32:a:633:A:N7	38:h:109:SER:HA	2.33	0.44
32:a:682:G:H3'	41:k:38:ASN:ND2	2.32	0.44
7:A:282:C:H2'	7:A:283:A:C8	2.52	0.44
7:A:670:U:H1'	7:A:2268:6MZ:H9C1	1.99	0.44
7:A:1416:G:N2	7:A:1459:G:H5''	2.32	0.44
7:A:1740:G:H2'	7:A:1741:C:C6	2.53	0.44
7:A:2335:U:O4	7:A:2428:G:O6	2.36	0.44
16:K:75:SER:HB2	21:P:71:ARG:HH21	1.82	0.44
27:V:31:ILE:N	27:V:47:LEU:O	2.43	0.44
32:a:362:A:H2'	32:a:363:A:C8	2.53	0.44
32:a:442:C:H2'	32:a:443:A:C8	2.52	0.44
32:a:1251:C:H3'	32:a:1252:G:H5''	1.97	0.44
32:a:1315:G:H2'	32:a:1316:A:C8	2.52	0.44
32:a:1407:U:H2'	32:a:1408:G:H8	1.81	0.44
34:d:183:ARG:O	34:d:188:VAL:HB	2.16	0.44
35:e:87:VAL:O	35:e:91:ILE:HG13	2.16	0.44
43:m:15:MET:HE1	43:m:34:LEU:HD21	1.98	0.44
47:q:46:LYS:HG3	47:q:47:HIS:ND1	2.32	0.44
7:A:1546:G:H2'	7:A:1547:C:C6	2.53	0.44
7:A:2102:C:H2'	7:A:2103:C:H6	1.82	0.44
7:A:2565:A:H2'	7:A:2566:A:C8	2.53	0.44
7:A:2707:A:H2'	7:A:2708:G:O4'	2.18	0.44
8:B:61:U:H2'	8:B:62:G:C8	2.53	0.44
8:B:85:U:H2'	8:B:86:C:C6	2.52	0.44
10:D:14:THR:OG1	10:D:15:GLN:N	2.50	0.44
28:W:72:LYS:O	28:W:73:ARG:HG2	2.18	0.44
32:a:1074:U:H3'	32:a:1075:G:C8	2.53	0.44
32:a:1325:A:H2'	32:a:1326:G:O4'	2.17	0.44
32:a:1386:U:O2'	32:a:1494:C:O2'	2.27	0.44
41:k:136:ARG:N	41:k:136:ARG:HD3	2.33	0.44
42:l:21:THR:OG1	42:l:24:LEU:HB2	2.18	0.44
48:r:70:ASN:O	48:r:74:VAL:HG22	2.18	0.44
7:A:285:G:H3'	7:A:286:G:H5''	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:324:G:N1	7:A:452:A:C2	2.69	0.44
7:A:633:U:H2'	7:A:634:U:C6	2.51	0.44
7:A:1569:C:N4	7:A:1633:A:OP2	2.50	0.44
32:a:270:C:C2	32:a:271:C:C5	3.06	0.44
35:e:67:LEU:HD12	35:e:81:TYR:HA	1.99	0.44
35:e:120:ALA:HB2	35:e:170:ALA:N	2.32	0.44
42:l:114:ARG:HB3	42:l:114:ARG:CZ	2.47	0.44
7:A:333:U:H2'	7:A:334:C:C6	2.52	0.44
7:A:338:G:H8	7:A:346:G:N2	2.15	0.44
7:A:1607:G:H2'	7:A:1608:G:H8	1.82	0.44
7:A:2761:G:HO2'	7:A:3002:A:HO2'	1.64	0.44
10:D:90:ASP:C	10:D:92:ALA:H	2.26	0.44
13:G:46:ASN:OD1	13:G:50:ALA:N	2.37	0.44
16:K:59:LYS:HB2	16:K:59:LYS:HE3	1.50	0.44
21:P:106:LYS:HB2	21:P:106:LYS:HE3	1.58	0.44
32:a:529:U:H2'	32:a:530:A:H8	1.83	0.44
32:a:598:A:OP1	32:a:622:G:N2	2.39	0.44
32:a:905:C:H2'	32:a:906:A:C8	2.52	0.44
32:a:941:C:H3'	43:m:106:ASN:ND2	2.33	0.44
32:a:1221:A:OP2	43:m:114:LYS:NZ	2.28	0.44
32:a:1312:C:H42	49:s:36:ARG:HB3	1.83	0.44
34:d:96:VAL:HG22	34:d:165:TRP:HH2	1.83	0.44
37:g:30:VAL:HG23	37:g:39:ALA:HB1	2.00	0.44
7:A:991:G:H2'	7:A:992:A:O4'	2.18	0.44
7:A:1331:C:H2'	7:A:1332:C:H6	1.82	0.44
7:A:1560:U:H5''	7:A:1561:C:C5	2.52	0.44
7:A:1690:A:C4	7:A:2940:G:C8	3.06	0.44
15:J:88:THR:OG1	15:J:91:GLU:HG3	2.18	0.44
17:L:4:LYS:HA	17:L:4:LYS:HD2	1.70	0.44
20:O:105:GLY:HA2	20:O:109:ALA:HB2	1.99	0.44
32:a:506:G:H2'	32:a:507:U:C6	2.53	0.44
32:a:529:U:H2'	32:a:530:A:C8	2.53	0.44
32:a:688:U:O2	32:a:776:G:N2	2.39	0.44
32:a:978:C:H2'	32:a:979:U:H6	1.82	0.44
32:a:1087:C:H2'	32:a:1088:C:C6	2.52	0.44
32:a:1100:C:C2	32:a:1101:A:C8	3.06	0.44
34:d:6:GLY:H	34:d:107:ARG:HH22	1.65	0.44
5:4:11:CYS:HB3	5:4:32:HIS:CE1	2.53	0.44
7:A:90:C:H3'	7:A:91:A:H2'	2.00	0.44
7:A:616:A:N1	7:A:2280:A:H2'	2.33	0.44
7:A:633:U:H3	7:A:650:G:H1	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1195:U:H1'	7:A:1198:A:OP2	2.18	0.44
7:A:1558:A:P	7:A:1646:G:H22	2.41	0.44
7:A:1566:G:N2	7:A:1637:U:O2	2.29	0.44
7:A:1592:U:O2	7:A:1613:G:N2	2.39	0.44
7:A:2379:A:N1	7:A:2387:U:H1'	2.32	0.44
7:A:2551:C:H5''	12:F:95:ARG:HD3	1.99	0.44
7:A:3048:C:H2'	7:A:3049:C:H6	1.83	0.44
7:A:3059:A:H3'	7:A:3060:C:O2	2.18	0.44
8:B:48:C:H2'	8:B:49:G:C8	2.53	0.44
8:B:83:C:H2'	8:B:84:C:O4'	2.18	0.44
10:D:33:PRO:C	10:D:34:ASN:HD22	2.26	0.44
26:U:8:THR:HA	26:U:22:LYS:HA	2.00	0.44
32:a:118:C:O2	32:a:238:G:N2	2.51	0.44
32:a:406:G:H2'	32:a:407:G:C8	2.53	0.44
32:a:1243:A:H2'	32:a:1244:A:C8	2.52	0.44
37:g:69:VAL:HG23	37:g:100:ALA:HB1	2.00	0.44
7:A:389:U:H2'	7:A:390:G:O4'	2.18	0.44
7:A:487:G:H2'	7:A:488:U:C6	2.52	0.44
7:A:764:G:H2'	7:A:765:C:C6	2.53	0.44
7:A:913:G:H5'	7:A:914:G:OP1	2.18	0.44
7:A:2154:A:H2'	7:A:2155:U:C6	2.53	0.44
7:A:2442:A:H2'	7:A:2443:A:C8	2.53	0.44
9:C:16:ALA:HB2	9:C:207:GLY:HA3	2.00	0.44
11:E:135:GLU:OE2	11:E:138:GLU:HA	2.18	0.44
20:O:31:PRO:HD2	20:O:95:VAL:HG12	1.99	0.44
32:a:118:C:OP1	32:a:310:C:O2'	2.36	0.44
32:a:551:A:H4'	32:a:552:U:H5''	1.99	0.44
32:a:1149:A:N6	32:a:1170:G:H1'	2.33	0.44
32:a:1233:G:H2'	32:a:1234:G:H8	1.83	0.44
33:c:71:ARG:H	33:c:71:ARG:HD2	1.82	0.44
38:h:58:LYS:HB2	38:h:58:LYS:HE3	1.69	0.44
38:h:113:LEU:HB3	38:h:117:GLN:OE1	2.18	0.44
39:i:38:VAL:HG21	39:i:100:LEU:HA	1.99	0.44
42:l:23:ALA:HA	42:l:61:VAL:HG21	2.00	0.44
47:q:76:VAL:HG11	47:q:114:LEU:HD11	2.00	0.44
47:q:111:ARG:NH1	47:q:133:GLU:OE1	2.38	0.44
7:A:2335:U:H2'	7:A:2336:C:H6	1.81	0.43
7:A:2367:U:H2'	7:A:2368:G:C5	2.52	0.43
7:A:2919:C:OP2	10:D:119:LYS:NZ	2.41	0.43
12:F:103:MET:HE2	12:F:103:MET:HB3	1.87	0.43
21:P:33:GLU:O	21:P:36:LYS:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:179:G:OP2	32:a:179:G:N2	2.27	0.43
32:a:485:G:H2'	32:a:487:A:C8	2.52	0.43
32:a:769:G:H2'	32:a:770:C:C6	2.52	0.43
32:a:995:A:H2'	32:a:996:G:C8	2.53	0.43
32:a:1264:U:H2'	32:a:1265:U:C6	2.53	0.43
34:d:108:MET:O	34:d:112:LEU:HG	2.18	0.43
36:f:28:ASN:HA	36:f:31:ARG:HB2	1.99	0.43
50:t:5:LYS:HB2	50:t:5:LYS:HE3	1.79	0.43
4:3:26:LYS:HE2	4:3:48:THR:HB	2.00	0.43
5:4:7:VAL:HG22	5:4:36:GLN:HG3	2.00	0.43
5:4:27:CYS:SG	5:4:28:SER:N	2.91	0.43
7:A:637:C:H1'	7:A:647:G:N2	2.32	0.43
7:A:673:A:C6	7:A:677:A:C8	3.06	0.43
7:A:1570:U:H3	7:A:1632:G:H2'	1.83	0.43
7:A:2269:A:N3	7:A:2693:G:O2'	2.36	0.43
7:A:2829:C:H2'	7:A:2830:G:C8	2.52	0.43
10:D:108:ASP:OD1	10:D:185:VAL:HG12	2.18	0.43
12:F:81:ILE:H	12:F:86:LEU:HB3	1.83	0.43
32:a:334:C:H2'	32:a:335:A:C8	2.50	0.43
32:a:406:G:H2'	32:a:407:G:H8	1.82	0.43
32:a:410:A:H1'	32:a:412:G:H1'	2.00	0.43
33:c:145:ASN:O	33:c:204:LYS:NZ	2.51	0.43
35:e:108:ILE:HB	35:e:113:THR:HG22	2.00	0.43
6:6:60:ARG:O	6:6:63:LYS:HG3	2.18	0.43
7:A:945:C:H2'	7:A:946:C:O2	2.18	0.43
7:A:1331:C:H2'	7:A:1332:C:C6	2.53	0.43
7:A:2880:A:H2'	7:A:2881:A:C8	2.53	0.43
8:B:8:G:P	20:O:32:ARG:HH22	2.42	0.43
10:D:20:SER:O	10:D:20:SER:OG	2.30	0.43
13:G:42:LYS:HB2	13:G:54:THR:OG1	2.18	0.43
32:a:1022:U:H4'	32:a:1024:G:OP2	2.18	0.43
32:a:1190:G:H2'	32:a:1191:U:C6	2.54	0.43
32:a:1417:U:H2'	32:a:1418:A:C8	2.53	0.43
32:a:1433:U:H2'	32:a:1434:G:O4'	2.17	0.43
40:j:23:ARG:HA	40:j:27:GLU:HB2	2.00	0.43
40:j:37:VAL:H	40:j:75:ASP:CG	2.26	0.43
42:l:32:GLY:HA2	42:l:57:LEU:HA	1.99	0.43
43:m:96:MET:HG3	43:m:97:PRO:CD	2.48	0.43
7:A:293:G:C8	7:A:338:G:H2'	2.52	0.43
7:A:1053:U:H2'	7:A:1054:G:H8	1.82	0.43
7:A:1779:C:H2'	7:A:1780:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2195:C:H2'	7:A:2196:C:C6	2.54	0.43
7:A:2887:U:H2'	7:A:2888:C:C6	2.53	0.43
7:A:2892:A:N1	7:A:2903:A:H5''	2.34	0.43
8:B:114:C:N3	8:B:115:A:O2'	2.48	0.43
11:E:124:ARG:HD3	11:E:124:ARG:HA	1.78	0.43
17:L:4:LYS:O	17:L:7:ASP:N	2.51	0.43
17:L:54:MET:HE2	17:L:54:MET:HB2	1.89	0.43
26:U:12:ILE:HG21	26:U:72:MET:HG3	2.01	0.43
32:a:1012:A:H2'	32:a:1013:G:C4	2.53	0.43
33:c:85:ARG:HD3	33:c:86:ILE:HD13	2.01	0.43
36:f:45:LYS:HB3	36:f:45:LYS:HE3	1.87	0.43
40:j:25:ILE:HG22	40:j:90:ILE:HD13	2.00	0.43
7:A:152:C:H2'	7:A:153:C:C6	2.54	0.43
7:A:1117:A:P	31:Z:11:SER:HB3	2.58	0.43
7:A:2103:C:H2'	7:A:2104:C:C6	2.53	0.43
12:F:23:LEU:HD13	12:F:36:PRO:HD2	2.00	0.43
12:F:147:GLU:H	12:F:147:GLU:CD	2.26	0.43
24:S:20:VAL:HG12	24:S:22:VAL:HG12	2.00	0.43
32:a:185:G:C6	32:a:199:G:C6	3.06	0.43
32:a:253:G:OP1	47:q:123:THR:N	2.48	0.43
32:a:665:G:H2'	32:a:666:A:C8	2.47	0.43
32:a:1285:G:H2'	32:a:1286:G:H8	1.83	0.43
32:a:1403:G:H2'	32:a:1404:U:H6	1.83	0.43
34:d:29:ARG:NH1	34:d:30:PRO:HD2	2.34	0.43
35:e:76:MET:HE2	35:e:102:PHE:HB3	2.00	0.43
36:f:9:ILE:HG22	36:f:86:LEU:HB2	2.00	0.43
36:f:63:ILE:HG22	36:f:65:VAL:HG23	2.00	0.43
40:j:75:ASP:OD1	40:j:76:ILE:N	2.51	0.43
43:m:91:ARG:HB2	43:m:98:VAL:HG12	2.00	0.43
45:o:5:ALA:O	45:o:9:LYS:HG2	2.18	0.43
49:s:13:GLU:HA	49:s:16:LEU:HD12	2.00	0.43
7:A:645:G:N2	7:A:646:A:N7	2.61	0.43
7:A:648:G:H2'	7:A:649:A:C8	2.52	0.43
7:A:730:C:N4	17:L:75:GLU:OE1	2.51	0.43
7:A:870:U:H2'	7:A:871:U:C6	2.54	0.43
7:A:1177:A:H1'	7:A:1241:G:H21	1.83	0.43
7:A:2525:A:C5	7:A:2527:G:C8	3.07	0.43
7:A:2530:U:H2'	7:A:2531:C:C6	2.53	0.43
12:F:68:THR:HG22	12:F:98:LEU:HD11	2.01	0.43
17:L:4:LYS:O	17:L:6:HIS:N	2.52	0.43
18:M:59:LYS:HD3	18:M:59:LYS:HA	1.74	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:65:U:H2'	32:a:66:C:C6	2.53	0.43
32:a:147:A:C5	32:a:148:A:C8	3.07	0.43
32:a:321:C:O2'	50:t:18:ARG:NH1	2.52	0.43
32:a:442:C:H2'	32:a:443:A:H8	1.82	0.43
32:a:687:A:H2'	32:a:688:U:C6	2.53	0.43
32:a:937:G:N1	32:a:1330:G:OP2	2.28	0.43
32:a:939:A:H2'	32:a:940:G:C8	2.54	0.43
32:a:1121:A:H2'	32:a:1122:G:H8	1.83	0.43
32:a:1324:A:H2'	32:a:1325:A:C8	2.54	0.43
32:a:1517:C:H2'	32:a:1518:G:C8	2.54	0.43
33:c:71:ARG:HD2	33:c:71:ARG:N	2.34	0.43
41:k:103:ARG:NH1	41:k:122:ASP:OD2	2.49	0.43
7:A:282:C:H2'	7:A:283:A:H8	1.83	0.43
7:A:355:C:H2'	7:A:356:A:H8	1.83	0.43
7:A:455:U:H2'	7:A:456:C:C6	2.54	0.43
7:A:1554:G:H2'	7:A:1555:A:C8	2.54	0.43
7:A:1567:U:C5	7:A:1632:G:H5''	2.54	0.43
7:A:1741:C:H2'	7:A:1742:U:H6	1.84	0.43
8:B:107:C:H2'	8:B:108:G:H8	1.83	0.43
8:B:111:G:H2'	8:B:112:A:C8	2.54	0.43
12:F:169:THR:OG1	12:F:171:ASP:OD1	2.23	0.43
20:O:27:THR:OG1	20:O:28:ALA:N	2.52	0.43
23:R:61:VAL:HG12	23:R:103:ILE:HG12	2.00	0.43
30:Y:13:LEU:H	30:Y:13:LEU:HD22	1.83	0.43
32:a:575:G:H2'	32:a:576:G:H8	1.83	0.43
32:a:586:G:H1'	32:a:587:C:H5	1.83	0.43
32:a:752:G:H2'	32:a:753:A:H8	1.84	0.43
32:a:1220:C:OP1	43:m:108:ARG:NH1	2.38	0.43
32:a:1255:G:H2'	32:a:1256:C:C6	2.54	0.43
32:a:1428:G:H2'	32:a:1429:C:C6	2.54	0.43
34:d:15:LEU:HD22	34:d:55:LYS:HG3	2.00	0.43
41:k:46:ASP:OD1	41:k:50:ASN:N	2.45	0.43
42:l:54:ARG:HD2	42:l:54:ARG:HA	1.87	0.43
44:n:13:LYS:HE2	44:n:13:LYS:HB3	1.78	0.43
7:A:2153:U:C2	7:A:2154:A:C8	3.07	0.43
7:A:2302:C:H2'	7:A:2303:C:C6	2.54	0.43
7:A:2696:G:H21	7:A:2697:A:H61	1.67	0.43
9:C:54:LYS:O	9:C:218:ARG:HD3	2.19	0.43
12:F:142:GLN:H	12:F:156:VAL:CG1	2.31	0.43
13:G:164:ARG:HB3	13:G:168:GLU:OE2	2.19	0.43
17:L:36:THR:HG23	17:L:41:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:T:25:ASP:N	25:T:25:ASP:OD1	2.50	0.43
29:X:18:VAL:HG22	29:X:24:ARG:HG2	2.00	0.43
31:Z:40:ASN:C	31:Z:44:ARG:HH21	2.27	0.43
32:a:60:G:H2'	32:a:61:C:C6	2.53	0.43
32:a:138:C:H2'	32:a:139:U:O4'	2.18	0.43
32:a:408:G:OP1	34:d:23:ASP:HB3	2.19	0.43
32:a:700:A:H2'	32:a:701:G:C8	2.53	0.43
33:c:157:LEU:H	33:c:196:ILE:HD11	1.84	0.43
38:h:95:PRO:HG3	38:h:127:VAL:HG21	1.99	0.43
43:m:12:ASP:H	43:m:46:ARG:HE	1.67	0.43
43:m:39:ILE:HD12	43:m:40:ASP:H	1.82	0.43
7:A:568:A:H1'	7:A:569:A:H5''	2.01	0.43
7:A:1603:C:O2	7:A:1604:G:N1	2.51	0.43
7:A:1655:C:H2'	7:A:1656:G:O4'	2.18	0.43
7:A:1657:A:H4'	7:A:1658:A:H5''	2.01	0.43
7:A:1667:G:H2'	7:A:1668:C:H6	1.84	0.43
7:A:1675:G:O2'	7:A:1755:G:O2'	2.20	0.43
7:A:2893:G:N2	7:A:2894:U:O4	2.45	0.43
7:A:3075:U:OP2	19:N:50:LYS:NZ	2.52	0.43
12:F:151:ASP:OD1	12:F:152:LYS:HG3	2.19	0.43
23:R:52:ASP:OD1	23:R:53:ALA:N	2.52	0.43
32:a:680:C:C2	32:a:681:G:C8	3.06	0.43
32:a:754:G:H2'	32:a:755:C:C6	2.53	0.43
34:d:110:ARG:O	34:d:114:SER:OG	2.24	0.43
39:i:134:ARG:O	39:i:136:LYS:NZ	2.52	0.43
45:o:6:GLU:H	45:o:6:GLU:HG3	1.60	0.43
47:q:116:GLU:H	47:q:116:GLU:HG3	1.62	0.43
49:s:11:VAL:HG11	49:s:41:ILE:HG23	1.99	0.43
7:A:338:G:N2	7:A:338:G:OP2	2.52	0.43
7:A:1070:G:H5''	17:L:34:ARG:O	2.19	0.43
7:A:1444:U:H5	7:A:1838:A:N1	2.17	0.43
7:A:2297:A:O2'	53:A:3201:WDP:O19	2.35	0.43
12:F:76:ARG:HG2	12:F:76:ARG:HH11	1.84	0.43
12:F:126:PRO:HD3	12:F:185:LYS:HG2	2.01	0.43
13:G:19:ILE:HD11	13:G:45:ARG:HH12	1.84	0.43
15:J:141:GLU:N	15:J:141:GLU:OE1	2.52	0.43
28:W:50:ASN:HB2	28:W:80:ILE:HB	2.01	0.43
32:a:447:A:P	32:a:476:G:H22	2.42	0.43
32:a:1242:A:H2	32:a:1363:G:H1'	1.84	0.43
32:a:1497:G:H4'	32:a:1498:G:C4	2.54	0.43
39:i:48:LYS:HD3	39:i:48:LYS:HA	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:291:C:H2'	7:A:292:C:H6	1.84	0.42
7:A:571:U:H4'	26:U:44:HIS:ND1	2.33	0.42
7:A:637:C:H2'	7:A:638:C:C6	2.54	0.42
7:A:1668:C:H2'	7:A:1669:A:H8	1.84	0.42
7:A:1682:U:H2'	7:A:1683:A:C8	2.53	0.42
7:A:1955:G:N2	7:A:1974:G:N1	2.65	0.42
7:A:2530:U:H2'	7:A:2531:C:H6	1.84	0.42
7:A:2936:U:H2'	7:A:2937:C:H6	1.83	0.42
13:G:30:LYS:NZ	13:G:82:GLN:HA	2.34	0.42
20:O:93:ASP:OD1	20:O:94:THR:HG23	2.18	0.42
24:S:100:GLN:OE1	24:S:102:ARG:NH2	2.52	0.42
32:a:104:A:H5'	32:a:105:C:C5	2.54	0.42
32:a:724:G:N2	48:r:62:ARG:HH22	2.16	0.42
32:a:1029:C:H2'	32:a:1030:U:C6	2.53	0.42
32:a:1285:G:H2'	32:a:1286:G:C8	2.54	0.42
40:j:37:VAL:N	40:j:75:ASP:OD2	2.51	0.42
7:A:152:C:H2'	7:A:153:C:H6	1.84	0.42
7:A:277:G:C6	7:A:312:G:C6	3.07	0.42
7:A:1177:A:H1'	7:A:1241:G:N2	2.34	0.42
7:A:1178:C:H1'	7:A:1242:U:H4'	2.01	0.42
7:A:2359:U:H3'	7:A:2360:G:C8	2.54	0.42
12:F:107:LEU:HD23	12:F:107:LEU:HA	1.88	0.42
24:S:21:ARG:HG2	24:S:21:ARG:NH1	2.34	0.42
32:a:18:G:H1'	35:e:60:ARG:HH12	1.83	0.42
32:a:414:C:H2'	32:a:415:G:O4'	2.19	0.42
32:a:1109:U:H2'	32:a:1110:C:C6	2.54	0.42
45:o:87:LEU:HD13	45:o:88:ARG:HG2	2.01	0.42
4:3:19:THR:HG23	7:A:755:G:H5''	2.01	0.42
5:4:22:ARG:HH22	7:A:1253:C:C4'	2.31	0.42
7:A:296:U:O4	7:A:297:A:N6	2.52	0.42
7:A:766:G:H2'	7:A:767:C:O4'	2.19	0.42
7:A:1701:U:H2'	7:A:1702:G:C8	2.55	0.42
7:A:1981:C:H2'	7:A:1982:C:H6	1.84	0.42
7:A:2633:C:OP1	17:L:62:LYS:NZ	2.53	0.42
7:A:2657:U:H2'	7:A:2658:C:C6	2.54	0.42
10:D:188:GLU:H	10:D:188:GLU:CD	2.26	0.42
15:J:69:LEU:HD23	15:J:89:ILE:HG22	2.02	0.42
18:M:30:GLY:O	18:M:134:ARG:NH2	2.52	0.42
32:a:238:G:N2	32:a:289:C:O2'	2.52	0.42
32:a:428:U:O2	32:a:430:A:N7	2.53	0.42
32:a:1403:G:H2'	32:a:1404:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:27:LEU:HD22	36:f:37:VAL:HG11	2.00	0.42
37:g:103:TRP:CE3	37:g:137:ARG:HG2	2.54	0.42
4:3:47:ARG:NH2	7:A:734:G:OP1	2.51	0.42
7:A:701:U:H2'	7:A:702:C:C6	2.54	0.42
7:A:970:G:H2'	7:A:971:C:C6	2.54	0.42
7:A:1607:G:H2'	7:A:1608:G:C8	2.55	0.42
7:A:2649:A:H2'	7:A:2650:A:C8	2.54	0.42
20:O:81:GLN:O	20:O:85:GLU:HG2	2.19	0.42
30:Y:7:PRO:HG3	30:Y:56:ARG:HD3	2.02	0.42
32:a:451:A:N1	46:p:92:ARG:HG2	2.33	0.42
32:a:638:C:H2'	32:a:639:A:C8	2.55	0.42
32:a:943:U:H2'	32:a:944:G:H8	1.82	0.42
32:a:974:U:OP2	32:a:975:U:O2'	2.35	0.42
32:a:1007:G:H2'	32:a:1008:A:C5	2.54	0.42
32:a:1429:C:H2'	32:a:1430:C:H6	1.84	0.42
37:g:63:LYS:HA	37:g:66:LEU:HG	2.00	0.42
38:h:104:ALA:HB3	38:h:115:ASP:OD1	2.19	0.42
47:q:63:GLY:HA3	47:q:78:LEU:HD23	2.00	0.42
47:q:115:MET:HE3	47:q:115:MET:O	2.20	0.42
50:t:58:LEU:HD23	50:t:76:LYS:HG3	2.01	0.42
2:1:23:TYR:HH	7:A:2585:C:HO2'	1.68	0.42
6:6:23:GLN:OE1	6:6:23:GLN:N	2.53	0.42
7:A:52:A:H2'	7:A:53:A:C8	2.54	0.42
7:A:184:A:H2'	7:A:185:C:H6	1.83	0.42
7:A:423:A:H2'	7:A:424:C:O4'	2.20	0.42
7:A:587:U:H2'	7:A:588:G:O4'	2.20	0.42
7:A:610:G:H2'	7:A:611:C:C6	2.54	0.42
7:A:1032:U:H2'	7:A:1033:C:C6	2.54	0.42
7:A:2829:C:H2'	7:A:2830:G:H8	1.85	0.42
12:F:149:ASP:H	12:F:152:LYS:HZ2	1.66	0.42
17:L:95:ASP:OD1	17:L:95:ASP:C	2.63	0.42
17:L:133:ARG:O	17:L:137:THR:HG23	2.19	0.42
32:a:38:G:H2'	32:a:39:C:C6	2.55	0.42
32:a:136:C:H4'	47:q:45:PRO:O	2.20	0.42
32:a:161:G:H2'	32:a:162:G:H8	1.85	0.42
32:a:322:U:H2'	32:a:323:G:O4'	2.19	0.42
32:a:647:G:N2	45:o:23:GLY:HA3	2.34	0.42
32:a:676:G:N1	32:a:695:A:OP2	2.48	0.42
34:d:60:TYR:CD2	34:d:89:LEU:HB3	2.54	0.42
36:f:48:LEU:HD22	36:f:52:ILE:HD12	2.01	0.42
40:j:22:ALA:HB1	40:j:73:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:18:CYS:SG	6:6:41:CYS:HB3	2.59	0.42
7:A:745:U:H2'	7:A:746:G:O4'	2.19	0.42
7:A:1577:C:H2'	7:A:1578:C:C6	2.55	0.42
7:A:2033:G:C5	9:C:177:MET:HE3	2.54	0.42
7:A:2577:G:H2'	7:A:2578:A:H8	1.84	0.42
8:B:33:G:O2'	8:B:43:G:N7	2.49	0.42
12:F:55:LYS:HD3	12:F:55:LYS:HA	1.84	0.42
29:X:61:ILE:C	29:X:61:ILE:HD12	2.45	0.42
32:a:172:C:H2'	32:a:173:G:C8	2.54	0.42
32:a:361:G:N2	32:a:364:U:OP2	2.50	0.42
32:a:409:G:H1'	32:a:431:A:N6	2.34	0.42
32:a:895:G:H2'	32:a:896:G:C8	2.53	0.42
34:d:30:PRO:C	34:d:32:PRO:HD3	2.45	0.42
38:h:21:TYR:CZ	38:h:70:ARG:HB3	2.54	0.42
7:A:384:U:O4	26:U:79:LYS:NZ	2.35	0.42
7:A:741:A:H5''	17:L:114:ASP:HB2	2.01	0.42
7:A:759:C:O2'	7:A:760:A:N7	2.45	0.42
7:A:1198:A:C2	7:A:1225:A:H5''	2.55	0.42
7:A:1575:A:H2'	7:A:1576:C:C6	2.54	0.42
7:A:1651:C:H2'	7:A:1652:A:C8	2.55	0.42
7:A:2109:G:H2'	7:A:2110:G:C8	2.55	0.42
7:A:2303:C:H2'	7:A:2304:C:H6	1.85	0.42
7:A:2504:A:H4'	7:A:2505:A:N3	2.34	0.42
12:F:159:MET:HE1	12:F:161:ILE:CD1	2.48	0.42
13:G:96:ARG:HE	13:G:98:GLN:NE2	2.17	0.42
27:V:72:LYS:NZ	27:V:74:GLN:HB2	2.35	0.42
27:V:87:ARG:HH22	27:V:91:GLN:HG2	1.84	0.42
32:a:158:A:N6	32:a:159:C:O2	2.52	0.42
32:a:413:A:H3'	32:a:414:C:H6	1.85	0.42
32:a:445:C:H2'	32:a:446:G:O4'	2.19	0.42
32:a:477:U:H2'	32:a:478:A:C8	2.48	0.42
32:a:500:A:OP1	34:d:46:TYR:HB3	2.19	0.42
32:a:528:G:H5''	42:l:110:ARG:NH1	2.34	0.42
32:a:667:A:H5''	41:k:125:PRO:HB3	2.02	0.42
32:a:1313:U:H5''	32:a:1314:C:OP2	2.20	0.42
32:a:1384:U:H2'	32:a:1385:G:C8	2.55	0.42
34:d:28:LYS:HE2	34:d:28:LYS:HB2	1.83	0.42
35:e:146:LEU:HD13	35:e:154:ILE:HG21	2.00	0.42
41:k:45:THR:HG22	41:k:51:VAL:HG22	2.01	0.42
41:k:66:ARG:O	41:k:69:THR:OG1	2.30	0.42
7:A:769:U:H2'	7:A:770:A:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:889:G:H2'	7:A:890:A:O4'	2.19	0.42
7:A:1213:A:C2	7:A:1214:A:H1'	2.55	0.42
7:A:1676:U:H2'	7:A:1677:A:H8	1.85	0.42
7:A:1731:A:H2'	7:A:1732:A:C8	2.54	0.42
32:a:152:U:O2	32:a:161:G:N2	2.38	0.42
32:a:375:G:H5''	46:p:6:LYS:HB2	2.01	0.42
32:a:590:U:O2'	38:h:123:VAL:HG13	2.20	0.42
32:a:638:C:H2'	32:a:639:A:H8	1.84	0.42
32:a:1305:U:H2'	32:a:1306:C:C6	2.55	0.42
40:j:59:LYS:HE2	40:j:62:ARG:HH21	1.84	0.42
42:l:37:VAL:HG21	42:l:74:LEU:HB3	2.02	0.42
43:m:91:ARG:NH2	43:m:96:MET:HG2	2.30	0.42
50:t:46:LYS:O	50:t:49:GLU:HG3	2.19	0.42
1:0:16:ARG:NH2	7:A:1395:G:OP1	2.33	0.42
7:A:646:A:H3'	7:A:647:G:H8	1.84	0.42
7:A:1133:C:H2'	7:A:1140:G:H2'	2.01	0.42
7:A:1191:G:H2'	7:A:1191:G:N3	2.35	0.42
7:A:1244:A:H2'	7:A:1245:U:C6	2.55	0.42
7:A:1977:G:H2'	7:A:1978:G:C8	2.55	0.42
8:B:113:A:C6	8:B:114:C:C2	3.08	0.42
19:N:18:LYS:HE2	19:N:18:LYS:HB3	1.45	0.42
32:a:108:G:H2'	32:a:109:U:H6	1.84	0.42
32:a:1105:C:O2'	44:n:60:SER:O	2.34	0.42
32:a:1219:A:O3'	43:m:115:ARG:NH1	2.51	0.42
32:a:1279:A:H2'	32:a:1280:A:H8	1.85	0.42
32:a:1319:C:H2'	32:a:1320:C:H6	1.85	0.42
36:f:68:ALA:HB3	36:f:71:THR:HG23	2.01	0.42
38:h:29:HIS:CD2	38:h:60:LEU:HB2	2.54	0.42
43:m:74:VAL:O	43:m:78:ILE:HG12	2.20	0.42
49:s:33:THR:HG23	49:s:51:VAL:HA	2.02	0.42
7:A:668:U:O4	23:R:82:LYS:HE3	2.20	0.42
7:A:904:G:OP1	7:A:906:G:O2'	2.37	0.42
7:A:1195:U:H4'	7:A:1197:G:N7	2.35	0.42
7:A:1732:A:H2'	7:A:1733:A:C8	2.54	0.42
7:A:2033:G:O2'	9:C:181:GLU:OE2	2.25	0.42
7:A:2159:C:H2'	7:A:2160:A:C8	2.51	0.42
7:A:2263:G:H2'	7:A:2264:A:C8	2.55	0.42
7:A:2343:G:C6	7:A:2420:U:O2	2.72	0.42
7:A:2412:C:H3'	7:A:2414:C:OP2	2.20	0.42
9:C:209:ALA:O	9:C:213:ARG:HG2	2.20	0.42
11:E:74:GLN:HE21	11:E:74:GLN:HB3	1.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:209:G:H2'	32:a:210:C:C6	2.54	0.42
32:a:548:G:H2'	32:a:549:G:C8	2.55	0.42
32:a:1109:U:H2'	32:a:1110:C:H6	1.85	0.42
38:h:7:ILE:O	38:h:11:LEU:HG	2.19	0.42
3:2:18:VAL:O	3:2:23:LEU:HD22	2.20	0.41
7:A:353:G:H2'	7:A:354:G:C8	2.55	0.41
7:A:636:U:HO2'	7:A:637:C:H6	1.68	0.41
7:A:893:A:H5'	9:C:210:GLY:HA2	2.01	0.41
7:A:1297:A:H2'	7:A:1298:U:H6	1.85	0.41
8:B:111:G:C2	8:B:112:A:C5	3.08	0.41
20:O:45:GLN:HA	20:O:57:ALA:HA	2.01	0.41
32:a:337:A:H2'	32:a:338:C:H6	1.85	0.41
32:a:1098:C:C4	32:a:1099:G:C8	3.08	0.41
32:a:1115:G:H5''	40:j:37:VAL:HG12	2.02	0.41
32:a:1229:C:O2'	32:a:1292:G:N2	2.52	0.41
32:a:1275:C:H2'	32:a:1276:U:O4'	2.20	0.41
39:i:76:VAL:HG13	39:i:77:ASP:H	1.84	0.41
42:l:66:TYR:HB3	42:l:96:LYS:HG2	2.01	0.41
7:A:35:G:H1'	7:A:543:A:C4	2.55	0.41
7:A:443:C:H2'	7:A:444:C:C6	2.55	0.41
7:A:703:G:H2'	7:A:704:C:C6	2.55	0.41
7:A:962:G:H2'	7:A:963:C:C6	2.55	0.41
7:A:1235:G:H2'	7:A:1236:G:N9	2.35	0.41
7:A:1235:G:H2'	7:A:1236:G:C8	2.55	0.41
7:A:1409:C:H2'	7:A:1410:A:H8	1.84	0.41
7:A:2028:U:H2'	7:A:2029:C:H6	1.86	0.41
7:A:2309:C:H2'	7:A:2310:C:C6	2.54	0.41
9:C:108:PRO:HD2	9:C:111:LEU:HD22	2.01	0.41
10:D:135:GLN:HB2	10:D:144:VAL:O	2.19	0.41
12:F:15:TYR:HA	12:F:19:ILE:CG1	2.51	0.41
22:Q:109:LEU:HD23	22:Q:109:LEU:HA	1.86	0.41
32:a:440:A:H61	32:a:484:A:N6	2.18	0.41
32:a:735:C:H2'	32:a:736:A:C8	2.49	0.41
32:a:971:A:H2	32:a:1308:G:H21	1.68	0.41
32:a:1002:G:H2'	32:a:1003:U:C6	2.54	0.41
32:a:1283:C:H2'	32:a:1284:C:C6	2.55	0.41
33:c:34:GLU:O	33:c:38:ILE:HG12	2.20	0.41
33:c:47:GLU:O	33:c:117:GLN:NE2	2.53	0.41
34:d:95:ASN:O	34:d:99:ARG:HG2	2.20	0.41
34:d:133:SER:OG	34:d:134:GLN:N	2.53	0.41
36:f:9:ILE:HD12	36:f:87:ARG:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:g:66:LEU:HA	37:g:69:VAL:HG22	2.02	0.41
37:g:104:LEU:HD22	37:g:123:GLU:HG3	2.02	0.41
46:p:84:LYS:HA	46:p:84:LYS:HD3	1.81	0.41
50:t:15:GLU:O	50:t:19:LEU:HD23	2.19	0.41
7:A:420:G:C4	7:A:421:G:H1'	2.56	0.41
7:A:786:U:H2'	7:A:787:G:H8	1.80	0.41
7:A:1558:A:H3'	7:A:1645:A:N6	2.35	0.41
7:A:1727:A:C2	9:C:75:VAL:HG22	2.54	0.41
7:A:1750:C:H2'	7:A:1751:C:H6	1.84	0.41
7:A:2649:A:H2'	7:A:2650:A:H8	1.86	0.41
19:N:56:LYS:NZ	19:N:90:ARG:O	2.53	0.41
21:P:37:GLU:HA	21:P:37:GLU:OE1	2.19	0.41
25:T:97:GLY:HA3	30:Y:40:GLN:HE22	1.85	0.41
32:a:398:G:H2'	32:a:399:C:C6	2.55	0.41
32:a:1042:G:H2'	32:a:1043:U:C6	2.55	0.41
32:a:1453:A:H2'	32:a:1454:G:O4'	2.19	0.41
33:c:91:GLU:HA	33:c:94:THR:HG22	2.01	0.41
43:m:60:ILE:HG13	43:m:61:GLU:N	2.35	0.41
7:A:128:C:H2'	7:A:129:C:H6	1.85	0.41
7:A:739:C:O2'	7:A:743:U:OP1	2.38	0.41
7:A:1860:C:H2'	7:A:1861:A:O4'	2.20	0.41
7:A:2404:U:H2'	7:A:2405:G:C8	2.55	0.41
7:A:2805:G:H2'	7:A:2806:C:C6	2.55	0.41
8:B:34:U:H2'	8:B:35:C:C6	2.55	0.41
17:L:4:LYS:HB3	17:L:6:HIS:CE1	2.55	0.41
18:M:60:ARG:HA	18:M:60:ARG:CZ	2.50	0.41
32:a:218:C:H4'	32:a:380:C:H5'	2.02	0.41
32:a:333:C:H2'	32:a:334:C:H6	1.85	0.41
35:e:72:ASP:CG	35:e:76:MET:HB2	2.45	0.41
41:k:71:PHE:O	41:k:74:GLN:HG3	2.20	0.41
43:m:29:ARG:HA	43:m:32:GLU:HG2	2.02	0.41
7:A:221:A:N3	7:A:236:U:O2'	2.44	0.41
7:A:285:G:H3'	7:A:286:G:C5'	2.50	0.41
7:A:765:C:H2'	7:A:766:G:C8	2.56	0.41
7:A:772:G:O2'	7:A:773:C:O4'	2.38	0.41
7:A:1784:U:H2'	7:A:1785:C:C6	2.55	0.41
7:A:1953:G:C2	7:A:1977:G:C2	3.09	0.41
7:A:2077:C:H2'	7:A:2078:U:C6	2.56	0.41
12:F:25:LYS:HA	12:F:25:LYS:HD3	1.95	0.41
12:F:45:MET:HG3	12:F:60:ALA:HB1	2.02	0.41
12:F:119:ARG:HA	12:F:119:ARG:NE	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:87:LYS:O	13:G:166:GLU:HB2	2.20	0.41
15:J:14:SER:O	15:J:52:ASP:HB3	2.21	0.41
32:a:491:G:H2'	32:a:492:C:C6	2.55	0.41
32:a:586:G:N3	32:a:587:C:N4	2.64	0.41
32:a:741:C:C2	32:a:742:U:C5	3.08	0.41
32:a:1259:C:N3	32:a:1319:C:H4'	2.35	0.41
38:h:29:HIS:HD2	38:h:60:LEU:HB2	1.85	0.41
39:i:84:ILE:C	39:i:84:ILE:HD12	2.45	0.41
7:A:163:A:OP2	7:A:164:U:O2'	2.28	0.41
7:A:356:A:H2'	7:A:357:G:C8	2.55	0.41
7:A:1767:A:H2'	7:A:1768:G:O4'	2.20	0.41
7:A:1826:C:H2'	7:A:1827:A:C8	2.55	0.41
7:A:1876:A:H2'	7:A:1877:G:O4'	2.20	0.41
7:A:1979:A:H2'	7:A:1980:U:H6	1.85	0.41
7:A:2065:G:H2'	7:A:2066:C:C6	2.56	0.41
7:A:2448:G:H21	7:A:2449:A:H5''	1.84	0.41
12:F:21:ASP:O	12:F:25:LYS:NZ	2.54	0.41
13:G:73:VAL:O	13:G:77:VAL:HG12	2.20	0.41
15:J:98:ASP:OD1	15:J:98:ASP:N	2.48	0.41
26:U:103:LYS:N	26:U:103:LYS:HD3	2.36	0.41
32:a:403:G:OP1	34:d:110:ARG:NE	2.54	0.41
32:a:915:G:H5''	35:e:57:LYS:HZ3	1.85	0.41
32:a:1140:U:H2'	32:a:1141:C:O4'	2.20	0.41
37:g:27:VAL:HG11	37:g:40:GLU:HG3	2.02	0.41
39:i:54:ARG:HD2	39:i:59:TYR:CD1	2.56	0.41
40:j:30:VAL:HG12	40:j:36:VAL:HG21	2.02	0.41
41:k:29:GLY:C	41:k:92:VAL:HG12	2.46	0.41
42:l:54:ARG:NH2	42:l:62:GLU:HB3	2.36	0.41
43:m:87:TYR:CZ	43:m:91:ARG:HD2	2.56	0.41
46:p:45:GLU:HB2	46:p:46:PRO:CD	2.49	0.41
5:4:14:CYS:HA	5:4:27:CYS:HB2	2.02	0.41
7:A:682:C:H2'	7:A:683:C:H6	1.84	0.41
7:A:1283:C:OP1	22:Q:92:ARG:NH2	2.43	0.41
7:A:1446:C:H2'	7:A:1447:U:H6	1.86	0.41
7:A:1668:C:H2'	7:A:1669:A:C8	2.56	0.41
7:A:1925:A:H2'	7:A:1926:C:O4'	2.20	0.41
7:A:1953:G:N2	7:A:1976:G:N2	2.68	0.41
7:A:2771:C:H2'	7:A:2772:A:O4'	2.21	0.41
7:A:2814:G:O2'	7:A:2817:C:OP2	2.30	0.41
8:B:4:C:OP1	8:B:60:C:O2'	2.33	0.41
16:K:4:GLN:NE2	16:K:5:GLU:OE2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:206:A:H2'	32:a:207:A:C4	2.55	0.41
32:a:379:G:C4	32:a:381:A:H5''	2.56	0.41
32:a:452:G:N1	32:a:471:U:C2	2.87	0.41
32:a:464:C:H2'	32:a:465:U:C6	2.56	0.41
32:a:929:C:C4	32:a:930:A:N7	2.89	0.41
32:a:1109:U:C2	32:a:1171:A:C6	3.09	0.41
32:a:1255:G:O6	32:a:1264:U:O4	2.38	0.41
32:a:1306:C:H2'	32:a:1307:U:C6	2.56	0.41
32:a:1402:C:H2'	32:a:1403:G:C8	2.51	0.41
38:h:21:TYR:OH	38:h:70:ARG:O	2.22	0.41
39:i:76:VAL:HG13	39:i:77:ASP:N	2.36	0.41
43:m:65:LYS:HB2	43:m:65:LYS:HE3	1.91	0.41
7:A:141:A:H2'	7:A:142:U:C6	2.56	0.41
7:A:339:C:H2'	7:A:340:U:C6	2.56	0.41
7:A:943:C:H2'	7:A:944:C:H6	1.86	0.41
7:A:990:A:H2'	7:A:991:G:O4'	2.21	0.41
7:A:2202:G:O2'	7:A:2205:C:OP1	2.39	0.41
8:B:43:G:N2	8:B:47:C:C2	2.89	0.41
19:N:33:ARG:HG3	19:N:114:GLU:HB3	2.02	0.41
19:N:74:ASP:O	19:N:78:THR:HG22	2.21	0.41
32:a:510:C:H2'	32:a:511:A:C8	2.56	0.41
32:a:667:A:H2'	32:a:668:U:H6	1.86	0.41
32:a:932:G:H2'	32:a:933:C:C6	2.55	0.41
32:a:1116:U:O3'	40:j:7:ARG:NH2	2.54	0.41
32:a:1341:A:H5''	39:i:144:LYS:HB2	2.02	0.41
47:q:46:LYS:HG3	47:q:47:HIS:H	1.85	0.41
7:A:299:G:H2'	7:A:300:G:C8	2.55	0.41
7:A:448:U:H2'	7:A:449:A:H8	1.85	0.41
7:A:833:G:O2'	7:A:855:G:N2	2.41	0.41
7:A:1157:A:N6	7:A:1254:G:H2'	2.36	0.41
7:A:1191:G:C6	7:A:1206:A:H1'	2.56	0.41
7:A:1409:C:H2'	7:A:1410:A:C8	2.56	0.41
7:A:1650:U:H2'	7:A:1651:C:H6	1.85	0.41
7:A:1690:A:H5''	7:A:1691:G:H5''	2.01	0.41
7:A:1692:U:O2'	7:A:1693:G:N7	2.54	0.41
7:A:1954:U:C2	7:A:1955:G:C8	3.09	0.41
7:A:2427:G:H2'	7:A:2428:G:H8	1.84	0.41
7:A:2604:A:H2'	7:A:2605:G:O4'	2.20	0.41
7:A:2705:C:H2'	7:A:2706:A:O4'	2.21	0.41
7:A:2986:A:H2'	7:A:2987:A:C8	2.56	0.41
7:A:3084:G:H4'	7:A:3085:A:H5'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:44:A:H5'	12:F:99:ARG:HD3	2.02	0.41
11:E:190:ASN:ND2	11:E:193:ASP:OD1	2.53	0.41
12:F:169:THR:OG1	12:F:172:GLU:OE1	2.38	0.41
15:J:88:THR:HG23	15:J:91:GLU:OE1	2.21	0.41
16:K:39:ILE:HA	16:K:39:ILE:HD13	1.76	0.41
20:O:32:ARG:NE	20:O:98:ASP:OD2	2.39	0.41
27:V:10:ARG:NH1	27:V:68:ASP:OD1	2.53	0.41
32:a:118:C:H2'	32:a:119:G:H8	1.85	0.41
32:a:184:C:H2'	32:a:185:G:O4'	2.21	0.41
32:a:409:G:H1'	32:a:431:A:H61	1.86	0.41
32:a:424:G:H2'	32:a:425:U:C6	2.56	0.41
32:a:444:U:H2'	32:a:445:C:H6	1.86	0.41
32:a:515:G:H2'	32:a:516:C:C6	2.56	0.41
32:a:539:G:H2'	32:a:540:C:C6	2.56	0.41
32:a:661:A:H2'	32:a:662:C:C6	2.55	0.41
32:a:675:U:O2'	41:k:51:VAL:O	2.27	0.41
32:a:798:A:H2'	32:a:799:C:C6	2.56	0.41
32:a:979:U:H2'	32:a:980:G:C8	2.56	0.41
32:a:1046:A:O2'	33:c:161:GLU:O	2.37	0.41
32:a:1051:U:O2'	40:j:54:SER:HB2	2.20	0.41
32:a:1096:A:H2'	32:a:1097:G:H8	1.86	0.41
32:a:1314:C:H4'	32:a:1315:G:H5'	2.02	0.41
32:a:1500:A:H2'	32:a:1501:G:H8	1.84	0.41
33:c:76:ILE:HD12	33:c:76:ILE:HA	1.92	0.41
35:e:70:VAL:HG11	35:e:99:ARG:HH11	1.86	0.41
40:j:12:ALA:HB3	40:j:18:ILE:HB	2.02	0.41
42:l:79:MET:O	42:l:103:ASP:HB3	2.21	0.41
42:l:110:ARG:HB3	42:l:119:ALA:HB2	2.01	0.41
43:m:70:LEU:HD23	43:m:70:LEU:HA	1.91	0.41
47:q:67:SER:HB3	47:q:75:VAL:HB	2.03	0.41
50:t:12:ARG:O	50:t:15:GLU:HG3	2.20	0.41
50:t:44:LYS:HD2	50:t:44:LYS:HA	1.85	0.41
2:1:35:ARG:HG2	2:1:53:GLU:HB3	2.03	0.41
7:A:306:G:H21	14:H:45:LYS:HZ1	1.68	0.41
7:A:1298:U:H2'	7:A:1299:C:C6	2.56	0.41
7:A:1958:C:H3'	7:A:1959:A:C8	2.55	0.41
7:A:2043:A:H2'	7:A:2044:A:C8	2.56	0.41
7:A:2608:G:H2'	7:A:2609:G:C8	2.56	0.41
7:A:2759:C:H2'	7:A:2760:U:C6	2.55	0.41
7:A:2978:A:H2'	7:A:2979:A:C8	2.56	0.41
8:B:23:G:N7	8:B:55:U:H2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:86:C:H2'	8:B:87:C:O4'	2.20	0.41
10:D:212:ILE:H	10:D:212:ILE:HG12	1.47	0.41
17:L:110:LYS:HG3	17:L:127:LYS:O	2.21	0.41
30:Y:23:ARG:NH2	30:Y:24:GLU:OE1	2.54	0.41
32:a:108:G:H1'	32:a:353:G:H5'	2.03	0.41
32:a:368:G:H2'	32:a:369:C:H6	1.86	0.41
32:a:625:C:H2'	32:a:626:G:H8	1.86	0.41
32:a:816:A:O2'	38:h:13:ARG:NE	2.53	0.41
32:a:816:A:H2'	32:a:817:C:C6	2.56	0.41
32:a:922:G:O6	32:a:1382:C:N4	2.54	0.41
32:a:974:U:H5'	44:n:21:TYR:CZ	2.56	0.41
32:a:1063:G:H2'	32:a:1064:U:C6	2.55	0.41
32:a:1091:C:H2'	32:a:1093:A:O5'	2.21	0.41
32:a:1340:U:H2'	32:a:1341:A:H8	1.85	0.41
32:a:1406:A:H2	32:a:1480:G:H22	1.68	0.41
35:e:124:VAL:HB	35:e:160:GLY:N	2.36	0.41
40:j:7:ARG:C	40:j:8:ILE:HD12	2.45	0.41
47:q:61:ARG:HD3	47:q:78:LEU:HD13	2.03	0.41
6:6:58:VAL:O	6:6:62:GLU:HG2	2.22	0.40
7:A:504:A:H2'	7:A:505:C:C6	2.56	0.40
7:A:679:G:O2'	7:A:1385:A:OP1	2.39	0.40
7:A:2741:A:C6	53:A:3201:WDP:C07	3.02	0.40
8:B:46:C:O2'	20:O:103:THR:HG21	2.21	0.40
11:E:24:ILE:HD13	11:E:24:ILE:HA	1.93	0.40
14:H:26:GLY:O	14:H:31:LEU:HD12	2.21	0.40
16:K:35:ILE:O	16:K:69:ARG:NH2	2.54	0.40
24:S:68:ALA:HB1	24:S:74:LEU:HD12	2.02	0.40
32:a:169:U:H5''	32:a:208:A:O4'	2.21	0.40
32:a:1197:U:H2'	32:a:1198:G:C8	2.56	0.40
32:a:1229:C:O3'	32:a:1292:G:N2	2.54	0.40
34:d:94:ASP:OD2	34:d:95:ASN:N	2.53	0.40
35:e:119:GLU:HG3	35:e:124:VAL:HG22	2.02	0.40
36:f:6:ILE:HG12	36:f:90:VAL:HG22	2.03	0.40
37:g:143:LYS:HG3	37:g:144:MET:N	2.36	0.40
38:h:81:SER:OG	38:h:126:GLU:OE2	2.26	0.40
40:j:87:LEU:O	40:j:90:ILE:HG13	2.20	0.40
42:l:99:ARG:HB2	42:l:117:TYR:HA	2.02	0.40
46:p:45:GLU:CD	46:p:45:GLU:H	2.29	0.40
6:6:42:HIS:CE1	12:F:121:PHE:HD2	2.39	0.40
7:A:12:U:O2'	7:A:13:A:O5'	2.37	0.40
7:A:428:A:H1'	7:A:429:A:C2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:496:C:H2'	7:A:497:C:C6	2.56	0.40
7:A:1038:A:H2'	7:A:1041:C:H5	1.85	0.40
7:A:1184:G:O2'	7:A:1213:A:N6	2.54	0.40
7:A:2315:C:H2'	7:A:2316:U:C6	2.56	0.40
7:A:2886:G:H2'	7:A:2887:U:H6	1.87	0.40
53:A:3201:WDP:C43	53:A:3201:WDP:C71	2.98	0.40
30:Y:16:GLU:H	30:Y:16:GLU:CD	2.27	0.40
32:a:659:A:H2'	32:a:660:G:H8	1.86	0.40
32:a:666:A:H4'	48:r:80:THR:HG21	2.04	0.40
32:a:681:G:H2'	32:a:682:G:C8	2.56	0.40
32:a:1152:G:C6	32:a:1153:C:C4	3.09	0.40
36:f:12:PRO:HB3	36:f:57:GLU:HB2	2.02	0.40
37:g:112:ARG:HD2	37:g:112:ARG:HA	1.77	0.40
40:j:81:PRO:HA	40:j:84:VAL:HG12	2.02	0.40
7:A:420:G:C5	7:A:421:G:H1'	2.57	0.40
7:A:436:G:H2'	7:A:437:C:H6	1.86	0.40
7:A:500:G:OP2	7:A:2644:A:O2'	2.31	0.40
7:A:1130:A:H2'	7:A:1131:G:O4'	2.21	0.40
7:A:2617:G:H2'	7:A:2618:U:C6	2.56	0.40
10:D:102:THR:OG1	10:D:104:GLU:OE2	2.25	0.40
11:E:121:LEU:HD23	11:E:121:LEU:HA	1.91	0.40
19:N:106:ASP:OD1	19:N:106:ASP:N	2.53	0.40
31:Z:29:ARG:HG2	31:Z:33:HIS:CE1	2.56	0.40
32:a:1051:U:H5''	40:j:53:ARG:HB3	2.03	0.40
32:a:1232:U:O2'	32:a:1233:G:H5'	2.22	0.40
32:a:1310:A:H4'	49:s:10:PHE:CG	2.56	0.40
32:a:1506:A:H2'	32:a:1507:C:H6	1.87	0.40
35:e:76:MET:HE1	35:e:103:PHE:N	2.36	0.40
39:i:78:ARG:HA	39:i:79:VAL:HA	1.80	0.40
40:j:11:LYS:HG2	40:j:71:LYS:HG2	2.03	0.40
43:m:107:ALA:HB3	43:m:111:LYS:HE2	2.04	0.40
7:A:283:A:N6	7:A:306:G:O6	2.54	0.40
7:A:340:U:H2'	7:A:341:A:C8	2.55	0.40
7:A:362:A:H2	7:A:442:G:O2'	2.05	0.40
7:A:428:A:H1'	7:A:429:A:H2	1.85	0.40
7:A:2340:A:N6	7:A:2424:A:N7	2.69	0.40
7:A:2656:G:H2'	7:A:2657:U:O4'	2.21	0.40
22:Q:91:ASP:OD1	22:Q:92:ARG:N	2.54	0.40
24:S:69:GLN:OE1	24:S:69:GLN:C	2.65	0.40
28:W:38:VAL:HG12	28:W:40:GLN:HG2	2.02	0.40
32:a:407:G:H5'	34:d:108:MET:HE2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:592:U:H3	32:a:628:G:H1	1.69	0.40
32:a:621:C:H2'	32:a:622:G:O4'	2.21	0.40
32:a:676:G:OP1	41:k:24:LYS:NZ	2.35	0.40
32:a:728:C:C2	32:a:729:U:C5	3.08	0.40
50:t:24:VAL:HG11	50:t:66:VAL:HG11	2.03	0.40
50:t:43:ASP:OD1	50:t:44:LYS:N	2.55	0.40
1:0:4:PRO:O	7:A:2254:U:O2'	2.35	0.40
7:A:294:G:H2'	7:A:295:G:O4'	2.22	0.40
7:A:364:A:H2'	7:A:365:G:O4'	2.21	0.40
7:A:496:C:H2'	7:A:497:C:H6	1.87	0.40
7:A:1260:G:H4'	15:J:84:LEU:HD22	2.03	0.40
7:A:1649:G:H2'	7:A:1650:U:C6	2.56	0.40
7:A:1701:U:H2'	7:A:1702:G:H8	1.86	0.40
8:B:20:A:N6	8:B:62:G:O6	2.54	0.40
17:L:75:GLU:HB3	17:L:103:VAL:HG23	2.03	0.40
32:a:101:C:H2'	32:a:102:G:O4'	2.22	0.40
32:a:114:A:H4'	32:a:115:A:C8	2.57	0.40
32:a:506:G:C6	32:a:507:U:C4	3.10	0.40
32:a:726:G:H2'	32:a:727:U:H6	1.86	0.40
32:a:1171:A:H2'	32:a:1172:A:C8	2.56	0.40
33:c:23:TYR:CG	40:j:97:ASP:HB2	2.56	0.40
34:d:132:VAL:HB	34:d:177:ILE:HG13	2.03	0.40
37:g:69:VAL:HG12	37:g:135:VAL:HG22	2.02	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	0	52/57 (91%)	52 (100%)	0	0	100	100
2	1	46/55 (84%)	45 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	40/47 (85%)	39 (98%)	1 (2%)	0	100	100
4	3	60/64 (94%)	60 (100%)	0	0	100	100
5	4	35/37 (95%)	35 (100%)	0	0	100	100
6	6	53/80 (66%)	46 (87%)	7 (13%)	0	100	100
9	C	270/279 (97%)	259 (96%)	11 (4%)	0	100	100
10	D	211/213 (99%)	198 (94%)	13 (6%)	0	100	100
11	E	205/207 (99%)	201 (98%)	4 (2%)	0	100	100
12	F	176/178 (99%)	162 (92%)	14 (8%)	0	100	100
13	G	172/177 (97%)	167 (97%)	5 (3%)	0	100	100
14	H	45/152 (30%)	38 (84%)	7 (16%)	0	100	100
15	J	144/195 (74%)	141 (98%)	3 (2%)	0	100	100
16	K	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
17	L	141/146 (97%)	128 (91%)	12 (8%)	1 (1%)	18	38
18	M	132/138 (96%)	122 (92%)	10 (8%)	0	100	100
19	N	114/180 (63%)	110 (96%)	4 (4%)	0	100	100
20	O	114/122 (93%)	107 (94%)	7 (6%)	0	100	100
21	P	110/113 (97%)	105 (96%)	5 (4%)	0	100	100
22	Q	120/129 (93%)	117 (98%)	3 (2%)	0	100	100
23	R	98/104 (94%)	88 (90%)	9 (9%)	1 (1%)	12	28
24	S	111/197 (56%)	108 (97%)	3 (3%)	0	100	100
25	T	96/100 (96%)	88 (92%)	8 (8%)	0	100	100
26	U	86/105 (82%)	73 (85%)	12 (14%)	1 (1%)	10	23
27	V	93/215 (43%)	90 (97%)	3 (3%)	0	100	100
28	W	69/86 (80%)	64 (93%)	5 (7%)	0	100	100
29	X	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
30	Y	63/77 (82%)	60 (95%)	3 (5%)	0	100	100
31	Z	57/65 (88%)	56 (98%)	1 (2%)	0	100	100
33	c	205/274 (75%)	191 (93%)	14 (7%)	0	100	100
34	d	198/201 (98%)	188 (95%)	10 (5%)	0	100	100
35	e	158/220 (72%)	145 (92%)	12 (8%)	1 (1%)	21	42
36	f	93/96 (97%)	90 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	g	150/156 (96%)	146 (97%)	4 (3%)	0	100	100
38	h	128/132 (97%)	123 (96%)	4 (3%)	1 (1%)	16	34
39	i	125/151 (83%)	107 (86%)	18 (14%)	0	100	100
40	j	97/101 (96%)	86 (89%)	11 (11%)	0	100	100
41	k	115/139 (83%)	108 (94%)	7 (6%)	0	100	100
42	l	120/124 (97%)	95 (79%)	24 (20%)	1 (1%)	16	34
43	m	114/124 (92%)	105 (92%)	9 (8%)	0	100	100
44	n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
45	o	85/89 (96%)	79 (93%)	5 (6%)	1 (1%)	10	23
46	p	89/162 (55%)	81 (91%)	7 (8%)	1 (1%)	11	25
47	q	91/135 (67%)	82 (90%)	9 (10%)	0	100	100
48	r	61/84 (73%)	58 (95%)	3 (5%)	0	100	100
49	s	81/93 (87%)	70 (86%)	11 (14%)	0	100	100
50	t	80/86 (93%)	80 (100%)	0	0	100	100
51	v	20/22 (91%)	20 (100%)	0	0	100	100
All	All	5161/6154 (84%)	4843 (94%)	310 (6%)	8 (0%)	44	66

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	R	51	THR
42	l	114	ARG
17	L	5	LEU
45	o	19	GLU
26	U	91	THR
46	p	46	PRO
35	e	191	PRO
38	h	68	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	0	44/47 (94%)	43 (98%)	1 (2%)	44	71
2	1	45/51 (88%)	44 (98%)	1 (2%)	45	72
3	2	36/40 (90%)	34 (94%)	2 (6%)	19	40
4	3	53/54 (98%)	53 (100%)	0	100	100
5	4	35/35 (100%)	34 (97%)	1 (3%)	37	65
6	6	49/66 (74%)	48 (98%)	1 (2%)	48	74
9	C	212/218 (97%)	210 (99%)	2 (1%)	70	87
10	D	163/163 (100%)	156 (96%)	7 (4%)	26	51
11	E	159/159 (100%)	158 (99%)	1 (1%)	78	91
12	F	147/147 (100%)	143 (97%)	4 (3%)	39	67
13	G	143/145 (99%)	140 (98%)	3 (2%)	47	73
14	H	36/121 (30%)	35 (97%)	1 (3%)	38	66
15	J	120/161 (74%)	115 (96%)	5 (4%)	26	52
16	K	100/101 (99%)	99 (99%)	1 (1%)	68	86
17	L	107/110 (97%)	102 (95%)	5 (5%)	23	48
18	M	110/114 (96%)	109 (99%)	1 (1%)	70	87
19	N	94/139 (68%)	93 (99%)	1 (1%)	65	84
20	O	88/93 (95%)	82 (93%)	6 (7%)	14	32
21	P	98/99 (99%)	97 (99%)	1 (1%)	68	86
22	Q	95/99 (96%)	93 (98%)	2 (2%)	47	73
23	R	81/83 (98%)	79 (98%)	2 (2%)	42	69
24	S	87/140 (62%)	85 (98%)	2 (2%)	44	71
25	T	82/83 (99%)	78 (95%)	4 (5%)	22	47
26	U	77/88 (88%)	74 (96%)	3 (4%)	28	55
27	V	75/164 (46%)	72 (96%)	3 (4%)	28	55
28	W	51/62 (82%)	49 (96%)	2 (4%)	28	55
29	X	52/52 (100%)	51 (98%)	1 (2%)	50	75
30	Y	58/66 (88%)	57 (98%)	1 (2%)	53	78
31	Z	51/55 (93%)	48 (94%)	3 (6%)	18	38
33	c	170/210 (81%)	167 (98%)	3 (2%)	51	76
34	d	176/177 (99%)	175 (99%)	1 (1%)	78	91
35	e	114/159 (72%)	112 (98%)	2 (2%)	51	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	f	84/85 (99%)	81 (96%)	3 (4%)	31	58
37	g	127/131 (97%)	120 (94%)	7 (6%)	19	41
38	h	106/108 (98%)	105 (99%)	1 (1%)	70	87
39	i	102/120 (85%)	98 (96%)	4 (4%)	28	55
40	j	89/90 (99%)	88 (99%)	1 (1%)	65	84
41	k	90/107 (84%)	87 (97%)	3 (3%)	33	61
42	l	104/105 (99%)	102 (98%)	2 (2%)	50	75
43	m	99/104 (95%)	99 (100%)	0	100	100
44	n	46/47 (98%)	44 (96%)	2 (4%)	26	51
45	o	77/79 (98%)	76 (99%)	1 (1%)	61	82
46	p	75/125 (60%)	74 (99%)	1 (1%)	61	82
47	q	83/105 (79%)	81 (98%)	2 (2%)	43	70
48	r	53/72 (74%)	51 (96%)	2 (4%)	29	56
49	s	75/85 (88%)	74 (99%)	1 (1%)	61	82
50	t	62/65 (95%)	61 (98%)	1 (2%)	55	79
51	v	18/18 (100%)	18 (100%)	0	100	100
All	All	4298/4947 (87%)	4194 (98%)	104 (2%)	43	70

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	25	THR
2	1	25	THR
3	2	32	SER
3	2	44	THR
5	4	34	GLN
6	6	21	THR
9	C	25	THR
9	C	177	MET
10	D	60	ARG
10	D	113	ASP
10	D	115	THR
10	D	135	GLN
10	D	185	VAL
10	D	206	VAL
10	D	212	ILE

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Mol	Chain	Res	Type
11	E	74	GLN
12	F	21	ASP
12	F	47	VAL
12	F	148	VAL
12	F	166	SER
13	G	133	THR
13	G	137	ILE
13	G	152	LEU
14	H	12	LEU
15	J	3	THR
15	J	11	THR
15	J	12	THR
15	J	17	VAL
15	J	133	SER
16	K	39	ILE
17	L	21	VAL
17	L	31	THR
17	L	72	THR
17	L	131	SER
17	L	144	THR
18	M	94	VAL
19	N	112	VAL
20	O	25	SER
20	O	33	LEU
20	O	35	VAL
20	O	103	THR
20	O	117	GLU
20	O	118	ASN
21	P	101	GLU
22	Q	53	ARG
22	Q	101	SER
23	R	23	VAL
23	R	62	THR
24	S	119	SER
24	S	120	ARG
25	T	3	THR
25	T	4	LEU
25	T	68	ARG
25	T	85	THR
26	U	38	VAL
26	U	45	THR
26	U	98	SER

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Mol	Chain	Res	Type
27	V	61	THR
27	V	69	ILE
27	V	98	VAL
28	W	49	VAL
28	W	57	ASP
29	X	51	VAL
30	Y	13	LEU
31	Z	9	VAL
31	Z	22	SER
31	Z	56	VAL
33	c	6	ASN
33	c	63	VAL
33	c	93	LEU
34	d	171	GLU
35	e	116	VAL
35	e	192	ILE
36	f	19	VAL
36	f	65	VAL
36	f	93	THR
37	g	12	LEU
37	g	13	VAL
37	g	24	THR
37	g	43	VAL
37	g	61	THR
37	g	84	THR
37	g	115	THR
38	h	26	SER
39	i	46	THR
39	i	79	VAL
39	i	85	PHE
39	i	151	ARG
40	j	48	VAL
41	k	26	VAL
41	k	28	HIS
41	k	87	HIS
42	l	55	VAL
42	l	77	HIS
44	n	13	LYS
44	n	25	SER
45	o	4	THR
46	p	62	VAL
47	q	93	THR

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Mol	Chain	Res	Type
47	q	105	VAL
48	r	27	ASP
48	r	73	GLU
49	s	41	ILE
50	t	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	37	HIS
9	C	70	ASN
9	C	135	ASN
9	C	227	ASN
10	D	76	ASN
10	D	179	ASN
11	E	74	GLN
11	E	97	HIS
11	E	127	ASN
12	F	62	ASN
14	H	46	GLN
17	L	57	HIS
18	M	28	ASN
19	N	61	HIS
20	O	17	HIS
22	Q	72	ASN
26	U	25	GLN
27	V	74	GLN
27	V	91	GLN
31	Z	3	GLN
33	c	152	GLN
34	d	24	GLN
34	d	167	GLN
35	e	41	ASN
40	j	101	GLN
41	k	38	ASN
41	k	59	HIS
42	l	109	ASN
43	m	55	HIS
46	p	15	ASN
46	p	52	ASN
50	t	70	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	a	1518/1537 (98%)	223 (14%)	0
7	A	3116/3138 (99%)	425 (13%)	2 (0%)
8	B	114/115 (99%)	16 (14%)	0
All	All	4748/4790 (99%)	664 (13%)	2 (0%)

All (664) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	13	A
7	A	35	G
7	A	63	A
7	A	71	A
7	A	74	U
7	A	75	G
7	A	94	C
7	A	118	A
7	A	119	A
7	A	120	U
7	A	125	A
7	A	142	U
7	A	143	G
7	A	167	A
7	A	176	G
7	A	183	A
7	A	198	A
7	A	201	A
7	A	217	G
7	A	218	A
7	A	224	A
7	A	225	A
7	A	231	U
7	A	232	G
7	A	250	G
7	A	269	G
7	A	271	U
7	A	279	A
7	A	283	A
7	A	286	G
7	A	287	G
7	A	288	U
7	A	289	A

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Mol	Chain	Res	Type
7	A	290	A
7	A	293	G
7	A	294	G
7	A	297	A
7	A	301	G
7	A	303	U
7	A	320	G
7	A	327	U
7	A	328	A
7	A	329	U
7	A	330	G
7	A	331	U
7	A	332	C
7	A	339	C
7	A	345	G
7	A	358	U
7	A	370	G
7	A	372	G
7	A	377	G
7	A	394	U
7	A	399	U
7	A	413	A
7	A	414	G
7	A	429	A
7	A	446	A
7	A	447	G
7	A	448	U
7	A	453	A
7	A	473	C
7	A	475	G
7	A	500	G
7	A	501	A
7	A	526	U
7	A	544	U
7	A	570	G
7	A	592	G
7	A	593	A
7	A	595	U
7	A	596	A
7	A	597	C
7	A	606	G
7	A	616	A

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Mol	Chain	Res	Type
7	A	618	U
7	A	619	C
7	A	620	C
7	A	621	G
7	A	637	C
7	A	639	U
7	A	641	U
7	A	642	C
7	A	643	C
7	A	645	G
7	A	653	U
7	A	665	G
7	A	673	A
7	A	675	G
7	A	676	A
7	A	677	A
7	A	689	G
7	A	694	G
7	A	706	A
7	A	719	U
7	A	741	A
7	A	750	A
7	A	756	A
7	A	758	C
7	A	759	C
7	A	760	A
7	A	768	A
7	A	772	G
7	A	774	G
7	A	776	G
7	A	779	U
7	A	780	G
7	A	781	A
7	A	782	A
7	A	783	U
7	A	815	U
7	A	843	U
7	A	844	A
7	A	846	G
7	A	847	A
7	A	852	G
7	A	859	C

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Mol	Chain	Res	Type
7	A	876	U
7	A	893	A
7	A	894	G
7	A	904	G
7	A	905	G
7	A	911	A
7	A	913	G
7	A	914	G
7	A	918	A
7	A	934	G
7	A	941	C
7	A	956	U
7	A	958	A
7	A	988	G
7	A	1007	G
7	A	1025	A
7	A	1026	C
7	A	1036	C
7	A	1039	A
7	A	1043	C
7	A	1059	A
7	A	1061	A
7	A	1074	G
7	A	1086	U
7	A	1087	A
7	A	1089	G
7	A	1096	A
7	A	1103	A
7	A	1112	A
7	A	1125	G
7	A	1142	G
7	A	1155	G
7	A	1162	U
7	A	1168	G
7	A	1175	A
7	A	1176	G
7	A	1177	A
7	A	1184	G
7	A	1189	U
7	A	1190	U
7	A	1191	G
7	A	1193	C

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Mol	Chain	Res	Type
7	A	1196	A
7	A	1199	A
7	A	1200	G
7	A	1202	A
7	A	1207	C
7	A	1208	C
7	A	1210	U
7	A	1212	G
7	A	1215	A
7	A	1216	G
7	A	1217	A
7	A	1219	U
7	A	1230	U
7	A	1234	U
7	A	1239	A
7	A	1240	A
7	A	1241	G
7	A	1261	U
7	A	1262	A
7	A	1264	C
7	A	1265	G
7	A	1271	C
7	A	1273	A
7	A	1304	U
7	A	1305	U
7	A	1306	G
7	A	1308	G
7	A	1309	G
7	A	1342	C
7	A	1381	G
7	A	1384	A
7	A	1387	G
7	A	1402	G
7	A	1403	A
7	A	1406	A
7	A	1431	A
7	A	1432	A
7	A	1451	C
7	A	1452	C
7	A	1453	A
7	A	1460	U
7	A	1481	C

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Mol	Chain	Res	Type
7	A	1483	U
7	A	1491	G
7	A	1496	A
7	A	1499	G
7	A	1510	U
7	A	1515	A
7	A	1542	G
7	A	1551	C
7	A	1552	G
7	A	1554	G
7	A	1560	U
7	A	1561	C
7	A	1562	A
7	A	1567	U
7	A	1568	A
7	A	1577	C
7	A	1580	A
7	A	1581	A
7	A	1582	A
7	A	1609	U
7	A	1610	G
7	A	1614	A
7	A	1615	G
7	A	1622	G
7	A	1624	C
7	A	1625	U
7	A	1636	U
7	A	1637	U
7	A	1646	G
7	A	1647	U
7	A	1657	A
7	A	1658	A
7	A	1666	C
7	A	1690	A
7	A	1693	G
7	A	1696	A
7	A	1697	A
7	A	1698	C
7	A	1699	A
7	A	1720	G
7	A	1722	G
7	A	1727	A

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Mol	Chain	Res	Type
7	A	1746	U
7	A	1754	A
7	A	1763	G
7	A	1773	U
7	A	1774	U
7	A	1797	G
7	A	1803	A
7	A	1806	A
7	A	1821	G
7	A	1832	G
7	A	1842	C
7	A	1843	A
7	A	1845	A
7	A	1881	U
7	A	1883	C
7	A	1884	G
7	A	1888	U
7	A	1889	A
7	A	1909	G
7	A	1950	A
7	A	1959	A
7	A	1960	C
7	A	1961	C
7	A	1963	U
7	A	1964	U
7	A	1990	G
7	A	1992	A
7	A	1998	U
7	A	2007	A
7	A	2010	G
7	A	2034	C
7	A	2035	G
7	A	2050	U
7	A	2063	A
7	A	2105	G
7	A	2106	C
7	A	2107	A
7	A	2108	A
7	A	2109	G
7	A	2124	U
7	A	2144	G
7	A	2151	A

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Mol	Chain	Res	Type
7	A	2157	A
7	A	2167	G
7	A	2168	G
7	A	2175	A
7	A	2176	A
7	A	2193	U
7	A	2203	C
7	A	2205	C
7	A	2208	A
7	A	2209	U
7	A	2210	G
7	A	2229	U
7	A	2231	U
7	A	2258	A
7	A	2259	C
7	A	2261	A
7	A	2268	6MZ
7	A	2269	A
7	A	2270	G
7	A	2281	C
7	A	2293	C
7	A	2294	G
7	A	2297	A
7	A	2298	A
7	A	2299	G
7	A	2300	A
7	A	2330	G
7	A	2340	A
7	A	2343	G
7	A	2346	U
7	A	2347	G
7	A	2348	U
7	A	2352	G
7	A	2353	G
7	A	2354	A
7	A	2355	U
7	A	2356	A
7	A	2357	G
7	A	2360	G
7	A	2361	G
7	A	2362	G
7	A	2364	G

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Mol	Chain	Res	Type
7	A	2365	A
7	A	2366	C
7	A	2367	U
7	A	2371	A
7	A	2375	C
7	A	2377	C
7	A	2378	G
7	A	2382	C
7	A	2384	A
7	A	2385	G
7	A	2387	U
7	A	2391	G
7	A	2393	G
7	A	2394	G
7	A	2395	A
7	A	2396	G
7	A	2398	C
7	A	2400	U
7	A	2401	U
7	A	2402	G
7	A	2403	U
7	A	2404	U
7	A	2405	G
7	A	2406	A
7	A	2407	A
7	A	2408	A
7	A	2412	C
7	A	2413	A
7	A	2416	C
7	A	2417	U
7	A	2419	A
7	A	2424	A
7	A	2435	A
7	A	2449	A
7	A	2463	A
7	A	2476	G
7	A	2477	G
7	A	2489	OMG
7	A	2517	G
7	A	2521	C
7	A	2525	A
7	A	2526	A

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Mol	Chain	Res	Type
7	A	2543	A
7	A	2546	G
7	A	2547	C
7	A	2550	U
7	A	2558	C
7	A	2560	A
7	A	2563	G
7	A	2573	A
7	A	2583	G
7	A	2585	C
7	A	2588	C
7	A	2615	A
7	A	2621	G
7	A	2623	A
7	A	2644	A
7	A	2661	U
7	A	2663	A
7	A	2667	G
7	A	2668	A
7	A	2679	C
7	A	2686	A
7	A	2707	A
7	A	2714	A
7	A	2728	G
7	A	2736	OMC
7	A	2743	G
7	A	2751	G
7	A	2756	A
7	A	2767	G
7	A	2773	G
7	A	2804	A
7	A	2805	G
7	A	2840	A
7	A	2847	U
7	A	2851	U
7	A	2868	A
7	A	2952	G
7	A	2962	C
7	A	2964	C
7	A	2986	A
7	A	2995	A
7	A	2996	A

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Mol	Chain	Res	Type
7	A	3003	A
7	A	3016	A
7	A	3018	C
7	A	3023	U
7	A	3037	G
7	A	3038	U
7	A	3040	G
7	A	3056	A
7	A	3070	A
7	A	3107	A
7	A	3118	A
7	A	3119	C
7	A	3120	C
7	A	3129	A
8	B	2	U
8	B	8	G
8	B	24	A
8	B	34	U
8	B	41	C
8	B	51	A
8	B	55	U
8	B	56	A
8	B	65	A
8	B	85	U
8	B	86	C
8	B	88	G
8	B	101	G
8	B	105	A
8	B	114	C
8	B	115	A
32	a	11	A
32	a	12	G
32	a	25	G
32	a	34	G
32	a	35	A
32	a	42	G
32	a	50	C
32	a	51	U
32	a	54	A
32	a	74	A
32	a	78	U
32	a	81	C

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Mol	Chain	Res	Type
32	a	82	U
32	a	84	C
32	a	86	G
32	a	89	A
32	a	90	U
32	a	91	A
32	a	116	C
32	a	125	G
32	a	127	U
32	a	167	A
32	a	169	U
32	a	178	G
32	a	185	G
32	a	189	U
32	a	194	G
32	a	204	G
32	a	206	A
32	a	208	A
32	a	213	U
32	a	214	U
32	a	216	A
32	a	217	G
32	a	219	G
32	a	244	C
32	a	246	G
32	a	247	C
32	a	250	G
32	a	265	G
32	a	266	C
32	a	279	C
32	a	280	G
32	a	288	G
32	a	327	U
32	a	328	A
32	a	346	G
32	a	350	G
32	a	351	C
32	a	353	G
32	a	366	U
32	a	368	G
32	a	371	C
32	a	381	A

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Mol	Chain	Res	Type
32	a	391	C
32	a	397	C
32	a	405	G
32	a	408	G
32	a	409	G
32	a	410	A
32	a	411	U
32	a	412	G
32	a	413	A
32	a	414	C
32	a	420	U
32	a	421	C
32	a	428	U
32	a	437	U
32	a	439	C
32	a	451	A
32	a	452	G
32	a	453	G
32	a	455	C
32	a	457	G
32	a	459	G
32	a	460	U
32	a	461	U
32	a	463	U
32	a	465	U
32	a	473	A
32	a	476	G
32	a	485	G
32	a	486	A
32	a	487	A
32	a	488	G
32	a	490	A
32	a	500	A
32	a	501	A
32	a	502	C
32	a	508	G
32	a	509	C
32	a	512	G
32	a	517	C
32	a	518	G7M
32	a	523	A
32	a	538	A

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Mol	Chain	Res	Type
32	a	550	A
32	a	551	A
32	a	553	U
32	a	563	A
32	a	564	A
32	a	565	A
32	a	566	G
32	a	567	A
32	a	568	G
32	a	606	C
32	a	610	U
32	a	623	U
32	a	624	G
32	a	633	A
32	a	640	G
32	a	644	A
32	a	656	G
32	a	677	U
32	a	678	A
32	a	686	A
32	a	694	G
32	a	709	A
32	a	712	G
32	a	740	A
32	a	746	G
32	a	768	A
32	a	784	U
32	a	785	A
32	a	806	A
32	a	808	C
32	a	827	G
32	a	830	U
32	a	833	U
32	a	835	C
32	a	836	C
32	a	837	U
32	a	838	U
32	a	865	A
32	a	866	A
32	a	883	G
32	a	895	G
32	a	900	A

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Mol	Chain	Res	Type
32	a	919	G
32	a	927	C
32	a	951	A
32	a	953	U
32	a	954	U
32	a	962	A
32	a	968	A
32	a	969	G
32	a	970	A
32	a	985	U
32	a	986	G
32	a	987	A
32	a	993	A
32	a	997	G
32	a	1008	A
32	a	1010	A
32	a	1012	A
32	a	1019	C
32	a	1020	C
32	a	1021	C
32	a	1022	U
32	a	1023	U
32	a	1024	G
32	a	1033	G
32	a	1035	G
32	a	1044	G
32	a	1056	U
32	a	1085	G
32	a	1086	U
32	a	1092	A
32	a	1099	G
32	a	1116	U
32	a	1126	G
32	a	1129	A
32	a	1131	G
32	a	1137	G
32	a	1138	A
32	a	1150	C
32	a	1151	U
32	a	1160	C
32	a	1161	A
32	a	1174	G

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Mol	Chain	Res	Type
32	a	1175	U
32	a	1176	G
32	a	1188	A
32	a	1189	A
32	a	1199	C
32	a	1204	U
32	a	1205	A
32	a	1206	U
32	a	1218	C
32	a	1219	A
32	a	1228	A
32	a	1230	A
32	a	1232	U
32	a	1233	G
32	a	1249	U
32	a	1250	G
32	a	1252	G
32	a	1254	U
32	a	1270	G
32	a	1272	A
32	a	1277	U
32	a	1279	A
32	a	1292	G
32	a	1297	G
32	a	1312	C
32	a	1314	C
32	a	1328	C
32	a	1349	A
32	a	1356	A
32	a	1357	C
32	a	1369	U
32	a	1371	C
32	a	1419	A
32	a	1435	G
32	a	1439	A
32	a	1444	U
32	a	1485	A
32	a	1486	A
32	a	1492	A
32	a	1496	A
32	a	1510	G
32	a	1522	G

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Mol	Chain	Res	Type
32	a	1523	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	338	G
7	A	913	G

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

13 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
32	MA6	a	1512	32	23,26,27	1.30	3 (13%)	33,38,41	2.13	9 (27%)
7	OMC	A	2736	7,54	19,22,23	1.60	3 (15%)	25,31,34	1.07	2 (8%)
32	5MC	a	960	32	19,22,23	2.39	7 (36%)	26,32,35	1.14	1 (3%)
32	2MG	a	959	32	23,26,27	2.75	4 (17%)	33,38,41	2.07	9 (27%)
32	G7M	a	518	32	23,26,27	2.65	5 (21%)	34,39,42	1.57	7 (20%)
32	4OC	a	1395	32	20,23,24	2.55	5 (25%)	25,32,35	0.92	1 (4%)
7	6MZ	A	2268	7	22,25,26	2.36	3 (13%)	29,36,39	2.33	9 (31%)
32	2MG	a	1509	32	23,26,27	2.73	5 (21%)	33,38,41	2.05	9 (27%)
32	UR3	a	1491	32	19,22,23	2.83	4 (21%)	26,32,35	1.40	3 (11%)
7	OMG	A	2791	7	23,26,27	2.39	6 (26%)	32,38,41	2.00	10 (31%)
7	OMG	A	2489	7	23,26,27	2.39	6 (26%)	32,38,41	1.97	10 (31%)
32	MA6	a	1511	32	23,26,27	1.31	3 (13%)	33,38,41	2.11	10 (30%)
7	5MU	A	2177	7	19,22,23	2.31	8 (42%)	27,32,35	2.41	6 (22%)

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
32	MA6	a	1512	32	-	1/11/29/30	0/3/3/3
7	OMC	A	2736	7,54	-	1/9/27/28	0/2/2/2
32	5MC	a	960	32	-	0/7/25/26	0/2/2/2
32	2MG	a	959	32	-	3/9/27/28	0/3/3/3
32	G7M	a	518	32	-	0/7/25/26	0/3/3/3
32	4OC	a	1395	32	-	0/9/29/30	0/2/2/2
7	6MZ	A	2268	7	-	2/9/27/28	0/3/3/3
32	2MG	a	1509	32	-	0/9/27/28	0/3/3/3
32	UR3	a	1491	32	-	1/7/25/26	0/2/2/2
7	OMG	A	2791	7	-	0/9/27/28	0/3/3/3
7	OMG	A	2489	7	-	3/9/27/28	0/3/3/3
32	MA6	a	1511	32	-	0/11/29/30	0/3/3/3
7	5MU	A	2177	7	-	0/7/25/26	0/2/2/2

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	a	518	G7M	O6-C6	10.54	1.43	1.23
32	a	1491	UR3	O4-C4	10.27	1.45	1.23
7	A	2268	6MZ	C6-N6	9.89	1.45	1.34
32	a	959	2MG	O6-C6	9.68	1.41	1.23
32	a	1509	2MG	O6-C6	9.54	1.41	1.23
32	a	1395	4OC	O2-C2	8.94	1.40	1.23
7	A	2489	OMG	O6-C6	8.82	1.40	1.23
7	A	2791	OMG	O6-C6	8.77	1.40	1.23
32	a	959	2MG	C2-N2	7.26	1.48	1.33
32	a	1509	2MG	C2-N2	7.16	1.48	1.33
32	a	960	5MC	C5-C4	-6.55	1.39	1.44
7	A	2736	OMC	C4-N4	5.44	1.47	1.33
7	A	2791	OMG	C2-N2	4.78	1.45	1.34
7	A	2489	OMG	C2-N2	4.73	1.45	1.34
32	a	1395	4OC	C4-N4	4.62	1.45	1.36
7	A	2177	5MU	C2-N1	-4.54	1.31	1.38
32	a	960	5MC	C4-N4	4.46	1.45	1.34
32	a	518	G7M	C5-N7	-4.28	1.34	1.39
32	a	1491	UR3	C2-N1	-4.11	1.32	1.38
32	a	1511	MA6	C6-N6	4.02	1.47	1.36
32	a	1512	MA6	C6-N6	3.98	1.47	1.36
7	A	2177	5MU	C4-C5	-3.88	1.38	1.44
7	A	2177	5MU	C4-N3	-3.86	1.31	1.38
7	A	2177	5MU	C2-N3	-3.77	1.31	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	a	1395	4OC	C2-N1	-3.75	1.32	1.40
32	a	960	5MC	C2-N1	-3.71	1.32	1.40
32	a	518	G7M	C2-N2	3.71	1.42	1.34
7	A	2177	5MU	C6-N1	-3.61	1.31	1.38
7	A	2489	OMG	C6-N1	-3.36	1.32	1.38
32	a	1491	UR3	C4-N3	-3.31	1.34	1.40
7	A	2791	OMG	C6-N1	-3.29	1.32	1.38
32	a	960	5MC	C6-N1	-3.21	1.32	1.38
32	a	1509	2MG	C6-N1	-3.07	1.33	1.38
32	a	1491	UR3	C2-N3	-2.92	1.33	1.39
32	a	518	G7M	C6-N1	-2.88	1.33	1.38
32	a	959	2MG	C6-N1	-2.88	1.33	1.38
7	A	2268	6MZ	C8-N9	-2.84	1.32	1.37
7	A	2177	5MU	O2-C2	-2.81	1.18	1.23
7	A	2177	5MU	O4-C4	-2.77	1.18	1.23
32	a	960	5MC	C6-C5	2.72	1.39	1.34
32	a	960	5MC	O2-C2	-2.63	1.18	1.23
7	A	2268	6MZ	C5-N7	-2.52	1.34	1.39
32	a	1511	MA6	C5-N7	-2.50	1.34	1.39
7	A	2736	OMC	C2-N1	-2.50	1.34	1.40
7	A	2177	5MU	C6-C5	2.48	1.38	1.34
7	A	2791	OMG	C8-N9	-2.46	1.32	1.37
32	a	1512	MA6	C5-N7	-2.42	1.34	1.39
7	A	2791	OMG	C5-N7	-2.38	1.34	1.39
32	a	1509	2MG	C8-N9	-2.36	1.32	1.37
7	A	2489	OMG	C8-N9	-2.33	1.32	1.37
32	a	959	2MG	C8-N9	-2.32	1.32	1.37
32	a	1395	4OC	C6-N1	-2.31	1.32	1.38
7	A	2489	OMG	C5-N7	-2.31	1.34	1.39
32	a	518	G7M	C2-N1	-2.30	1.32	1.37
32	a	1511	MA6	C4-N9	-2.15	1.33	1.37
32	a	1512	MA6	C4-N9	-2.15	1.33	1.37
7	A	2791	OMG	C2-N1	-2.10	1.32	1.37
32	a	960	5MC	C2-N3	-2.06	1.32	1.36
7	A	2489	OMG	C2-N1	-2.05	1.32	1.37
32	a	1395	4OC	C2-N3	-2.02	1.32	1.36
32	a	1509	2MG	CM2-N2	-2.02	1.42	1.45
7	A	2736	OMC	C2-N3	-2.02	1.32	1.36

All (86) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	a	959	2MG	C2-N3-C4	6.65	120.33	112.00
7	A	2268	6MZ	C9-N6-C6	-6.53	116.79	122.85
32	a	1509	2MG	C2-N3-C4	6.45	120.06	112.00
7	A	2177	5MU	C4-N3-C2	-5.77	119.78	127.34
32	a	959	2MG	C5-C4-N3	-5.66	119.38	128.39
7	A	2177	5MU	N3-C2-N1	5.56	122.14	114.89
7	A	2177	5MU	C5-C6-N1	-5.53	117.31	123.31
7	A	2489	OMG	C5-C4-N3	-5.45	119.72	128.39
32	a	1509	2MG	C5-C4-N3	-5.43	119.75	128.39
7	A	2791	OMG	C5-C4-N3	-5.39	119.81	128.39
7	A	2268	6MZ	C5-C4-N3	-5.19	119.56	126.72
7	A	2177	5MU	C5-C4-N3	4.92	119.60	115.32
32	a	1511	MA6	N1-C2-N3	-4.92	121.13	128.58
32	a	1512	MA6	N1-C2-N3	-4.88	121.19	128.58
7	A	2791	OMG	C2-N3-C4	4.84	120.63	112.30
7	A	2489	OMG	C2-N3-C4	4.80	120.58	112.30
32	a	1491	UR3	C4-N3-C2	-4.60	120.88	124.58
32	a	1512	MA6	C5-C4-N3	-4.60	120.39	126.72
32	a	1511	MA6	C5-C4-N3	-4.57	120.42	126.72
32	a	1511	MA6	C2-N1-C6	4.50	122.81	111.83
32	a	1512	MA6	C2-N1-C6	4.46	122.72	111.83
7	A	2268	6MZ	N1-C2-N3	-4.41	121.91	128.58
32	a	960	5MC	C5-C6-N1	-4.20	118.75	123.31
32	a	1512	MA6	C4-C5-N7	-4.01	106.00	110.58
32	a	1511	MA6	C4-C5-N7	-3.95	106.07	110.58
7	A	2177	5MU	O4-C4-C5	-3.92	120.43	124.92
32	a	959	2MG	N9-C4-N3	3.90	133.76	125.95
7	A	2268	6MZ	N3-C4-N9	3.85	133.72	127.17
7	A	2791	OMG	N9-C4-N3	3.82	133.58	125.95
32	a	518	G7M	C2-N3-C4	3.80	118.84	112.30
7	A	2489	OMG	N9-C4-N3	3.70	133.36	125.95
32	a	518	G7M	C5-C6-N1	3.68	119.45	111.84
32	a	1512	MA6	C5-N7-C8	3.64	109.17	103.45
32	a	518	G7M	C5-C4-N3	-3.60	121.35	128.15
32	a	1511	MA6	C5-N7-C8	3.59	109.10	103.45
32	a	1509	2MG	N9-C4-N3	3.59	133.14	125.95
7	A	2268	6MZ	C2-N3-C4	3.48	120.32	111.83
32	a	1512	MA6	N9-C8-N7	-3.46	109.03	113.94
32	a	1512	MA6	C2-N3-C4	3.34	119.99	111.83
32	a	1511	MA6	N9-C8-N7	-3.33	109.20	113.94
32	a	1511	MA6	C2-N3-C4	3.31	119.91	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	a	518	G7M	O6-C6-C5	-3.21	120.84	128.01
7	A	2791	OMG	C6-C5-N7	3.21	136.13	130.29
7	A	2489	OMG	C6-C5-N7	3.19	136.10	130.29
32	a	518	G7M	C6-C5-N7	3.09	136.05	132.17
7	A	2177	5MU	O2-C2-N1	-3.02	118.87	122.80
7	A	2268	6MZ	N9-C8-N7	-2.97	109.72	113.94
32	a	518	G7M	N9-C4-N3	2.91	131.77	125.95
7	A	2489	OMG	C2-N1-C6	-2.89	119.86	125.11
7	A	2791	OMG	C5-C6-N1	2.89	120.60	113.25
7	A	2791	OMG	C2-N1-C6	-2.88	119.90	125.11
32	a	1512	MA6	N3-C4-N9	2.85	132.02	127.17
32	a	1511	MA6	N3-C4-N9	2.84	132.00	127.17
7	A	2489	OMG	C5-C6-N1	2.84	120.48	113.25
32	a	1509	2MG	N1-C2-N2	2.84	119.46	116.56
7	A	2736	OMC	O2-C2-N3	-2.73	118.02	122.33
7	A	2791	OMG	O6-C6-C5	-2.65	119.55	126.53
7	A	2268	6MZ	C5-N7-C8	2.64	107.60	103.45
32	a	1491	UR3	C5-C4-N3	2.61	118.48	115.04
7	A	2268	6MZ	C4-C5-N7	-2.56	107.66	110.58
7	A	2489	OMG	O6-C6-C5	-2.55	119.80	126.53
32	a	1509	2MG	C4-C5-N7	-2.54	106.64	110.67
7	A	2489	OMG	C4-C5-N7	-2.47	106.75	110.67
7	A	2791	OMG	C8-N7-C5	2.47	108.65	104.26
7	A	2268	6MZ	C4-N9-C8	2.44	108.30	105.74
32	a	959	2MG	C4-C5-N7	-2.44	106.81	110.67
32	a	959	2MG	N1-C2-N2	2.43	119.04	116.56
32	a	1509	2MG	C8-N7-C5	2.43	108.59	104.26
32	a	959	2MG	C8-N7-C5	2.42	108.57	104.26
7	A	2791	OMG	C4-C5-N7	-2.41	106.85	110.67
32	a	518	G7M	C2-N1-C6	-2.41	120.75	125.11
7	A	2489	OMG	C8-N7-C5	2.39	108.52	104.26
7	A	2791	OMG	N9-C8-N7	-2.37	109.00	113.40
32	a	1512	MA6	C4-N9-C8	2.35	108.20	105.74
32	a	1509	2MG	C6-C5-N7	2.32	134.51	130.29
32	a	1509	2MG	N9-C8-N7	-2.31	109.12	113.40
32	a	959	2MG	N9-C8-N7	-2.21	109.31	113.40
7	A	2489	OMG	N9-C8-N7	-2.21	109.31	113.40
32	a	1511	MA6	C4-N9-C8	2.20	108.05	105.74
32	a	1491	UR3	C5-C6-N1	-2.15	118.34	121.84
32	a	1395	4OC	C5-C4-N3	-2.15	119.24	122.60
32	a	959	2MG	C6-C5-N7	2.11	134.13	130.29
32	a	1511	MA6	C4-C5-C6	2.07	118.05	115.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	a	1509	2MG	CM2-N2-C2	-2.05	119.24	123.65
32	a	959	2MG	O6-C6-C5	-2.04	121.16	126.53
7	A	2736	OMC	N1-C2-N3	2.01	122.29	118.80

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2489	OMG	O4'-C4'-C5'-O5'
7	A	2489	OMG	C1'-C2'-O2'-CM2
32	a	959	2MG	N1-C2-N2-CM2
32	a	959	2MG	N3-C2-N2-CM2
7	A	2268	6MZ	O4'-C4'-C5'-O5'
7	A	2268	6MZ	C3'-C4'-C5'-O5'
7	A	2489	OMG	C3'-C4'-C5'-O5'
32	a	1512	MA6	O4'-C4'-C5'-O5'
32	a	1491	UR3	O4'-C4'-C5'-O5'
32	a	959	2MG	C4'-C5'-O5'-P
7	A	2736	OMC	O4'-C4'-C5'-O5'

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	a	1512	MA6	1	0
32	a	518	G7M	2	0
32	a	1395	4OC	2	0
7	A	2268	6MZ	1	0
32	a	1509	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 454 ligands modelled in this entry, 453 are monoatomic - leaving 1 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
53	WDP	A	3201	-	84,90,90	2.46	20 (23%)	101,132,132	2.25	17 (16%)

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
53	WDP	A	3201	-	-	37/103/158/158	1/4/5/5

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	A	3201	WDP	C18-N20	8.83	1.50	1.35
53	A	3201	WDP	S26-N25	7.61	1.73	1.61
53	A	3201	WDP	O17-C18	6.26	1.46	1.34
53	A	3201	WDP	C62-N61	-6.20	1.33	1.46
53	A	3201	WDP	O50-C51	5.94	1.47	1.34
53	A	3201	WDP	C04-N03	-5.54	1.22	1.27
53	A	3201	WDP	C14-C15	5.18	1.62	1.53
53	A	3201	WDP	O40-C41	4.66	1.47	1.34
53	A	3201	WDP	C43-C41	4.62	1.59	1.50
53	A	3201	WDP	C29-S26	4.30	1.83	1.76
53	A	3201	WDP	C59-N61	-4.03	1.35	1.48
53	A	3201	WDP	O17-C15	-3.43	1.41	1.46
53	A	3201	WDP	C24-C21	3.21	1.57	1.53
53	A	3201	WDP	O74-C73	2.81	1.49	1.41
53	A	3201	WDP	C24-N25	2.78	1.50	1.47
53	A	3201	WDP	C82-C79	-2.69	1.46	1.52
53	A	3201	WDP	C53-C51	2.40	1.56	1.51
53	A	3201	WDP	O27-S26	2.31	1.46	1.43
53	A	3201	WDP	C60-C59	2.18	1.59	1.52
53	A	3201	WDP	O19-C18	-2.16	1.17	1.21

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	A	3201	WDP	O28-S26-O27	-15.10	101.18	119.52
53	A	3201	WDP	O17-C18-N20	7.72	119.98	109.88
53	A	3201	WDP	C05-C04-N03	-5.83	120.13	126.93
53	A	3201	WDP	O40-C41-C43	4.75	119.94	111.43
53	A	3201	WDP	O50-C51-C53	4.08	120.25	111.53
53	A	3201	WDP	O19-C18-N20	-3.18	119.98	124.91
53	A	3201	WDP	O17-C18-O19	-3.15	120.04	125.64
53	A	3201	WDP	O28-S26-N25	2.74	111.29	107.03
53	A	3201	WDP	O27-S26-N25	2.74	111.29	107.03
53	A	3201	WDP	O08-C06-C05	2.70	112.39	108.62
53	A	3201	WDP	O28-S26-C29	2.65	111.32	107.98
53	A	3201	WDP	O27-S26-C29	2.58	111.24	107.98
53	A	3201	WDP	C07-C06-C05	-2.50	108.78	113.27
53	A	3201	WDP	C49-O50-C51	-2.48	113.64	117.76
53	A	3201	WDP	C76-C75-C77	-2.33	108.82	113.08
53	A	3201	WDP	O50-C51-O52	-2.27	119.86	123.95
53	A	3201	WDP	O10-C11-C67	2.05	110.65	108.23

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
53	A	3201	WDP	C16-C15-O17-C18
53	A	3201	WDP	C22-C21-C24-N25
53	A	3201	WDP	C23-C21-C24-N25
53	A	3201	WDP	N20-C21-C24-N25
53	A	3201	WDP	C22-C21-N20-C18
53	A	3201	WDP	C24-C21-N20-C18
53	A	3201	WDP	C23-C21-N20-C18
53	A	3201	WDP	C21-C24-N25-S26
53	A	3201	WDP	C05-C04-N03-O02
53	A	3201	WDP	C85-C04-N03-O02
53	A	3201	WDP	C12-C11-C67-C55
53	A	3201	WDP	O17-C18-N20-C21
53	A	3201	WDP	O19-C18-N20-C21
53	A	3201	WDP	N20-C18-O17-C15
53	A	3201	WDP	O19-C18-O17-C15
53	A	3201	WDP	C15-C35-C37-C38
53	A	3201	WDP	O36-C35-C37-C38
53	A	3201	WDP	C37-C39-O40-C41
53	A	3201	WDP	C47-C39-O40-C41
53	A	3201	WDP	C43-C41-O40-C39
53	A	3201	WDP	C49-C69-C71-O72

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Mol	Chain	Res	Type	Atoms
53	A	3201	WDP	C70-C69-C71-O72
53	A	3201	WDP	C04-N03-O02-C01
53	A	3201	WDP	O42-C41-O40-C39
53	A	3201	WDP	O08-C09-O10-C11
53	A	3201	WDP	C24-N25-S26-O28
53	A	3201	WDP	O10-C11-C67-C55
53	A	3201	WDP	C12-C11-C67-C68
53	A	3201	WDP	C24-N25-S26-C29
53	A	3201	WDP	C24-N25-S26-O27
53	A	3201	WDP	C41-C43-C44-C45
53	A	3201	WDP	C82-C73-O72-C71
53	A	3201	WDP	O10-C11-C67-C68
53	A	3201	WDP	C37-C39-C47-C49
53	A	3201	WDP	C41-C43-C44-C46
53	A	3201	WDP	C82-C79-O80-C81
53	A	3201	WDP	C38-C37-C39-O40

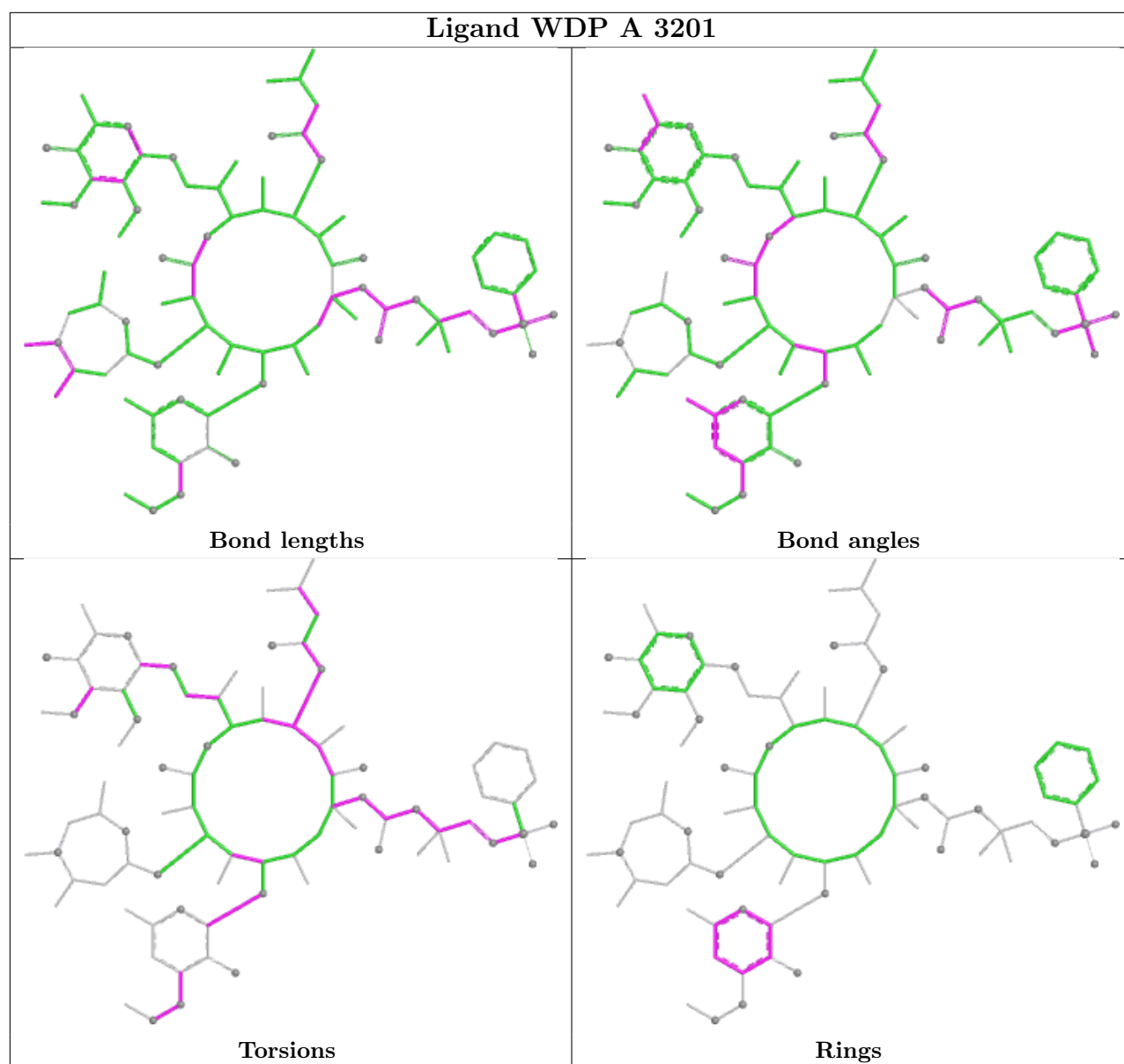
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
53	A	3201	WDP	C04-C05-C06-C09-C85-O08

1 monomer is involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
53	A	3201	WDP	21	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.

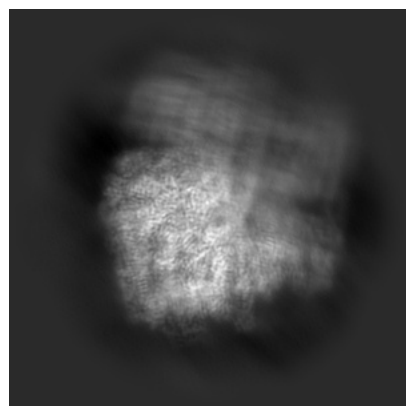
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25100. These allow visual inspection of the internal detail of the map and identification of artifacts.

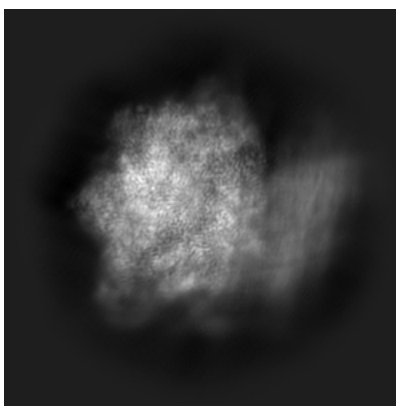
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

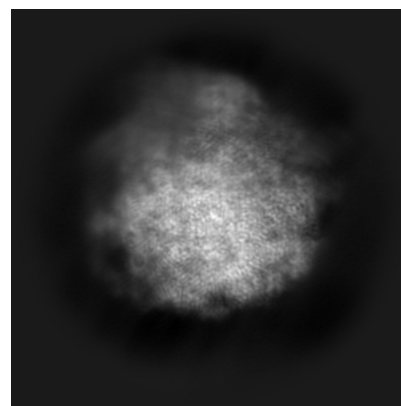
6.1.1 Primary map



X

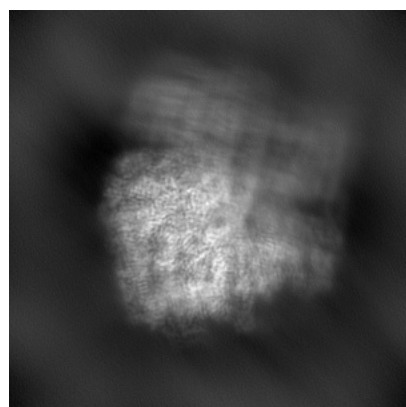


Y

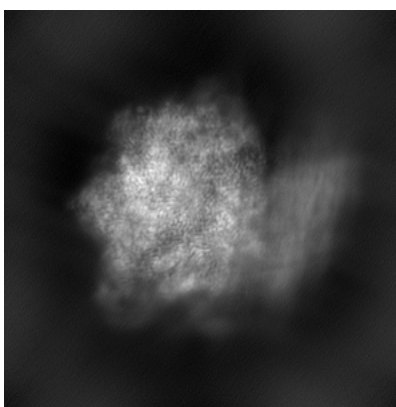


Z

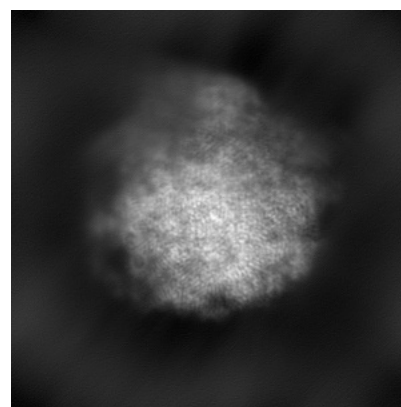
6.1.2 Raw map



X



Y

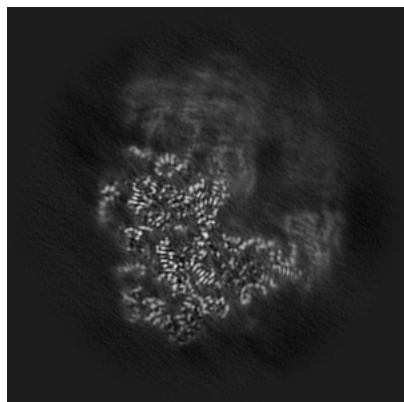


Z

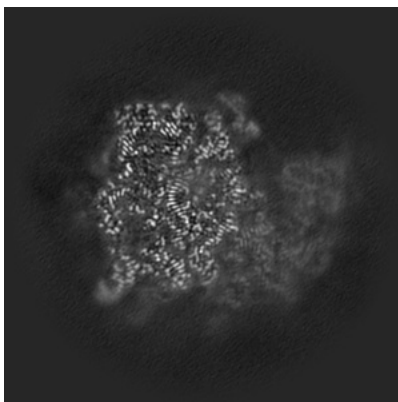
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

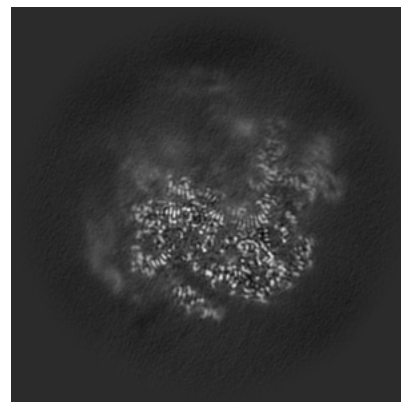
6.2.1 Primary map



X Index: 210

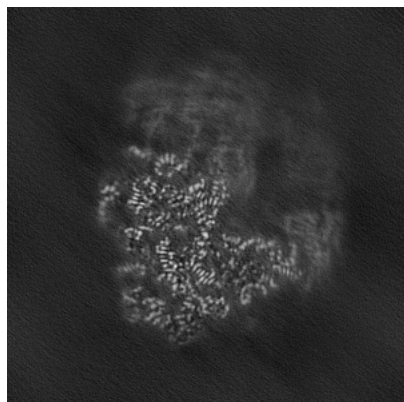


Y Index: 210

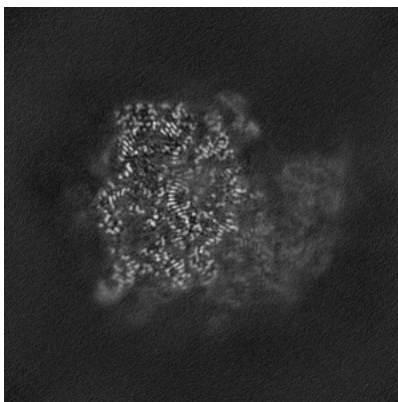


Z Index: 210

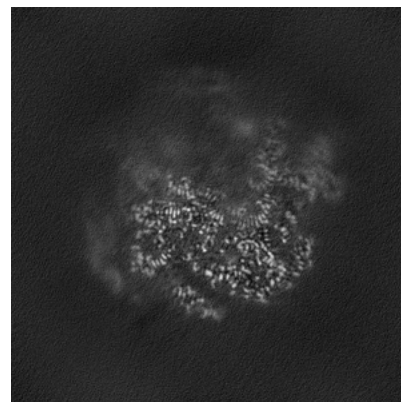
6.2.2 Raw map



X Index: 210



Y Index: 210

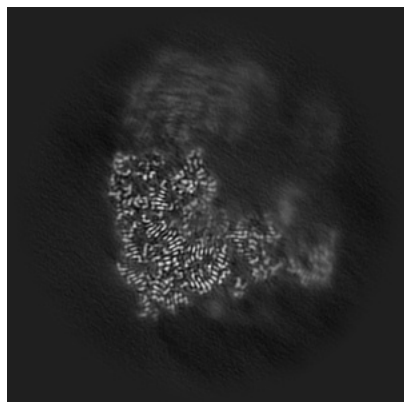


Z Index: 210

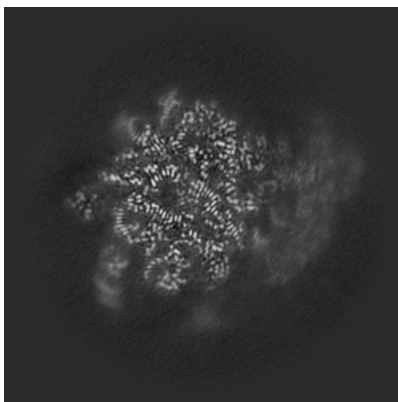
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

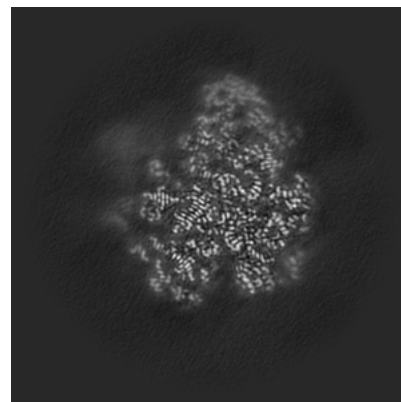
6.3.1 Primary map



X Index: 244

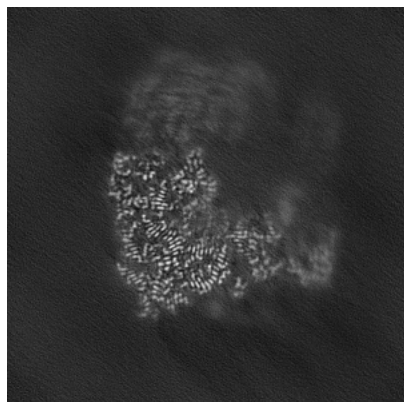


Y Index: 172

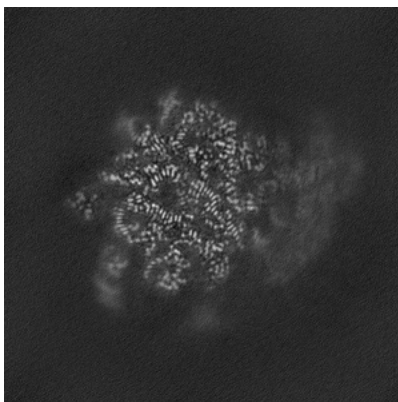


Z Index: 158

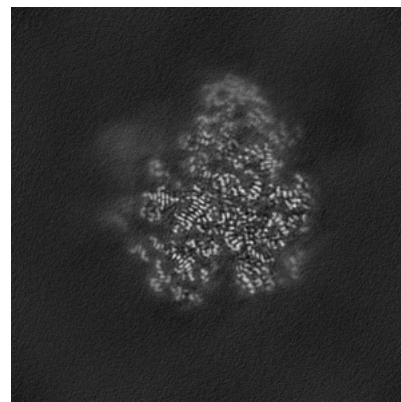
6.3.2 Raw map



X Index: 244



Y Index: 172

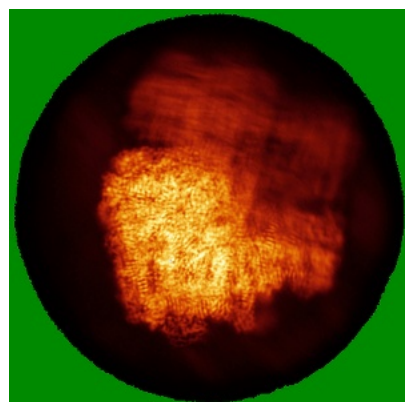


Z Index: 158

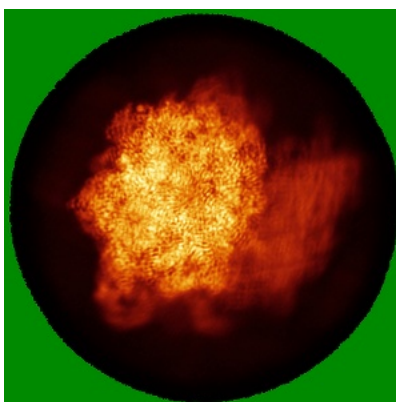
The images above show the largest variance slices of the map in three orthogonal directions.

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

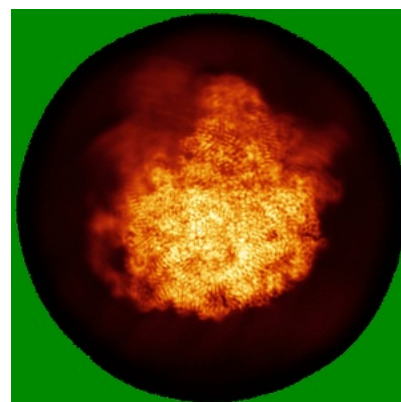
6.4.1 Primary map



X

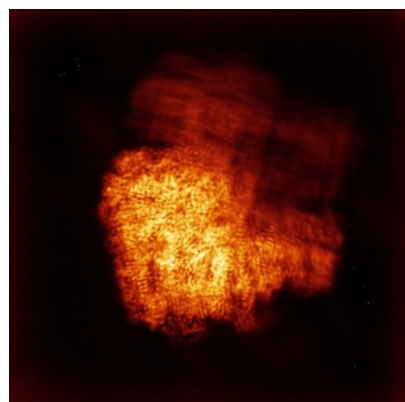


Y

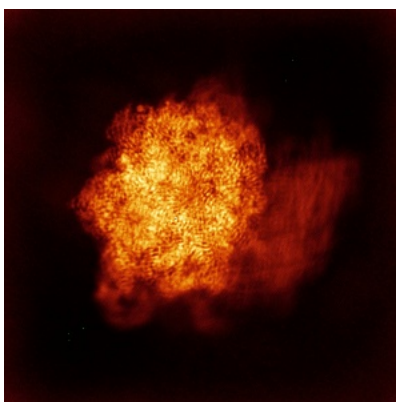


Z

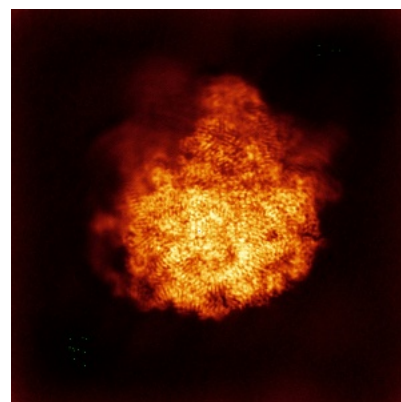
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

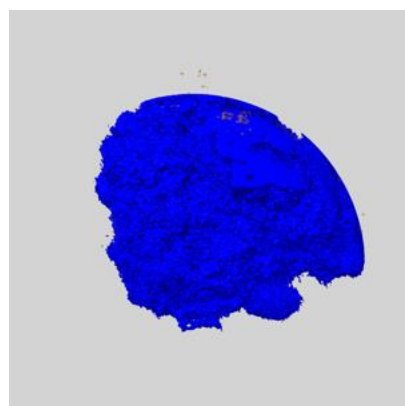
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

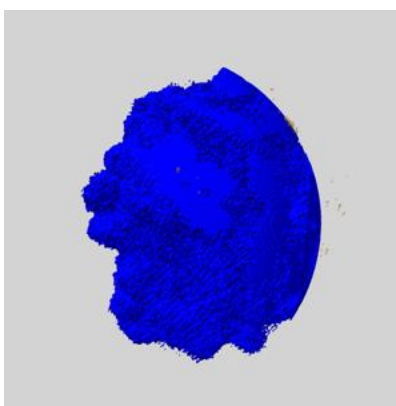
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

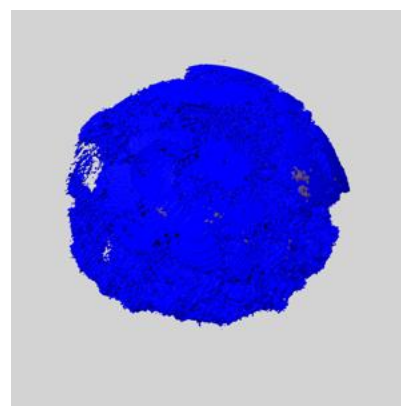
6.6.1 emd_25100_msk_1.map [i](#)



X



Y

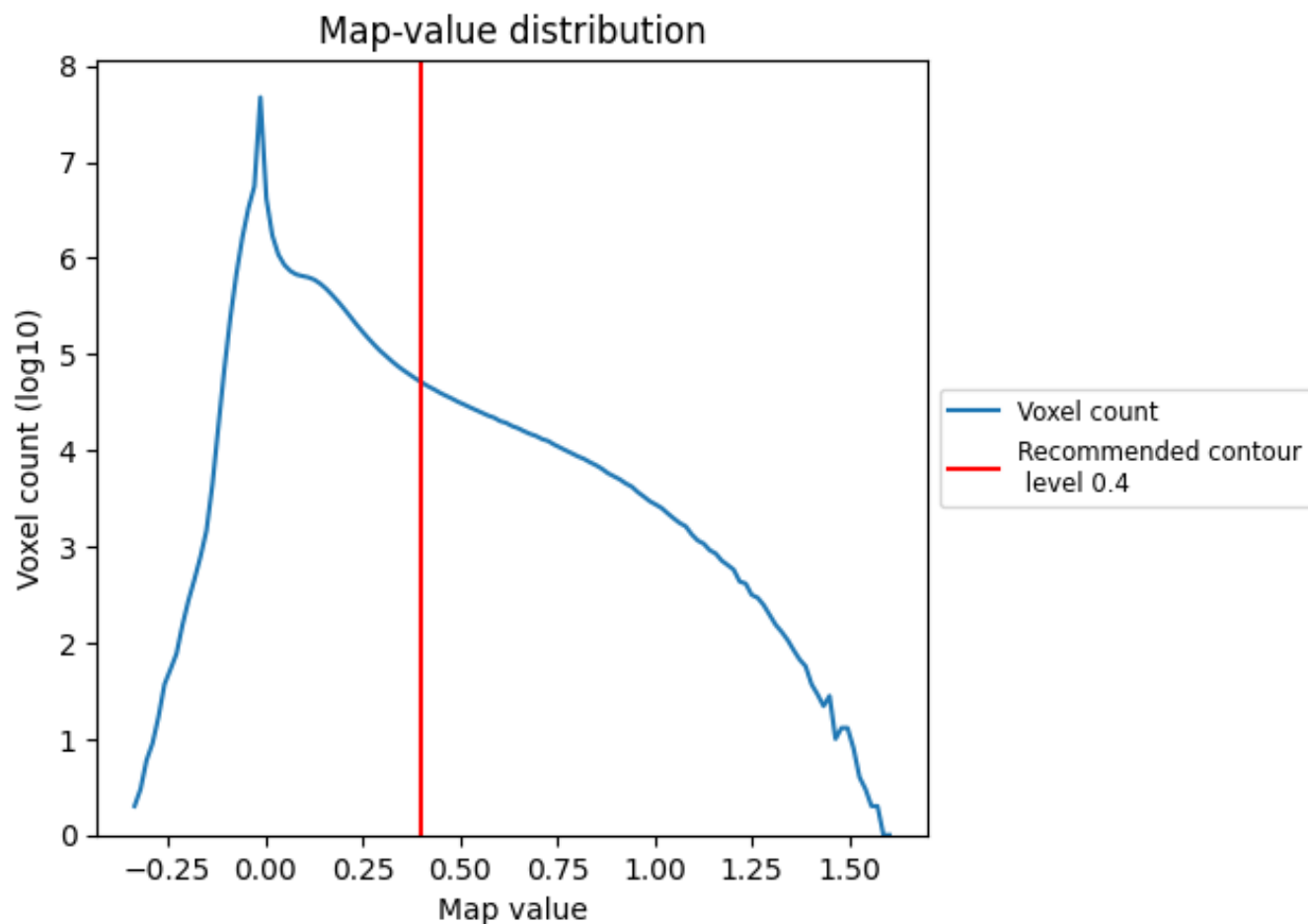


Z

7 Map analysis [i](#)

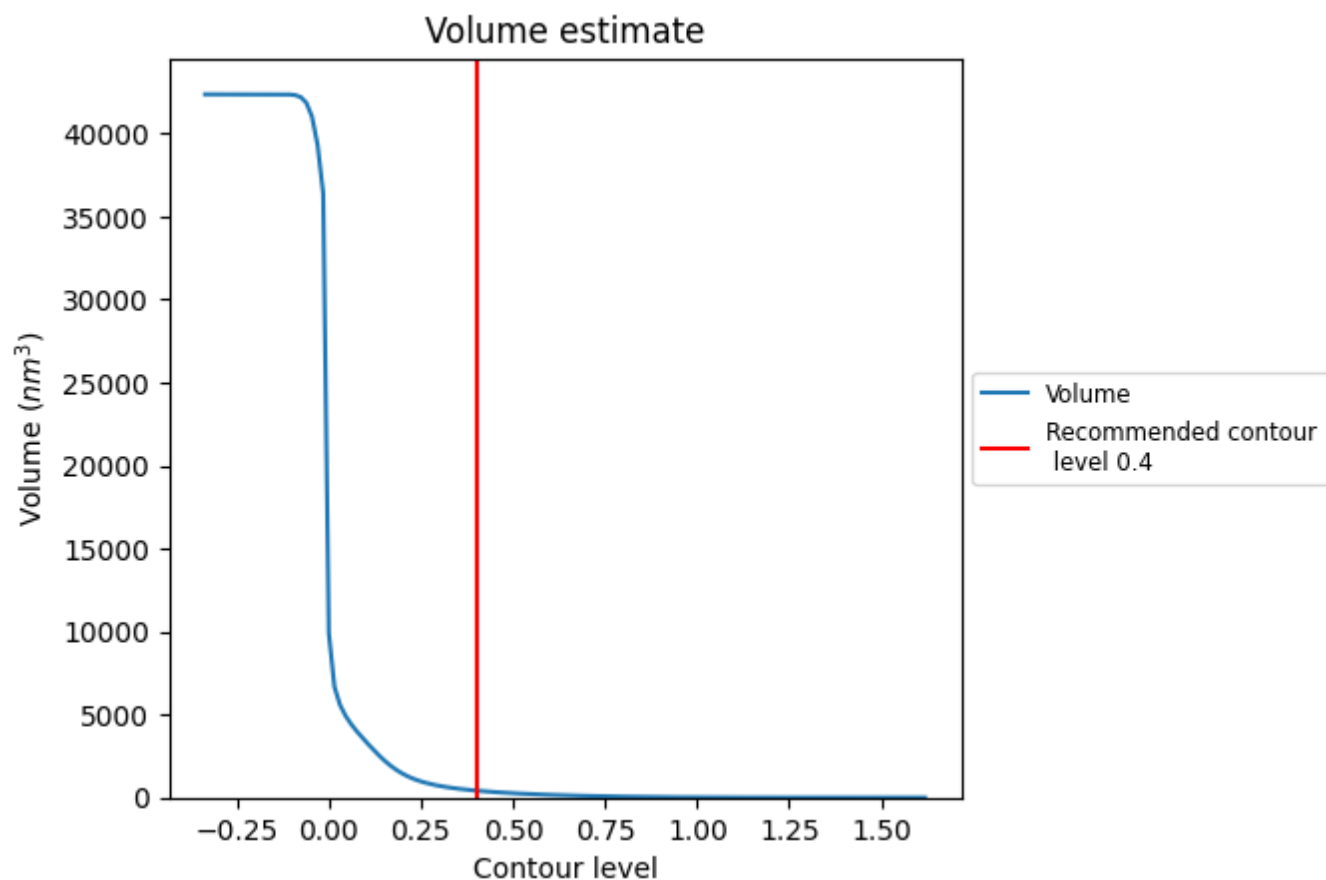
This section contains the results of statistical analysis of the map.

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.

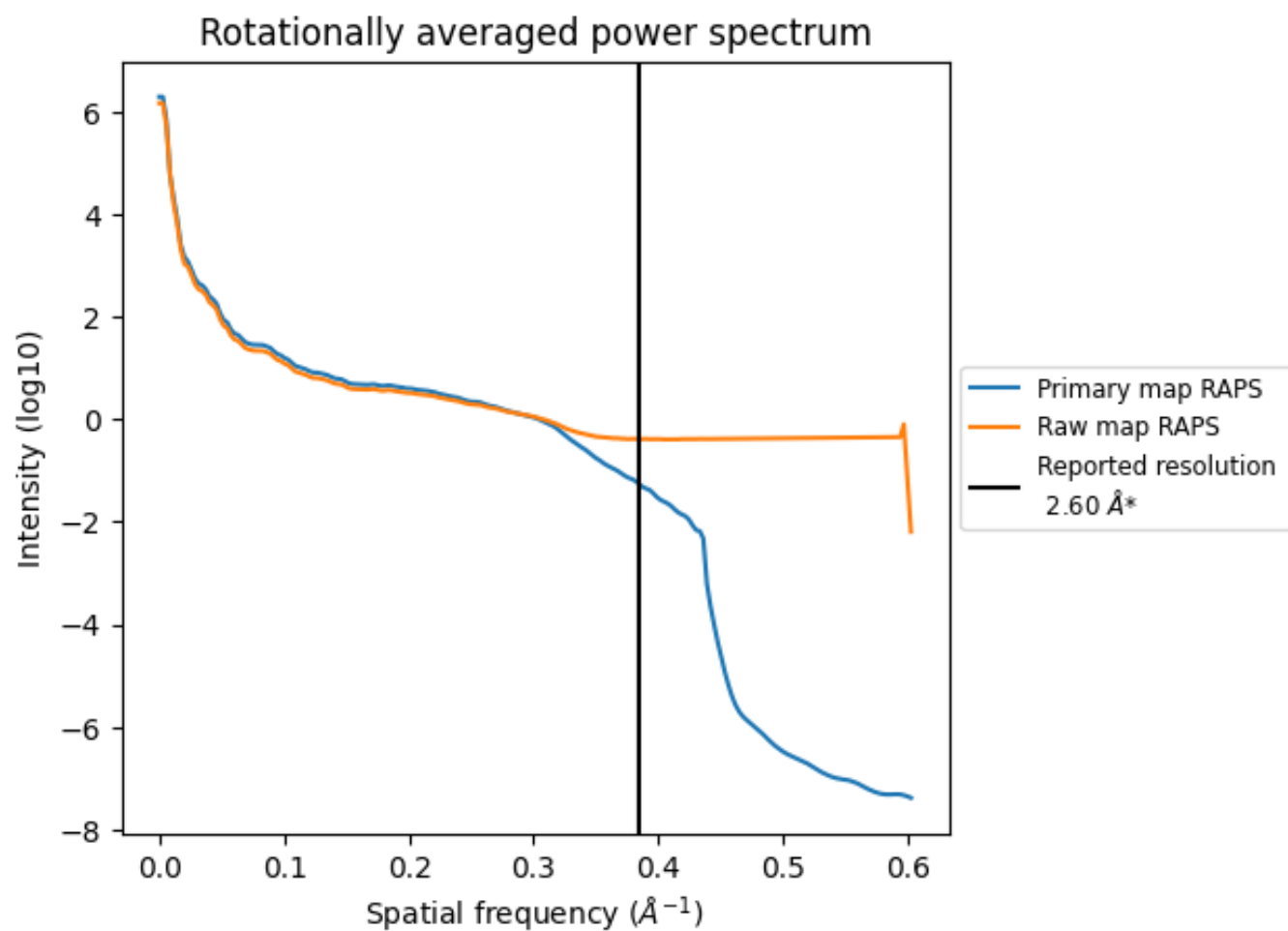
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 418 nm³; this corresponds to an approximate mass of 377 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 ⓘ

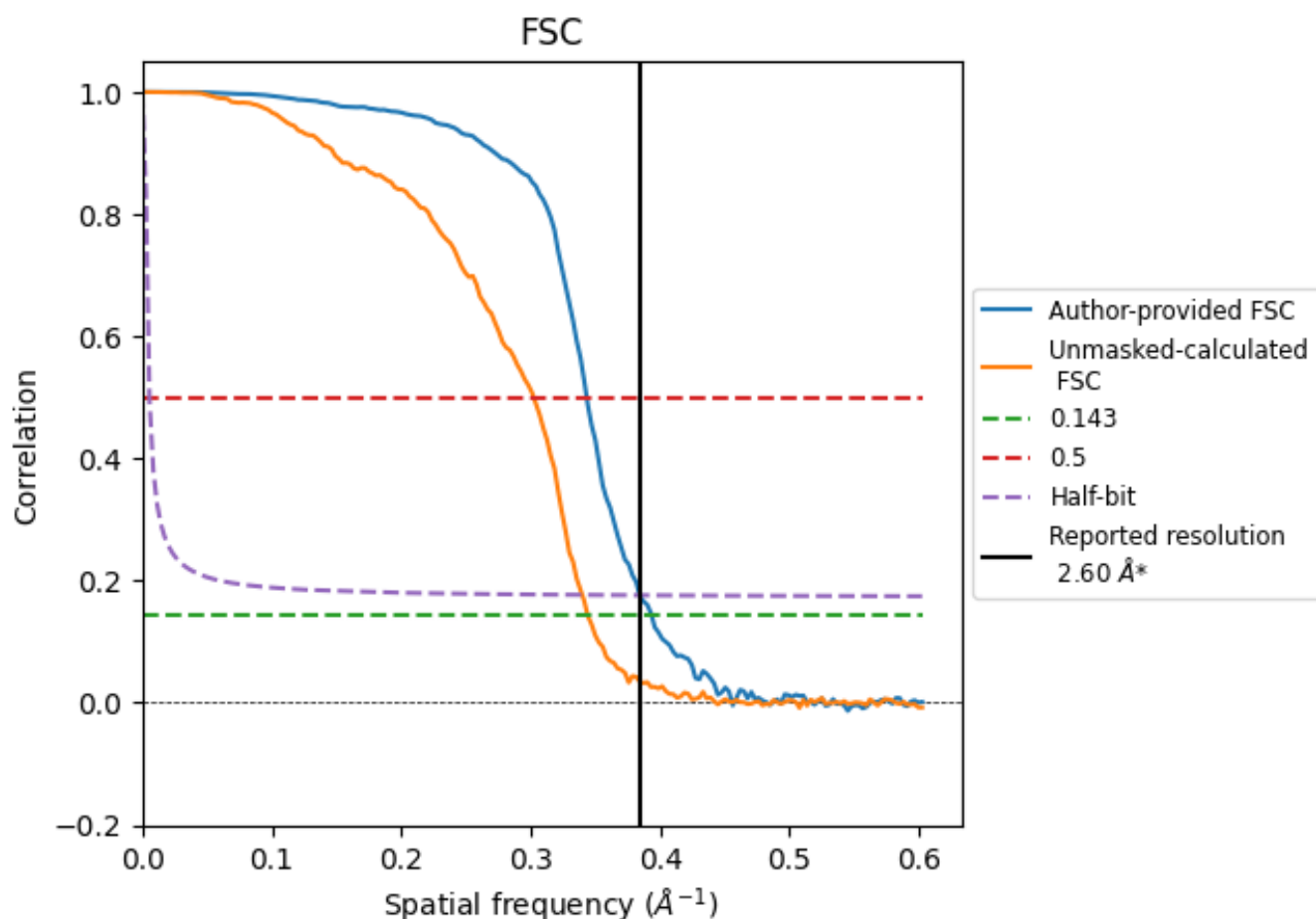


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.385 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

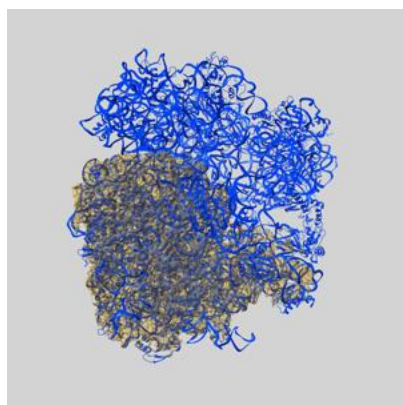
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.54	2.91	2.60
Unmasked-calculated*	2.91	3.31	2.94

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.91 differs from the reported value 2.6 by more than 10 %

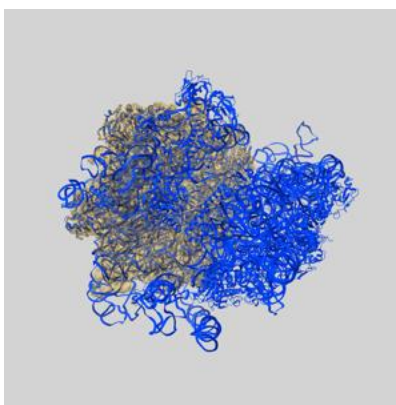
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25100 and PDB model 7SFR. Per-residue inclusion information can be found in section 3 on page 15.

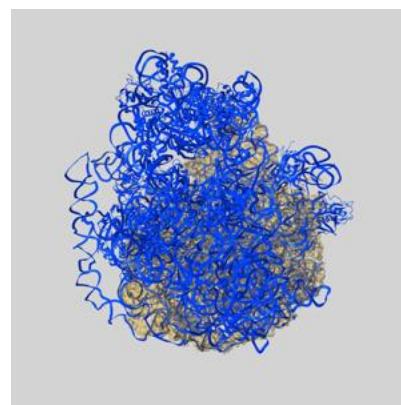
9.1 Map-model overlay [i](#)



X



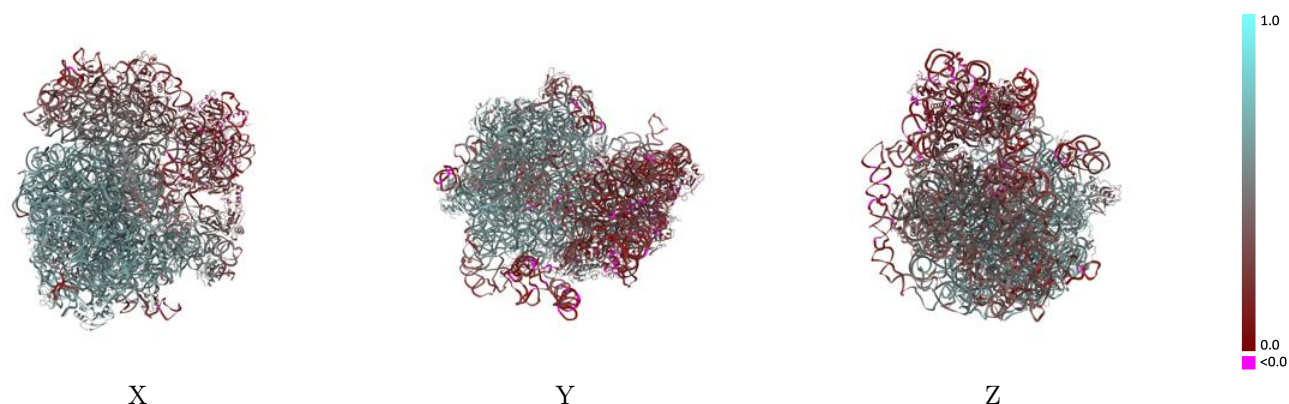
Y



Z

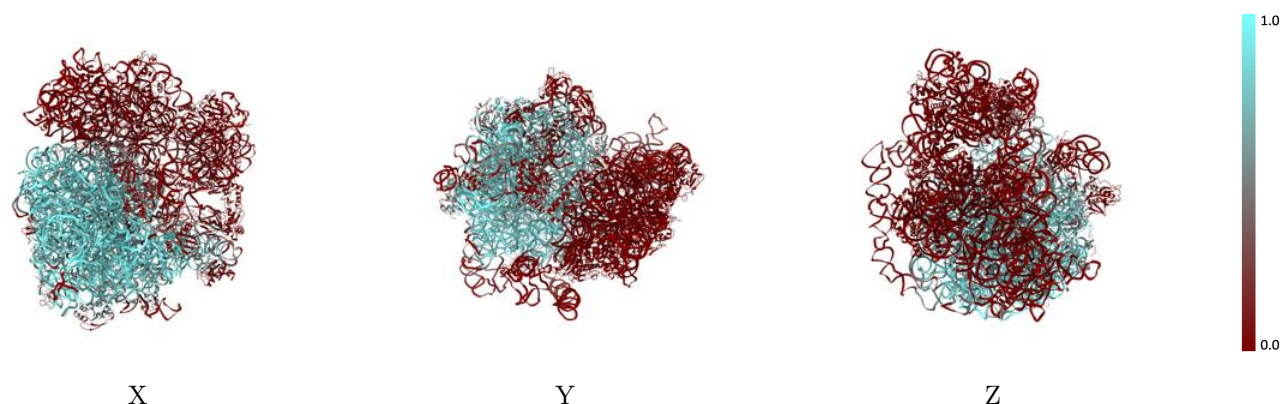
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



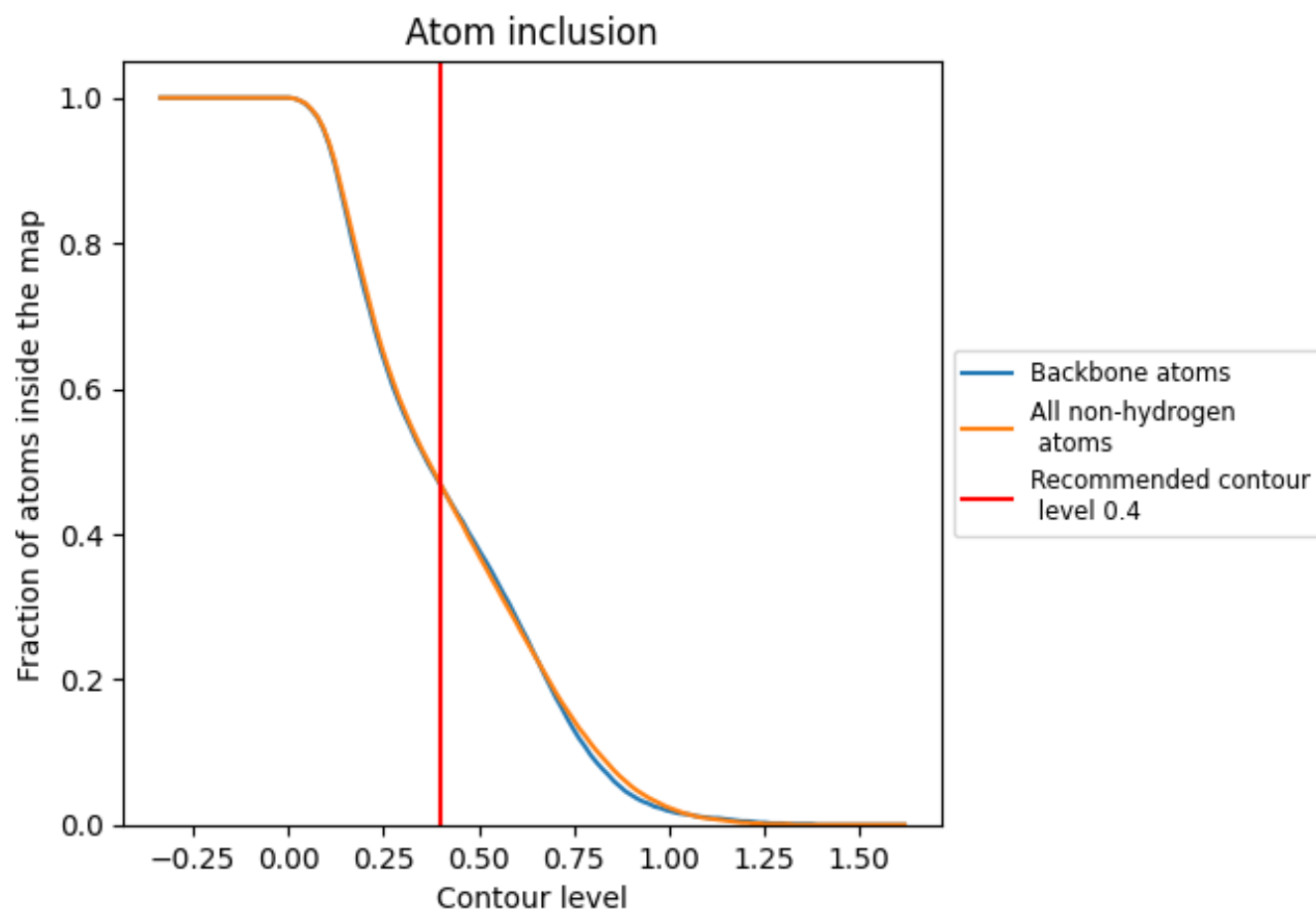
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 47% of all backbone atoms, 47% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4680	 0.4680
0	 0.4540	 0.6090
1	 0.6700	 0.5810
2	 0.9570	 0.6490
3	 0.7060	 0.6210
4	 0.1910	 0.5570
6	 0.0000	 0.2530
A	 0.7680	 0.5450
B	 0.5460	 0.4700
C	 0.8570	 0.6210
D	 0.7290	 0.6040
E	 0.6070	 0.5910
F	 0.0140	 0.3610
G	 0.0400	 0.4250
H	 0.0260	 0.3940
J	 0.8130	 0.6090
K	 0.6930	 0.6030
L	 0.6590	 0.5850
M	 0.1200	 0.5530
N	 0.8350	 0.6250
O	 0.2180	 0.4590
P	 0.6230	 0.5890
Q	 0.8520	 0.6190
R	 0.6470	 0.6010
S	 0.8140	 0.6220
T	 0.6410	 0.5780
U	 0.4140	 0.5220
V	 0.0440	 0.4840
W	 0.7620	 0.5990
X	 0.7660	 0.6190
Y	 0.5870	 0.5510
Z	 0.6990	 0.5880
a	 0.0180	 0.3330
c	 0.0000	 0.2250
d	 0.0000	 0.2260



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Chain	Atom inclusion	Q-score
e	 0.0000	 0.3140
f	 0.0000	 0.4430
g	 0.0000	 0.2290
h	 0.0000	 0.3360
i	 0.0000	 0.1610
j	 0.0000	 0.1700
k	 0.0000	 0.4060
l	 0.0000	 0.3460
m	 0.0000	 0.2100
n	 0.0000	 0.2030
o	 0.0000	 0.4150
p	 0.0000	 0.3030
q	 0.0000	 0.3330
r	 0.0000	 0.4080
s	 0.0000	 0.1790
t	 0.0000	 0.3420
v	 0.0170	 0.5040