



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 09:58 PM UTC

PDB ID : 9C8K / pdb_00009c8k
EMDB ID : EMD-45307
Title : Rabbit Hemorrhagic Disease Virus reinitiation stimulating TURBS RNA
bound to rabbit ribosome
Authors : Sherlock, M.E.; Kieft, J.S.
Deposited on : 2024-06-12
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

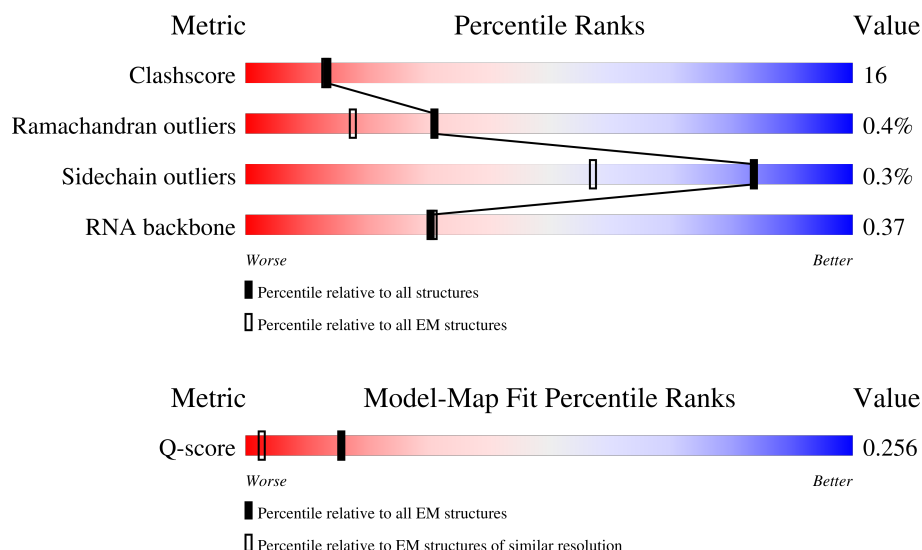
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	A	295	
2	B	264	
3	C	293	

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Mol	Chain	Length	Quality of chain
4	D	243	
5	E	263	
6	F	204	
7	G	249	
8	H	194	
9	I	208	
10	J	194	
11	K	165	
12	L	158	
13	M	132	
14	N	151	
15	O	151	
16	P	145	
17	Q	146	
18	R	135	
19	S	152	
20	T	145	
21	U	119	
22	V	83	
23	W	130	
24	X	143	
25	Y	133	
26	Z	125	
27	a	115	
28	b	84	

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Mol	Chain	Length	Quality of chain
29	c	69	71%68%19%12%
30	d	56	73%59%29%9%
31	e	59	53%75%19%7%
32	f	156	42%37%9%53%
33	g	317	99%74%26%
34	1	1869	25%43%36%12%9%
35	2	91	5%20%8%70%

2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 134479 atoms, of which 58947 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 Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	215	Total	C	H	N	O	S	0	0
			3409	1083	1705	298	315	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	290	ALA	THR	conflict	UNP G1TLT8
A	293	ASP	GLU	conflict	UNP G1TLT8

- Molecule 2 is a protein called eS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	212	Total	C	H	N	O	S	0	0
			3517	1093	1795	308	307	14		

- Molecule 3 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	222	Total	C	H	N	O	S	0	0
			3533	1114	1809	296	304	10		

- Molecule 4 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	220	Total	C	H	N	O	S	0	0
			3513	1090	1804	308	304	7		

- Molecule 5 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	257	Total	C	H	N	O	S	0	0
			4170	1298	2139	381	344	8		

- Molecule 6 is a protein called uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	190	Total	C	H	N	O	S	0	0
			3060	939	1558	285	271	7		

- Molecule 7 is a protein called eS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	232	Total	C	H	N	O	S	0	0
			3929	1176	2045	379	322	7		

- Molecule 8 is a protein called eS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	183	Total	C	H	N	O	S	0	0
			3045	941	1566	272	265	1		

- Molecule 9 is a protein called eS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	207	Total	C	H	N	O	S	0	0
			3482	1064	1786	334	293	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 10 is a protein called uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	179	Total	C	H	N	O	S	0	0
			3110	953	1615	299	241	2		

- Molecule 11 is a protein called S10_pectin domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	98	Total	C	H	N	O	S	0	0
			1681	539	854	148	134	6		

- Molecule 12 is a protein called uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	153	Total	C	H	N	O	S	0	0
			2593	804	1335	235	213	6		

- Molecule 13 is a protein called eS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	120	Total	C	H	N	O	S	0	0
			1893	584	962	164	174	9		

- Molecule 14 is a protein called uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	149	Total	C	H	N	O	S	0	0
			2492	770	1290	228	203	1		

- Molecule 15 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	136	Total	C	H	N	O	S	0	0
			2056	621	1040	199	190	6		

- Molecule 16 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	120	Total	C	H	N	O	S	0	0
			2046	636	1047	188	168	7		

- Molecule 17 is a protein called uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	139	Total	C	H	N	O	S	0	0
			2284	704	1175	210	192	3		

- Molecule 18 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	121	Total	C	H	N	O	S	0	0
			2021	618	1036	183	181	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	134	PRO	ALA	conflict	UNP G1TU13

- Molecule 19 is a protein called uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	139	Total	C	H	N	O	S	0	0
			2365	725	1211	233	195	1		

- Molecule 20 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	T	143	Total	C	H	N	O	S	0	0
			2258	697	1146	214	198	3		

- Molecule 21 is a protein called uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	U	97	Total	C	H	N	O	S	0	0
			1607	483	838	144	138	4		

- Molecule 22 is a protein called eS21.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	V	81	Total	C	H	N	O	S	0	0
			1239	380	622	114	118	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	3	ASN	SER	conflict	UNP G1TM82
V	4	ASP	ASN	conflict	UNP G1TM82
V	33	GLN	PRO	conflict	UNP G1TM82
V	50	PHE	SER	conflict	UNP G1TM82
V	75	ALA	SER	conflict	UNP G1TM82
V	76	ASP	HIS	conflict	UNP G1TM82
V	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 23 is a protein called uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	W	129	Total	C	H	N	O	S	0	0
			2115	659	1081	193	176	6		

- Molecule 24 is a protein called uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	X	139	Total	C	H	N	O	S	0	0
			2228	682	1148	214	181	3		

- Molecule 25 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	125	Total	C	H	N	O	S	0	0
			2102	642	1087	199	169	5		

- Molecule 26 is a protein called eS25.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	73	Total	C	H	N	O	S	0	0
			1226	374	641	108	102	1		

- Molecule 27 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	a	97	Total	C	H	N	O	S	0	0
			1598	481	824	160	128	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	28	ARG	CYS	conflict	UNP G1TFE8
a	56	ALA	VAL	conflict	UNP G1TFE8
a	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 28 is a protein called eS27.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	b	80	Total	C	H	N	O	S	0	0
			1272	391	647	116	111	7		

- Molecule 29 is a protein called eS28.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	c	61	Total	C	H	N	O	S	0	0
			984	291	504	96	91	2		

- Molecule 30 is a protein called uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	d	51	Total	C	H	N	O	S	0	0
			858	269	431	87	66	5		

- Molecule 31 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	e	55	Total	C	H	N	O	S	0	0
			921	272	484	96	68	1		

- Molecule 32 is a protein called eS31.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	f	73	Total	C	H	N	O	S	0	0
			1224	379	623	115	100	7		

- Molecule 33 is a protein called Receptor for Activated C Kinase 1 (RACK1).

Mol	Chain	Residues	Atoms						AltConf	Trace
33	g	314	Total	C	H	N	O	S	0	0
			4839	1537	2399	425	466	12		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	1	1708	Total	C	H	N	O	P	0	0
			54862	16274	18406	6546	11928	1708		

- Molecule 35 is a RNA chain called RHDV Reinitiation stimulating element RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	2	27	Total	C	H	N	O	P	0	0
			871	258	294	108	186	25		

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	Q	2	Total	Mg	0
			2	2	
36	X	1	Total	Mg	0
			1	1	

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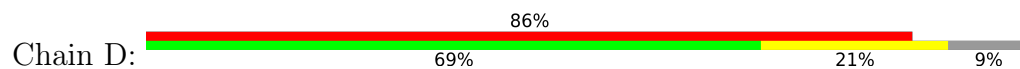
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Mol	Chain	Residues	Atoms		AltConf
36	1	71	Total	Mg	0
			71	71	

- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

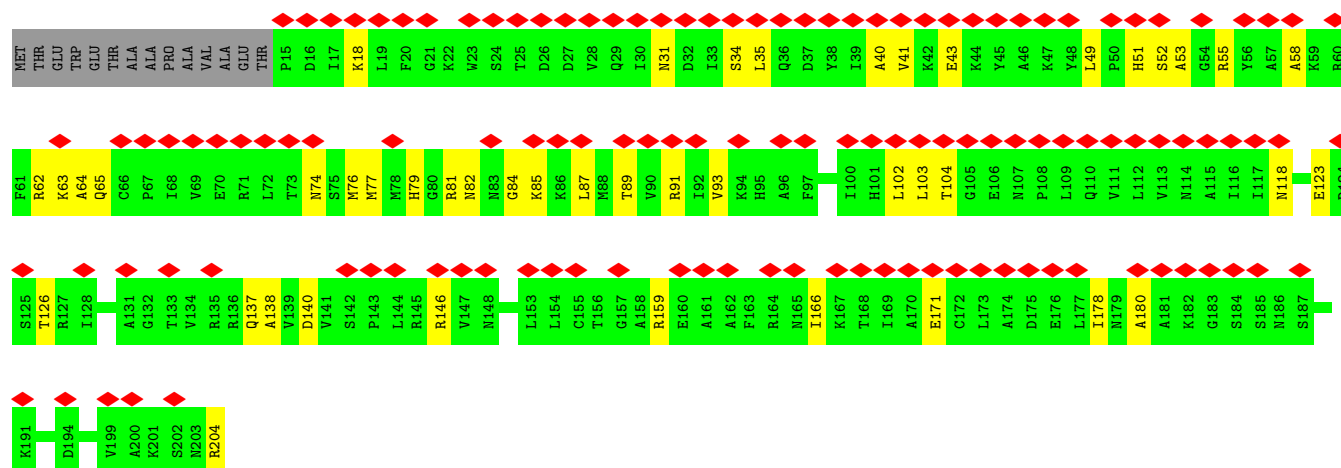
Mol	Chain	Residues	Atoms		AltConf
37	a	1	Total	Zn	0
			1	1	
37	d	1	Total	Zn	0
			1	1	

Chain C:

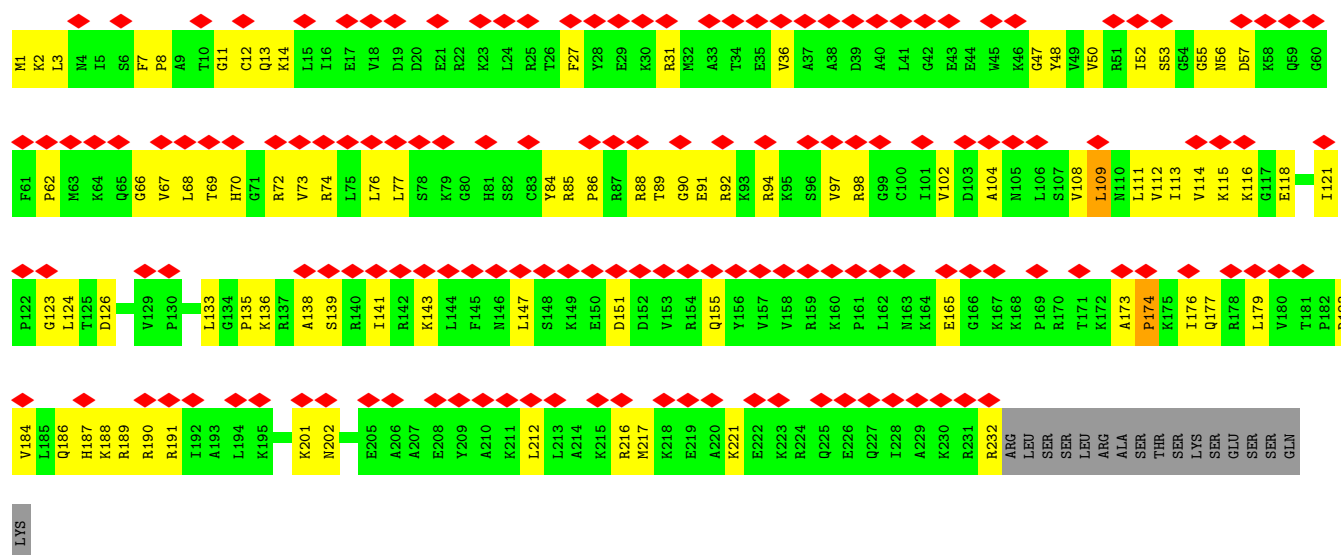




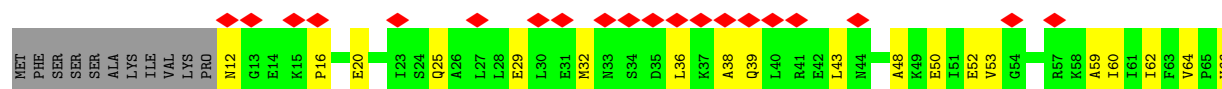
• Molecule 6: uS7

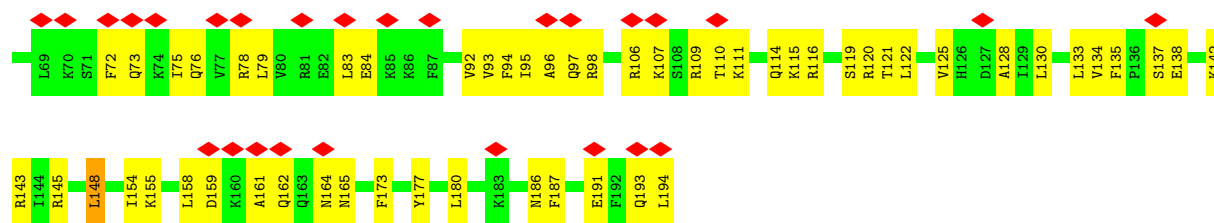


• Molecule 7: eS6

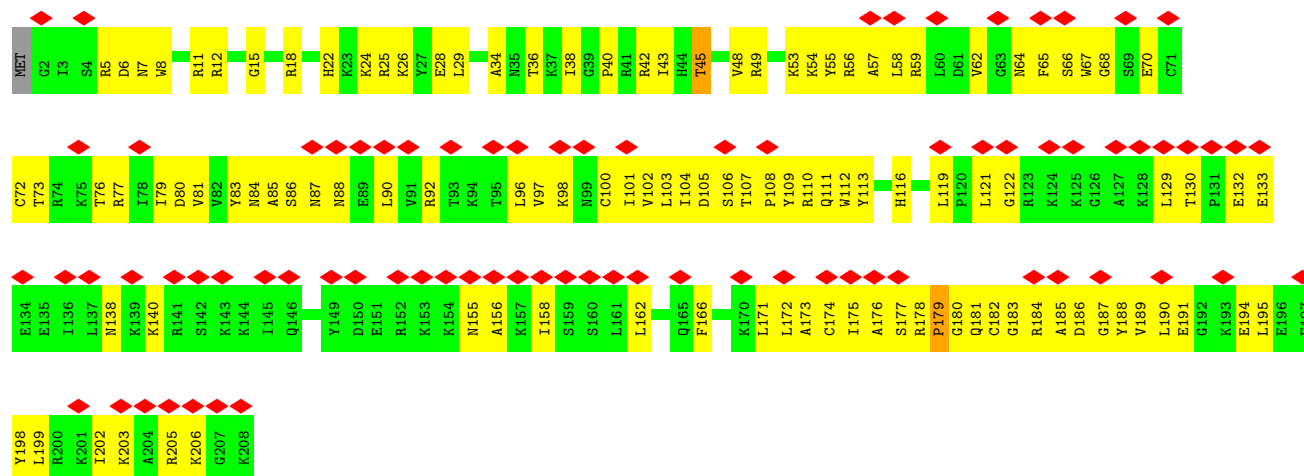
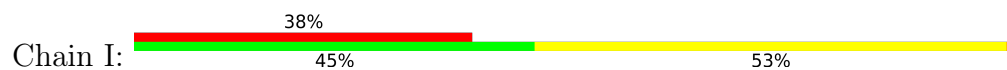


• Molecule 8: eS7

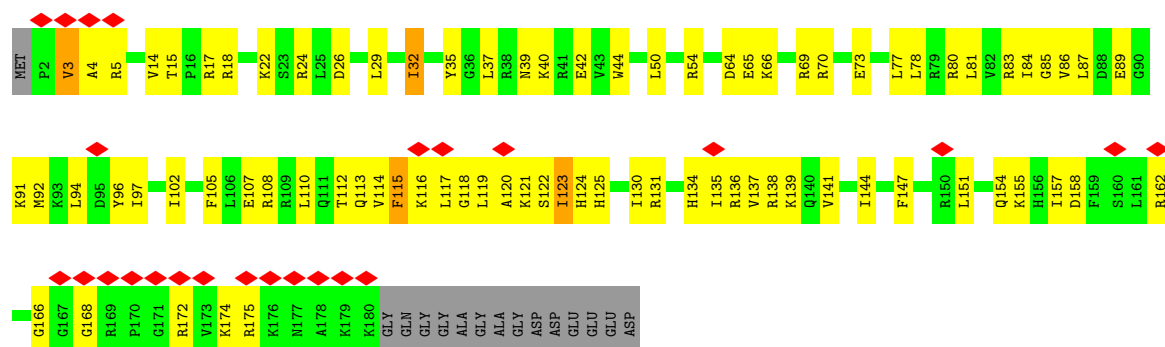




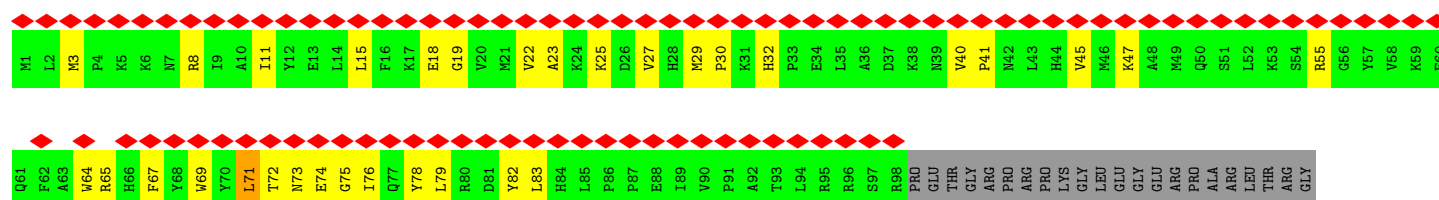
• Molecule 9: eS8



• Molecule 10: uS4



• Molecule 11: S10_pectin domain-containing protein



GLU
ALA
ASP
ILE
THR
TYR
ARG
SER
VAL
PRO
PRO
GLY
ALA
ASP
LYS
ALA
GLU
ALA
GLY
ALA
GLY
SER
ALA
THR
GLU
PHE
GLN
PHE
ARG
GLY
GLY
GLY
PHE
PHE
GLY
ARG
GLY
ARG
GLY
GLN
PRO
PRO
GLN

• Molecule 12: uS17

Chain L: 22% 70% 27%

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

M82 Q83 R84 T85 I96 E103 N108 M109 S110 V111 D119 L120 Q121 I122 G123 D124 I125 C131 R132 L133 L134 S136 K136 F140 L143 A148 A149 G150 T151 K152 K153 Q154 F155 Q156 K157 F158

• Molecule 13: eS12

Chain M: 91% 76% 15% 9%

MET ALA GLU ILE ALA GLY V11 M12 D13 V14 H15 T16 A17 L18 Q19 E20 V21 K23 T24 A25 L26 I27 H28 D29 G30 L31 A32 R33 G34 I35 E37 A38 A39 K40 A41 L42 D43 K44 R45 Q46 A47 H48 L49 C50 V51 L52 A53 S54 N55 C56 D57 E58 P59 M60

Y61 V62 F63 L64 V65 E66 A67 L68 C69 A70 E71 H72 Q73 T74 W75 L76 I77 K78 V79 D80 N81 H82 K83 V86 K84 L85 G86 E87 W88 H89 G90 L91 Q92 A93 I94 D95 R96 E97 G98 A99 P100 A101 K102 V103 G104 G105 C106 S107 C108 V109 V110 V111 K112 D113 Y114 G115 K116 E117 S118 Q119 A120

K121 D122 V123 I124 E126 Y127 F128 K129 L130 LYS LYS

• Molecule 14: uS15

Chain N: 68% 30%

MET G2 R3 H4 H5 L11 A15 L16 R20 T29 V33 I37 S48 V52 I53 D56 R64 F65 V66 T67 K70 I71 L72 P82 D83 L88 I92 A95 V96 R99 K100 H101 L102 R106 K107 D108 K109 K112 F113 R114 T118

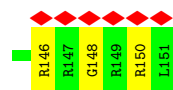
E119 S120 R121 R124 L125 Y128 Y129 K130 T131 K132 R133 W139 K140 Y141 T145 A146 S147 A148 L149 V150 ALA

• Molecule 15: Small ribosomal subunit protein uS11

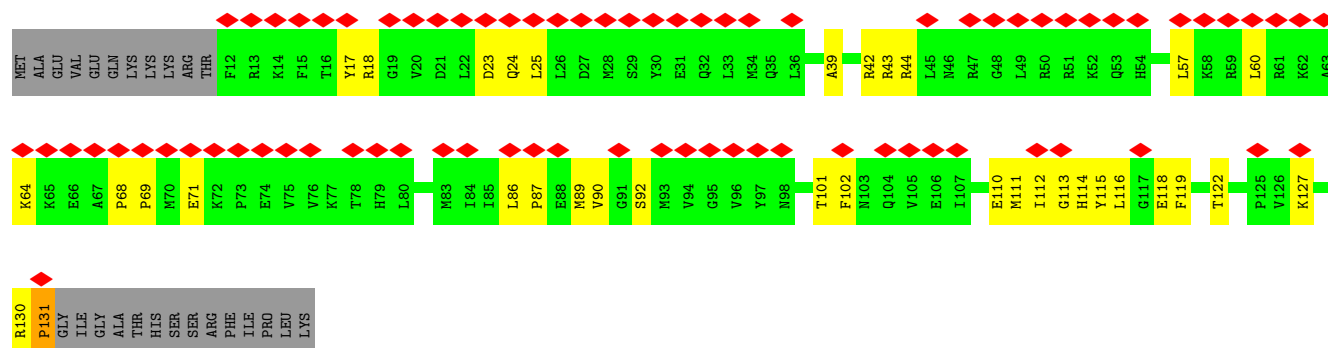
Chain O: 15% 46% 41% 10%

MET ALA PRO ARG LYS LYS GLU LYS VAL ILE S16 L17 V21 A22 E23 G24 V27 V30 C31 H32 I33 F34 A35 S36 F37 N38 D39 T40 F41 V42 H43 V44 T45 D46 K50 E51 T52 I53 C54 R55 V56 T57 G58 M60 K61 V62 K63 R66 D67

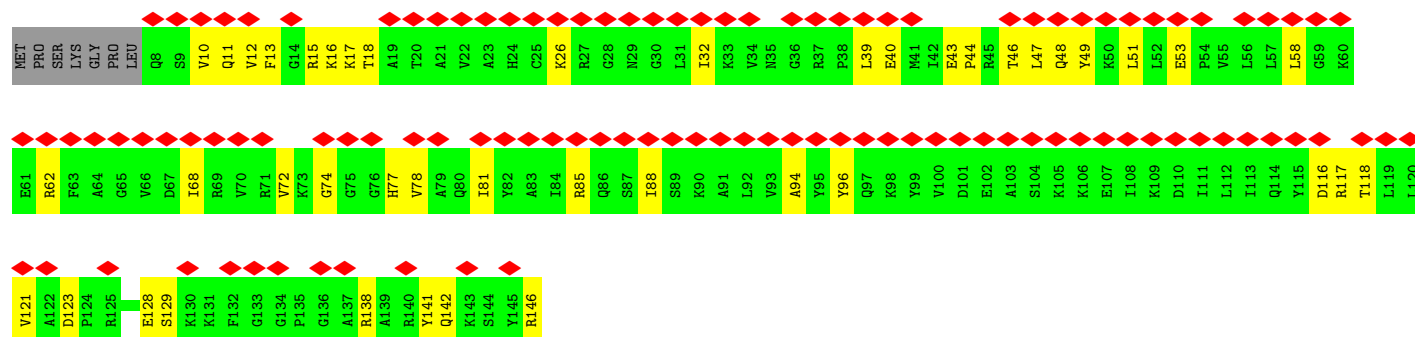
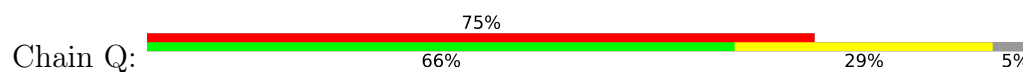
E68 S69 S70 P71 Y72 M75 L76 A77 A78 V81 A82 Q83 R84 C85 K86 E87 I90 T91 A92 L93 H94 I95 G101 G102 N103 R104 T105 K106 T107 P108 G109 A112 Q113 R117 A118 L119 A120 S121 S122 G123 M124 E130 D131 V132 I135 P136 S137 D138 S139 T140 R141 R142



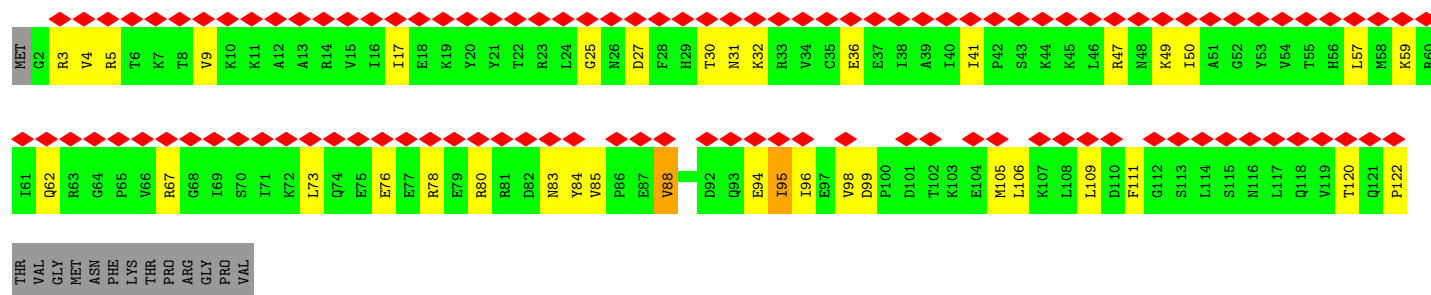
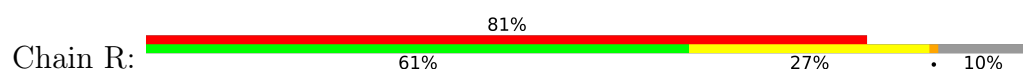
• Molecule 16: 40S ribosomal protein uS19



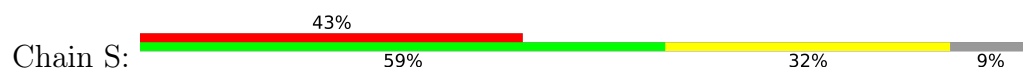
• Molecule 17: uS9

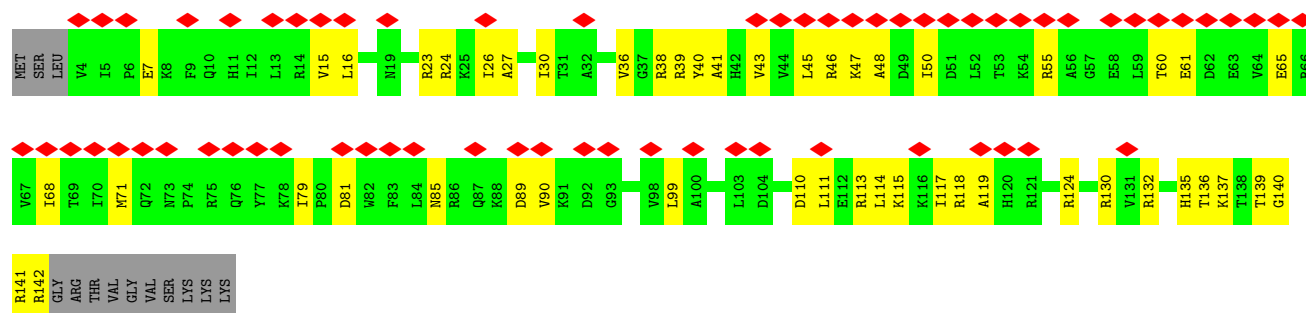


• Molecule 18: Small ribosomal subunit protein eS17

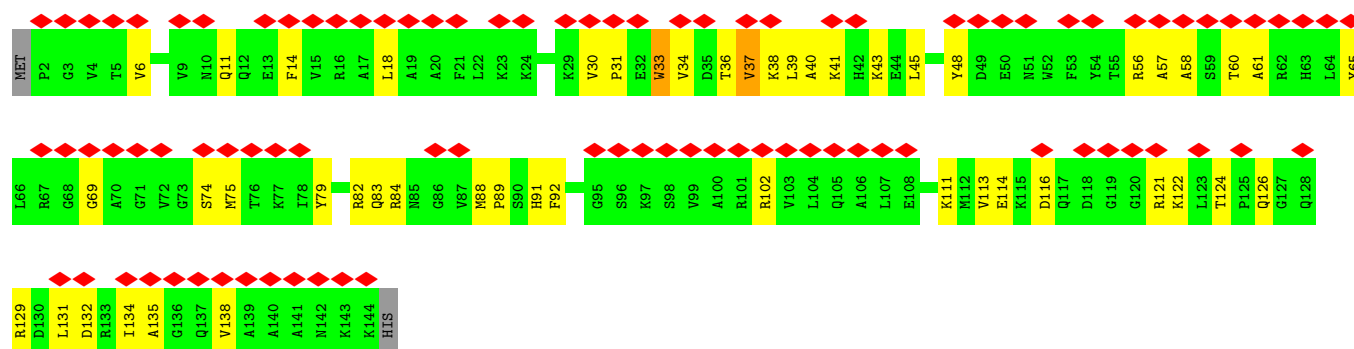


• Molecule 19: uS13

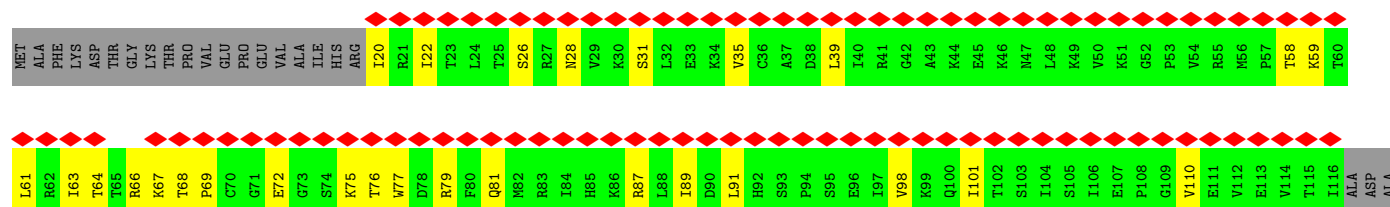
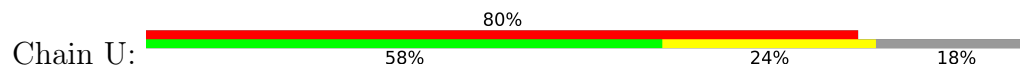




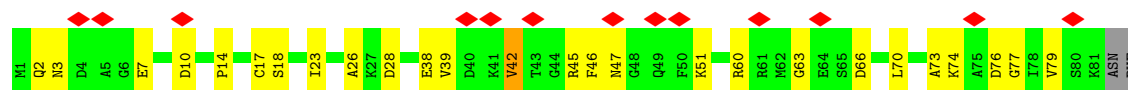
- Molecule 20: 40S ribosomal protein eS19



- Molecule 21: uS10

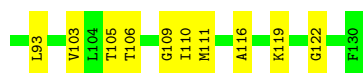


- Molecule 22: eS21

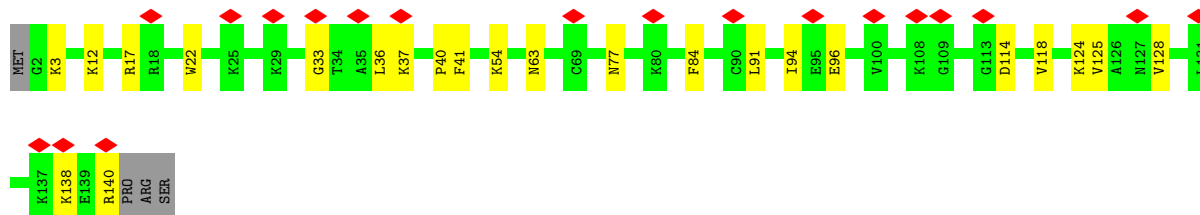
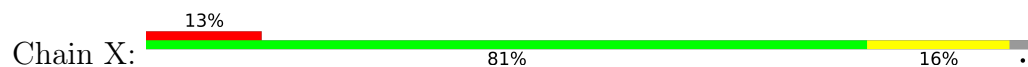


- Molecule 23: uS8

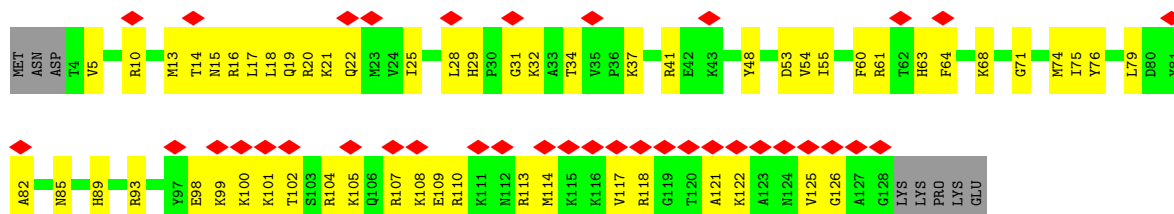




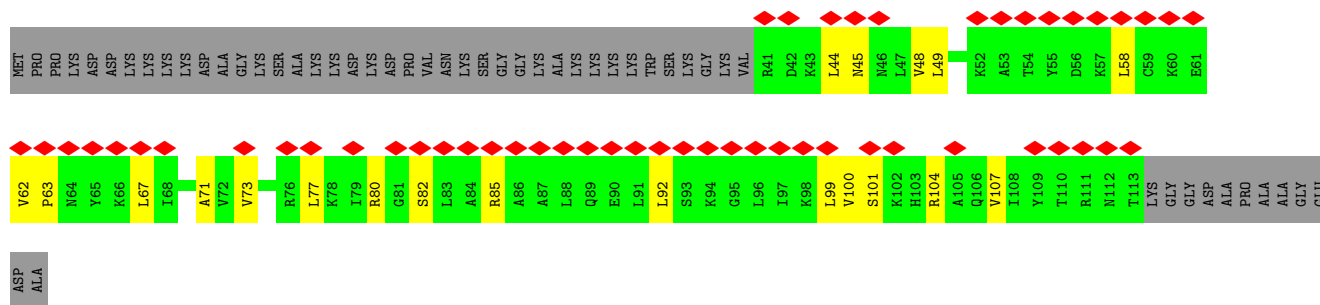
- Molecule 24: uS12



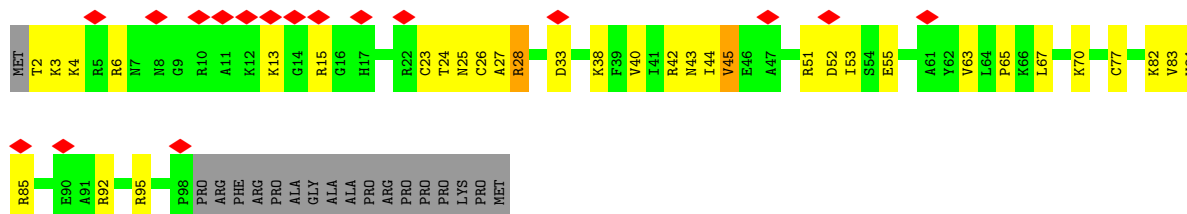
- Molecule 25: Small ribosomal subunit protein eS24



- Molecule 26: eS25

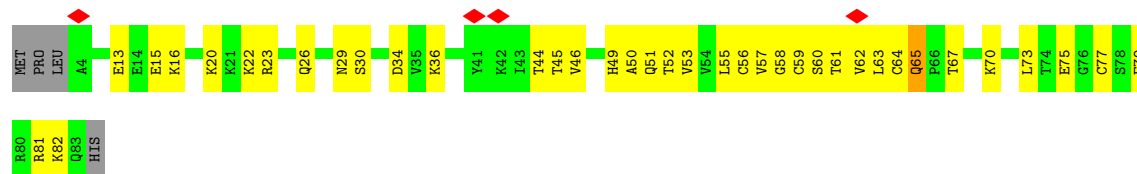


- Molecule 27: 40S ribosomal protein S26



- Molecule 28: eS27

Chain b: 



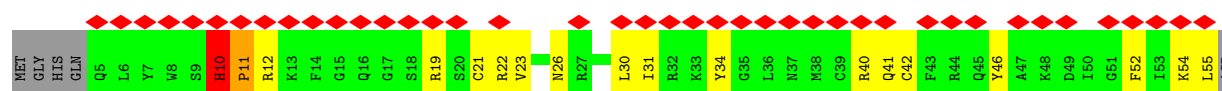
- Molecule 29: eS28

Chain c: 

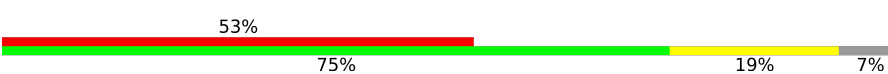


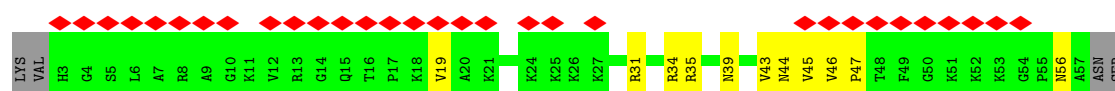
- Molecule 30: uS14

Chain d: 



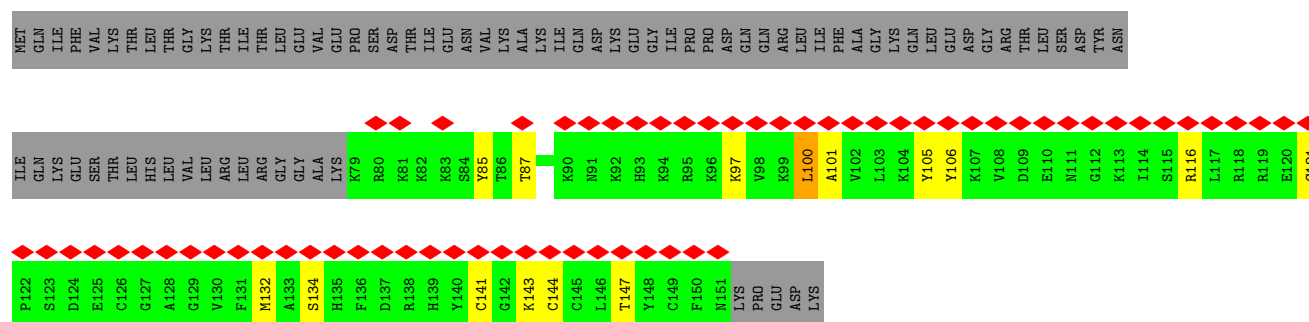
- Molecule 31: 40S ribosomal protein eS30

Chain e: 

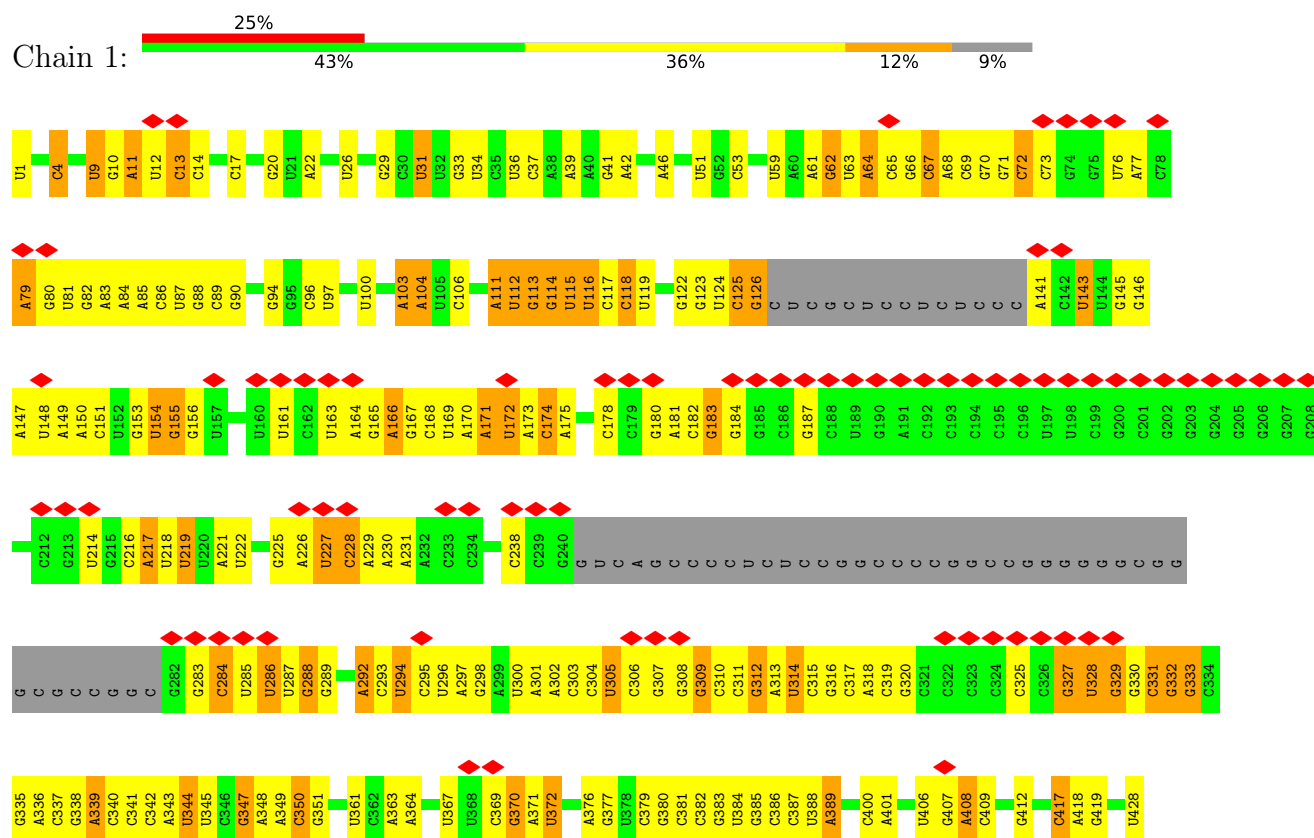


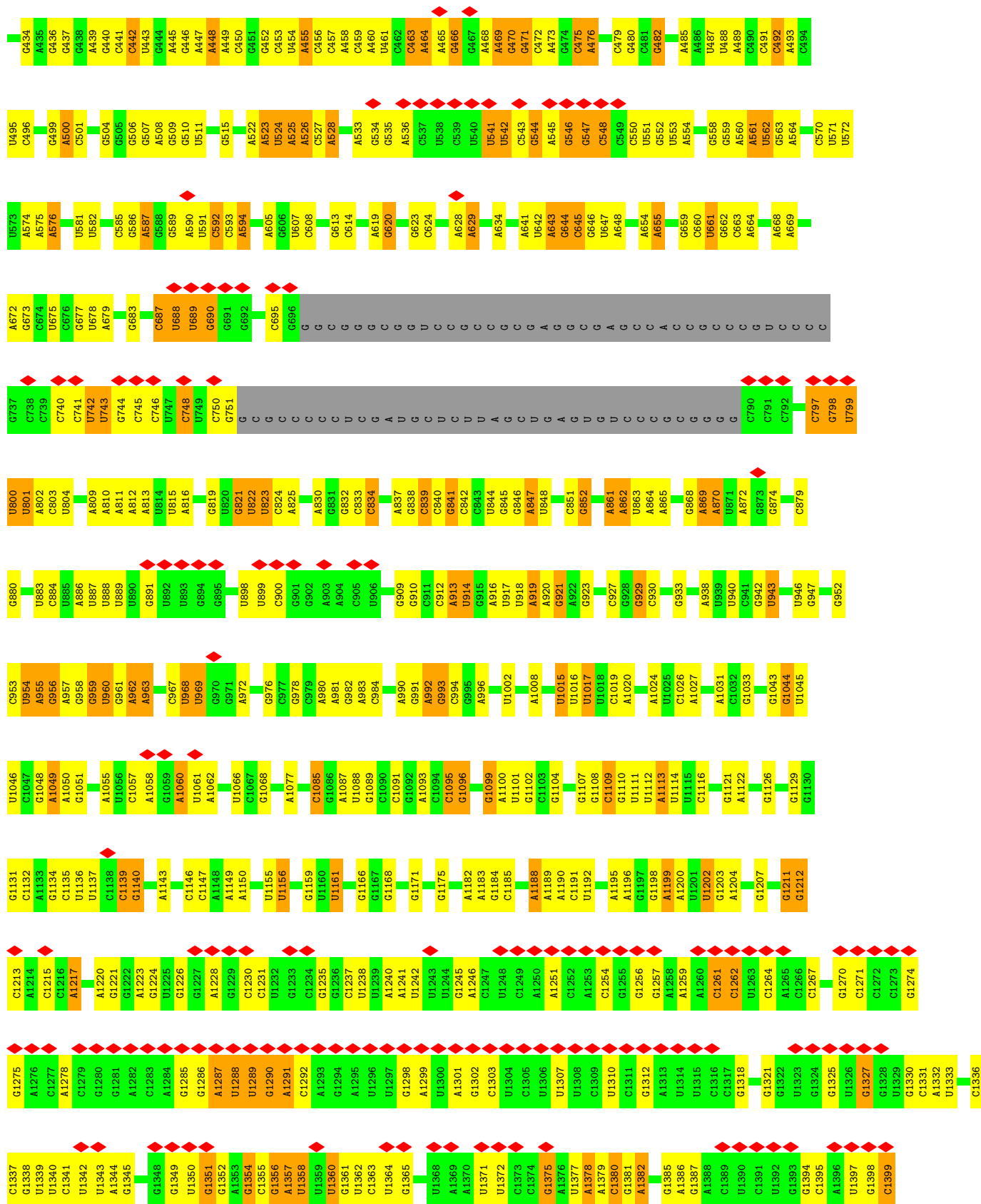
- Molecule 32: eS31

Chain f: 



- Molecule 33: Receptor for Activated C Kinase 1 (RACK1)





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	61643	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.94	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	3.029	Depositor
Minimum map value	-1.682	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.43	Depositor
Map size (Å)	388.0, 388.0, 388.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.97, 0.97, 0.97	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.20	0/1741	0.51	0/2366
2	B	0.19	0/1749	0.49	0/2340
3	C	0.17	0/1761	0.43	0/2379
4	D	0.13	0/1736	0.34	0/2338
5	E	0.62	3/2072 (0.1%)	0.75	4/2793 (0.1%)
6	F	0.13	0/1524	0.38	0/2048
7	G	0.70	4/1907 (0.2%)	0.90	5/2538 (0.2%)
8	H	0.18	0/1501	0.48	0/2009
9	I	0.75	4/1725 (0.2%)	0.95	5/2298 (0.2%)
10	J	0.21	0/1520	0.46	0/2030
11	K	0.14	0/851	0.38	0/1147
12	L	0.19	0/1281	0.45	0/1710
13	M	0.11	0/941	0.29	0/1264
14	N	0.19	0/1226	0.47	0/1649
15	O	1.00	4/1029 (0.4%)	1.07	6/1380 (0.4%)
16	P	0.17	0/1019	0.44	1/1361 (0.1%)
17	Q	0.14	0/1126	0.36	0/1506
18	R	0.15	0/997	0.37	0/1338
19	S	0.13	0/1172	0.36	0/1570
20	T	0.14	0/1131	0.35	0/1515
21	U	0.11	0/778	0.27	0/1045
22	V	0.16	0/623	0.40	0/833
23	W	0.21	0/1051	0.53	0/1406
24	X	0.14	0/1097	0.43	0/1464
25	Y	0.17	0/1032	0.41	0/1371
26	Z	0.14	0/591	0.37	0/794
27	a	0.17	0/786	0.43	0/1053
28	b	0.24	0/637	0.53	0/854
29	c	0.13	0/482	0.42	0/645
30	d	0.86	3/437 (0.7%)	1.59	6/580 (1.0%)
31	e	0.13	0/443	0.38	0/583
32	f	0.24	0/613	0.66	3/811 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.10	0/2497	0.27	0/3399
34	1	0.11	0/40767	0.29	2/63536 (0.0%)
35	2	0.10	0/644	0.26	0/1003
All	All	0.26	18/80487 (0.0%)	0.43	32/116956 (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
15	O	0	2
28	b	0	1
30	d	0	1
32	f	0	1
All	All	0	5

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	O	71	PRO	CB-CG	22.57	2.62	1.49
9	I	179	PRO	CB-CG	22.35	2.61	1.49
7	G	174	PRO	CB-CG	22.04	2.59	1.49
5	E	43	PRO	CG-CD	-21.65	0.77	1.50
15	O	71	PRO	CG-CD	-18.24	0.88	1.50
9	I	179	PRO	CG-CD	-17.90	0.89	1.50
7	G	174	PRO	CG-CD	-17.49	0.91	1.50
30	d	10	HIS	C-N	-9.85	1.10	1.33
30	d	11	PRO	CG-CD	-9.81	1.17	1.50
30	d	11	PRO	CB-CG	-9.47	1.02	1.49
5	E	43	PRO	N-CD	9.01	1.60	1.47
5	E	43	PRO	CB-CG	8.61	1.92	1.49
15	O	71	PRO	CA-CB	-7.49	1.43	1.53
15	O	71	PRO	N-CD	7.12	1.57	1.47
7	G	174	PRO	N-CD	6.76	1.57	1.47
9	I	179	PRO	N-CA	-5.86	1.39	1.47
7	G	174	PRO	CA-CB	-5.54	1.45	1.53
9	I	179	PRO	CA-CB	-5.09	1.46	1.53

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	179	PRO	CB-CG-CD	-30.93	7.13	106.10
7	G	174	PRO	CB-CG-CD	-29.33	12.24	106.10
15	O	71	PRO	CB-CG-CD	-24.59	27.42	106.10
30	d	11	PRO	CB-CG-CD	23.05	179.85	106.10
5	E	43	PRO	N-CD-CG	-22.69	69.16	103.20
7	G	174	PRO	N-CA-CB	-20.41	81.82	103.25
30	d	11	PRO	N-CD-CG	-18.81	74.98	103.20
30	d	11	PRO	CA-CB-CG	-17.25	71.73	104.50
9	I	179	PRO	N-CA-CB	-15.33	87.15	103.25
15	O	71	PRO	N-CA-CB	-13.24	90.24	103.48
15	O	71	PRO	N-CD-CG	-12.39	84.62	103.20
5	E	43	PRO	CA-CB-CG	-11.89	81.90	104.50
9	I	179	PRO	CA-N-CD	-11.77	95.52	112.00
9	I	179	PRO	CA-CB-CG	-11.53	82.60	104.50
7	G	174	PRO	CA-CB-CG	-11.24	83.15	104.50
7	G	174	PRO	CA-N-CD	-11.13	96.42	112.00
15	O	71	PRO	CA-CB-CG	-10.11	85.30	104.50
34	1	1357	A	OP2-P-O3'	-9.55	79.34	108.00
15	O	136	PRO	CA-N-CD	-9.30	98.98	112.00
34	1	1357	A	OP1-P-O3'	-8.92	81.23	108.00
30	d	11	PRO	CA-N-CD	-8.52	100.07	112.00
7	G	174	PRO	N-CD-CG	-7.64	91.74	103.20
32	f	144	CYS	CA-CB-SG	7.14	130.82	114.40
32	f	143	LYS	CA-C-N	7.05	132.64	120.58
32	f	143	LYS	C-N-CA	7.05	132.64	120.58
5	E	43	PRO	CA-N-CD	-6.57	102.80	112.00
15	O	71	PRO	CA-N-CD	-5.98	103.62	112.00
5	E	43	PRO	N-CA-CB	-5.69	98.15	103.27
16	P	131	PRO	CA-N-CD	-5.30	104.57	112.00
30	d	11	PRO	CA-C-N	5.27	131.60	121.54
30	d	11	PRO	C-N-CA	5.27	131.60	121.54
9	I	179	PRO	N-CD-CG	-5.17	95.45	103.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	O	141	ARG	Peptide
15	O	142	ARG	Peptide
28	b	65	GLN	Peptide
30	d	10	HIS	Peptide
32	f	141	CYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1704	1705	1704	104	0
2	B	1722	1795	1794	90	0
3	C	1724	1809	1808	78	0
4	D	1709	1804	1803	43	0
5	E	2031	2139	2138	89	0
6	F	1502	1558	1557	42	0
7	G	1884	2045	2044	110	0
8	H	1479	1566	1564	78	0
9	I	1696	1786	1785	133	0
10	J	1495	1615	1615	71	0
11	K	827	854	854	24	0
12	L	1258	1335	1334	38	0
13	M	931	962	961	14	0
14	N	1202	1290	1289	38	0
15	O	1016	1040	1039	76	0
16	P	999	1047	1046	35	0
17	Q	1109	1175	1174	35	0
18	R	985	1036	1035	36	0
19	S	1154	1211	1210	54	0
20	T	1112	1146	1146	43	0
21	U	769	838	837	24	0
22	V	617	622	622	24	0
23	W	1034	1081	1080	50	0
24	X	1080	1148	1147	22	0
25	Y	1015	1087	1086	61	0
26	Z	585	641	640	17	0
27	a	774	824	823	29	0
28	b	625	647	646	36	0
29	c	480	504	503	12	0
30	d	427	431	428	23	0
31	e	437	484	483	12	0
32	f	601	623	622	9	0
33	g	2440	2399	2396	61	0
34	1	36456	18406	18410	794	0
35	2	577	294	298	6	0
36	1	71	0	0	0	0
36	Q	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	X	1	0	0	0	0
37	a	1	0	0	0	0
37	d	1	0	0	0	0
All	All	75532	58947	58921	2026	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All (2026) 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:G:174:PRO:N	7:G:174:PRO:CG	1.84	1.41
15:O:71:PRO:CG	15:O:71:PRO:N	1.73	1.41
9:I:179:PRO:CG	9:I:179:PRO:N	1.84	1.37
9:I:179:PRO:CD	9:I:179:PRO:HG2	1.66	1.16
7:G:174:PRO:CD	7:G:174:PRO:HG2	1.68	1.14
15:O:71:PRO:CD	15:O:71:PRO:HG2	1.65	1.14
7:G:174:PRO:CD	7:G:174:PRO:HG3	1.68	1.12
9:I:179:PRO:CD	9:I:179:PRO:HG3	1.66	1.11
15:O:71:PRO:CD	15:O:71:PRO:HG3	1.65	1.10
9:I:179:PRO:CG	9:I:179:PRO:HD3	1.56	1.07
7:G:174:PRO:CG	7:G:174:PRO:HD2	1.58	1.07
28:b:67:THR:OG1	34:1:929:G:O4'	1.73	1.07
9:I:179:PRO:CG	9:I:179:PRO:HD2	1.56	1.06
15:O:71:PRO:CG	15:O:71:PRO:HD3	1.57	1.06
15:O:71:PRO:CG	15:O:71:PRO:HD2	1.57	1.06
7:G:174:PRO:CG	7:G:174:PRO:HD3	1.58	1.05
34:1:90:G:OP1	34:1:445:A:N6	1.94	1.01
34:1:1113:A:OP1	35:2:5:U:O2'	1.78	1.01
34:1:436:G:OP2	34:1:471:G:O2'	1.80	0.99
5:E:191:ARG:NH2	5:E:212:ASP:OD2	1.96	0.98
7:G:92:ARG:NH2	34:1:441:C:O2	1.95	0.98
1:A:102:ARG:O	18:R:67:ARG:NH2	1.98	0.96
15:O:44:VAL:HG12	15:O:53:ILE:HD12	1.46	0.96
4:D:145:GLN:O	34:1:1332:A:O2'	1.83	0.96
34:1:147:A:N6	34:1:170:A:OP2	1.99	0.95
34:1:62:G:O2'	34:1:172:U:OP1	1.83	0.94
9:I:186:ASP:OD2	34:1:219:U:O2'	1.84	0.93
34:1:84:A:O2'	34:1:150:A:O3'	1.86	0.93
2:B:137:LEU:HD11	2:B:172:MET:SD	2.08	0.93
34:1:641:A:O2'	34:1:645:C:OP1	1.88	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:202:GLN:NE2	2:B:206:PRO:O	2.02	0.92
34:1:216:C:O2	34:1:309:G:N2	2.02	0.92
34:1:933:G:O6	34:1:992:A:N6	2.03	0.91
28:b:30:SER:OG	34:1:1016:U:OP1	1.88	0.91
34:1:146:G:O6	34:1:173:A:N6	2.02	0.91
7:G:174:PRO:CG	7:G:174:PRO:CD	0.91	0.91
34:1:66:G:O6	34:1:82:G:O2'	1.89	0.91
17:Q:15:ARG:NH1	34:1:1395:C:OP1	2.04	0.90
15:O:71:PRO:N	15:O:71:PRO:HG3	1.77	0.89
34:1:1735:A:N7	34:1:1799:G:N2	2.19	0.89
9:I:12:ARG:NH1	34:1:104:A:OP1	2.05	0.89
9:I:179:PRO:CG	9:I:179:PRO:CD	0.89	0.89
14:N:120:SER:OG	34:1:677:G:OP1	1.88	0.89
17:Q:128:GLU:OE1	17:Q:138:ARG:NH1	2.05	0.89
27:a:26:CYS:N	27:a:77:CYS:SG	2.45	0.88
34:1:113:G:N2	34:1:295:C:O2'	2.06	0.88
7:G:84:TYR:OH	7:G:91:GLU:O	1.91	0.88
15:O:71:PRO:CG	15:O:71:PRO:CD	0.88	0.88
30:d:42:CYS:SG	34:1:1495:G:N2	2.46	0.88
8:H:121:THR:OG1	34:1:688:U:OP1	1.90	0.88
14:N:114:ARG:NH2	34:1:996:A:OP1	2.07	0.88
2:B:175:GLU:O	2:B:179:ASN:ND2	2.06	0.88
34:1:1349:G:O6	34:1:1380:C:N4	2.06	0.88
5:E:54:TYR:O	25:Y:15:ASN:ND2	2.07	0.87
12:L:136:LYS:NZ	34:1:372:U:OP1	2.07	0.87
34:1:1419:C:O2	34:1:1420:G:N2	2.07	0.87
9:I:40:PRO:O	9:I:59:ARG:NE	2.07	0.87
7:G:47:GLY:N	7:G:118:GLU:OE2	2.08	0.87
19:S:85:ASN:OD1	34:1:1610:G:N2	2.06	0.87
15:O:70:SER:C	15:O:71:PRO:HG3	2.00	0.86
34:1:289:G:N2	34:1:295:C:O2	2.09	0.86
9:I:182:CYS:O	34:1:305:U:N3	2.08	0.86
14:N:96:VAL:HG22	14:N:146:ALA:HB1	1.57	0.86
33:g:87:LEU:HD11	33:g:108:VAL:HG11	1.55	0.86
34:1:1533:A:N3	34:1:1536:G:O2'	2.09	0.86
3:C:68:ARG:NH1	3:C:276:THR:OG1	2.09	0.86
34:1:218:U:O4	34:1:303:C:N4	2.09	0.85
20:T:83:GLN:NE2	34:1:1627:C:OP1	2.08	0.85
9:I:194:GLU:OE2	12:L:11:GLN:NE2	2.09	0.85
34:1:1693:G:O2'	34:1:1835:A:OP2	1.93	0.85
4:D:94:ARG:O	4:D:101:GLN:NE2	2.09	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:100:ARG:NH2	5:E:118:GLU:O	2.10	0.85
7:G:2:LYS:NZ	34:1:156:G:OP1	2.09	0.85
3:C:114:LYS:N	3:C:121:ARG:O	2.10	0.84
34:1:1211:G:O2'	34:1:1212:G:OP1	1.95	0.84
34:1:84:A:N3	34:1:150:A:O2'	2.09	0.84
12:L:85:THR:OG1	12:L:111:VAL:O	1.96	0.84
17:Q:26:LYS:NZ	34:1:1409:A:OP1	2.11	0.84
34:1:1095:C:O2'	34:1:1096:G:OP1	1.95	0.84
34:1:955:A:N6	34:1:969:U:O2	2.09	0.84
3:C:187:ARG:NH2	34:1:1143:A:OP2	2.10	0.84
34:1:171:A:O2'	34:1:173:A:OP2	1.96	0.84
34:1:1681:U:O2	34:1:1683:C:N4	2.10	0.84
25:Y:34:THR:O	34:1:570:C:O2'	1.95	0.84
34:1:115:U:O2'	34:1:381:C:O2	1.96	0.83
34:1:832:G:O6	34:1:842:C:N4	2.10	0.83
33:g:170:TRP:NE1	33:g:195:LEU:O	2.11	0.83
5:E:255:ARG:NH2	34:1:819:G:O2'	2.12	0.83
4:D:22:ASN:O	4:D:26:THR:HG23	1.78	0.83
34:1:363:A:N6	34:1:400:C:O2	2.10	0.83
5:E:196:THR:OG1	5:E:211:LYS:NZ	2.11	0.83
10:J:37:LEU:HD23	10:J:42:GLU:HG3	1.60	0.83
6:F:76:MET:O	6:F:159:ARG:NH2	2.11	0.82
19:S:139:THR:OG1	34:1:1231:C:OP2	1.95	0.82
7:G:173:ALA:C	7:G:174:PRO:CG	2.53	0.82
34:1:822:U:O2'	34:1:823:U:OP1	1.97	0.82
25:Y:93:ARG:NH1	34:1:575:A:OP1	2.12	0.82
34:1:149:A:OP2	34:1:168:C:N4	2.11	0.82
10:J:175:ARG:NE	34:1:559:G:OP1	2.12	0.82
34:1:1658:G:O6	34:1:1666:C:N4	2.12	0.82
7:G:50:VAL:HG11	7:G:111:LEU:HD22	1.59	0.81
34:1:146:G:N2	34:1:174:C:O2	2.13	0.81
34:1:1245:G:O2'	34:1:1492:U:OP1	1.98	0.81
19:S:142:ARG:NH2	34:1:1228:A:OP1	2.13	0.81
34:1:493:A:O2'	34:1:574:A:OP1	1.98	0.81
15:O:70:SER:CA	15:O:71:PRO:HG3	2.11	0.81
34:1:748:C:O2	34:1:750:C:N4	2.13	0.81
9:I:8:TRP:O	9:I:18:ARG:NH1	2.13	0.81
5:E:134:LYS:NZ	5:E:149:TYR:OH	2.12	0.81
1:A:186:ARG:NH1	1:A:186:ARG:O	2.14	0.81
34:1:1261:C:O2	34:1:1618:C:N4	2.14	0.80
4:D:127:MET:HE2	4:D:127:MET:HA	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:70:SER:C	15:O:71:PRO:CG	2.54	0.80
34:1:227:U:O2'	34:1:228:C:OP2	1.97	0.80
15:O:141:ARG:NH2	34:1:1857:G:OP2	2.15	0.80
18:R:32:LYS:NZ	34:1:1451:G:OP1	2.15	0.80
28:b:70:LYS:NZ	34:1:1107:G:OP1	2.14	0.80
3:C:205:VAL:O	3:C:224:THR:OG1	2.00	0.79
8:H:145:ARG:NH1	23:W:49:GLU:OE2	2.15	0.79
11:K:25:LYS:N	11:K:65:ARG:O	2.15	0.79
15:O:70:SER:CB	15:O:71:PRO:HG3	2.13	0.79
5:E:42:LEU:HD21	5:E:47:PHE:HB2	1.65	0.79
15:O:137:SER:N	34:1:943:U:O2	2.16	0.79
34:1:1587:G:OP1	34:1:1587:G:N2	2.16	0.79
34:1:218:U:O2	34:1:304:C:O2'	2.00	0.79
7:G:183:ARG:NE	34:1:316:G:OP2	2.15	0.78
8:H:39:GLN:O	8:H:43:LEU:N	2.15	0.78
1:A:74:VAL:HG13	1:A:121:LEU:HD22	1.65	0.78
30:d:30:LEU:HD21	34:1:1659:U:H4'	1.66	0.78
34:1:659:G:O2'	34:1:662:G:O2'	1.95	0.78
34:1:1362:U:OP2	34:1:1363:C:N4	2.15	0.78
10:J:113:GLN:OE1	10:J:154:GLN:NE2	2.17	0.78
15:O:71:PRO:CG	15:O:71:PRO:CB	2.62	0.78
34:1:1648:G:N2	34:1:1675:A:OP2	2.15	0.78
7:G:191:ARG:NH1	34:1:312:G:O2'	2.16	0.78
34:1:231:A:OP2	34:1:889:U:O2'	2.01	0.77
35:2:5:U:O2'	35:2:6:G:OP2	2.02	0.77
15:O:50:LYS:NZ	34:1:976:G:N3	2.31	0.77
23:W:55:ASP:OD1	23:W:56:HIS:N	2.17	0.77
34:1:141:A:OP1	34:1:178:C:O2'	2.03	0.77
34:1:659:G:HO2'	34:1:662:G:HO2'	1.21	0.77
34:1:918:U:O2'	34:1:919:A:OP2	2.00	0.77
15:O:141:ARG:NH1	34:1:1857:G:OP1	2.17	0.77
1:A:208:GLU:OE1	1:A:208:GLU:N	2.17	0.77
9:I:92:ARG:NE	9:I:92:ARG:O	2.18	0.77
19:S:141:ARG:NE	34:1:1523:C:OP2	2.18	0.77
5:E:197:ASN:OD1	5:E:198:ARG:N	2.18	0.77
10:J:22:LYS:NZ	10:J:26:ASP:OD1	2.18	0.77
4:D:161:GLY:N	34:1:1482:C:O2	2.18	0.76
34:1:1413:G:N2	34:1:1424:G:O6	2.19	0.76
32:f:105:TYR:O	32:f:116:ARG:NH1	2.19	0.76
34:1:594:A:N1	34:1:642:U:O2'	2.19	0.76
1:A:104:THR:OG1	18:R:67:ARG:NH2	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:80:ARG:NH1	34:1:1598:G:OP1	2.18	0.76
34:1:143:U:O2	34:1:313:A:O2'	1.99	0.76
15:O:83:GLN:NE2	15:O:87:GLU:OE2	2.18	0.76
9:I:113:TYR:OH	9:I:119:LEU:O	2.00	0.76
34:1:406:U:O2'	34:1:408:A:OP1	2.02	0.76
34:1:63:U:O2	34:1:85:A:N6	2.19	0.76
2:B:136:ARG:NH2	34:1:942:G:OP1	2.19	0.75
8:H:145:ARG:NE	23:W:51:GLU:OE1	2.20	0.75
19:S:140:GLY:N	34:1:1230:C:OP2	2.18	0.75
34:1:11:A:N3	34:1:1356:G:O2'	2.17	0.75
3:C:116:THR:O	34:1:1203:G:O2'	2.03	0.75
25:Y:110:ARG:NH1	25:Y:126:GLY:O	2.19	0.75
6:F:82:ASN:OD1	34:1:1535:U:O2'	2.03	0.75
10:J:162:ARG:O	10:J:166:GLY:N	2.20	0.75
5:E:197:ASN:ND2	5:E:199:GLU:OE2	2.18	0.75
16:P:23:ASP:OD1	16:P:24:GLN:N	2.20	0.75
1:A:184:ARG:NH2	1:A:193:HIS:O	2.20	0.75
4:D:134:CYS:SG	4:D:135:GLU:N	2.60	0.75
28:b:59:CYS:SG	28:b:61:THR:HG23	2.26	0.75
3:C:85:SER:OG	22:V:28:ASP:O	2.05	0.74
8:H:164:ASN:OD1	8:H:165:ASN:N	2.20	0.74
10:J:64:ASP:OD1	10:J:65:GLU:N	2.20	0.74
16:P:110:GLU:OE1	16:P:110:GLU:N	2.20	0.74
17:Q:146:ARG:NE	17:Q:146:ARG:O	2.19	0.74
9:I:176:ALA:N	9:I:186:ASP:O	2.20	0.74
19:S:30:ILE:HG22	19:S:36:VAL:HG11	1.68	0.74
34:1:463:C:O2'	34:1:466:G:O6	2.04	0.74
6:F:18:LYS:NZ	6:F:43:GLU:O	2.20	0.74
7:G:85:ARG:NH1	7:G:86:PRO:O	2.20	0.74
4:D:123:LEU:HD22	4:D:154:ASP:OD2	1.88	0.74
34:1:87:U:O4	34:1:500:A:N6	2.19	0.74
5:E:17:HIS:O	5:E:51:ARG:NH2	2.20	0.74
20:T:11:GLN:OE1	34:1:1541:G:O2'	2.05	0.74
7:G:92:ARG:O	34:1:453:C:O2'	2.03	0.73
34:1:64:A:N6	34:1:83:A:OP2	2.21	0.73
34:1:740:C:O2'	34:1:741:C:O2	2.06	0.73
9:I:178:ARG:C	9:I:179:PRO:CG	2.61	0.73
33:g:24:THR:OG1	33:g:27:PHE:O	2.04	0.73
14:N:70:LYS:NZ	34:1:1020:A:OP2	2.20	0.73
1:A:79:SER:O	1:A:84:GLN:NE2	2.22	0.73
8:H:194:LEU:OXT	28:b:16:LYS:NZ	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:76:THR:HG21	9:I:104:ILE:HG23	1.70	0.72
12:L:57:ASP:OD1	12:L:60:CYS:N	2.22	0.72
34:1:528:A:N7	34:1:558:G:N2	2.37	0.72
10:J:18:ARG:NH2	34:1:4:C:O2'	2.22	0.72
12:L:35:ARG:NH2	12:L:53:GLY:O	2.22	0.72
1:A:12:GLU:OE1	1:A:12:GLU:N	2.23	0.72
9:I:36:THR:HG21	9:I:96:LEU:HB2	1.69	0.72
1:A:147:LEU:HD21	1:A:171:VAL:HG22	1.69	0.72
17:Q:10:VAL:HG11	17:Q:94:ALA:HB1	1.72	0.72
21:U:20:ILE:HG21	21:U:98:VAL:HG11	1.72	0.72
8:H:84:GLU:OE1	8:H:92:VAL:HG23	1.89	0.72
24:X:54:LYS:NZ	24:X:96:GLU:OE2	2.21	0.72
1:A:89:LYS:O	1:A:89:LYS:NZ	2.22	0.72
10:J:5:ARG:NH2	34:1:39:A:OP1	2.23	0.72
12:L:108:ASN:OD1	12:L:109:MET:N	2.23	0.72
10:J:107:GLU:HA	10:J:112:THR:HG21	1.72	0.72
34:1:1337:C:O2	34:1:1490:G:N2	2.16	0.72
3:C:69:LEU:HD21	3:C:273:LEU:HG	1.72	0.71
27:a:43:ASN:OD1	27:a:44:ILE:N	2.23	0.71
17:Q:68:ILE:HD12	17:Q:88:ILE:HD12	1.71	0.71
23:W:37:PHE:CE1	23:W:103:VAL:HG21	2.26	0.71
25:Y:41:ARG:NE	25:Y:55:ILE:O	2.19	0.71
34:1:541:U:O4	34:1:543:C:N4	2.23	0.71
5:E:200:ARG:NH1	5:E:201:HIS:O	2.23	0.71
13:M:33:ARG:HD2	13:M:91:LEU:HD21	1.73	0.71
1:A:25:LEU:O	1:A:164:ASN:ND2	2.24	0.71
7:G:13:GLN:O	7:G:124:LEU:HD21	1.89	0.71
34:1:689:U:O2'	34:1:690:G:O4'	2.09	0.71
34:1:1706:G:HO2'	34:1:1850:A:HO2'	1.38	0.71
17:Q:116:ASP:OD1	17:Q:117:ARG:N	2.24	0.71
34:1:962:A:O2'	34:1:963:A:OP1	2.07	0.71
27:a:95:ARG:O	34:1:1866:A:O2'	2.06	0.71
23:W:85:ASP:O	23:W:85:ASP:OD2	2.08	0.71
5:E:134:LYS:N	34:1:298:G:OP1	2.24	0.70
24:X:84:PHE:HB2	24:X:118:VAL:HG11	1.73	0.70
4:D:167:TYR:OH	4:D:202:LYS:O	2.07	0.70
10:J:69:ARG:NH1	10:J:73:GLU:OE1	2.23	0.70
9:I:12:ARG:NH2	34:1:103:A:OP1	2.25	0.70
34:1:493:A:N1	34:1:510:G:O2'	2.22	0.70
34:1:929:G:O2'	34:1:930:C:O5'	2.06	0.70
10:J:117:LEU:O	10:J:117:LEU:HD23	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:136:LYS:NZ	34:1:64:A:OP1	2.24	0.70
34:1:1350:U:H3	34:1:1379:A:H61	1.39	0.70
19:S:16:LEU:HD22	19:S:99:LEU:CD2	2.22	0.70
12:L:131:CYS:SG	12:L:132:ARG:N	2.64	0.70
16:P:42:ARG:NH2	34:1:1613:G:OP1	2.25	0.70
33:g:124:SER:OG	33:g:126:ASP:OD1	2.04	0.70
34:1:1757:G:N2	34:1:1776:G:N3	2.40	0.70
8:H:60:ILE:CG2	8:H:92:VAL:HG22	2.22	0.69
8:H:106:ARG:NH2	34:1:863:U:O4	2.25	0.69
10:J:134:HIS:C	10:J:135:ILE:HD13	2.17	0.69
2:B:97:LEU:HD22	2:B:228:LEU:HD21	1.74	0.69
25:Y:98:GLU:O	25:Y:100:LYS:NZ	2.25	0.69
6:F:91:ARG:NH2	34:1:1593:C:OP1	2.25	0.69
20:T:65:TYR:OH	34:1:1423:C:O2'	2.11	0.69
5:E:183:VAL:HG22	5:E:220:THR:HG21	1.74	0.69
10:J:40:LYS:NZ	34:1:641:A:OP1	2.26	0.69
16:P:44:ARG:NH1	34:1:1620:A:OP1	2.25	0.69
1:A:23:THR:OG1	1:A:164:ASN:N	2.25	0.69
2:B:106:THR:OG1	2:B:108:ASP:OD1	2.07	0.69
18:R:3:ARG:NH2	34:1:1468:C:OP2	2.25	0.69
34:1:327:G:O2'	34:1:329:G:N7	2.22	0.69
34:1:628:A:O2'	34:1:629:A:OP1	2.09	0.69
15:O:27:VAL:O	15:O:92:ALA:N	2.26	0.69
34:1:1226:G:O2'	34:1:1640:A:N6	2.26	0.69
1:A:80:ARG:NH2	1:A:125:THR:O	2.24	0.69
7:G:74:ARG:NH2	34:1:455:A:OP1	2.25	0.69
7:G:155:GLN:OE1	7:G:155:GLN:N	2.26	0.69
8:H:119:SER:O	34:1:913:A:N6	2.26	0.69
20:T:92:PHE:N	34:1:1655:C:OP1	2.26	0.69
34:1:1397:U:O2'	34:1:1399:C:OP2	2.10	0.68
5:E:81:THR:OG1	5:E:81:THR:O	2.10	0.68
5:E:49:ARG:NH2	34:1:496:C:OP1	2.25	0.68
11:K:64:TRP:HZ3	30:d:23:VAL:HG22	1.58	0.68
34:1:39:A:H62	34:1:515:G:H21	1.40	0.68
2:B:114:VAL:O	2:B:114:VAL:HG12	1.93	0.68
9:I:45:THR:N	34:1:307:G:O2'	2.26	0.68
20:T:41:LYS:NZ	20:T:82:ARG:O	2.25	0.68
24:X:96:GLU:OE1	24:X:96:GLU:N	2.27	0.68
34:1:88:G:N2	34:1:499:G:O3'	2.27	0.68
6:F:91:ARG:NH2	17:Q:46:THR:OG1	2.27	0.68
34:1:1351:G:N2	34:1:1378:A:O2'	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:ASN:ND2	3:C:85:SER:O	2.26	0.68
17:Q:58:LEU:O	17:Q:62:ARG:NH1	2.26	0.68
28:b:65:GLN:OE1	28:b:65:GLN:N	2.27	0.68
17:Q:40:GLU:O	17:Q:48:GLN:NE2	2.26	0.67
14:N:112:LYS:NZ	34:1:1031:A:O3'	2.18	0.67
19:S:110:ASP:OD1	19:S:113:ARG:NH1	2.28	0.67
34:1:39:A:H62	34:1:515:G:N2	1.92	0.67
5:E:63:LYS:NZ	25:Y:85:ASN:OD1	2.19	0.67
10:J:136:ARG:N	10:J:158:ASP:O	2.27	0.67
25:Y:32:LYS:O	34:1:581:U:O2'	2.11	0.67
9:I:88:ASN:OD1	9:I:205:ARG:NH1	2.26	0.67
10:J:134:HIS:O	10:J:135:ILE:HD13	1.94	0.67
34:1:111:A:O2'	34:1:112:U:OP2	2.11	0.67
23:W:21:GLY:O	23:W:23:ARG:NH1	2.27	0.67
27:a:83:VAL:HG12	27:a:84:VAL:HG23	1.76	0.67
6:F:166:ILE:HD11	34:1:1599:U:OP2	1.95	0.67
14:N:141:TYR:HE2	14:N:146:ALA:HB2	1.60	0.67
34:1:1452:A:O2'	34:1:1475:G:N1	2.28	0.67
2:B:127:VAL:HG12	2:B:128:LYS:H	1.59	0.67
15:O:70:SER:HB2	15:O:71:PRO:HG3	1.76	0.67
1:A:39:TYR:OH	18:R:109:LEU:N	2.28	0.66
19:S:38:ARG:NH1	34:1:1603:G:O4'	2.28	0.66
33:g:283:PRO:O	33:g:303:THR:OG1	2.14	0.66
10:J:122:SER:O	10:J:125:HIS:N	2.27	0.66
12:L:22:ARG:NH2	12:L:30:LYS:O	2.29	0.66
2:B:137:LEU:HD12	2:B:137:LEU:C	2.19	0.66
2:B:160:GLN:NE2	34:1:1122:A:OP1	2.22	0.66
10:J:139:LYS:HA	10:J:139:LYS:HE3	1.76	0.66
1:A:82:THR:HA	1:A:204:TYR:CG	2.31	0.66
25:Y:17:LEU:O	25:Y:19:GLN:NE2	2.27	0.66
25:Y:29:HIS:ND1	25:Y:31:GLY:O	2.27	0.66
26:Z:92:LEU:HD22	26:Z:99:LEU:HD23	1.78	0.66
1:A:90:PHE:CE2	1:A:179:ALA:HB2	2.30	0.66
25:Y:105:LYS:NZ	34:1:507:G:O6	2.27	0.66
27:a:23:CYS:SG	27:a:24:THR:N	2.69	0.66
34:1:88:G:H2'	34:1:89:C:O4'	1.96	0.66
34:1:1341:C:N3	34:1:1484:A:N6	2.43	0.66
5:E:153:VAL:HG22	7:G:216:ARG:NH2	2.11	0.65
15:O:132:VAL:HG23	15:O:132:VAL:O	1.96	0.65
22:V:45:ARG:NH1	22:V:47:ASN:OD1	2.30	0.65
5:E:160:VAL:HG23	5:E:172:PHE:HB3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:124:ARG:NH2	34:1:1024:A:OP2	2.30	0.65
34:1:1617:G:N2	34:1:1620:A:OP2	2.26	0.65
19:S:114:LEU:HA	19:S:117:ILE:HD12	1.77	0.65
1:A:65:ILE:CD1	1:A:74:VAL:HG11	2.26	0.65
1:A:88:LEU:O	18:R:80:ARG:NH2	2.29	0.65
7:G:13:GLN:CD	34:1:153:G:H21	2.04	0.65
29:c:38:THR:O	29:c:39:SER:OG	2.13	0.65
34:1:535:G:O2'	34:1:536:A:N7	2.26	0.65
7:G:14:LYS:HB2	7:G:124:LEU:HD11	1.77	0.65
7:G:186:GLN:OE1	34:1:317:C:N4	2.29	0.65
10:J:39:ASN:ND2	34:1:642:U:OP1	2.30	0.65
15:O:138:ASP:O	15:O:139:SER:OG	2.10	0.65
34:1:1394:G:N2	34:1:1475:G:N3	2.45	0.65
7:G:14:LYS:CB	7:G:124:LEU:HD11	2.25	0.65
10:J:110:LEU:O	10:J:114:VAL:HG23	1.95	0.65
17:Q:116:ASP:OD2	17:Q:118:THR:OG1	2.14	0.65
8:H:158:LEU:HD11	8:H:187:PHE:HD2	1.61	0.65
9:I:198:TYR:HH	12:L:11:GLN:CD	2.05	0.65
4:D:160:SER:OG	34:1:1385:G:OP1	2.11	0.65
15:O:54:CYS:SG	15:O:55:ARG:N	2.70	0.65
30:d:19:ARG:NH2	30:d:31:ILE:O	2.29	0.65
33:g:52:TYR:CD2	33:g:309:VAL:HG21	2.32	0.65
34:1:464:A:O2'	34:1:466:G:O6	2.14	0.65
33:g:18:VAL:HG21	33:g:307:VAL:HG22	1.79	0.64
9:I:65:PHE:O	9:I:73:THR:HG23	1.97	0.64
10:J:108:ARG:NH2	10:J:154:GLN:OE1	2.30	0.64
16:P:39:ALA:N	34:1:1613:G:OP2	2.24	0.64
19:S:39:ARG:HD2	20:T:39:LEU:HD23	1.78	0.64
3:C:69:LEU:HG	3:C:273:LEU:HD21	1.79	0.64
6:F:79:HIS:N	34:1:1223:A:OP1	2.30	0.64
8:H:52:GLU:OE1	8:H:52:GLU:N	2.31	0.64
8:H:20:GLU:OE2	8:H:48:ALA:N	2.31	0.64
12:L:154:GLN:OE1	12:L:156:GLN:NE2	2.31	0.64
15:O:91:THR:OG1	15:O:92:ALA:N	2.28	0.64
17:Q:53:GLU:OE1	17:Q:85:ARG:NH2	2.29	0.64
34:1:440:G:OP1	34:1:1798:C:O2'	2.11	0.64
4:D:76:ARG:HB2	11:K:22:VAL:HG11	1.78	0.64
2:B:52:THR:OG1	2:B:56:LYS:O	2.16	0.63
34:1:1095:C:HO2'	34:1:1096:G:P	2.20	0.63
2:B:87:ILE:O	2:B:98:THR:OG1	2.14	0.63
34:1:216:C:O2'	34:1:217:A:O5'	2.15	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:1204:A:N6	34:1:1693:G:O6	2.30	0.63
1:A:77:ILE:HD12	1:A:122:LEU:HD21	1.80	0.63
9:I:100:CYS:O	9:I:102:VAL:HG23	1.97	0.63
15:O:138:ASP:OD1	15:O:139:SER:N	2.30	0.63
17:Q:18:THR:OG1	34:1:1672:U:OP1	2.16	0.63
1:A:47:TYR:O	1:A:48:ILE:HD13	1.98	0.63
34:1:214:U:OP1	34:1:304:C:N4	2.32	0.63
1:A:24:HIS:HD2	1:A:48:ILE:HD12	1.64	0.63
12:L:96:ILE:HD11	12:L:103:GLU:OE2	1.97	0.63
15:O:85:CYS:HB3	15:O:90:ILE:HD11	1.79	0.63
19:S:27:ALA:HB2	19:S:45:LEU:HD22	1.81	0.63
28:b:15:GLU:O	28:b:23:ARG:NH1	2.31	0.63
34:1:61:A:N1	34:1:335:G:O2'	2.24	0.63
34:1:350:C:O2'	34:1:383:G:N1	2.31	0.63
18:R:5:ARG:NH1	18:R:9:VAL:HG11	2.13	0.62
33:g:32:LEU:HB3	33:g:71:ILE:HD11	1.80	0.62
3:C:105:GLU:OE1	3:C:212:LYS:NZ	2.32	0.62
3:C:232:THR:HG21	34:1:13:C:H4'	1.81	0.62
27:a:45:VAL:HG11	27:a:53:ILE:HD11	1.80	0.62
34:1:13:C:H42	34:1:1198:G:H1	1.47	0.62
5:E:150:PRO:HB3	5:E:169:ILE:HD11	1.80	0.62
9:I:184:ARG:NH1	34:1:303:C:O2'	2.32	0.62
1:A:198:MET:SD	1:A:199:PRO:HD2	2.39	0.62
25:Y:25:ILE:O	25:Y:71:GLY:N	2.29	0.62
9:I:87:ASN:HB3	9:I:90:LEU:HD12	1.80	0.62
12:L:82:MET:HG2	12:L:85:THR:HG23	1.81	0.62
8:H:191:GLU:O	8:H:193:GLN:NE2	2.33	0.62
33:g:192:THR:OG1	33:g:213:ASP:OD2	2.16	0.62
5:E:246:LEU:O	5:E:247:THR:OG1	2.15	0.62
34:1:126:G:O2'	34:1:181:A:N6	2.33	0.62
8:H:114:GLN:NE2	34:1:869:A:O5'	2.32	0.62
10:J:18:ARG:O	10:J:24:ARG:NH2	2.32	0.62
5:E:31:PRO:HG2	5:E:38:LEU:HD23	1.82	0.62
20:T:38:LYS:NZ	34:1:1567:G:O2'	2.33	0.62
34:1:456:C:O2'	34:1:1801:A:O2'	2.17	0.62
14:N:83:ASP:O	14:N:83:ASP:OD2	2.18	0.61
25:Y:5:VAL:HG12	25:Y:29:HIS:CD2	2.35	0.61
10:J:121:LYS:O	10:J:122:SER:OG	2.13	0.61
34:1:851:C:O3'	34:1:852:G:N2	2.29	0.61
5:E:232:ASN:OD1	5:E:232:ASN:O	2.18	0.61
33:g:87:LEU:HD23	33:g:111:VAL:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:92:ARG:NH1	34:1:441:C:O2'	2.33	0.61
8:H:137:SER:OG	8:H:138:GLU:N	2.32	0.61
9:I:162:LEU:HD11	9:I:191:GLU:OE1	2.01	0.61
18:R:9:VAL:HG13	18:R:50:ILE:HA	1.81	0.61
34:1:524:U:OP1	34:1:525:A:O2'	2.17	0.61
9:I:5:ARG:HH22	34:1:382:C:H41	1.47	0.61
20:T:134:ILE:O	20:T:138:VAL:HG23	1.99	0.61
23:W:56:HIS:NE2	34:1:918:U:O3'	2.33	0.61
34:1:11:A:C8	34:1:1357:A:H1'	2.35	0.61
34:1:1488:C:H3'	34:1:1489:A:H4'	1.81	0.61
34:1:1631:U:O4	34:1:1632:G:N1	2.34	0.61
6:F:62:ARG:O	6:F:64:ALA:N	2.33	0.61
8:H:191:GLU:OE1	8:H:191:GLU:N	2.34	0.61
9:I:56:ARG:NH2	34:1:380:G:OP2	2.33	0.61
9:I:105:ASP:OD1	9:I:106:SER:N	2.34	0.61
10:J:136:ARG:NE	10:J:139:LYS:O	2.34	0.61
14:N:56:ASP:OD1	28:b:52:THR:HG22	2.00	0.61
2:B:124:HIS:ND1	2:B:124:HIS:O	2.34	0.61
3:C:116:THR:OG1	3:C:119:GLY:O	2.14	0.61
8:H:134:VAL:HG22	8:H:173:PHE:CE2	2.36	0.61
12:L:154:GLN:NE2	14:N:133:ARG:O	2.29	0.61
19:S:36:VAL:HG13	19:S:40:TYR:HD2	1.66	0.61
8:H:38:ALA:HB2	8:H:75:ILE:HD12	1.82	0.61
19:S:16:LEU:HD22	19:S:99:LEU:HD23	1.83	0.61
1:A:81:ASN:ND2	1:A:204:TYR:OH	2.34	0.61
5:E:158:ASP:OD1	5:E:159:THR:N	2.33	0.61
1:A:209:GLU:OE1	1:A:210:ILE:N	2.34	0.61
3:C:65:LYS:HE3	3:C:273:LEU:HD13	1.83	0.61
23:W:20:ARG:NE	34:1:1096:G:OP1	2.33	0.61
32:f:101:ALA:O	34:1:1287:A:N6	2.33	0.61
34:1:70:G:N2	34:1:71:G:N3	2.49	0.61
34:1:1217:A:H2	34:1:1684:C:H42	1.46	0.61
19:S:24:ARG:NH1	34:1:1602:U:O2'	2.34	0.60
2:B:89:GLU:HG2	2:B:228:LEU:HD22	1.83	0.60
1:A:69:GLU:OE1	3:C:270:THR:HG21	2.01	0.60
1:A:103:PHE:O	1:A:107:THR:OG1	2.17	0.60
2:B:103:MET:HB2	2:B:215:VAL:HG12	1.83	0.60
14:N:92:ILE:O	14:N:96:VAL:HG23	2.01	0.60
30:d:12:ARG:NH1	34:1:1262:C:O2'	2.34	0.60
11:K:64:TRP:CZ3	30:d:23:VAL:HG22	2.37	0.60
25:Y:99:LYS:NZ	34:1:492:C:OP1	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:150:A:OP2	34:1:151:C:N4	2.31	0.60
19:S:46:ARG:HD2	20:T:37:VAL:HG22	1.82	0.60
5:E:32:SER:N	5:E:81:THR:OG1	2.35	0.60
15:O:146:ARG:NH2	34:1:1858:G:N7	2.50	0.60
34:1:677:G:N1	34:1:1027:A:OP2	2.25	0.60
1:A:209:GLU:OE1	1:A:210:ILE:HG23	2.01	0.60
6:F:65:GLN:N	6:F:65:GLN:OE1	2.35	0.60
23:W:32:LYS:NZ	34:1:687:C:OP1	2.31	0.60
34:1:344:U:H2'	34:1:345:U:O4'	2.02	0.60
1:A:76:VAL:CG1	1:A:87:VAL:HG13	2.31	0.60
12:L:44:PHE:CE2	12:L:143:LEU:HD23	2.37	0.60
19:S:132:ARG:NH2	34:1:1608:U:OP2	2.35	0.60
34:1:66:G:O4'	34:1:83:A:N6	2.35	0.60
9:I:162:LEU:HD21	9:I:195:LEU:HD22	1.84	0.59
30:d:10:HIS:O	30:d:12:ARG:N	2.35	0.59
34:1:84:A:O2'	34:1:150:A:O2'	2.19	0.59
34:1:342:C:H2'	34:1:343:A:O4'	2.02	0.59
23:W:8:ALA:HA	23:W:74:VAL:HG21	1.83	0.59
12:L:39:ASN:O	34:1:292:A:O2'	2.19	0.59
9:I:171:LEU:HD11	9:I:189:VAL:HG13	1.84	0.59
16:P:118:GLU:OE1	19:S:117:ILE:HG21	2.03	0.59
21:U:61:LEU:HD11	30:d:34:TYR:CZ	2.37	0.59
34:1:1577:G:O2'	34:1:1579:A:N3	2.29	0.59
4:D:4:GLN:N	4:D:4:GLN:OE1	2.36	0.59
20:T:114:GLU:HB2	20:T:124:THR:HG22	1.84	0.59
8:H:159:ASP:OD2	8:H:161:ALA:N	2.35	0.59
34:1:1137:U:O2'	34:1:1139:C:OP1	2.13	0.59
1:A:39:TYR:CD2	18:R:105:MET:HE3	2.38	0.59
33:g:133:ASN:OD1	33:g:134:THR:N	2.35	0.59
6:F:140:ASP:HB2	29:c:46:VAL:HG22	1.84	0.59
20:T:61:ALA:HB1	20:T:131:LEU:HD11	1.85	0.59
25:Y:10:ARG:NH2	34:1:832:G:OP2	2.35	0.59
34:1:316:G:H2'	34:1:317:C:O4'	2.02	0.59
2:B:35:ALA:HB2	2:B:44:ILE:HD11	1.84	0.59
6:F:159:ARG:NE	34:1:1535:U:O4	2.36	0.59
9:I:73:THR:O	34:1:301:A:O2'	2.21	0.59
10:J:85:GLY:HA2	10:J:151:LEU:HD13	1.85	0.59
3:C:145:LYS:N	34:1:1349:G:OP1	2.31	0.59
23:W:8:ALA:CA	23:W:74:VAL:HG21	2.32	0.59
27:a:13:LYS:NZ	34:1:992:A:OP2	2.20	0.59
34:1:844:U:H2'	34:1:845:G:H8	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:181:LEU:O	2:B:185:VAL:HG23	2.03	0.58
2:B:218:LEU:HD23	2:B:218:LEU:H	1.67	0.58
4:D:39:VAL:HG22	4:D:48:ILE:HG23	1.85	0.58
14:N:48:SER:O	34:1:1017:U:O2'	2.21	0.58
27:a:6:ARG:NE	34:1:1147:C:OP1	2.36	0.58
28:b:13:GLU:OE1	28:b:13:GLU:N	2.36	0.58
34:1:1085:C:N4	34:1:1087:A:N3	2.51	0.58
1:A:90:PHE:O	1:A:94:THR:HG22	2.02	0.58
2:B:82:ARG:NH2	2:B:188:LEU:O	2.36	0.58
9:I:178:ARG:HA	9:I:179:PRO:CG	2.33	0.58
34:1:331:C:H3'	34:1:332:G:H5''	1.85	0.58
34:1:1746:U:O4	34:1:1789:G:N2	2.36	0.58
3:C:205:VAL:O	3:C:205:VAL:HG23	2.03	0.58
7:G:102:VAL:HG12	7:G:104:ALA:H	1.69	0.58
34:1:1060:A:O2'	34:1:1062:A:N7	2.30	0.58
9:I:55:TYR:OH	34:1:309:G:OP2	2.19	0.58
10:J:89:GLU:OE1	10:J:89:GLU:N	2.34	0.58
16:P:89:MET:HE1	16:P:116:LEU:HD21	1.85	0.58
25:Y:79:LEU:O	25:Y:82:ALA:HB3	2.03	0.58
31:e:45:VAL:O	31:e:45:VAL:HG12	2.03	0.58
34:1:439:A:H4'	34:1:1799:G:H4'	1.84	0.58
2:B:130:THR:OG1	2:B:178:THR:O	2.21	0.58
14:N:33:VAL:O	14:N:37:ILE:HG13	2.04	0.58
34:1:125:C:N3	34:1:339:A:N6	2.52	0.58
34:1:338:G:O2'	34:1:339:A:O5'	2.20	0.58
34:1:440:G:O2'	34:1:1737:G:N3	2.35	0.58
6:F:58:ALA:O	34:1:1679:A:N6	2.36	0.58
9:I:177:SER:O	9:I:179:PRO:HG2	2.03	0.58
9:I:188:TYR:OH	9:I:194:GLU:OE1	2.22	0.58
15:O:135:ILE:O	34:1:943:U:O2'	2.16	0.58
34:1:34:U:H4'	34:1:564:A:H4'	1.85	0.58
34:1:863:U:O4	34:1:864:A:N6	2.35	0.58
34:1:1730:U:O4	34:1:1731:A:N6	2.37	0.58
1:A:19:LEU:HG	18:R:96:ILE:HD13	1.85	0.58
21:U:28:ASN:ND2	21:U:31:SER:OG	2.36	0.58
34:1:1707:U:O2	34:1:1849:G:N2	2.37	0.58
1:A:76:VAL:HG12	1:A:87:VAL:HG22	1.84	0.58
4:D:23:GLU:OE1	30:d:46:TYR:OH	2.18	0.58
7:G:36:VAL:HG21	7:G:52:ILE:HD11	1.84	0.58
31:e:56:ASN:OD1	34:1:605:A:O2'	2.17	0.58
34:1:10:G:N2	34:1:1358:U:O5'	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:31:ARG:HA	29:c:43:ILE:HG22	1.86	0.57
1:A:7:VAL:HG21	22:V:42:VAL:HA	1.87	0.57
4:D:162:ASP:HB2	34:1:1481:G:H21	1.69	0.57
20:T:39:LEU:HD22	20:T:43:LYS:O	2.05	0.57
25:Y:21:LYS:NZ	25:Y:48:TYR:OH	2.35	0.57
34:1:912:C:O2'	34:1:914:U:O2'	2.18	0.57
19:S:15:VAL:HG12	19:S:16:LEU:HG	1.87	0.57
34:1:350:C:O2'	34:1:383:G:N2	2.36	0.57
16:P:116:LEU:HD23	16:P:119:PHE:CE2	2.39	0.57
31:e:44:ASN:ND2	34:1:550:C:O2	2.37	0.57
5:E:64:ILE:HG12	25:Y:18:LEU:HD21	1.85	0.57
7:G:76:LEU:HD11	7:G:92:ARG:HD2	1.86	0.57
20:T:57:ALA:O	20:T:60:THR:OG1	2.22	0.57
34:1:170:A:H3'	34:1:171:A:C8	2.40	0.57
8:H:98:ARG:NH2	8:H:125:VAL:O	2.37	0.57
23:W:106:THR:HG22	23:W:122:GLY:O	2.04	0.57
29:c:24:GLN:OE1	34:1:1683:C:N4	2.34	0.57
34:1:470:G:O2'	34:1:471:G:O4'	2.23	0.57
34:1:482:G:N2	34:1:485:A:OP2	2.38	0.57
4:D:75:LYS:NZ	11:K:18:GLU:O	2.34	0.57
14:N:130:LYS:NZ	14:N:139:TRP:O	2.34	0.57
34:1:437:G:N2	34:1:1801:A:OP1	2.38	0.57
2:B:127:VAL:HG11	2:B:176:VAL:CG1	2.35	0.57
2:B:208:HIS:O	2:B:210:VAL:HG23	2.04	0.57
10:J:35:TYR:O	10:J:123:ILE:HG21	2.05	0.57
4:D:122:VAL:O	4:D:126:ILE:HG22	2.05	0.56
34:1:88:G:C6	34:1:89:C:C5	2.93	0.56
1:A:177:MET:O	1:A:181:GLU:HG2	2.06	0.56
2:B:137:LEU:HB3	2:B:215:VAL:HG23	1.85	0.56
9:I:158:ILE:HD13	9:I:166:PHE:CE2	2.40	0.56
11:K:29:MET:SD	11:K:30:PRO:HD3	2.45	0.56
28:b:34:ASP:OD2	28:b:82:LYS:NZ	2.38	0.56
34:1:1340:U:OP2	34:1:1341:C:O2'	2.22	0.56
2:B:32:ASP:OD1	2:B:32:ASP:N	2.34	0.56
10:J:115:PHE:CD1	10:J:120:ALA:HB3	2.40	0.56
19:S:23:ARG:O	26:Z:48:VAL:HG11	2.05	0.56
23:W:74:VAL:HG12	23:W:75:ILE:N	2.20	0.56
33:g:7:LEU:HD12	33:g:309:VAL:O	2.06	0.56
34:1:524:U:H3	34:1:594:A:H62	1.52	0.56
8:H:186:ASN:OD1	8:H:187:PHE:N	2.38	0.56
9:I:110:ARG:NH1	9:I:121:LEU:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:179:PRO:O	9:I:183:GLY:CA	2.53	0.56
33:g:201:SER:OG	33:g:203:ASP:OD1	2.17	0.56
2:B:29:ASP:O	2:B:49:VAL:N	2.38	0.56
9:I:199:LEU:O	9:I:203:LYS:HG3	2.05	0.56
34:1:349:A:O2'	34:1:350:C:O4'	2.24	0.56
34:1:1235:G:OP1	34:1:1246:A:N6	2.38	0.56
4:D:161:GLY:O	34:1:1482:C:O2'	2.23	0.56
34:1:10:G:C2	34:1:1357:A:H2'	2.41	0.56
9:I:56:ARG:NH2	34:1:379:C:O5'	2.38	0.56
1:A:74:VAL:O	1:A:97:THR:N	2.38	0.56
12:L:23:VAL:O	12:L:23:VAL:HG13	2.04	0.56
27:a:4:LYS:NZ	34:1:1863:A:OP2	2.37	0.56
3:C:60:TRP:CH2	3:C:67:GLY:HA3	2.41	0.56
25:Y:79:LEU:H	25:Y:79:LEU:HD23	1.70	0.56
28:b:50:ALA:HB3	28:b:64:CYS:SG	2.46	0.56
34:1:1650:A:N6	34:1:1674:G:O2'	2.36	0.56
8:H:48:ALA:HB2	8:H:62:ILE:HG22	1.86	0.55
17:Q:51:LEU:O	17:Q:51:LEU:HD23	2.05	0.55
18:R:59:LYS:NZ	34:1:1456:G:OP1	2.37	0.55
23:W:27:ILE:HG22	23:W:29:PRO:HD2	1.88	0.55
34:1:1102:G:C4	34:1:1131:G:N2	2.74	0.55
1:A:178:LEU:O	1:A:182:VAL:HG23	2.07	0.55
5:E:70:ILE:HD12	5:E:70:ILE:N	2.21	0.55
7:G:118:GLU:N	7:G:118:GLU:OE1	2.39	0.55
12:L:37:TYR:OH	12:L:51:ILE:HG23	2.07	0.55
23:W:25:VAL:HG12	23:W:26:LEU:H	1.70	0.55
23:W:28:ARG:HG3	23:W:29:PRO:HD3	1.87	0.55
34:1:1718:G:N2	34:1:1815:A:OP2	2.39	0.55
8:H:120:ARG:NH2	34:1:913:A:OP1	2.40	0.55
10:J:15:THR:HG21	34:1:22:A:O2'	2.06	0.55
11:K:71:LEU:HD21	11:K:76:ILE:HD11	1.88	0.55
24:X:12:LYS:NZ	34:1:1161:U:OP1	2.27	0.55
28:b:26:GLN:OE1	28:b:26:GLN:O	2.23	0.55
1:A:104:THR:O	1:A:107:THR:OG1	2.24	0.55
1:A:206:ASP:HB3	1:A:210:ILE:HD11	1.88	0.55
23:W:47:ILE:HG22	23:W:69:LEU:HD11	1.89	0.55
25:Y:13:MET:SD	25:Y:14:THR:N	2.77	0.55
32:f:147:THR:HG1	34:1:1292:C:HO2'	1.53	0.55
34:1:343:A:H2'	34:1:344:U:O4'	2.07	0.55
1:A:7:VAL:HG21	22:V:42:VAL:H	1.70	0.55
1:A:23:THR:HG1	1:A:164:ASN:N	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:GLY:HA3	1:A:150:THR:HG23	1.89	0.55
9:I:34:ALA:HB3	9:I:56:ARG:HD2	1.87	0.55
5:E:115:THR:HG22	5:E:116:VAL:H	1.72	0.55
7:G:27:PHE:CZ	7:G:102:VAL:HG11	2.42	0.55
10:J:64:ASP:OD2	10:J:66:LYS:NZ	2.28	0.55
34:1:440:G:O3'	34:1:1737:G:N2	2.39	0.55
4:D:172:VAL:O	4:D:173:ARG:NH1	2.35	0.55
14:N:109:LYS:NZ	34:1:1033:G:OP1	2.37	0.55
25:Y:25:ILE:N	25:Y:71:GLY:O	2.40	0.55
1:A:168:ALA:HB1	1:A:203:PHE:O	2.06	0.55
12:L:36:TYR:HH	34:1:294:U:P	2.30	0.55
33:g:216:ALA:O	33:g:230:LEU:N	2.38	0.55
33:g:276:SER:O	33:g:277:THR:OG1	2.24	0.55
15:O:45:THR:C	15:O:53:ILE:HD11	2.31	0.55
2:B:41:ILE:HD11	2:B:74:LEU:HD12	1.89	0.55
2:B:135:LEU:HD13	2:B:137:LEU:HB3	1.88	0.55
3:C:88:ILE:HG23	3:C:93:ILE:HD12	1.89	0.55
6:F:118:ASN:ND2	6:F:180:ALA:O	2.38	0.55
14:N:99:ARG:NH2	14:N:119:GLU:OE1	2.40	0.55
17:Q:141:TYR:OH	34:1:1668:U:OP2	2.19	0.55
34:1:318:A:N1	34:1:332:G:N2	2.55	0.55
34:1:1049:A:OP2	34:1:1068:G:N1	2.31	0.55
34:1:1354:G:N1	34:1:1357:A:OP2	2.40	0.55
8:H:98:ARG:HE	8:H:125:VAL:HG23	1.71	0.54
9:I:38:ILE:HD11	9:I:79:ILE:O	2.07	0.54
18:R:5:ARG:NH1	18:R:49:LYS:O	2.40	0.54
23:W:8:ALA:HB2	23:W:74:VAL:HG21	1.89	0.54
25:Y:74:MET:HE2	25:Y:74:MET:HA	1.89	0.54
34:1:1362:U:O4	34:1:1382:A:N6	2.40	0.54
3:C:230:THR:O	3:C:230:THR:HG22	2.07	0.54
7:G:27:PHE:HE1	7:G:109:LEU:HD13	1.73	0.54
27:a:2:THR:OG1	27:a:3:LYS:N	2.40	0.54
28:b:53:VAL:HB	28:b:55:LEU:HD21	1.88	0.54
33:g:178:ASN:O	33:g:182:CYS:N	2.41	0.54
34:1:217:A:H2'	34:1:218:U:C6	2.43	0.54
34:1:229:A:O2'	34:1:888:U:O2	2.21	0.54
34:1:440:G:N1	34:1:453:C:O2	2.34	0.54
34:1:1220:A:N3	34:1:1677:U:O2'	2.24	0.54
34:1:1583:C:OP2	34:1:1584:G:O2'	2.15	0.54
5:E:34:GLY:N	34:1:345:U:O2'	2.37	0.54
34:1:1240:A:N6	34:1:1241:A:N1	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:132:ASP:N	3:C:136:HIS:O	2.37	0.54
9:I:138:ASN:OD1	9:I:140:LYS:NZ	2.29	0.54
9:I:179:PRO:O	9:I:183:GLY:HA2	2.06	0.54
10:J:80:ARG:O	10:J:84:ILE:HG13	2.07	0.54
18:R:17:ILE:HD12	18:R:57:LEU:HD13	1.88	0.54
2:B:85:LYS:C	2:B:86:LEU:HD12	2.33	0.54
3:C:69:LEU:CG	3:C:273:LEU:HD21	2.38	0.54
5:E:108:ARG:NH2	34:1:846:G:OP2	2.39	0.54
19:S:65:GLU:O	19:S:68:ILE:HG22	2.08	0.54
23:W:71:LYS:NZ	34:1:1155:U:O3'	2.41	0.54
3:C:128:VAL:HG12	3:C:154:ALA:HB1	1.90	0.54
20:T:116:ASP:OD1	20:T:122:LYS:NZ	2.28	0.54
25:Y:37:LYS:N	34:1:571:U:OP1	2.41	0.54
28:b:20:LYS:NZ	34:1:1015:U:OP2	2.34	0.54
34:1:469:A:H2'	34:1:470:G:O5'	2.08	0.54
34:1:1361:G:N7	34:1:1362:U:N3	2.56	0.54
1:A:142:LEU:C	1:A:142:LEU:HD12	2.33	0.54
9:I:81:VAL:HG22	9:I:96:LEU:HD21	1.89	0.54
10:J:91:LYS:C	10:J:92:MET:HE2	2.33	0.54
34:1:475:C:O2'	34:1:476:A:OP1	2.17	0.54
12:L:36:TYR:OH	34:1:294:U:OP1	2.25	0.54
16:P:69:PRO:O	16:P:71:GLU:N	2.40	0.54
25:Y:93:ARG:NH2	34:1:575:A:OP2	2.40	0.54
5:E:45:ILE:HA	5:E:61:VAL:HG11	1.89	0.54
10:J:122:SER:O	10:J:124:HIS:N	2.41	0.54
33:g:236:ILE:HG21	33:g:239:LEU:HD21	1.90	0.54
3:C:173:LYS:O	3:C:175:GLY:N	2.41	0.53
10:J:157:ILE:H	10:J:157:ILE:HD12	1.70	0.53
25:Y:113:ARG:O	25:Y:117:VAL:HG22	2.08	0.53
2:B:145:LYS:NZ	2:B:151:ARG:O	2.41	0.53
3:C:115:GLN:N	34:1:1358:U:OP1	2.41	0.53
3:C:166:ARG:NH1	22:V:10:ASP:OD2	2.40	0.53
3:C:207:ALA:HB1	3:C:208:PRO:HD2	1.90	0.53
7:G:74:ARG:NH1	34:1:455:A:OP1	2.39	0.53
7:G:173:ALA:HB1	7:G:174:PRO:HG2	1.91	0.53
23:W:47:ILE:HD12	23:W:63:VAL:CG1	2.37	0.53
24:X:3:LYS:NZ	34:1:661:U:OP2	2.41	0.53
34:1:1442:U:H2'	34:1:1443:C:O4'	2.09	0.53
4:D:106:ARG:NE	4:D:174:HIS:O	2.41	0.53
9:I:72:CYS:HG	9:I:112:TRP:CG	2.27	0.53
9:I:162:LEU:CD2	9:I:195:LEU:HD22	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:121:VAL:HG13	34:1:1474:A:H4'	1.90	0.53
34:1:419:G:N2	34:1:661:U:O2	2.41	0.53
34:1:800:U:H2'	34:1:801:U:O4'	2.09	0.53
34:1:879:C:H3'	34:1:880:G:H21	1.73	0.53
2:B:47:THR:OG1	15:O:46:ASP:OD2	2.22	0.53
9:I:34:ALA:HB1	9:I:58:LEU:HD23	1.90	0.53
14:N:128:TYR:O	14:N:131:THR:HG22	2.09	0.53
18:R:95:ILE:HD13	18:R:122:PRO:O	2.08	0.53
18:R:106:LEU:HD23	18:R:109:LEU:HD22	1.90	0.53
1:A:151:ASP:N	1:A:151:ASP:OD1	2.42	0.53
19:S:43:VAL:HA	20:T:37:VAL:HG21	1.90	0.53
19:S:135:HIS:O	19:S:139:THR:OG1	2.26	0.53
24:X:63:ASN:CG	34:1:624:C:H41	2.16	0.53
34:1:1211:G:HO2'	34:1:1212:G:P	2.24	0.53
34:1:1796:G:H2'	34:1:1797:U:C2	2.44	0.53
19:S:16:LEU:HD22	19:S:99:LEU:HD21	1.89	0.53
22:V:51:LYS:NZ	22:V:76:ASP:OD2	2.41	0.53
5:E:61:VAL:HG12	5:E:80:VAL:CG2	2.39	0.53
10:J:168:GLY:O	10:J:172:ARG:NE	2.41	0.53
24:X:91:LEU:O	24:X:91:LEU:HD23	2.09	0.53
34:1:742:U:O2'	34:1:743:U:O5'	2.26	0.53
8:H:130:LEU:HD13	8:H:177:TYR:CD1	2.44	0.53
15:O:148:GLY:O	27:a:28:ARG:NH2	2.42	0.53
21:U:81:GLN:HE21	30:d:55:LEU:HD12	1.74	0.53
29:c:43:ILE:HD11	29:c:66:ARG:HH21	1.73	0.53
3:C:114:LYS:HA	34:1:1358:U:P	2.49	0.53
7:G:88:ARG:O	7:G:89:THR:C	2.52	0.53
9:I:178:ARG:CA	9:I:179:PRO:CG	2.86	0.53
34:1:1554:C:H1'	34:1:1555:U:OP2	2.09	0.53
14:N:102:LEU:HD11	14:N:112:LYS:HA	1.90	0.53
34:1:628:A:H3'	34:1:629:A:C5'	2.39	0.53
34:1:810:A:H61	34:1:851:C:N4	2.07	0.53
2:B:52:THR:OG1	2:B:57:ILE:HA	2.09	0.52
12:L:124:ASP:OD1	12:L:124:ASP:N	2.41	0.52
34:1:1455:A:H61	34:1:1471:C:N4	2.06	0.52
10:J:5:ARG:NH2	34:1:39:A:P	2.83	0.52
15:O:82:ALA:HB2	15:O:119:LEU:HD12	1.91	0.52
18:R:27:ASP:OD2	18:R:30:THR:N	2.42	0.52
25:Y:89:HIS:CG	34:1:493:A:H4'	2.45	0.52
28:b:53:VAL:HG12	28:b:62:VAL:HG13	1.90	0.52
33:g:32:LEU:CB	33:g:71:ILE:HD11	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:66:G:OP1	34:1:82:G:N2	2.35	0.52
34:1:94:G:HO2'	34:1:508:A:HO2'	1.55	0.52
34:1:1622:U:H4'	34:1:1623:A:H5''	1.91	0.52
34:1:1720:U:H3'	34:1:1721:U:H5''	1.91	0.52
2:B:151:ARG:HB3	34:1:1101:U:OP1	2.09	0.52
7:G:1:MET:SD	7:G:109:LEU:HD11	2.50	0.52
7:G:173:ALA:HB1	7:G:174:PRO:CG	2.39	0.52
8:H:66:VAL:HG23	8:H:97:GLN:O	2.09	0.52
33:g:85:GLY:HA2	33:g:108:VAL:HG23	1.91	0.52
34:1:587:A:O5'	34:1:592:C:N4	2.40	0.52
1:A:121:LEU:HD23	1:A:122:LEU:N	2.24	0.52
6:F:166:ILE:O	34:1:1598:G:N2	2.43	0.52
22:V:17:CYS:SG	22:V:18:SER:N	2.82	0.52
32:f:97:LYS:NZ	34:1:1290:G:O6	2.26	0.52
34:1:417:C:H2'	34:1:418:A:C5'	2.40	0.52
34:1:798:G:H2'	34:1:800:U:OP2	2.10	0.52
11:K:82:TYR:CE2	11:K:83:LEU:HD23	2.45	0.52
16:P:119:PHE:N	16:P:119:PHE:CD1	2.77	0.52
28:b:59:CYS:SG	28:b:60:SER:N	2.82	0.52
33:g:296:GLN:NE2	33:g:312:VAL:O	2.43	0.52
34:1:11:A:C5	34:1:1357:A:H1'	2.44	0.52
33:g:164:ILE:HG23	33:g:176:VAL:HG13	1.90	0.52
12:L:49:GLU:O	12:L:53:GLY:N	2.42	0.52
13:M:17:ALA:HB1	13:M:124:ILE:HD13	1.92	0.52
16:P:43:ARG:NH1	34:1:1615:U:OP2	2.42	0.52
24:X:124:LYS:NZ	34:1:29:G:OP1	2.32	0.52
34:1:1455:A:N6	34:1:1456:G:O6	2.43	0.52
1:A:76:VAL:HB	1:A:87:VAL:HG13	1.92	0.52
6:F:77:MET:HE1	34:1:1674:G:O2'	2.09	0.52
7:G:31:ARG:NH1	7:G:68:LEU:HD22	2.24	0.52
9:I:100:CYS:HB3	9:I:175:ILE:HD12	1.91	0.52
11:K:40:VAL:HG23	11:K:40:VAL:O	2.10	0.52
21:U:79:ARG:NH2	21:U:81:GLN:OE1	2.41	0.52
1:A:34:MET:SD	1:A:34:MET:C	2.93	0.52
14:N:96:VAL:CG2	14:N:146:ALA:HB1	2.36	0.52
15:O:39:ASP:OD1	15:O:40:THR:N	2.42	0.52
19:S:90:VAL:O	19:S:90:VAL:HG12	2.10	0.52
19:S:136:THR:HG22	19:S:136:THR:O	2.08	0.52
20:T:14:PHE:CE2	20:T:18:LEU:HD22	2.45	0.52
20:T:69:GLY:N	20:T:121:ARG:O	2.39	0.52
34:1:172:U:N3	34:1:337:C:O2'	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:THR:HG23	1:A:96:ALA:H	1.75	0.52
7:G:48:TYR:HE2	7:G:113:ILE:HG21	1.75	0.52
8:H:53:VAL:HG23	8:H:53:VAL:O	2.08	0.52
9:I:45:THR:HG22	34:1:307:G:H1'	1.91	0.52
9:I:97:VAL:HB	34:1:377:G:H4'	1.91	0.52
10:J:144:ILE:HD13	34:1:824:C:C2	2.45	0.52
34:1:1568:C:H2'	34:1:1569:A:O4'	2.10	0.52
1:A:11:LYS:O	1:A:15:VAL:HG22	2.10	0.51
1:A:80:ARG:HE	1:A:126:ASP:HB3	1.74	0.51
1:A:196:GLU:OE1	1:A:196:GLU:N	2.41	0.51
6:F:204:ARG:O	29:c:63:ARG:NE	2.42	0.51
19:S:137:LYS:HG2	34:1:1521:C:H41	1.75	0.51
27:a:63:VAL:HG22	27:a:65:PRO:HD3	1.91	0.51
33:g:154:VAL:HG12	33:g:167:SER:CB	2.40	0.51
34:1:459:C:C4	34:1:460:A:C6	2.98	0.51
34:1:492:C:N4	34:1:507:G:OP2	2.39	0.51
34:1:1740:C:H2'	34:1:1741:U:C6	2.45	0.51
5:E:163:ASP:OD1	5:E:164:LEU:N	2.42	0.51
6:F:102:LEU:C	26:Z:67:LEU:HD11	2.34	0.51
7:G:13:GLN:NE2	34:1:153:G:H21	2.07	0.51
7:G:133:LEU:HD11	34:1:150:A:N1	2.24	0.51
9:I:11:ARG:NH2	34:1:367:U:OP1	2.42	0.51
9:I:111:GLN:OE1	9:I:111:GLN:N	2.44	0.51
20:T:18:LEU:HD23	20:T:58:ALA:HB1	1.92	0.51
34:1:150:A:C6	34:1:151:C:H1'	2.46	0.51
34:1:1402:A:N6	34:1:1441:U:O2'	2.43	0.51
34:1:1828:C:H2'	34:1:1829:G:O4'	2.10	0.51
5:E:116:VAL:HG13	5:E:117:GLU:OE2	2.10	0.51
8:H:109:ARG:NH1	34:1:797:C:O4'	2.43	0.51
13:M:14:VAL:HG22	13:M:127:TYR:CZ	2.45	0.51
28:b:67:THR:OG1	34:1:929:G:C1'	2.58	0.51
34:1:309:G:H2'	34:1:310:C:O4'	2.11	0.51
1:A:8:LEU:HD23	1:A:191:ARG:HH22	1.75	0.51
1:A:185:MET:SD	1:A:185:MET:N	2.84	0.51
9:I:79:ILE:HB	9:I:103:LEU:HB3	1.93	0.51
14:N:11:LEU:HD23	14:N:11:LEU:O	2.11	0.51
22:V:73:ALA:C	22:V:79:VAL:HG12	2.35	0.51
23:W:8:ALA:CB	23:W:74:VAL:HG21	2.41	0.51
24:X:128:VAL:HG21	24:X:140:ARG:C	2.35	0.51
34:1:151:C:O2	34:1:167:G:N1	2.38	0.51
34:1:962:A:N1	34:1:1055:A:O2'	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:192:VAL:HG21	5:E:242:LYS:O	2.11	0.51
8:H:122:LEU:HD21	34:1:742:U:O2	2.11	0.51
16:P:130:ARG:HB3	16:P:131:PRO:HD2	1.93	0.51
17:Q:43:GLU:HB2	17:Q:44:PRO:HD3	1.91	0.51
26:Z:73:VAL:O	26:Z:77:LEU:HG	2.11	0.51
27:a:42:ARG:O	27:a:67:LEU:N	2.40	0.51
2:B:71:LEU:HD11	2:B:82:ARG:HB3	1.92	0.51
3:C:216:MET:HA	3:C:216:MET:HE2	1.93	0.51
9:I:38:ILE:O	9:I:38:ILE:CG1	2.58	0.51
9:I:76:THR:HG23	9:I:108:PRO:HG2	1.92	0.51
25:Y:107:ARG:NH1	34:1:506:G:OP2	2.41	0.51
34:1:1043:G:HO2'	34:1:1044:G:C5'	2.24	0.51
3:C:115:GLN:OE1	3:C:115:GLN:HA	2.11	0.51
8:H:194:LEU:HD21	28:b:81:ARG:NH2	2.26	0.51
12:L:76:VAL:HG22	12:L:125:ILE:HD13	1.92	0.51
13:M:14:VAL:HG22	13:M:127:TYR:CE1	2.46	0.51
20:T:126:GLN:OE1	20:T:129:ARG:NH2	2.43	0.51
23:W:76:SER:HB2	23:W:77:PRO:HD3	1.92	0.51
28:b:44:THR:O	28:b:46:VAL:HG13	2.11	0.51
29:c:21:THR:N	29:c:27:CYS:O	2.29	0.51
30:d:12:ARG:NH1	34:1:1262:C:O3'	2.37	0.51
32:f:100:LEU:HD12	32:f:100:LEU:O	2.11	0.51
34:1:824:C:N4	34:1:825:A:C6	2.79	0.51
7:G:57:ASP:OD2	7:G:72:ARG:NE	2.36	0.51
34:1:123:G:H2'	34:1:124:U:O4'	2.11	0.51
10:J:136:ARG:HD3	10:J:139:LYS:HE3	1.93	0.51
30:d:21:CYS:HB3	30:d:26:ASN:O	2.11	0.51
34:1:84:A:O2'	34:1:150:A:C3'	2.59	0.51
8:H:95:ILE:HD12	8:H:180:LEU:HD11	1.92	0.50
16:P:86:LEU:HD12	16:P:87:PRO:O	2.11	0.50
22:V:14:PRO:HB2	22:V:23:ILE:HG23	1.93	0.50
23:W:105:THR:HG22	23:W:105:THR:O	2.11	0.50
1:A:173:LEU:O	1:A:177:MET:HG2	2.11	0.50
7:G:56:ASN:N	7:G:108:VAL:O	2.40	0.50
8:H:114:GLN:NE2	34:1:869:A:O4'	2.44	0.50
15:O:83:GLN:O	15:O:87:GLU:HG2	2.12	0.50
19:S:141:ARG:NH2	34:1:1521:C:O2'	2.44	0.50
25:Y:118:ARG:NH2	34:1:163:U:O4	2.45	0.50
34:1:1736:G:H1	34:1:1798:C:N4	2.09	0.50
5:E:66:MET:O	5:E:66:MET:SD	2.70	0.50
5:E:118:GLU:CD	5:E:118:GLU:H	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:156:VAL:HG23	5:E:157:ASN:N	2.27	0.50
11:K:3:MET:N	11:K:3:MET:SD	2.85	0.50
20:T:30:VAL:HG13	20:T:30:VAL:O	2.12	0.50
22:V:70:LEU:HD23	22:V:70:LEU:C	2.37	0.50
33:g:304:ASP:OD2	33:g:308:ARG:NH1	2.39	0.50
34:1:677:G:H2'	34:1:678:U:C6	2.46	0.50
34:1:1735:A:N6	34:1:1799:G:O2'	2.44	0.50
3:C:256:TRP:CH2	23:W:66:THR:HG21	2.46	0.50
8:H:64:VAL:HG22	8:H:72:PHE:CE2	2.46	0.50
8:H:95:ILE:CD1	8:H:180:LEU:HD11	2.41	0.50
12:L:16:ILE:HD11	12:L:36:TYR:HB2	1.93	0.50
12:L:48:LYS:O	12:L:51:ILE:N	2.44	0.50
12:L:57:ASP:OD2	12:L:84:ARG:NH1	2.45	0.50
14:N:108:ASP:OD1	14:N:108:ASP:N	2.43	0.50
15:O:124:MET:HE2	15:O:124:MET:HA	1.92	0.50
17:Q:32:ILE:HD13	17:Q:39:LEU:HD22	1.93	0.50
23:W:68:ARG:NH1	23:W:70:ASN:OD1	2.44	0.50
30:d:10:HIS:NE2	34:1:1261:C:H2'	2.26	0.50
34:1:9:U:N3	34:1:12:U:OP2	2.43	0.50
3:C:61:MET:SD	3:C:61:MET:O	2.69	0.50
3:C:230:THR:HG23	3:C:236:PHE:CD1	2.46	0.50
5:E:156:VAL:HG23	5:E:157:ASN:H	1.76	0.50
7:G:121:ILE:HG22	7:G:123:GLY:H	1.77	0.50
9:I:53:LYS:NZ	34:1:308:G:OP1	2.30	0.50
18:R:109:LEU:HD23	18:R:111:PHE:HB2	1.94	0.50
23:W:62:VAL:O	23:W:62:VAL:HG23	2.11	0.50
28:b:61:THR:OG1	28:b:63:LEU:CD1	2.59	0.50
31:e:46:VAL:N	31:e:47:PRO:CD	2.75	0.50
34:1:13:C:C2	34:1:1355:C:C4	2.99	0.50
10:J:84:ILE:O	10:J:108:ARG:NH2	2.44	0.50
11:K:75:GLY:O	11:K:79:LEU:N	2.45	0.50
16:P:118:GLU:OE1	19:S:117:ILE:HD13	2.12	0.50
23:W:28:ARG:HB2	34:1:921:G:N7	2.26	0.50
33:g:21:ILE:HD13	33:g:299:PHE:HB3	1.94	0.50
34:1:62:G:H2'	34:1:63:U:H5'	1.93	0.50
10:J:77:LEU:O	10:J:81:LEU:HD23	2.11	0.50
24:X:3:LYS:NZ	34:1:663:C:OP2	2.37	0.50
33:g:18:VAL:HG21	33:g:307:VAL:CG2	2.42	0.50
3:C:195:LEU:O	3:C:196:ILE:HD13	2.11	0.50
3:C:256:TRP:CZ3	23:W:66:THR:HG21	2.46	0.50
7:G:48:TYR:CE2	7:G:113:ILE:HG21	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:98:ARG:NH2	8:H:128:ALA:HB3	2.27	0.50
9:I:98:LYS:HA	9:I:177:SER:O	2.12	0.50
21:U:69:PRO:O	30:d:40:ARG:NH1	2.44	0.50
22:V:2:GLN:OE1	22:V:2:GLN:N	2.45	0.50
30:d:30:LEU:HD21	34:1:1659:U:C4'	2.37	0.50
1:A:122:LEU:HD23	1:A:123:VAL:N	2.26	0.50
7:G:176:ILE:HG21	7:G:179:LEU:HD23	1.94	0.50
14:N:148:ALA:HB3	14:N:149:LEU:HD12	1.93	0.50
20:T:111:LYS:O	20:T:124:THR:OG1	2.19	0.50
28:b:56:CYS:O	28:b:60:SER:N	2.43	0.50
29:c:38:THR:OG1	29:c:39:SER:N	2.43	0.50
33:g:218:LEU:HD21	33:g:248:LEU:HD22	1.94	0.50
34:1:1325:G:O2'	34:1:1327:G:OP1	2.29	0.50
4:D:126:ILE:HD11	4:D:188:ILE:HD13	1.94	0.49
5:E:85:GLY:O	5:E:101:LEU:HD12	2.11	0.49
7:G:94:ARG:HG3	34:1:454:U:O3'	2.12	0.49
8:H:158:LEU:HD11	8:H:187:PHE:CD2	2.46	0.49
10:J:136:ARG:NE	10:J:141:VAL:HG23	2.27	0.49
23:W:18:GLU:HG3	23:W:69:LEU:HB2	1.94	0.49
33:g:87:LEU:HD21	33:g:122:SER:CB	2.41	0.49
34:1:90:G:OP1	34:1:446:G:N1	2.45	0.49
34:1:312:G:O2'	34:1:314:U:OP2	2.30	0.49
34:1:801:U:H2'	34:1:802:A:O4'	2.11	0.49
8:H:32:MET:N	8:H:32:MET:HE2	2.27	0.49
22:V:3:ASN:OD1	22:V:7:GLU:N	2.40	0.49
25:Y:101:LYS:NZ	25:Y:102:THR:O	2.45	0.49
28:b:61:THR:OG1	28:b:63:LEU:HD12	2.12	0.49
33:g:52:TYR:CG	33:g:309:VAL:HG21	2.47	0.49
34:1:12:U:C2	34:1:13:C:C5	3.00	0.49
34:1:547:G:H3'	34:1:548:C:H5''	1.93	0.49
34:1:1289:U:O2'	34:1:1290:G:O4'	2.30	0.49
34:1:1290:G:H2'	34:1:1291:A:O4'	2.12	0.49
34:1:1380:C:N4	34:1:1381:G:O6	2.46	0.49
2:B:127:VAL:HG12	2:B:128:LYS:N	2.26	0.49
7:G:177:GLN:NE2	34:1:172:U:OP2	2.46	0.49
7:G:201:LYS:NZ	34:1:124:U:OP1	2.42	0.49
9:I:67:TRP:N	9:I:72:CYS:O	2.45	0.49
17:Q:12:VAL:HG12	17:Q:13:PHE:H	1.76	0.49
34:1:1108:G:C2	34:1:1109:C:C4	2.99	0.49
7:G:173:ALA:CA	7:G:174:PRO:CG	2.90	0.49
8:H:159:ASP:OD2	8:H:162:GLN:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:36:GLU:HA	18:R:47:ARG:HE	1.77	0.49
34:1:1:U:O2'	34:1:417:C:N4	2.45	0.49
34:1:466:G:H3'	34:1:466:G:N3	2.27	0.49
34:1:620:G:H2'	34:1:620:G:N3	2.27	0.49
34:1:918:U:O2	34:1:918:U:H2'	2.12	0.49
34:1:1213:C:H42	34:1:1686:G:H1	1.60	0.49
16:P:18:ARG:NH1	19:S:89:ASP:OD1	2.45	0.49
25:Y:102:THR:O	25:Y:102:THR:HG23	2.12	0.49
28:b:63:LEU:HG	28:b:73:LEU:HD23	1.94	0.49
34:1:154:U:H2'	34:1:155:G:O4'	2.13	0.49
34:1:417:C:H2'	34:1:418:A:H5''	1.94	0.49
34:1:457:C:N4	34:1:458:A:H62	2.11	0.49
34:1:822:U:C2'	34:1:823:U:OP1	2.59	0.49
2:B:188:LEU:CD2	2:B:212:VAL:HG21	2.43	0.49
5:E:194:VAL:N	5:E:211:LYS:O	2.37	0.49
7:G:90:GLY:HA2	34:1:442:C:O2	2.13	0.49
20:T:89:PRO:O	20:T:91:HIS:ND1	2.45	0.49
24:X:63:ASN:ND2	34:1:623:G:O6	2.46	0.49
34:1:116:U:H3	34:1:347:G:H22	1.59	0.49
3:C:64:THR:HG22	3:C:64:THR:O	2.13	0.49
5:E:56:LEU:HD23	25:Y:22:GLN:OE1	2.13	0.49
7:G:3:LEU:HD22	7:G:111:LEU:CD1	2.43	0.49
8:H:20:GLU:HG2	8:H:48:ALA:HB3	1.94	0.49
8:H:64:VAL:HG13	8:H:72:PHE:HE2	1.77	0.49
9:I:42:ARG:HA	9:I:42:ARG:CZ	2.43	0.49
13:M:79:VAL:HG21	13:M:85:LEU:HD21	1.95	0.49
14:N:95:ALA:HB2	14:N:118:ILE:CG2	2.43	0.49
15:O:42:VAL:HG11	15:O:81:VAL:HG11	1.95	0.49
19:S:81:ASP:OD1	19:S:81:ASP:N	2.44	0.49
20:T:74:SER:N	34:1:1562:C:OP1	2.45	0.49
34:1:69:C:N4	34:1:70:G:O6	2.46	0.49
34:1:80:G:C6	34:1:81:U:C4	3.00	0.49
34:1:285:U:O2'	34:1:286:U:P	2.70	0.49
34:1:469:A:C2'	34:1:470:G:O5'	2.61	0.49
34:1:659:G:O4'	34:1:662:G:N2	2.44	0.49
2:B:104:ASP:O	2:B:105:LEU:HD12	2.13	0.49
5:E:92:ILE:HD11	25:Y:17:LEU:HD21	1.95	0.49
8:H:36:LEU:CD1	8:H:75:ILE:HG21	2.43	0.49
9:I:171:LEU:HD21	9:I:189:VAL:CG1	2.43	0.49
12:L:36:TYR:OH	34:1:294:U:P	2.70	0.49
34:1:388:U:H2'	34:1:389:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:525:A:H2'	34:1:526:A:C1'	2.43	0.49
34:1:929:G:HO2'	34:1:930:C:P	2.34	0.49
34:1:1043:G:O2'	34:1:1044:G:O5'	2.30	0.49
34:1:1290:G:N2	34:1:1310:U:O2	2.46	0.49
34:1:1508:A:O2'	34:1:1510:G:N7	2.40	0.49
2:B:40:ASN:ND2	2:B:76:ASN:HB2	2.28	0.49
3:C:196:ILE:HG22	3:C:197:PRO:HD2	1.93	0.49
5:E:36:HIS:NE2	5:E:85:GLY:HA3	2.28	0.49
5:E:47:PHE:CE2	5:E:52:LEU:HD11	2.47	0.49
6:F:103:LEU:HD23	6:F:104:THR:HG23	1.93	0.49
9:I:84:ASN:ND2	9:I:86:SER:OG	2.45	0.49
18:R:4:VAL:HG22	34:1:1466:G:H5''	1.95	0.49
18:R:62:GLN:O	33:g:280:LYS:NZ	2.35	0.49
25:Y:20:ARG:HB3	25:Y:76:TYR:CE1	2.48	0.49
31:e:34:ARG:NH2	34:1:641:A:OP2	2.44	0.49
34:1:71:G:C2'	34:1:79:A:H61	2.26	0.49
10:J:114:VAL:HG12	10:J:120:ALA:HB2	1.94	0.49
20:T:45:LEU:HD13	20:T:48:TYR:OH	2.13	0.49
27:a:27:ALA:O	27:a:28:ARG:HG2	2.12	0.49
33:g:190:GLY:O	33:g:217:MET:HE1	2.13	0.49
34:1:1364:U:H5	34:1:1375:G:H21	1.61	0.49
1:A:76:VAL:HG12	1:A:87:VAL:HG13	1.95	0.48
3:C:230:THR:HG23	3:C:236:PHE:CG	2.48	0.48
5:E:162:ILE:HD13	5:E:169:ILE:HG23	1.94	0.48
17:Q:43:GLU:HB2	17:Q:44:PRO:CD	2.43	0.48
21:U:63:ILE:HD12	30:d:52:PHE:CE1	2.48	0.48
23:W:68:ARG:NH1	23:W:68:ARG:O	2.32	0.48
6:F:34:SER:O	6:F:35:LEU:HD12	2.13	0.48
14:N:15:ALA:C	14:N:16:LEU:HD12	2.39	0.48
16:P:68:PRO:HB2	16:P:69:PRO:HD3	1.95	0.48
23:W:82:GLN:NE2	34:1:804:U:OP1	2.35	0.48
28:b:15:GLU:OE1	28:b:15:GLU:N	2.46	0.48
34:1:1521:C:O2'	34:1:1522:A:OP2	2.30	0.48
34:1:1538:C:H42	34:1:1594:A:N6	2.11	0.48
34:1:1717:C:H2'	34:1:1718:G:O4'	2.13	0.48
7:G:184:VAL:HG13	34:1:315:C:OP2	2.12	0.48
11:K:3:MET:SD	11:K:47:LYS:NZ	2.86	0.48
1:A:176:TRP:HE1	1:A:195:TRP:CD1	2.31	0.48
3:C:84:PHE:CE2	3:C:264:SER:HA	2.48	0.48
5:E:162:ILE:O	5:E:162:ILE:HG23	2.14	0.48
8:H:50:GLU:OE2	8:H:59:ALA:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:64:VAL:HB	8:H:96:ALA:HA	1.95	0.48
13:M:53:ALA:HB2	13:M:85:LEU:HD12	1.95	0.48
23:W:75:ILE:HD11	23:W:93:LEU:HD11	1.94	0.48
34:1:36:U:O2'	34:1:37:C:O5'	2.22	0.48
2:B:174:ARG:NH2	2:B:175:GLU:OE2	2.46	0.48
9:I:6:ASP:HB3	9:I:28:GLU:OE1	2.13	0.48
11:K:25:LYS:O	11:K:27:VAL:HG13	2.14	0.48
18:R:83:ASN:OD1	18:R:83:ASN:N	2.43	0.48
31:e:39:ASN:ND2	34:1:551:U:OP1	2.45	0.48
34:1:1797:U:N3	34:1:1798:C:N4	2.60	0.48
2:B:38:MET:SD	2:B:38:MET:N	2.87	0.48
7:G:70:HIS:O	7:G:98:ARG:NH1	2.47	0.48
10:J:118:GLY:C	10:J:119:LEU:HD22	2.39	0.48
18:R:85:VAL:O	18:R:88:VAL:HG23	2.13	0.48
21:U:31:SER:O	21:U:35:VAL:HG12	2.14	0.48
21:U:72:GLU:CD	34:1:1490:G:H21	2.21	0.48
23:W:25:VAL:HG12	23:W:26:LEU:N	2.28	0.48
26:Z:58:LEU:HD13	26:Z:77:LEU:HD22	1.96	0.48
28:b:53:VAL:HA	28:b:64:CYS:HB2	1.95	0.48
34:1:39:A:N6	34:1:515:G:H21	2.09	0.48
34:1:327:G:O2'	34:1:328:U:OP2	2.32	0.48
34:1:909:G:N2	34:1:910:G:N3	2.60	0.48
34:1:1351:G:N2	34:1:1378:A:O3'	2.46	0.48
2:B:167:LYS:NZ	2:B:170:GLU:OE1	2.27	0.48
8:H:134:VAL:HG22	8:H:173:PHE:CD2	2.47	0.48
16:P:111:MET:SD	19:S:117:ILE:HG23	2.53	0.48
19:S:38:ARG:HH21	20:T:45:LEU:HD11	1.77	0.48
31:e:31:ARG:NH2	34:1:526:A:O3'	2.45	0.48
34:1:898:U:H2'	34:1:899:U:O4'	2.14	0.48
3:C:60:TRP:HZ2	3:C:93:ILE:HG13	1.77	0.48
5:E:122:LYS:NZ	5:E:143:ASP:OD2	2.46	0.48
8:H:148:LEU:O	8:H:148:LEU:HD23	2.13	0.48
34:1:1200:A:C2	34:1:1357:A:N6	2.82	0.48
3:C:131:GLY:HA3	3:C:137:VAL:HA	1.96	0.48
3:C:132:ASP:OD1	3:C:133:TYR:N	2.47	0.48
3:C:241:PHE:HA	3:C:244:ILE:HG22	1.96	0.48
6:F:85:LYS:NZ	34:1:1591:C:OP1	2.36	0.48
6:F:89:THR:O	6:F:93:VAL:HG23	2.14	0.48
15:O:90:ILE:HD12	15:O:91:THR:N	2.29	0.48
2:B:75:GLN:OE1	2:B:75:GLN:N	2.47	0.48
3:C:68:ARG:HD2	3:C:276:THR:HB	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:184:VAL:HG22	34:1:315:C:OP2	2.13	0.48
9:I:182:CYS:O	34:1:305:U:C4	2.67	0.48
17:Q:142:GLN:NE2	34:1:1643:U:O2	2.46	0.48
33:g:87:LEU:HD23	33:g:111:VAL:CG2	2.43	0.48
34:1:14:C:O2	34:1:1198:G:C2	2.67	0.48
34:1:124:U:C4	34:1:125:C:N4	2.81	0.48
34:1:824:C:H2'	34:1:825:A:O4'	2.12	0.48
34:1:956:G:O2'	34:1:972:A:N1	2.35	0.48
34:1:1543:U:H2'	34:1:1544:C:O4'	2.14	0.48
1:A:42:LYS:HD3	1:A:48:ILE:HD11	1.95	0.47
7:G:92:ARG:HH22	34:1:441:C:C2'	2.27	0.47
9:I:67:TRP:CD1	9:I:70:GLU:H	2.32	0.47
9:I:83:TYR:CE2	9:I:85:ALA:HB2	2.49	0.47
9:I:97:VAL:HB	34:1:377:G:O3'	2.14	0.47
31:e:43:VAL:HG11	34:1:550:C:O2'	2.14	0.47
33:g:68:ASP:OD1	33:g:69:VAL:N	2.47	0.47
34:1:344:U:C4	34:1:345:U:C4	3.02	0.47
2:B:158:HIS:O	2:B:158:HIS:CG	2.67	0.47
2:B:176:VAL:HG23	2:B:184:VAL:HG11	1.95	0.47
3:C:210:PRO:O	3:C:214:LEU:HD23	2.15	0.47
7:G:69:THR:HG21	7:G:73:VAL:HG11	1.97	0.47
15:O:78:ALA:HA	15:O:81:VAL:HG12	1.97	0.47
27:a:33:ASP:N	27:a:33:ASP:OD1	2.47	0.47
34:1:468:A:H2'	34:1:469:A:O4'	2.13	0.47
34:1:993:G:OP2	34:1:1132:C:O2'	2.31	0.47
34:1:1673:U:H2'	34:1:1674:G:O4'	2.14	0.47
6:F:126:THR:HG21	6:F:137:GLN:H	1.79	0.47
8:H:20:GLU:CG	8:H:48:ALA:HB3	2.44	0.47
8:H:76:GLN:HB3	8:H:135:PHE:CE1	2.49	0.47
8:H:79:LEU:O	8:H:83:LEU:HG	2.14	0.47
12:L:122:ILE:HG22	12:L:123:GLY:N	2.30	0.47
23:W:110:ILE:H	23:W:110:ILE:HD12	1.80	0.47
26:Z:104:ARG:NH1	34:1:1594:A:N7	2.62	0.47
34:1:64:A:N1	34:1:83:A:N7	2.63	0.47
13:M:94:ILE:HG22	13:M:95:ASP:O	2.14	0.47
15:O:27:VAL:N	15:O:91:THR:OG1	2.47	0.47
21:U:28:ASN:OD1	21:U:28:ASN:N	2.47	0.47
27:a:84:VAL:O	27:a:84:VAL:HG12	2.14	0.47
34:1:1202:U:H1'	34:1:1358:U:H4'	1.95	0.47
34:1:1286:G:H3'	34:1:1287:A:H5''	1.97	0.47
34:1:1474:A:H2'	34:1:1475:G:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ARG:HA	1:A:88:LEU:HD12	1.96	0.47
1:A:195:TRP:CD1	1:A:197:VAL:H	2.33	0.47
3:C:65:LYS:CG	3:C:273:LEU:HD22	2.44	0.47
9:I:66:SER:OG	34:1:221:A:O4'	2.23	0.47
10:J:78:LEU:HD21	10:J:92:MET:HA	1.96	0.47
15:O:70:SER:CA	15:O:71:PRO:CG	2.86	0.47
23:W:76:SER:HB3	34:1:1159:G:OP1	2.14	0.47
27:a:51:ARG:O	27:a:55:GLU:HB2	2.14	0.47
34:1:455:A:H1'	34:1:1735:A:C2	2.49	0.47
34:1:1226:G:N1	34:1:1639:G:OP2	2.47	0.47
2:B:146:ARG:NE	2:B:146:ARG:HA	2.29	0.47
7:G:48:TYR:CD1	7:G:116:LYS:O	2.67	0.47
18:R:94:GLU:HG2	18:R:95:ILE:HD12	1.97	0.47
20:T:39:LEU:HD13	20:T:43:LYS:H	1.79	0.47
34:1:11:A:C2	34:1:1356:G:N3	2.83	0.47
2:B:98:THR:HG1	2:B:99:ASN:H	1.63	0.47
7:G:13:GLN:OE1	34:1:166:A:H1'	2.14	0.47
9:I:178:ARG:NH1	34:1:380:G:O6	2.43	0.47
15:O:35:ALA:HB2	15:O:112:ALA:HB3	1.96	0.47
15:O:52:THR:HG21	34:1:952:G:H21	1.80	0.47
21:U:66:ARG:O	21:U:67:LYS:HB2	2.15	0.47
33:g:228:TYR:OH	33:g:261:LEU:O	2.32	0.47
34:1:113:G:H4'	34:1:114:G:OP2	2.15	0.47
34:1:470:G:H2'	34:1:471:G:O4'	2.14	0.47
34:1:511:U:O2'	34:1:576:A:N1	2.36	0.47
34:1:522:A:N6	34:1:644:G:OP1	2.48	0.47
34:1:824:C:C4	34:1:825:A:C5	3.03	0.47
34:1:1267:C:O2	34:1:1516:G:N2	2.47	0.47
34:1:1338:G:C5	34:1:1490:G:C2	3.03	0.47
3:C:124:PHE:N	3:C:144:SER:O	2.37	0.47
3:C:215:MET:HE3	3:C:215:MET:O	2.15	0.47
4:D:96:LEU:HD21	4:D:198:ILE:O	2.14	0.47
5:E:151:ASP:OD1	7:G:212:LEU:HD21	2.15	0.47
9:I:174:CYS:HB3	9:I:188:TYR:CE2	2.50	0.47
17:Q:121:VAL:HG13	34:1:1474:A:H5''	1.95	0.47
23:W:109:GLY:O	23:W:111:MET:HG3	2.15	0.47
25:Y:41:ARG:NH2	25:Y:53:ASP:O	2.48	0.47
25:Y:108:LYS:HB3	34:1:53:C:O3'	2.15	0.47
34:1:173:A:HO2'	34:1:174:C:H6	1.62	0.47
34:1:1659:U:OP2	34:1:1660:C:N4	2.48	0.47
15:O:130:GLU:OE1	15:O:130:GLU:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:440:G:H5''	34:1:1798:C:O2	2.14	0.47
34:1:678:U:C2	34:1:1027:A:N6	2.83	0.47
34:1:690:G:O6	34:1:741:C:O2'	2.31	0.47
34:1:1686:G:H2'	34:1:1687:C:C6	2.50	0.47
2:B:59:SER:O	2:B:63:LYS:HG2	2.15	0.47
3:C:205:VAL:O	3:C:205:VAL:CG2	2.63	0.47
3:C:255:LEU:HD23	22:V:23:ILE:HD11	1.97	0.47
7:G:50:VAL:CG1	7:G:111:LEU:HD22	2.37	0.47
33:g:164:ILE:HD11	33:g:185:LYS:NZ	2.30	0.47
34:1:343:A:C5	34:1:344:U:C4	3.03	0.47
4:D:9:ARG:HA	4:D:12:VAL:HG12	1.96	0.46
7:G:11:GLY:HA2	34:1:166:A:O2'	2.15	0.46
27:a:15:ARG:NH2	34:1:993:G:C5	2.83	0.46
34:1:1171:G:N2	34:1:1188:A:OP2	2.48	0.46
6:F:74:ASN:HB3	34:1:1675:A:O3'	2.15	0.46
8:H:72:PHE:O	8:H:76:GLN:HB2	2.16	0.46
9:I:38:ILE:O	9:I:38:ILE:HG12	2.14	0.46
19:S:7:GLU:OE1	26:Z:49:LEU:HD21	2.16	0.46
22:V:60:ARG:O	22:V:63:GLY:N	2.44	0.46
23:W:36:ARG:O	23:W:40:VAL:HG23	2.16	0.46
26:Z:62:VAL:N	26:Z:63:PRO:CD	2.78	0.46
26:Z:92:LEU:HD22	26:Z:99:LEU:CD2	2.45	0.46
27:a:51:ARG:HA	27:a:51:ARG:CZ	2.45	0.46
34:1:122:G:C5	34:1:123:G:N7	2.82	0.46
1:A:8:LEU:HD13	1:A:59:LEU:HD21	1.97	0.46
1:A:37:TYR:CE1	1:A:53:ARG:HB3	2.50	0.46
5:E:56:LEU:HD12	5:E:57:THR:HB	1.97	0.46
5:E:56:LEU:HD12	5:E:57:THR:N	2.30	0.46
5:E:103:TYR:CE2	5:E:184:ILE:HG22	2.50	0.46
13:M:113:ASP:OD1	13:M:113:ASP:N	2.46	0.46
15:O:138:ASP:HB2	34:1:984:C:H1'	1.97	0.46
18:R:98:VAL:HG11	18:R:120:THR:HG22	1.97	0.46
34:1:546:G:C4'	34:1:547:G:OP2	2.64	0.46
34:1:1109:C:H2'	34:1:1110:G:O4'	2.16	0.46
34:1:1199:A:H2	34:1:1355:C:H41	1.62	0.46
2:B:181:LEU:O	2:B:184:VAL:HG22	2.15	0.46
4:D:25:LEU:HD22	4:D:29:LEU:HD11	1.97	0.46
7:G:66:GLY:HA3	34:1:1790:A:H1'	1.98	0.46
7:G:188:LYS:O	7:G:191:ARG:HG2	2.15	0.46
9:I:107:THR:HA	9:I:110:ARG:HG2	1.97	0.46
10:J:134:HIS:HA	10:J:162:ARG:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:101:THR:O	16:P:102:PHE:C	2.58	0.46
25:Y:60:PHE:O	25:Y:61:ARG:NE	2.49	0.46
32:f:121:CYS:HA	32:f:132:MET:HE3	1.98	0.46
34:1:883:U:H2'	34:1:884:C:O4'	2.15	0.46
1:A:107:THR:O	1:A:116:PHE:HA	2.15	0.46
3:C:65:LYS:HG2	3:C:273:LEU:HD22	1.97	0.46
3:C:73:MET:N	3:C:73:MET:SD	2.89	0.46
5:E:255:ARG:NH2	34:1:819:G:HO2'	2.07	0.46
7:G:8:PRO:HA	34:1:166:A:O3'	2.16	0.46
9:I:107:THR:HG22	9:I:111:GLN:NE2	2.31	0.46
10:J:29:LEU:O	10:J:29:LEU:HD12	2.16	0.46
12:L:121:GLN:C	12:L:122:ILE:HD12	2.40	0.46
12:L:132:ARG:O	12:L:134:LEU:HD13	2.15	0.46
14:N:141:TYR:HD2	14:N:145:THR:HG1	1.62	0.46
19:S:27:ALA:HB1	19:S:41:ALA:HB1	1.97	0.46
23:W:15:ASN:HD21	23:W:71:LYS:HA	1.81	0.46
33:g:87:LEU:HD13	33:g:104:HIS:NE2	2.31	0.46
34:1:551:U:H2'	34:1:552:G:C8	2.51	0.46
34:1:1445:U:O4	34:1:1446:A:N6	2.49	0.46
2:B:226:GLY:O	2:B:230:GLU:HG2	2.16	0.46
5:E:138:HIS:ND1	5:E:148:ARG:HB3	2.31	0.46
9:I:64:ASN:OD1	9:I:185:ALA:O	2.33	0.46
10:J:131:ARG:NH1	34:1:522:A:O3'	2.45	0.46
18:R:73:LEU:HD23	18:R:78:ARG:HH12	1.80	0.46
20:T:60:THR:HG22	20:T:75:MET:HE1	1.98	0.46
24:X:36:LEU:HD22	34:1:407:G:C5	2.51	0.46
34:1:216:C:O2'	34:1:217:A:C5'	2.64	0.46
34:1:548:C:OP1	34:1:548:C:H4'	2.15	0.46
34:1:959:G:H2'	34:1:960:U:C2	2.50	0.46
34:1:1111:U:C4	34:1:1112:U:C4	3.04	0.46
34:1:1796:G:H2'	34:1:1797:U:N1	2.30	0.46
2:B:135:LEU:C	2:B:135:LEU:HD12	2.41	0.46
2:B:203:SER:O	34:1:1121:G:O2'	2.33	0.46
8:H:115:LYS:HG2	8:H:116:ARG:H	1.79	0.46
10:J:14:VAL:HG22	10:J:44:TRP:HB3	1.96	0.46
16:P:64:LYS:NZ	16:P:92:SER:OG	2.29	0.46
16:P:90:VAL:HG21	16:P:112:ILE:HD11	1.97	0.46
16:P:114:HIS:NE2	19:S:117:ILE:HD11	2.31	0.46
25:Y:89:HIS:HB2	34:1:574:A:H4'	1.97	0.46
27:a:70:LYS:HD2	27:a:70:LYS:N	2.31	0.46
34:1:1365:G:O6	34:1:1375:G:N2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:31:ARG:HH12	7:G:68:LEU:HD22	1.80	0.46
11:K:23:ALA:HB2	11:K:45:VAL:HG11	1.97	0.46
14:N:95:ALA:HB2	14:N:118:ILE:HG21	1.98	0.46
14:N:141:TYR:CE2	14:N:146:ALA:HB2	2.47	0.46
24:X:125:VAL:O	24:X:128:VAL:N	2.49	0.46
34:1:1104:G:C6	34:1:1129:G:C6	3.04	0.46
34:1:1109:C:C4	34:1:1110:G:C5	3.03	0.46
2:B:110:MET:HE1	2:B:213:ARG:HD2	1.97	0.46
2:B:142:PHE:O	2:B:207:LEU:HA	2.16	0.46
5:E:72:ILE:HG22	5:E:73:ASP:HB2	1.96	0.46
6:F:51:HIS:ND1	17:Q:47:LEU:HD21	2.30	0.46
6:F:77:MET:HE3	6:F:84:GLY:H	1.81	0.46
9:I:26:LYS:HD2	9:I:29:LEU:HD21	1.97	0.46
9:I:155:ASN:O	9:I:156:ALA:C	2.59	0.46
10:J:50:LEU:O	10:J:54:ARG:HG2	2.16	0.46
10:J:112:THR:O	10:J:116:LYS:HG2	2.16	0.46
10:J:131:ARG:HH22	34:1:522:A:H4'	1.80	0.46
11:K:55:ARG:NH2	34:1:1278:A:OP1	2.48	0.46
12:L:36:TYR:OH	34:1:294:U:O5'	2.32	0.46
18:R:95:ILE:HG21	18:R:122:PRO:C	2.41	0.46
21:U:22:ILE:CD1	21:U:91:LEU:HD12	2.45	0.46
23:W:74:VAL:CG1	23:W:75:ILE:N	2.79	0.46
34:1:122:G:C2	34:1:343:A:C2	3.03	0.46
34:1:370:G:H4'	34:1:371:A:OP1	2.15	0.46
34:1:593:C:O2'	34:1:594:A:O5'	2.30	0.46
34:1:1211:G:H2'	34:1:1212:G:C8	2.50	0.46
2:B:68:GLU:OE1	2:B:68:GLU:N	2.46	0.46
5:E:47:PHE:CZ	5:E:52:LEU:HD11	2.51	0.46
7:G:143:LYS:NZ	34:1:146:G:OP1	2.49	0.46
20:T:14:PHE:CD1	20:T:138:VAL:HG21	2.51	0.46
23:W:39:THR:O	23:W:43:LYS:HG2	2.16	0.46
23:W:56:HIS:HE2	34:1:919:A:P	2.38	0.46
25:Y:121:ALA:O	25:Y:125:VAL:HG23	2.15	0.46
34:1:845:G:C6	34:1:846:G:N1	2.84	0.46
34:1:870:A:N3	34:1:916:A:N6	2.64	0.46
1:A:102:ARG:CZ	1:A:104:THR:HA	2.46	0.45
4:D:16:ILE:HG21	30:d:22:ARG:NH1	2.31	0.45
7:G:88:ARG:NH2	34:1:452:G:OP1	2.50	0.45
7:G:217:MET:HE3	7:G:221:LYS:NZ	2.32	0.45
9:I:62:VAL:HG12	9:I:77:ARG:HA	1.98	0.45
15:O:61:LYS:C	15:O:62:VAL:HG23	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:72:TYR:CZ	15:O:76:LEU:HD21	2.51	0.45
15:O:94:HIS:C	15:O:95:ILE:HD13	2.41	0.45
27:a:82:LYS:O	27:a:85:ARG:NH2	2.49	0.45
34:1:830:A:C5	34:1:845:G:C2	3.04	0.45
34:1:1337:C:N3	34:1:1490:G:N1	2.55	0.45
34:1:1377:U:C4	34:1:1380:C:OP1	2.69	0.45
34:1:1507:G:O2'	34:1:1508:A:C5'	2.64	0.45
5:E:213:ALA:HB2	5:E:242:LYS:NZ	2.30	0.45
7:G:53:SER:HB3	34:1:165:G:H4'	1.98	0.45
7:G:92:ARG:NH2	34:1:441:C:O2'	2.50	0.45
9:I:38:ILE:HD11	9:I:79:ILE:C	2.41	0.45
9:I:43:ILE:HG12	9:I:57:ALA:CB	2.47	0.45
9:I:45:THR:HB	34:1:307:G:O2'	2.15	0.45
9:I:172:LEU:HD12	9:I:190:LEU:HD12	1.97	0.45
9:I:173:ALA:HA	9:I:188:TYR:O	2.16	0.45
19:S:136:THR:O	19:S:136:THR:CG2	2.64	0.45
20:T:84:ARG:NH2	34:1:1605:G:OP1	2.48	0.45
21:U:66:ARG:HG3	21:U:68:THR:HG22	1.98	0.45
24:X:128:VAL:HG13	24:X:138:LYS:HE2	1.98	0.45
34:1:563:G:O6	34:1:586:G:H2'	2.16	0.45
34:1:628:A:H3'	34:1:629:A:H5''	1.99	0.45
34:1:815:U:O4	34:1:816:A:N6	2.50	0.45
2:B:171:ILE:HG21	2:B:197:ILE:HG12	1.98	0.45
2:B:176:VAL:HG23	2:B:184:VAL:CG1	2.47	0.45
3:C:108:LYS:HD2	3:C:233:LEU:HD23	1.97	0.45
4:D:188:ILE:HG23	4:D:188:ILE:O	2.16	0.45
5:E:32:SER:OG	5:E:79:ASP:OD2	2.33	0.45
5:E:130:THR:O	5:E:137:PRO:HA	2.17	0.45
7:G:189:ARG:HD3	34:1:330:G:P	2.57	0.45
8:H:106:ARG:HH12	34:1:802:A:H61	1.64	0.45
12:L:84:ARG:O	12:L:84:ARG:HG3	2.17	0.45
16:P:60:LEU:CD2	16:P:89:MET:HG3	2.47	0.45
25:Y:14:THR:HG23	25:Y:14:THR:O	2.17	0.45
34:1:523:A:C6	34:1:524:U:H1'	2.51	0.45
34:1:1350:U:H3	34:1:1379:A:N6	2.10	0.45
1:A:169:HIS:O	1:A:203:PHE:CE1	2.69	0.45
1:A:181:GLU:O	1:A:185:MET:HE2	2.16	0.45
2:B:176:VAL:O	2:B:176:VAL:HG22	2.16	0.45
2:B:180:ASP:OD1	2:B:183:GLU:N	2.38	0.45
8:H:53:VAL:O	8:H:53:VAL:CG2	2.64	0.45
24:X:33:GLY:O	24:X:37:LYS:NZ	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:114:MET:HG2	25:Y:126:GLY:HA3	1.98	0.45
34:1:70:G:C2	34:1:80:G:C6	3.05	0.45
34:1:1352:G:C6	34:1:1360:U:H1'	2.51	0.45
34:1:1736:G:H2'	34:1:1737:G:C8	2.51	0.45
1:A:170:SER:O	1:A:174:MET:HE2	2.16	0.45
4:D:131:ALA:HB1	4:D:188:ILE:HD11	1.98	0.45
9:I:107:THR:O	9:I:111:GLN:NE2	2.48	0.45
17:Q:72:VAL:HG12	17:Q:74:GLY:H	1.81	0.45
18:R:5:ARG:NE	34:1:1454:A:OP1	2.50	0.45
19:S:111:LEU:O	19:S:115:LYS:HG3	2.14	0.45
34:1:13:C:H2'	34:1:14:C:H5'	1.97	0.45
34:1:113:G:H3'	34:1:114:G:H5'	1.98	0.45
1:A:63:ARG:NH2	22:V:38:GLU:O	2.48	0.45
2:B:136:ARG:HB2	2:B:218:LEU:HD22	1.98	0.45
4:D:68:GLU:OE2	11:K:71:LEU:N	2.26	0.45
9:I:107:THR:N	9:I:108:PRO:CD	2.79	0.45
9:I:129:LEU:O	9:I:130:THR:OG1	2.30	0.45
9:I:132:GLU:O	9:I:133:GLU:HG2	2.17	0.45
11:K:15:LEU:O	11:K:19:GLY:N	2.41	0.45
34:1:293:C:H2'	34:1:295:C:C6	2.51	0.45
1:A:80:ARG:HE	1:A:126:ASP:CB	2.29	0.45
2:B:36:PRO:O	2:B:38:MET:N	2.46	0.45
2:B:97:LEU:HD23	2:B:97:LEU:C	2.41	0.45
4:D:170:THR:HG23	4:D:185:LYS:HE3	1.98	0.45
9:I:24:LYS:HG3	9:I:24:LYS:O	2.16	0.45
10:J:154:GLN:CG	10:J:154:GLN:O	2.65	0.45
11:K:8:ARG:O	11:K:11:ILE:HG22	2.17	0.45
16:P:127:LYS:O	34:1:1238:U:H4'	2.16	0.45
19:S:55:ARG:NH2	26:Z:82:SER:OG	2.41	0.45
25:Y:63:HIS:ND1	25:Y:68:LYS:O	2.45	0.45
31:e:19:VAL:HG23	34:1:634:A:O2'	2.17	0.45
34:1:1661:A:O2'	34:1:1662:U:O5'	2.35	0.45
1:A:147:LEU:CD2	1:A:171:VAL:HG22	2.42	0.45
6:F:55:ARG:NH2	17:Q:123:ASP:O	2.50	0.45
6:F:103:LEU:HD13	6:F:178:ILE:HD13	1.99	0.45
10:J:122:SER:O	10:J:122:SER:OG	2.35	0.45
12:L:38:LYS:NZ	12:L:66:VAL:O	2.49	0.45
15:O:16:SER:OG	15:O:17:LEU:N	2.50	0.45
15:O:86:LYS:NZ	15:O:122:SER:OG	2.49	0.45
15:O:113:GLN:OE1	27:a:45:VAL:HG13	2.17	0.45
16:P:116:LEU:HD23	16:P:119:PHE:HE2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:130:ARG:HE	16:P:130:ARG:C	2.24	0.45
18:R:5:ARG:HH11	18:R:9:VAL:HG11	1.80	0.45
23:W:106:THR:O	34:1:862:A:H1'	2.17	0.45
24:X:114:ASP:HB2	34:1:619:A:N1	2.32	0.45
24:X:128:VAL:HG13	24:X:138:LYS:CE	2.47	0.45
34:1:149:A:N6	34:1:168:C:O2	2.33	0.45
34:1:678:U:C2	34:1:679:A:C8	3.05	0.45
34:1:1357:A:H5'	34:1:1358:U:OP2	2.17	0.45
34:1:1729:U:H2'	34:1:1730:U:C6	2.51	0.45
5:E:19:MET:HE3	5:E:108:ARG:HD3	1.99	0.45
5:E:121:TYR:HB3	5:E:161:GLN:HE21	1.82	0.45
7:G:13:GLN:CG	34:1:153:G:H2'	2.47	0.45
9:I:79:ILE:HG22	9:I:80:ASP:OD1	2.17	0.45
25:Y:89:HIS:CD2	34:1:493:A:H4'	2.51	0.45
33:g:61:GLY:HA2	34:1:1398:G:C2	2.52	0.45
33:g:186:THR:HG22	33:g:187:ASN:N	2.31	0.45
34:1:348:A:N6	34:1:349:A:N1	2.64	0.45
5:E:132:GLY:O	34:1:297:A:H4'	2.16	0.45
5:E:161:GLN:HB3	5:E:170:ILE:O	2.17	0.45
9:I:11:ARG:NH1	9:I:15:GLY:O	2.50	0.45
10:J:70:ARG:CZ	10:J:94:LEU:HD12	2.46	0.45
18:R:76:GLU:O	18:R:80:ARG:NH1	2.50	0.45
34:1:317:C:H2'	34:1:318:A:C8	2.52	0.45
1:A:27:GLY:N	1:A:150:THR:OG1	2.49	0.44
1:A:75:SER:HA	1:A:97:THR:HB	1.99	0.44
3:C:251:LEU:HD13	23:W:68:ARG:HD2	1.99	0.44
7:G:174:PRO:CG	7:G:174:PRO:CA	2.82	0.44
8:H:12:ASN:C	8:H:12:ASN:OD1	2.61	0.44
8:H:66:VAL:HG11	34:1:913:A:O2'	2.16	0.44
9:I:43:ILE:HG12	9:I:57:ALA:HB2	1.98	0.44
9:I:65:PHE:HA	9:I:187:GLY:O	2.17	0.44
9:I:86:SER:O	34:1:389:A:H1'	2.16	0.44
9:I:87:ASN:HB2	34:1:389:A:H1'	2.00	0.44
16:P:57:LEU:HD21	16:P:86:LEU:HD11	2.00	0.44
20:T:84:ARG:NH1	34:1:1537:A:O3'	2.50	0.44
28:b:56:CYS:HB3	28:b:59:CYS:SG	2.57	0.44
34:1:463:C:C2'	34:1:466:G:O6	2.65	0.44
34:1:470:G:C2'	34:1:471:G:O4'	2.64	0.44
34:1:563:G:N7	34:1:586:G:C2	2.85	0.44
34:1:1464:C:O2	34:1:1464:C:O4'	2.35	0.44
1:A:203:PHE:O	1:A:204:TYR:CB	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:154:ILE:HD13	5:E:154:ILE:N	2.33	0.44
7:G:188:LYS:HG3	7:G:189:ARG:N	2.31	0.44
9:I:42:ARG:HA	9:I:42:ARG:NE	2.33	0.44
9:I:97:VAL:HG22	9:I:100:CYS:HB2	2.00	0.44
15:O:35:ALA:HB2	15:O:112:ALA:CB	2.47	0.44
19:S:47:LYS:HG3	19:S:79:ILE:HD11	1.99	0.44
25:Y:32:LYS:HA	34:1:582:U:H4'	1.98	0.44
25:Y:117:VAL:CG2	25:Y:122:LYS:HA	2.48	0.44
34:1:96:C:H5	34:1:434:G:H22	1.66	0.44
34:1:511:U:O2'	34:1:576:A:C6	2.70	0.44
34:1:929:G:C2'	34:1:930:C:O5'	2.65	0.44
34:1:1664:A:O2'	34:1:1665:G:P	2.75	0.44
34:1:1739:C:C5	34:1:1740:C:C4	3.05	0.44
34:1:1741:U:C5	34:1:1742:C:C5	3.05	0.44
3:C:168:GLY:N	3:C:179:THR:O	2.40	0.44
8:H:16:PRO:HA	8:H:20:GLU:OE1	2.17	0.44
10:J:39:ASN:N	10:J:42:GLU:OE2	2.45	0.44
10:J:78:LEU:HD21	10:J:92:MET:CA	2.48	0.44
16:P:122:THR:OG1	34:1:1622:U:O2	2.28	0.44
17:Q:129:SER:O	34:1:1479:G:O2'	2.36	0.44
22:V:74:LYS:O	22:V:77:GLY:N	2.50	0.44
24:X:36:LEU:HD22	34:1:407:G:C6	2.53	0.44
33:g:87:LEU:HD21	33:g:122:SER:HB3	1.98	0.44
34:1:86:C:H2'	34:1:87:U:O4'	2.17	0.44
34:1:458:A:H2'	34:1:459:C:C6	2.52	0.44
34:1:463:C:H5'	34:1:464:A:OP1	2.17	0.44
34:1:1189:A:C2	34:1:1190:A:C4	3.05	0.44
2:B:114:VAL:O	2:B:114:VAL:CG1	2.63	0.44
7:G:67:VAL:HG23	34:1:1791:A:H4'	1.99	0.44
7:G:187:HIS:CG	34:1:315:C:C5	3.05	0.44
9:I:202:ILE:O	9:I:206:LYS:HG2	2.17	0.44
10:J:18:ARG:O	10:J:24:ARG:NH1	2.46	0.44
14:N:33:VAL:HG21	14:N:67:THR:OG1	2.17	0.44
26:Z:48:VAL:HG22	26:Z:80:ARG:NH1	2.32	0.44
34:1:65:C:O2'	34:1:67:C:OP1	2.29	0.44
34:1:171:A:N7	34:1:173:A:C6	2.85	0.44
34:1:335:G:C2	34:1:336:A:N7	2.86	0.44
34:1:1288:U:P	34:1:1312:G:H22	2.41	0.44
3:C:107:LEU:HB3	3:C:233:LEU:HD21	2.00	0.44
7:G:189:ARG:HD3	34:1:330:G:OP2	2.17	0.44
13:M:77:ILE:HD12	13:M:128:PHE:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:88:LEU:HB2	14:N:125:LEU:HD23	2.00	0.44
15:O:61:LYS:O	15:O:63:LYS:N	2.47	0.44
18:R:98:VAL:HG12	18:R:99:ASP:N	2.32	0.44
20:T:56:ARG:O	20:T:56:ARG:HD3	2.18	0.44
31:e:39:ASN:O	34:1:550:C:O2'	2.36	0.44
34:1:1156:U:O5'	34:1:1156:U:O2	2.36	0.44
34:1:1381:G:H3'	34:1:1382:A:H5''	1.98	0.44
34:1:1749:G:N2	34:1:1786:U:O2	2.50	0.44
1:A:211:GLU:OE2	18:R:84:TYR:CD2	2.71	0.44
9:I:57:ALA:CB	9:I:180:GLY:HA2	2.48	0.44
11:K:74:GLU:O	11:K:78:TYR:N	2.50	0.44
20:T:113:VAL:HG13	20:T:121:ARG:HB2	1.99	0.44
25:Y:54:VAL:HG22	25:Y:54:VAL:O	2.17	0.44
25:Y:64:PHE:CD1	25:Y:64:PHE:N	2.84	0.44
25:Y:108:LYS:NZ	34:1:507:G:OP1	2.33	0.44
25:Y:109:GLU:C	25:Y:113:ARG:HE	2.26	0.44
34:1:153:G:C2	34:1:166:A:C5	3.06	0.44
34:1:155:G:H2'	34:1:156:G:C8	2.51	0.44
34:1:887:U:H2'	34:1:887:U:O2	2.17	0.44
34:1:1270:G:H2'	34:1:1271:C:O4'	2.18	0.44
1:A:7:VAL:HG21	22:V:42:VAL:CA	2.47	0.44
20:T:36:THR:O	20:T:36:THR:HG22	2.17	0.44
21:U:58:THR:HG22	21:U:59:LYS:N	2.32	0.44
25:Y:74:MET:SD	25:Y:75:ILE:N	2.91	0.44
34:1:149:A:N7	34:1:168:C:O2	2.50	0.44
34:1:832:G:N1	34:1:842:C:N3	2.60	0.44
34:1:1278:A:N6	34:1:1318:G:O6	2.51	0.44
2:B:105:LEU:HD13	2:B:213:ARG:HA	2.00	0.44
6:F:51:HIS:HE1	17:Q:78:VAL:HG22	1.82	0.44
7:G:92:ARG:O	34:1:454:U:H5'	2.18	0.44
7:G:111:LEU:O	7:G:112:VAL:HG23	2.17	0.44
8:H:154:ILE:HG22	8:H:155:LYS:N	2.33	0.44
21:U:64:THR:HG22	21:U:77:TRP:CE3	2.53	0.44
22:V:73:ALA:O	22:V:76:ASP:HB3	2.18	0.44
34:1:9:U:O2	34:1:11:A:C5	2.71	0.44
34:1:9:U:O2	34:1:11:A:C6	2.70	0.44
34:1:11:A:C4	34:1:1357:A:H1'	2.52	0.44
34:1:13:C:C5	34:1:14:C:C5	3.06	0.44
34:1:164:A:N6	34:1:165:G:C6	2.86	0.44
34:1:181:A:H1'	34:1:182:C:C4	2.52	0.44
34:1:479:C:H2'	34:1:480:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:LEU:HD13	1:A:59:LEU:CD2	2.48	0.44
1:A:38:ILE:HD12	1:A:48:ILE:O	2.18	0.44
2:B:40:ASN:ND2	2:B:74:LEU:O	2.51	0.44
13:M:122:ASP:N	13:M:122:ASP:OD1	2.51	0.44
15:O:132:VAL:O	15:O:132:VAL:CG2	2.65	0.44
16:P:130:ARG:NH1	34:1:1237:C:OP1	2.51	0.44
17:Q:10:VAL:HG12	17:Q:11:GLN:N	2.33	0.44
28:b:22:LYS:HA	34:1:921:G:H21	1.82	0.44
34:1:173:A:C6	34:1:174:C:N4	2.86	0.44
34:1:464:A:C2'	34:1:466:G:O6	2.66	0.44
34:1:496:C:O2	34:1:496:C:O4'	2.35	0.44
34:1:647:U:H2'	34:1:648:A:H8	1.83	0.44
34:1:830:A:OP2	34:1:846:G:N2	2.51	0.44
34:1:1338:G:C6	34:1:1339:U:C4	3.05	0.44
3:C:72:ASP:HB2	3:C:74:LYS:HG2	2.00	0.43
3:C:267:GLN:O	3:C:270:THR:OG1	2.34	0.43
4:D:134:CYS:HB2	4:D:188:ILE:HD13	1.99	0.43
7:G:12:CYS:SG	7:G:124:LEU:HD22	2.58	0.43
9:I:25:ARG:HA	34:1:448:A:H5''	2.00	0.43
13:M:35:ILE:HD11	13:M:61:TYR:OH	2.17	0.43
28:b:22:LYS:HA	34:1:921:G:N2	2.33	0.43
33:g:94:THR:O	33:g:94:THR:HG22	2.19	0.43
34:1:89:C:O2'	34:1:90:G:H5'	2.18	0.43
1:A:177:MET:N	1:A:177:MET:SD	2.91	0.43
1:A:203:PHE:O	1:A:204:TYR:HB3	2.17	0.43
2:B:178:THR:O	2:B:179:ASN:C	2.60	0.43
5:E:100:ARG:HG2	5:E:114:ILE:HD13	2.00	0.43
7:G:76:LEU:HD11	7:G:92:ARG:CD	2.47	0.43
10:J:3:VAL:HG23	10:J:4:ALA:N	2.31	0.43
10:J:32:ILE:HD11	10:J:39:ASN:O	2.18	0.43
11:K:72:THR:HG22	11:K:73:ASN:N	2.33	0.43
14:N:64:ARG:HH22	34:1:919:A:P	2.41	0.43
20:T:40:ALA:HB2	34:1:1540:G:OP1	2.17	0.43
24:X:77:ASN:OD1	24:X:77:ASN:C	2.61	0.43
33:g:7:LEU:HD11	33:g:9:GLY:O	2.18	0.43
34:1:500:A:H3'	34:1:501:C:H6	1.81	0.43
34:1:1088:U:H4'	34:1:1089:G:OP2	2.18	0.43
1:A:5:LEU:HA	1:A:8:LEU:HD12	2.00	0.43
2:B:123:ALA:HB2	2:B:165:ARG:HG3	2.00	0.43
3:C:230:THR:O	3:C:230:THR:CG2	2.66	0.43
5:E:42:LEU:HD23	5:E:43:PRO:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:129:ILE:HG13	5:E:138:HIS:O	2.18	0.43
9:I:57:ALA:HB3	9:I:180:GLY:HA2	2.00	0.43
14:N:3:ARG:NH1	34:1:923:G:OP1	2.48	0.43
14:N:70:LYS:HE2	34:1:1019:C:OP2	2.19	0.43
15:O:59:GLY:HA2	15:O:68:GLU:CD	2.43	0.43
20:T:30:VAL:HG23	20:T:34:VAL:HG23	2.00	0.43
24:X:17:ARG:NH1	34:1:659:G:OP2	2.51	0.43
27:a:40:VAL:HG23	27:a:40:VAL:O	2.18	0.43
34:1:63:U:H5''	34:1:64:A:OP2	2.18	0.43
34:1:1611:G:H2'	34:1:1612:G:O4'	2.18	0.43
34:1:1737:G:O6	34:1:1796:G:N1	2.52	0.43
1:A:106:GLY:O	1:A:110:ASN:OD1	2.36	0.43
2:B:97:LEU:HD21	2:B:232:HIS:CE1	2.53	0.43
5:E:92:ILE:O	5:E:93:GLU:C	2.62	0.43
5:E:95:THR:HA	25:Y:16:ARG:NH2	2.33	0.43
5:E:132:GLY:O	5:E:135:GLY:N	2.52	0.43
5:E:134:LYS:O	5:E:134:LYS:HG2	2.18	0.43
5:E:183:VAL:CG2	5:E:220:THR:HG21	2.47	0.43
5:E:252:ARG:HD2	5:E:252:ARG:O	2.18	0.43
22:V:66:ASP:OD2	22:V:66:ASP:C	2.61	0.43
24:X:40:PRO:O	24:X:41:PHE:HB2	2.19	0.43
26:Z:48:VAL:HA	26:Z:80:ARG:HB2	2.01	0.43
34:1:113:G:C2	34:1:293:C:N4	2.86	0.43
34:1:126:G:O2'	34:1:181:A:N1	2.51	0.43
34:1:149:A:C4	34:1:150:A:C8	3.07	0.43
34:1:437:G:N2	34:1:457:C:O2	2.50	0.43
34:1:447:A:O3'	34:1:448:A:H4'	2.19	0.43
34:1:559:G:C4	34:1:561:A:C8	3.06	0.43
34:1:1337:C:H2'	34:1:1338:G:H8	1.82	0.43
3:C:205:VAL:HG22	3:C:223:TYR:HA	2.00	0.43
7:G:114:VAL:HG12	7:G:115:LYS:HG3	1.99	0.43
8:H:133:LEU:HD13	8:H:173:PHE:HB3	2.01	0.43
8:H:148:LEU:HA	23:W:42:MET:SD	2.59	0.43
9:I:81:VAL:HG13	9:I:100:CYS:SG	2.59	0.43
10:J:137:VAL:HG21	10:J:147:PHE:CE2	2.54	0.43
15:O:117:ARG:HG3	27:a:52:ASP:OD2	2.18	0.43
20:T:60:THR:HA	20:T:75:MET:HE1	2.00	0.43
23:W:9:ASP:OD1	34:1:1093:A:O2'	2.36	0.43
33:g:31:ILE:HG13	33:g:45:LEU:HD21	2.00	0.43
33:g:167:SER:OG	33:g:177:TRP:NE1	2.49	0.43
34:1:153:G:H1	34:1:165:G:H1	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:316:G:H2'	34:1:317:C:C6	2.54	0.43
34:1:562:U:H2'	34:1:563:G:C8	2.53	0.43
34:1:844:U:O2'	34:1:845:G:O4'	2.28	0.43
1:A:141:ASN:ND2	3:C:87:PRO:HD3	2.34	0.43
2:B:127:VAL:HG11	2:B:176:VAL:HG11	1.99	0.43
2:B:181:LEU:HD23	2:B:181:LEU:N	2.33	0.43
9:I:175:ILE:HA	9:I:186:ASP:O	2.19	0.43
10:J:83:ARG:O	10:J:151:LEU:N	2.43	0.43
12:L:78:THR:OG1	12:L:79:LYS:N	2.52	0.43
14:N:72:LEU:HB2	34:1:1019:C:OP1	2.18	0.43
19:S:130:ARG:CZ	34:1:1608:U:H4'	2.49	0.43
34:1:331:C:H3'	34:1:332:G:C5'	2.49	0.43
34:1:799:U:H2'	34:1:800:U:O4'	2.17	0.43
1:A:7:VAL:HG21	22:V:42:VAL:N	2.32	0.43
1:A:14:ASP:OD1	1:A:17:LYS:NZ	2.49	0.43
3:C:77:SER:HB2	3:C:79:GLU:OE1	2.19	0.43
3:C:144:SER:HB2	34:1:1349:G:H5''	2.00	0.43
7:G:7:PHE:N	7:G:7:PHE:CD1	2.85	0.43
7:G:69:THR:HG21	7:G:73:VAL:CG1	2.48	0.43
7:G:135:PRO:HG2	7:G:141:ILE:HG12	2.01	0.43
15:O:32:HIS:N	15:O:43:HIS:O	2.43	0.43
17:Q:16:LYS:HG3	17:Q:17:LYS:H	1.83	0.43
19:S:117:ILE:HG22	19:S:117:ILE:O	2.19	0.43
31:e:43:VAL:HG13	31:e:44:ASN:N	2.34	0.43
34:1:183:G:H2'	34:1:184:G:C8	2.54	0.43
34:1:340:C:H2'	34:1:341:C:O4'	2.19	0.43
34:1:388:U:H2'	34:1:389:A:C8	2.53	0.43
34:1:542:U:N3	34:1:544:G:O4'	2.51	0.43
34:1:899:U:H2'	34:1:900:C:O4'	2.19	0.43
34:1:1139:C:O2'	34:1:1140:G:O5'	2.32	0.43
1:A:25:LEU:HA	1:A:47:TYR:O	2.18	0.43
1:A:113:GLN:OE1	1:A:114:ALA:HB2	2.19	0.43
2:B:67:PHE:N	2:B:86:LEU:O	2.50	0.43
2:B:140:VAL:HG12	2:B:141:GLY:N	2.34	0.43
7:G:27:PHE:CZ	7:G:109:LEU:HD22	2.54	0.43
7:G:90:GLY:O	34:1:452:G:N3	2.51	0.43
9:I:98:LYS:O	9:I:175:ILE:C	2.62	0.43
16:P:60:LEU:HD11	16:P:92:SER:CB	2.49	0.43
19:S:48:ALA:HB3	19:S:50:ILE:HD12	2.01	0.43
25:Y:28:LEU:HD13	25:Y:68:LYS:HE3	2.00	0.43
30:d:11:PRO:HD3	34:1:1618:C:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:79:LEU:HG	33:g:111:VAL:HG21	1.99	0.43
34:1:180:G:H2'	34:1:181:A:H2'	2.01	0.43
34:1:288:G:C2	34:1:289:G:C5	3.06	0.43
34:1:742:U:O2	34:1:742:U:O4'	2.37	0.43
34:1:1109:C:C2	34:1:1110:G:C8	3.07	0.43
34:1:1641:A:H2'	34:1:1642:U:O4'	2.18	0.43
34:1:1806:A:H2'	34:1:1807:C:O4'	2.19	0.43
35:2:11:A:C5	35:2:12:C:C5	3.06	0.43
1:A:76:VAL:CB	1:A:87:VAL:HG13	2.49	0.43
1:A:88:LEU:O	18:R:80:ARG:NE	2.51	0.43
2:B:73:ASP:C	2:B:73:ASP:OD1	2.61	0.43
3:C:85:SER:OG	22:V:26:ALA:O	2.37	0.43
3:C:191:VAL:HG11	3:C:236:PHE:HD1	1.84	0.43
5:E:191:ARG:HG3	5:E:192:VAL:N	2.34	0.43
17:Q:39:LEU:HD21	17:Q:51:LEU:HD22	2.01	0.43
19:S:89:ASP:HB3	34:1:1611:G:O3'	2.19	0.43
19:S:115:LYS:O	19:S:118:ARG:N	2.42	0.43
20:T:132:ASP:OD2	34:1:1415:C:O2'	2.30	0.43
21:U:61:LEU:HD11	30:d:34:TYR:CE1	2.54	0.43
28:b:34:ASP:OD1	28:b:45:THR:HG22	2.18	0.43
33:g:150:TRP:N	33:g:150:TRP:CD1	2.85	0.43
34:1:1211:G:O2'	34:1:1212:G:P	2.75	0.43
34:1:1848:U:H2'	34:1:1850:A:OP2	2.19	0.43
1:A:142:LEU:HD12	1:A:143:PRO:O	2.19	0.43
2:B:25:PHE:CE1	15:O:53:ILE:HA	2.54	0.43
2:B:68:GLU:H	2:B:68:GLU:CD	2.27	0.43
2:B:76:ASN:C	2:B:77:ASP:OD1	2.62	0.43
2:B:176:VAL:O	2:B:177:GLN:C	2.62	0.43
3:C:69:LEU:HD21	3:C:273:LEU:CG	2.45	0.43
4:D:71:ALA:HB1	4:D:75:LYS:HE2	2.01	0.43
5:E:148:ARG:NH2	7:G:202:ASN:OD1	2.51	0.43
8:H:106:ARG:NH1	34:1:802:A:H61	2.17	0.43
8:H:142:LYS:C	8:H:143:ARG:HG2	2.44	0.43
10:J:86:VAL:HG23	10:J:87:LEU:N	2.34	0.43
10:J:174:LYS:NZ	34:1:561:A:OP1	2.38	0.43
19:S:36:VAL:HG22	19:S:71:MET:HE1	2.00	0.43
26:Z:44:LEU:HD23	26:Z:45:ASN:N	2.33	0.43
27:a:25:ASN:HB2	27:a:77:CYS:SG	2.58	0.43
29:c:37:ASP:C	29:c:38:THR:HG22	2.44	0.43
33:g:31:ILE:HG13	33:g:45:LEU:HD11	1.99	0.43
34:1:909:G:H2'	34:1:910:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:1199:A:H2	34:1:1355:C:N4	2.17	0.43
34:1:1420:G:N3	34:1:1420:G:H2'	2.33	0.43
5:E:138:HIS:HA	5:E:148:ARG:HA	2.00	0.42
9:I:48:VAL:CG1	34:1:381:C:H5'	2.48	0.42
10:J:131:ARG:NH2	34:1:522:A:O3'	2.49	0.42
14:N:149:LEU:HD12	14:N:149:LEU:N	2.34	0.42
34:1:183:G:O2'	34:1:184:G:O4'	2.34	0.42
34:1:1795:G:C6	34:1:1796:G:C5	3.07	0.42
7:G:11:GLY:HA3	34:1:167:G:O4'	2.19	0.42
9:I:162:LEU:HG	9:I:195:LEU:CD2	2.48	0.42
10:J:110:LEU:HG	10:J:130:ILE:HD11	2.01	0.42
15:O:138:ASP:O	15:O:139:SER:CB	2.67	0.42
19:S:36:VAL:CG2	19:S:71:MET:HE1	2.49	0.42
25:Y:20:ARG:HB3	25:Y:76:TYR:CD1	2.54	0.42
33:g:189:ILE:HG22	33:g:190:GLY:N	2.34	0.42
34:1:148:U:C5	34:1:169:U:C4	3.07	0.42
3:C:232:THR:HG23	3:C:232:THR:O	2.18	0.42
9:I:54:LYS:CG	9:I:181:GLN:O	2.67	0.42
9:I:101:ILE:HA	9:I:173:ALA:O	2.20	0.42
10:J:155:LYS:O	10:J:155:LYS:NZ	2.43	0.42
13:M:55:ASN:N	13:M:80:ASP:O	2.48	0.42
15:O:136:PRO:O	15:O:136:PRO:HD2	2.20	0.42
16:P:17:TYR:HB3	16:P:25:LEU:HD11	2.00	0.42
17:Q:62:ARG:NE	17:Q:96:TYR:OH	2.51	0.42
25:Y:63:HIS:CE1	25:Y:68:LYS:HB3	2.54	0.42
27:a:92:ARG:NE	34:1:1865:C:OP2	2.50	0.42
33:g:69:VAL:HG23	33:g:80:SER:HB3	2.02	0.42
34:1:112:U:O2'	34:1:114:G:H2'	2.18	0.42
34:1:641:A:C2'	34:1:645:C:OP1	2.67	0.42
34:1:800:U:O2	34:1:865:A:C2	2.72	0.42
34:1:833:C:H3'	34:1:834:C:C6	2.54	0.42
34:1:1643:U:H2'	34:1:1644:C:C6	2.55	0.42
4:D:134:CYS:N	4:D:154:ASP:O	2.52	0.42
5:E:42:LEU:HD23	5:E:43:PRO:C	2.45	0.42
5:E:191:ARG:NH1	5:E:245:ARG:H	2.16	0.42
9:I:104:ILE:HB	9:I:171:LEU:HB3	2.01	0.42
9:I:191:GLU:N	9:I:195:LEU:HB2	2.34	0.42
11:K:64:TRP:O	11:K:65:ARG:NH2	2.53	0.42
20:T:56:ARG:HD3	20:T:60:THR:HG23	2.02	0.42
23:W:62:VAL:O	23:W:62:VAL:CG2	2.67	0.42
33:g:96:THR:O	33:g:97:THR:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:221:A:C6	34:1:301:A:N1	2.88	0.42
34:1:742:U:O2'	34:1:743:U:P	2.76	0.42
34:1:839:C:H1'	34:1:841:G:H1'	2.01	0.42
1:A:105:PRO:HA	1:A:136:GLU:OE2	2.19	0.42
6:F:77:MET:HE3	6:F:84:GLY:N	2.35	0.42
6:F:81:ARG:NH2	34:1:1536:G:O3'	2.52	0.42
9:I:198:TYR:OH	12:L:11:GLN:HB2	2.20	0.42
18:R:25:GLY:O	18:R:31:ASN:ND2	2.52	0.42
19:S:15:VAL:HG13	19:S:68:ILE:HD12	2.01	0.42
21:U:66:ARG:HH22	21:U:75:LYS:HG2	1.83	0.42
23:W:28:ARG:CB	34:1:921:G:N7	2.82	0.42
30:d:54:LYS:O	30:d:55:LEU:HB2	2.20	0.42
32:f:85:TYR:HB3	32:f:87:THR:OG1	2.19	0.42
33:g:109:LEU:HD21	33:g:125:ARG:HB2	2.01	0.42
34:1:187:G:H1'	34:1:300:U:H5''	2.01	0.42
34:1:1807:C:H2'	34:1:1808:U:O4'	2.19	0.42
1:A:103:PHE:C	1:A:103:PHE:CD2	2.97	0.42
2:B:30:TRP:CD1	2:B:30:TRP:N	2.87	0.42
3:C:178:HIS:CD2	3:C:179:THR:HG22	2.54	0.42
3:C:253:PRO:HA	3:C:256:TRP:CD1	2.54	0.42
8:H:73:GLN:HA	8:H:135:PHE:CZ	2.55	0.42
21:U:87:ARG:NH2	34:1:1447:G:OP1	2.39	0.42
24:X:22:TRP:CE3	24:X:22:TRP:HA	2.54	0.42
26:Z:100:VAL:HG12	26:Z:101:SER:N	2.35	0.42
33:g:196:ASN:ND2	33:g:236:ILE:O	2.46	0.42
34:1:87:U:C2'	34:1:88:G:H5'	2.49	0.42
34:1:460:A:H2'	34:1:461:U:H6	1.84	0.42
34:1:594:A:N6	34:1:643:A:O5'	2.48	0.42
34:1:1110:G:C6	34:1:1111:U:C4	3.08	0.42
34:1:1553:C:H3'	34:1:1554:C:H5'	2.01	0.42
1:A:37:TYR:CD1	1:A:162:PRO:HG2	2.54	0.42
1:A:63:ARG:NE	22:V:39:VAL:HG22	2.34	0.42
2:B:35:ALA:HB1	2:B:36:PRO:HD2	2.02	0.42
2:B:126:ASP:C	2:B:126:ASP:OD1	2.61	0.42
3:C:78:LEU:HD11	3:C:97:PHE:HB3	2.02	0.42
6:F:35:LEU:HD13	6:F:146:ARG:NH2	2.34	0.42
6:F:49:LEU:HG	17:Q:49:TYR:HB2	2.01	0.42
8:H:64:VAL:HG13	8:H:72:PHE:CE2	2.53	0.42
8:H:75:ILE:HG22	8:H:75:ILE:O	2.19	0.42
8:H:94:PHE:CD1	8:H:94:PHE:N	2.88	0.42
9:I:84:ASN:O	9:I:85:ALA:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:32:HIS:ND1	11:K:32:HIS:O	2.51	0.42
11:K:67:PHE:HB2	11:K:69:TRP:CH2	2.55	0.42
13:M:80:ASP:OD1	13:M:80:ASP:N	2.50	0.42
21:U:39:LEU:HD21	21:U:89:ILE:HD11	2.02	0.42
28:b:49:HIS:CD2	34:1:1015:U:H5'	2.54	0.42
34:1:645:C:H2'	34:1:646:G:H8	1.84	0.42
34:1:1490:G:N1	34:1:1491:G:C6	2.88	0.42
1:A:42:LYS:HG2	1:A:43:SER:N	2.35	0.42
2:B:125:VAL:HG22	2:B:126:ASP:O	2.20	0.42
4:D:208:VAL:HG13	18:R:41:ILE:HG12	2.02	0.42
7:G:183:ARG:NH2	34:1:316:G:OP1	2.53	0.42
9:I:22:HIS:CE1	9:I:25:ARG:HE	2.38	0.42
9:I:81:VAL:CG2	9:I:96:LEU:HD21	2.50	0.42
12:L:35:ARG:HG3	12:L:36:TYR:H	1.85	0.42
14:N:20:ARG:HG3	14:N:65:PHE:CZ	2.55	0.42
15:O:40:THR:OG1	15:O:41:PHE:N	2.52	0.42
22:V:45:ARG:CG	22:V:46:PHE:N	2.83	0.42
25:Y:54:VAL:HG22	25:Y:76:TYR:HB2	2.02	0.42
26:Z:85:ARG:NE	26:Z:107:VAL:HG21	2.34	0.42
28:b:57:VAL:HG13	28:b:58:GLY:N	2.35	0.42
30:d:12:ARG:HG2	30:d:12:ARG:O	2.19	0.42
34:1:954:U:H2'	34:1:955:A:C8	2.55	0.42
34:1:1107:G:C6	34:1:1126:G:C6	3.07	0.42
1:A:90:PHE:CD2	1:A:179:ALA:HB2	2.54	0.42
2:B:39:PHE:CD2	2:B:74:LEU:HD23	2.54	0.42
2:B:108:ASP:OD1	2:B:108:ASP:N	2.52	0.42
7:G:27:PHE:CE1	7:G:109:LEU:HD22	2.55	0.42
8:H:39:GLN:NE2	8:H:72:PHE:HA	2.35	0.42
8:H:191:GLU:N	8:H:191:GLU:CD	2.78	0.42
9:I:133:GLU:HG3	9:I:133:GLU:O	2.20	0.42
9:I:166:PHE:N	9:I:166:PHE:CD1	2.88	0.42
11:K:71:LEU:O	11:K:71:LEU:HD23	2.20	0.42
19:S:26:ILE:HG23	19:S:45:LEU:HD21	2.01	0.42
21:U:20:ILE:HG21	21:U:98:VAL:HG21	2.01	0.42
33:g:283:PRO:O	33:g:285:GLN:N	2.51	0.42
34:1:1336:C:H2'	34:1:1337:C:O4'	2.20	0.42
1:A:50:ASN:C	1:A:51:LEU:HD12	2.45	0.42
3:C:60:TRP:CZ3	3:C:62:PRO:HA	2.55	0.42
3:C:206:SER:HB3	3:C:224:THR:HG21	2.01	0.42
4:D:9:ARG:NH2	34:1:1553:C:O2	2.53	0.42
4:D:106:ARG:HG3	4:D:175:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:41:VAL:O	6:F:41:VAL:HG22	2.19	0.42
9:I:8:TRP:CZ2	9:I:22:HIS:HB2	2.55	0.42
9:I:110:ARG:HH12	9:I:122:GLY:HA3	1.84	0.42
10:J:50:LEU:HD11	10:J:105:PHE:CD1	2.54	0.42
15:O:34:PHE:CD2	15:O:34:PHE:C	2.97	0.42
15:O:90:ILE:HD12	15:O:90:ILE:C	2.45	0.42
16:P:43:ARG:NH2	34:1:1615:U:OP2	2.53	0.42
20:T:88:MET:SD	34:1:1665:G:OP1	2.78	0.42
33:g:283:PRO:N	33:g:284:PRO:CD	2.83	0.42
34:1:173:A:C5	34:1:174:C:C4	3.08	0.42
34:1:174:C:C4	34:1:175:A:N7	2.87	0.42
34:1:417:C:C2'	34:1:418:A:H5''	2.50	0.42
34:1:436:G:N2	34:1:458:A:C4	2.88	0.42
34:1:1101:U:H2'	34:1:1102:G:H8	1.84	0.42
3:C:60:TRP:HB3	3:C:71:LYS:CE	2.50	0.41
3:C:92:GLU:HA	3:C:95:ASP:HB3	2.02	0.41
3:C:267:GLN:HA	3:C:270:THR:OG1	2.20	0.41
4:D:157:MET:HE3	4:D:158:ILE:H	1.85	0.41
5:E:73:ASP:O	5:E:73:ASP:OD1	2.38	0.41
7:G:139:SER:CB	34:1:145:G:OP2	2.67	0.41
7:G:147:LEU:HD13	7:G:151:ASP:O	2.20	0.41
8:H:66:VAL:HG11	34:1:913:A:H1'	2.01	0.41
15:O:40:THR:HG23	15:O:58:GLY:HA3	2.02	0.41
17:Q:12:VAL:HG12	17:Q:13:PHE:N	2.34	0.41
25:Y:5:VAL:HG12	25:Y:29:HIS:HD2	1.82	0.41
34:1:981:A:H2'	34:1:982:G:C8	2.55	0.41
34:1:1385:G:C5	34:1:1386:A:N7	2.88	0.41
34:1:1454:A:H4'	34:1:1455:A:O5'	2.19	0.41
2:B:71:LEU:HD21	2:B:82:ARG:O	2.20	0.41
5:E:126:VAL:O	5:E:156:VAL:O	2.39	0.41
15:O:66:ARG:NE	34:1:960:U:C4	2.88	0.41
15:O:131:ASP:OD1	15:O:131:ASP:C	2.63	0.41
34:1:315:C:N3	34:1:336:A:N6	2.67	0.41
34:1:316:G:C2	34:1:317:C:C2	3.08	0.41
34:1:343:A:C6	34:1:344:U:N3	2.89	0.41
34:1:1182:A:C5	34:1:1183:A:H1'	2.55	0.41
34:1:1212:G:H2'	34:1:1213:C:C6	2.55	0.41
34:1:1395:C:H1'	34:1:1474:A:C4	2.55	0.41
34:1:1462:U:O2'	34:1:1464:C:N3	2.48	0.41
34:1:1745:A:N6	34:1:1789:G:C2'	2.83	0.41
1:A:157:VAL:HG12	1:A:158:ASP:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:113:LEU:O	4:D:114:ALA:C	2.63	0.41
5:E:252:ARG:HD2	5:E:252:ARG:C	2.46	0.41
7:G:94:ARG:HG2	34:1:454:U:H5''	2.03	0.41
7:G:138:ALA:HA	7:G:141:ILE:HD12	2.03	0.41
8:H:38:ALA:HB2	8:H:75:ILE:CD1	2.48	0.41
12:L:82:MET:CG	12:L:85:THR:HG23	2.50	0.41
14:N:5:HIS:CD2	14:N:121:ARG:HE	2.38	0.41
16:P:110:GLU:OE1	16:P:110:GLU:CA	2.68	0.41
33:g:45:LEU:HD22	33:g:52:TYR:CE2	2.55	0.41
33:g:169:GLY:O	33:g:195:LEU:HD21	2.20	0.41
34:1:283:G:H2'	34:1:284:C:OP1	2.19	0.41
34:1:991:G:C6	34:1:1134:G:H4'	2.55	0.41
34:1:1184:G:C6	34:1:1185:C:C4	3.08	0.41
34:1:1749:G:H2'	34:1:1750:C:C6	2.55	0.41
2:B:153:THR:HB	2:B:155:TYR:CD2	2.55	0.41
7:G:13:GLN:HG3	34:1:153:G:H2'	2.02	0.41
7:G:186:GLN:HA	7:G:189:ARG:HE	1.86	0.41
9:I:54:LYS:HG2	9:I:181:GLN:O	2.20	0.41
9:I:67:TRP:HB2	9:I:109:TYR:CE2	2.55	0.41
10:J:50:LEU:HD21	10:J:102:ILE:HA	2.03	0.41
17:Q:32:ILE:HG12	17:Q:68:ILE:HD11	2.02	0.41
18:R:99:ASP:N	18:R:99:ASP:OD1	2.53	0.41
23:W:51:GLU:HG3	23:W:52:ILE:N	2.36	0.41
27:a:15:ARG:CZ	34:1:994:C:C4	3.02	0.41
31:e:35:ARG:NH1	34:1:527:C:OP1	2.54	0.41
33:g:79:LEU:HD23	33:g:111:VAL:HG22	2.02	0.41
34:1:524:U:H5''	34:1:525:A:O2'	2.19	0.41
34:1:1748:G:H2'	34:1:1749:G:O4'	2.21	0.41
35:2:4:C:C2	35:2:51:G:C2	3.09	0.41
6:F:87:LEU:HD12	34:1:1591:C:O2'	2.20	0.41
6:F:123:GLU:HB3	6:F:138:ALA:HB1	2.03	0.41
7:G:165:GLU:OE2	34:1:69:C:OP1	2.37	0.41
7:G:232:ARG:HD3	7:G:232:ARG:HA	1.93	0.41
9:I:97:VAL:O	9:I:175:ILE:HG21	2.21	0.41
9:I:190:LEU:HD23	9:I:190:LEU:HA	1.92	0.41
10:J:96:TYR:O	10:J:97:ILE:C	2.64	0.41
13:M:64:LEU:HD22	32:f:106:TYR:HB3	2.03	0.41
15:O:55:ARG:NH2	15:O:57:THR:HG23	2.35	0.41
20:T:33:TRP:HH2	20:T:102:ARG:HG3	1.86	0.41
23:W:116:ALA:O	23:W:119:LYS:N	2.49	0.41
27:a:38:LYS:HE2	34:1:1867:U:O2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:23:ARG:NH2	28:b:29:ASN:OD1	2.54	0.41
34:1:117:C:H5''	34:1:118:C:OP1	2.21	0.41
34:1:313:A:H4'	34:1:314:U:OP2	2.20	0.41
34:1:412:G:O2'	34:1:813:A:N6	2.53	0.41
34:1:797:C:C4'	34:1:798:G:OP2	2.69	0.41
34:1:887:U:O2'	34:1:888:U:H5''	2.20	0.41
34:1:1135:C:H2'	34:1:1136:U:O4'	2.20	0.41
4:D:57:ASN:O	4:D:65:ARG:HD2	2.20	0.41
4:D:110:LEU:HD13	4:D:177:LEU:HD21	2.02	0.41
5:E:139:LEU:HB2	5:E:150:PRO:HG3	2.02	0.41
7:G:66:GLY:HA2	34:1:1745:A:C8	2.56	0.41
7:G:190:ARG:HB2	34:1:332:G:O2'	2.20	0.41
8:H:78:ARG:HG2	8:H:78:ARG:O	2.20	0.41
8:H:93:VAL:HG11	8:H:133:LEU:HD22	2.03	0.41
8:H:110:THR:HG21	34:1:797:C:OP1	2.20	0.41
15:O:77:ALA:O	15:O:81:VAL:HG12	2.20	0.41
25:Y:20:ARG:HB2	25:Y:74:MET:SD	2.60	0.41
25:Y:105:LYS:NZ	34:1:53:C:O2'	2.53	0.41
27:a:15:ARG:NH1	34:1:994:C:C4	2.89	0.41
28:b:79:PHE:CD1	28:b:79:PHE:C	2.99	0.41
34:1:88:G:H21	34:1:500:A:P	2.44	0.41
34:1:338:G:N1	34:1:339:A:C2	2.88	0.41
34:1:499:G:C6	34:1:501:C:C2	3.09	0.41
34:1:527:C:C2	34:1:559:G:N2	2.89	0.41
34:1:1794:C:H2'	34:1:1795:G:O4'	2.19	0.41
1:A:24:HIS:HB2	1:A:48:ILE:HG23	2.02	0.41
4:D:131:ALA:CB	4:D:188:ILE:HD11	2.50	0.41
5:E:228:ILE:HD11	5:E:236:ILE:HB	2.03	0.41
7:G:55:GLY:O	7:G:62:PRO:HA	2.20	0.41
8:H:75:ILE:O	8:H:79:LEU:HD12	2.21	0.41
8:H:93:VAL:HG12	8:H:94:PHE:N	2.35	0.41
12:L:111:VAL:HG23	12:L:140:PHE:HB2	2.03	0.41
14:N:52:VAL:O	14:N:53:ILE:C	2.61	0.41
15:O:50:LYS:HG2	34:1:976:G:H1'	2.03	0.41
25:Y:76:TYR:CD2	25:Y:82:ALA:HB2	2.56	0.41
25:Y:104:ARG:O	25:Y:105:LYS:HB2	2.21	0.41
33:g:214:GLY:O	33:g:232:GLY:N	2.43	0.41
34:1:84:A:C2'	34:1:150:A:O2'	2.68	0.41
34:1:88:G:H2'	34:1:89:C:O2	2.20	0.41
34:1:219:U:C4	34:1:303:C:N3	2.88	0.41
34:1:592:C:O2	34:1:592:C:O4'	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:1168:G:C2	34:1:1192:U:O2	2.74	0.41
34:1:1190:A:H2'	34:1:1191:C:O4'	2.20	0.41
34:1:1298:G:H2'	34:1:1299:A:O4'	2.20	0.41
34:1:1499:U:H2'	34:1:1500:G:C8	2.55	0.41
2:B:174:ARG:HG2	2:B:174:ARG:HH11	1.86	0.41
5:E:78:VAL:HG23	5:E:79:ASP:N	2.36	0.41
7:G:74:ARG:CZ	34:1:455:A:OP1	2.69	0.41
9:I:7:ASN:ND2	34:1:351:G:OP1	2.53	0.41
9:I:67:TRP:CZ3	9:I:191:GLU:OE2	2.74	0.41
9:I:112:TRP:O	9:I:116:HIS:ND1	2.54	0.41
9:I:175:ILE:HG22	9:I:176:ALA:N	2.36	0.41
15:O:27:VAL:O	15:O:90:ILE:O	2.38	0.41
15:O:30:VAL:O	15:O:45:THR:N	2.41	0.41
15:O:103:ASN:O	15:O:142:ARG:NH1	2.54	0.41
16:P:115:TYR:O	16:P:116:LEU:HB2	2.19	0.41
21:U:64:THR:HG23	21:U:77:TRP:HB3	2.01	0.41
25:Y:19:GLN:N	25:Y:19:GLN:CD	2.77	0.41
28:b:36:LYS:O	28:b:77:CYS:HA	2.21	0.41
34:1:293:C:O2'	34:1:295:C:C6	2.70	0.41
34:1:314:U:H2'	34:1:315:C:C6	2.55	0.41
34:1:800:U:O2	34:1:865:A:N1	2.54	0.41
34:1:1451:G:H21	34:1:1474:A:H61	1.68	0.41
1:A:18:PHE:HZ	1:A:177:MET:HG3	1.85	0.41
1:A:112:ILE:HG23	1:A:113:GLN:HG3	2.03	0.41
2:B:110:MET:CE	2:B:213:ARG:HD2	2.51	0.41
2:B:137:LEU:CB	2:B:215:VAL:HG23	2.51	0.41
3:C:69:LEU:HD11	3:C:273:LEU:HD11	2.03	0.41
3:C:236:PHE:O	3:C:240:THR:HG22	2.20	0.41
5:E:133:VAL:HG12	5:E:136:ILE:HD11	2.02	0.41
5:E:216:ASN:N	5:E:216:ASN:OD1	2.53	0.41
6:F:140:ASP:CB	29:c:46:VAL:HG22	2.49	0.41
7:G:13:GLN:HB3	34:1:154:U:H4'	2.03	0.41
7:G:14:LYS:HB3	7:G:124:LEU:HD11	2.01	0.41
7:G:27:PHE:C	7:G:27:PHE:CD2	2.95	0.41
7:G:76:LEU:HD12	7:G:77:LEU:N	2.36	0.41
9:I:68:GLY:O	34:1:222:U:H4'	2.21	0.41
10:J:121:LYS:O	10:J:122:SER:CB	2.69	0.41
15:O:72:TYR:OH	15:O:76:LEU:HD21	2.21	0.41
15:O:82:ALA:HB2	15:O:119:LEU:CD1	2.51	0.41
15:O:117:ARG:O	15:O:121:ARG:HG2	2.21	0.41
19:S:124:ARG:NH1	19:S:130:ARG:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:79:TYR:CD1	20:T:79:TYR:C	2.99	0.41
21:U:67:LYS:HD2	21:U:76:THR:HG22	2.02	0.41
29:c:19:GLY:O	29:c:28:THR:HG23	2.20	0.41
30:d:41:GLN:HB3	34:1:1495:G:C6	2.56	0.41
32:f:134:SER:O	34:1:1307:U:O2'	2.39	0.41
33:g:296:GLN:O	33:g:312:VAL:HG23	2.21	0.41
34:1:417:C:H2'	34:1:418:A:H5'	2.03	0.41
34:1:802:A:H2'	34:1:803:C:H5'	2.03	0.41
34:1:1045:U:H2'	34:1:1046:U:O4'	2.21	0.41
34:1:1188:A:C2	34:1:1189:A:C4	3.09	0.41
34:1:1343:U:H2'	34:1:1344:A:O4'	2.21	0.41
34:1:1586:U:O2	34:1:1586:U:O4'	2.38	0.41
3:C:131:GLY:HA3	3:C:137:VAL:HG12	2.03	0.41
4:D:127:MET:HA	4:D:127:MET:CE	2.44	0.41
6:F:103:LEU:O	6:F:104:THR:OG1	2.28	0.41
7:G:97:VAL:HG12	7:G:98:ARG:O	2.21	0.41
9:I:66:SER:HB2	34:1:221:A:H4'	2.02	0.41
10:J:17:ARG:HG2	10:J:17:ARG:HH11	1.86	0.41
33:g:151:VAL:HG22	33:g:168:CYS:O	2.20	0.41
33:g:292:SER:OG	33:g:294:ASP:OD1	2.32	0.41
34:1:11:A:H8	34:1:11:A:O5'	2.04	0.41
34:1:310:C:H2'	34:1:311:C:C6	2.56	0.41
34:1:475:C:HO2'	34:1:476:A:P	2.37	0.41
34:1:571:U:H2'	34:1:572:U:C6	2.57	0.41
34:1:1453:C:H2'	34:1:1454:A:H5'	2.02	0.41
1:A:63:ARG:HD3	22:V:39:VAL:HG22	2.04	0.40
4:D:157:MET:HE3	4:D:158:ILE:C	2.46	0.40
5:E:147:ILE:HD12	5:E:167:GLY:O	2.21	0.40
5:E:183:VAL:HG12	5:E:189:LEU:HA	2.02	0.40
6:F:31:ASN:OD1	6:F:31:ASN:N	2.52	0.40
7:G:126:ASP:OD1	7:G:126:ASP:N	2.50	0.40
8:H:135:PHE:CD1	8:H:135:PHE:C	2.97	0.40
9:I:48:VAL:HG12	9:I:49:ARG:N	2.35	0.40
10:J:138:ARG:NH1	34:1:821:G:N7	2.68	0.40
15:O:72:TYR:HA	15:O:75:MET:HB3	2.03	0.40
16:P:112:ILE:HG22	16:P:113:GLY:N	2.37	0.40
16:P:118:GLU:HB3	19:S:119:ALA:HA	2.02	0.40
20:T:6:VAL:HG12	20:T:135:ALA:HB2	2.03	0.40
30:d:10:HIS:O	30:d:11:PRO:C	2.63	0.40
33:g:126:ASP:OD1	33:g:126:ASP:N	2.51	0.40
34:1:149:A:P	34:1:168:C:H42	2.40	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1:227:U:HO2'	34:1:228:C:P	2.33	0.40
34:1:318:A:C6	34:1:333:G:C6	3.09	0.40
34:1:458:A:C6	34:1:459:C:C4	3.10	0.40
34:1:525:A:H2'	34:1:526:A:O4'	2.21	0.40
34:1:654:A:OP2	34:1:655:A:O2'	2.36	0.40
34:1:946:U:C2	34:1:947:G:C8	3.09	0.40
35:2:3:C:C2	35:2:52:G:C2	3.09	0.40
1:A:50:ASN:HB2	18:R:109:LEU:HD11	2.03	0.40
5:E:229:GLY:HA2	5:E:235:TRP:CD1	2.57	0.40
8:H:107:LYS:HD3	34:1:861:A:H62	1.85	0.40
9:I:45:THR:CG2	34:1:307:G:H1'	2.51	0.40
28:b:63:LEU:HG	28:b:73:LEU:CD2	2.51	0.40
33:g:87:LEU:HD12	33:g:87:LEU:N	2.36	0.40
34:1:96:C:O2	34:1:96:C:O4'	2.39	0.40
34:1:288:G:C2	34:1:296:U:O2	2.75	0.40
34:1:587:A:H2'	34:1:587:A:N3	2.36	0.40
34:1:847:A:H2'	34:1:847:A:N3	2.36	0.40
34:1:957:A:C6	34:1:958:G:C5	3.09	0.40
34:1:1099:G:C2	34:1:1100:A:C8	3.09	0.40
34:1:1559:C:H2'	34:1:1560:U:O4'	2.21	0.40
34:1:1582:C:H2'	34:1:1583:C:C6	2.56	0.40
2:B:51:ARG:O	2:B:52:THR:C	2.63	0.40
2:B:75:GLN:CB	2:B:78:GLU:HG2	2.52	0.40
4:D:123:LEU:HA	4:D:126:ILE:HG22	2.03	0.40
6:F:40:ALA:O	6:F:41:VAL:C	2.63	0.40
6:F:52:SER:OG	6:F:53:ALA:N	2.54	0.40
15:O:138:ASP:HB2	34:1:984:C:O2'	2.21	0.40
17:Q:77:HIS:O	17:Q:81:ILE:HG12	2.22	0.40
19:S:110:ASP:HA	19:S:113:ARG:HG2	2.03	0.40
21:U:26:SER:OG	21:U:110:VAL:HG13	2.22	0.40
21:U:101:ILE:O	21:U:101:ILE:HG22	2.21	0.40
34:1:71:G:H5'	34:1:72:C:OP2	2.22	0.40
34:1:361:U:C2	34:1:1175:G:N3	2.90	0.40
34:1:455:A:O5'	34:1:455:A:H8	2.04	0.40
34:1:585:C:H2'	34:1:586:G:O4'	2.20	0.40
34:1:1551:U:O5'	34:1:1551:U:O2	2.39	0.40
34:1:1718:G:O3'	34:1:1719:A:H8	2.05	0.40
1:A:65:ILE:HG21	1:A:182:VAL:HG22	2.03	0.40
2:B:205:TYR:HD1	2:B:206:PRO:HD2	1.87	0.40
3:C:124:PHE:O	3:C:144:SER:N	2.44	0.40
5:E:211:LYS:HZ2	5:E:211:LYS:HG2	1.72	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:35:LEU:HD13	6:F:146:ARG:CZ	2.52	0.40
8:H:25:GLN:O	8:H:29:GLU:HG2	2.22	0.40
8:H:111:LYS:HZ1	34:1:745:C:C4'	2.34	0.40
9:I:191:GLU:HB2	12:L:19:ASN:OD1	2.22	0.40
14:N:82:PRO:O	14:N:83:ASP:HB3	2.22	0.40
19:S:38:ARG:HB3	20:T:45:LEU:HD21	2.02	0.40
19:S:60:THR:HG22	19:S:61:GLU:N	2.36	0.40
23:W:50:PHE:HE1	23:W:52:ILE:HD11	1.87	0.40
25:Y:54:VAL:HG21	25:Y:76:TYR:O	2.22	0.40
34:1:316:G:C2	34:1:335:G:C4	3.10	0.40
34:1:558:G:H2'	34:1:559:G:C8	2.57	0.40
34:1:594:A:N1	34:1:642:U:C2'	2.84	0.40
34:1:962:A:HO2'	34:1:963:A:P	2.39	0.40
34:1:967:C:C4	34:1:968:U:C4	3.10	0.40
2:B:99:ASN:ND2	2:B:228:LEU:HD13	2.37	0.40
4:D:25:LEU:HD23	4:D:28:GLU:OE2	2.21	0.40
6:F:171:GLU:OE1	26:Z:71:ALA:HB3	2.21	0.40
9:I:199:LEU:HA	9:I:202:ILE:HD12	2.04	0.40
28:b:51:GLN:OE1	34:1:927:C:O2	2.39	0.40
29:c:20:ARG:HG3	34:1:1680:G:O2'	2.21	0.40
34:1:31:U:O2	34:1:644:G:C6	2.75	0.40
34:1:454:U:H6	34:1:454:U:O5'	2.05	0.40
34:1:491:C:H5'	34:1:574:A:C2	2.56	0.40
34:1:980:A:H2'	34:1:981:A:C8	2.57	0.40
34:1:1026:C:O2'	34:1:1161:U:H4'	2.21	0.40
34:1:1378:A:O3'	34:1:1379:A:O4'	2.40	0.40
34:1:1413:G:H21	34:1:1424:G:H1	1.69	0.40
35:2:5:U:C2'	35:2:6:G:OP2	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	213/295 (72%)	188 (88%)	25 (12%)	0	100	100
2	B	210/264 (80%)	160 (76%)	47 (22%)	3 (1%)	9	34
3	C	220/293 (75%)	196 (89%)	23 (10%)	1 (0%)	24	57
4	D	218/243 (90%)	204 (94%)	13 (6%)	1 (0%)	24	57
5	E	255/263 (97%)	217 (85%)	37 (14%)	1 (0%)	30	61
6	F	188/204 (92%)	162 (86%)	25 (13%)	1 (0%)	24	57
7	G	230/249 (92%)	202 (88%)	28 (12%)	0	100	100
8	H	181/194 (93%)	162 (90%)	19 (10%)	0	100	100
9	I	205/208 (99%)	167 (82%)	38 (18%)	0	100	100
10	J	177/194 (91%)	156 (88%)	19 (11%)	2 (1%)	11	39
11	K	96/165 (58%)	85 (88%)	10 (10%)	1 (1%)	12	41
12	L	151/158 (96%)	133 (88%)	18 (12%)	0	100	100
13	M	118/132 (89%)	112 (95%)	6 (5%)	0	100	100
14	N	147/151 (97%)	126 (86%)	20 (14%)	1 (1%)	18	49
15	O	134/151 (89%)	111 (83%)	21 (16%)	2 (2%)	8	32
16	P	118/145 (81%)	98 (83%)	20 (17%)	0	100	100
17	Q	137/146 (94%)	126 (92%)	11 (8%)	0	100	100
18	R	119/135 (88%)	111 (93%)	6 (5%)	2 (2%)	7	30
19	S	137/152 (90%)	125 (91%)	12 (9%)	0	100	100
20	T	141/145 (97%)	133 (94%)	6 (4%)	2 (1%)	9	34
21	U	95/119 (80%)	93 (98%)	2 (2%)	0	100	100
22	V	79/83 (95%)	76 (96%)	2 (2%)	1 (1%)	9	35
23	W	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
24	X	137/143 (96%)	123 (90%)	14 (10%)	0	100	100
25	Y	123/133 (92%)	115 (94%)	8 (6%)	0	100	100
26	Z	71/125 (57%)	68 (96%)	3 (4%)	0	100	100
27	a	95/115 (83%)	80 (84%)	14 (15%)	1 (1%)	11	39
28	b	78/84 (93%)	56 (72%)	21 (27%)	1 (1%)	9	35
29	c	59/69 (86%)	52 (88%)	6 (10%)	1 (2%)	7	30
30	d	49/56 (88%)	46 (94%)	3 (6%)	0	100	100
31	e	53/59 (90%)	47 (89%)	6 (11%)	0	100	100
32	f	71/156 (46%)	66 (93%)	5 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	g	312/317 (98%)	292 (94%)	20 (6%)	0	100	100
All	All	4744/5476 (87%)	4200 (88%)	523 (11%)	21 (0%)	31	61

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	93	GLU
6	F	63	LYS
10	J	3	VAL
22	V	42	VAL
3	C	174	ILE
15	O	139	SER
18	R	88	VAL
4	D	217	ILE
10	J	123	ILE
15	O	141	ARG
28	b	75	GLU
18	R	95	ILE
29	c	38	THR
2	B	179	ASN
2	B	210	VAL
14	N	29	THR
20	T	31	PRO
27	a	45	VAL
11	K	41	PRO
2	B	205	TYR
20	T	37	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	180/243 (74%)	180 (100%)	0	100	100
2	B	193/231 (84%)	192 (100%)	1 (0%)	81	85
3	C	188/225 (84%)	188 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	183/202 (91%)	183 (100%)	0	100	100
5	E	220/225 (98%)	218 (99%)	2 (1%)	70	80
6	F	160/170 (94%)	160 (100%)	0	100	100
7	G	202/218 (93%)	201 (100%)	1 (0%)	81	85
8	H	164/174 (94%)	163 (99%)	1 (1%)	78	83
9	I	179/180 (99%)	178 (99%)	1 (1%)	78	83
10	J	160/168 (95%)	158 (99%)	2 (1%)	61	77
11	K	89/136 (65%)	88 (99%)	1 (1%)	65	78
12	L	138/142 (97%)	138 (100%)	0	100	100
13	M	102/108 (94%)	102 (100%)	0	100	100
14	N	130/131 (99%)	130 (100%)	0	100	100
15	O	106/119 (89%)	105 (99%)	1 (1%)	70	80
16	P	109/130 (84%)	109 (100%)	0	100	100
17	Q	115/121 (95%)	115 (100%)	0	100	100
18	R	110/122 (90%)	110 (100%)	0	100	100
19	S	121/132 (92%)	121 (100%)	0	100	100
20	T	113/115 (98%)	112 (99%)	1 (1%)	70	80
21	U	90/107 (84%)	90 (100%)	0	100	100
22	V	65/67 (97%)	65 (100%)	0	100	100
23	W	112/113 (99%)	112 (100%)	0	100	100
24	X	111/115 (96%)	110 (99%)	1 (1%)	70	80
25	Y	107/115 (93%)	107 (100%)	0	100	100
26	Z	65/103 (63%)	65 (100%)	0	100	100
27	a	84/98 (86%)	83 (99%)	1 (1%)	63	78
28	b	72/76 (95%)	72 (100%)	0	100	100
29	c	54/62 (87%)	54 (100%)	0	100	100
30	d	45/49 (92%)	45 (100%)	0	100	100
31	e	44/48 (92%)	44 (100%)	0	100	100
32	f	66/140 (47%)	65 (98%)	1 (2%)	57	75
33	g	272/275 (99%)	272 (100%)	0	100	100
All	All	4149/4660 (89%)	4135 (100%)	14 (0%)	84	87

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	232	HIS
5	E	81	THR
5	E	134	LYS
7	G	109	LEU
8	H	148	LEU
9	I	45	THR
10	J	32	ILE
10	J	115	PHE
11	K	71	LEU
15	O	150	ARG
20	T	33	TRP
24	X	94	ILE
27	a	28	ARG
32	f	100	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	169	HIS
1	A	193	HIS
2	B	40	ASN
3	C	277	HIS
4	D	101	GLN
5	E	36	HIS
6	F	107	ASN
7	G	187	HIS
9	I	9	HIS
9	I	22	HIS
9	I	35	ASN
10	J	140	GLN
12	L	11	GLN
13	M	48	HIS
14	N	90	HIS
15	O	20	GLN
15	O	94	HIS
16	P	32	GLN
19	S	42	HIS
21	U	85	HIS
23	W	113	HIS
24	X	87	ASN
28	b	26	GLN

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Mol	Chain	Res	Type
32	f	139	HIS
33	g	14	HIS
33	g	76	GLN
33	g	147	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	1	1701/1869 (91%)	393 (23%)	16 (0%)
35	2	25/91 (27%)	3 (12%)	1 (4%)
All	All	1726/1960 (88%)	396 (22%)	17 (0%)

All (396) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	1	4	C
34	1	9	U
34	1	11	A
34	1	13	C
34	1	17	C
34	1	20	G
34	1	26	U
34	1	31	U
34	1	33	G
34	1	41	G
34	1	42	A
34	1	46	A
34	1	51	U
34	1	59	U
34	1	62	G
34	1	64	A
34	1	67	C
34	1	68	A
34	1	72	C
34	1	73	C
34	1	76	U
34	1	77	A
34	1	79	A
34	1	97	U
34	1	100	U
34	1	103	A

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Mol	Chain	Res	Type
34	1	104	A
34	1	106	C
34	1	111	A
34	1	112	U
34	1	113	G
34	1	114	G
34	1	115	U
34	1	116	U
34	1	118	C
34	1	119	U
34	1	125	C
34	1	126	G
34	1	143	U
34	1	154	U
34	1	155	G
34	1	161	U
34	1	166	A
34	1	171	A
34	1	172	U
34	1	174	C
34	1	183	G
34	1	217	A
34	1	219	U
34	1	225	G
34	1	226	A
34	1	227	U
34	1	228	C
34	1	230	A
34	1	238	C
34	1	284	C
34	1	286	U
34	1	287	U
34	1	288	G
34	1	292	A
34	1	294	U
34	1	302	A
34	1	305	U
34	1	306	C
34	1	309	G
34	1	312	G
34	1	314	U
34	1	319	C

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Mol	Chain	Res	Type
34	1	320	G
34	1	325	C
34	1	327	G
34	1	328	U
34	1	329	G
34	1	331	C
34	1	332	G
34	1	333	G
34	1	339	A
34	1	344	U
34	1	347	G
34	1	350	C
34	1	364	A
34	1	370	G
34	1	372	U
34	1	376	A
34	1	384	U
34	1	385	G
34	1	386	C
34	1	387	C
34	1	389	A
34	1	401	A
34	1	408	A
34	1	409	C
34	1	417	C
34	1	428	U
34	1	442	C
34	1	443	U
34	1	448	A
34	1	449	A
34	1	450	C
34	1	455	A
34	1	463	C
34	1	464	A
34	1	465	A
34	1	466	G
34	1	469	A
34	1	470	G
34	1	471	G
34	1	472	C
34	1	473	A
34	1	476	A

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Mol	Chain	Res	Type
34	1	482	G
34	1	487	U
34	1	488	U
34	1	489	A
34	1	492	C
34	1	495	U
34	1	500	A
34	1	504	G
34	1	509	G
34	1	523	A
34	1	524	U
34	1	525	A
34	1	526	A
34	1	528	A
34	1	533	A
34	1	534	G
34	1	541	U
34	1	542	U
34	1	544	G
34	1	545	A
34	1	546	G
34	1	547	G
34	1	548	C
34	1	553	U
34	1	554	A
34	1	560	A
34	1	561	A
34	1	562	U
34	1	576	A
34	1	587	A
34	1	589	G
34	1	590	A
34	1	591	U
34	1	592	C
34	1	594	A
34	1	607	U
34	1	608	C
34	1	613	G
34	1	614	C
34	1	620	G
34	1	629	A
34	1	643	A

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Mol	Chain	Res	Type
34	1	644	G
34	1	645	C
34	1	655	A
34	1	660	C
34	1	661	U
34	1	664	A
34	1	668	A
34	1	669	A
34	1	672	A
34	1	673	G
34	1	675	U
34	1	683	G
34	1	687	C
34	1	688	U
34	1	689	U
34	1	690	G
34	1	695	C
34	1	742	U
34	1	743	U
34	1	744	G
34	1	746	C
34	1	748	C
34	1	751	G
34	1	798	G
34	1	799	U
34	1	800	U
34	1	801	U
34	1	809	A
34	1	811	A
34	1	812	A
34	1	821	G
34	1	823	U
34	1	834	C
34	1	837	A
34	1	838	G
34	1	839	C
34	1	840	C
34	1	841	G
34	1	847	A
34	1	848	U
34	1	852	G
34	1	861	A

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Mol	Chain	Res	Type
34	1	862	A
34	1	868	G
34	1	870	A
34	1	872	A
34	1	874	G
34	1	886	A
34	1	891	G
34	1	913	A
34	1	914	U
34	1	917	U
34	1	919	A
34	1	920	A
34	1	921	G
34	1	929	G
34	1	938	A
34	1	940	U
34	1	943	U
34	1	953	C
34	1	954	U
34	1	955	A
34	1	956	G
34	1	959	G
34	1	960	U
34	1	961	G
34	1	963	A
34	1	968	U
34	1	969	U
34	1	978	G
34	1	983	A
34	1	990	A
34	1	992	A
34	1	993	G
34	1	1002	U
34	1	1008	A
34	1	1015	U
34	1	1017	U
34	1	1044	G
34	1	1048	G
34	1	1049	A
34	1	1050	A
34	1	1051	G
34	1	1057	C

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Mol	Chain	Res	Type
34	1	1058	A
34	1	1060	A
34	1	1061	U
34	1	1066	U
34	1	1077	A
34	1	1085	C
34	1	1091	C
34	1	1095	C
34	1	1096	G
34	1	1099	G
34	1	1109	C
34	1	1113	A
34	1	1114	U
34	1	1116	C
34	1	1139	C
34	1	1140	G
34	1	1146	C
34	1	1149	A
34	1	1150	A
34	1	1156	U
34	1	1161	U
34	1	1166	G
34	1	1188	A
34	1	1195	A
34	1	1196	A
34	1	1199	A
34	1	1202	U
34	1	1207	G
34	1	1212	G
34	1	1215	C
34	1	1217	A
34	1	1221	G
34	1	1224	G
34	1	1242	U
34	1	1251	A
34	1	1254	C
34	1	1256	G
34	1	1257	G
34	1	1259	A
34	1	1261	C
34	1	1262	C
34	1	1264	C

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Mol	Chain	Res	Type
34	1	1274	G
34	1	1275	G
34	1	1285	G
34	1	1287	A
34	1	1288	U
34	1	1289	U
34	1	1290	G
34	1	1291	A
34	1	1301	A
34	1	1302	G
34	1	1303	C
34	1	1321	G
34	1	1327	G
34	1	1330	G
34	1	1331	C
34	1	1333	U
34	1	1342	U
34	1	1345	G
34	1	1351	G
34	1	1354	G
34	1	1356	G
34	1	1358	U
34	1	1360	U
34	1	1371	U
34	1	1372	U
34	1	1375	G
34	1	1378	A
34	1	1380	C
34	1	1382	A
34	1	1387	G
34	1	1399	C
34	1	1409	A
34	1	1420	G
34	1	1439	A
34	1	1442	U
34	1	1452	A
34	1	1454	A
34	1	1456	G
34	1	1463	U
34	1	1476	A
34	1	1477	U
34	1	1478	U

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Mol	Chain	Res	Type
34	1	1479	G
34	1	1484	A
34	1	1489	A
34	1	1494	U
34	1	1497	G
34	1	1498	A
34	1	1501	C
34	1	1505	U
34	1	1507	G
34	1	1508	A
34	1	1519	U
34	1	1520	G
34	1	1521	C
34	1	1522	A
34	1	1527	C
34	1	1531	A
34	1	1533	A
34	1	1535	U
34	1	1536	G
34	1	1537	A
34	1	1539	U
34	1	1544	C
34	1	1548	G
34	1	1553	C
34	1	1554	C
34	1	1555	U
34	1	1558	C
34	1	1580	A
34	1	1586	U
34	1	1588	A
34	1	1599	U
34	1	1601	A
34	1	1604	G
34	1	1606	G
34	1	1617	G
34	1	1621	U
34	1	1622	U
34	1	1623	A
34	1	1624	U
34	1	1646	C
34	1	1660	C
34	1	1661	A

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Mol	Chain	Res	Type
34	1	1662	U
34	1	1663	A
34	1	1665	G
34	1	1671	G
34	1	1678	A
34	1	1691	U
34	1	1699	A
34	1	1721	U
34	1	1726	G
34	1	1737	G
34	1	1742	C
34	1	1745	A
34	1	1750	C
34	1	1757	G
34	1	1783	C
34	1	1784	G
34	1	1823	A
34	1	1829	G
34	1	1831	A
34	1	1834	A
34	1	1835	A
34	1	1838	U
34	1	1843	G
34	1	1849	G
34	1	1861	G
34	1	1862	G
34	1	1863	A
34	1	1864	U
34	1	1865	C
34	1	1866	A
34	1	1869	A
35	2	5	U
35	2	6	G
35	2	45	C

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	1	227	U
34	1	332	G
34	1	369	C
34	1	463	C

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Mol	Chain	Res	Type
34	1	475	C
34	1	546	G
34	1	547	G
34	1	561	A
34	1	797	C
34	1	822	U
34	1	869	A
34	1	962	A
34	1	1095	C
34	1	1211	G
34	1	1554	C
34	1	1756	C
35	2	5	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 76 ligands modelled in this entry, 76 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	d	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	d	10:HIS	C	11:PRO	N	1.10

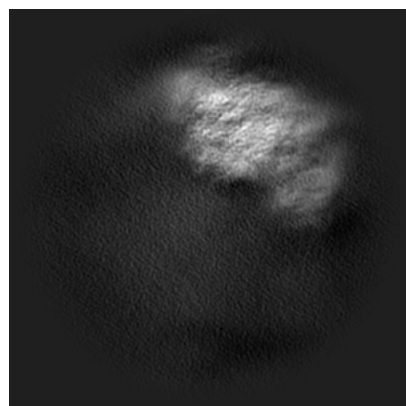
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45307. These allow visual inspection of the internal detail of the map and identification of artifacts.

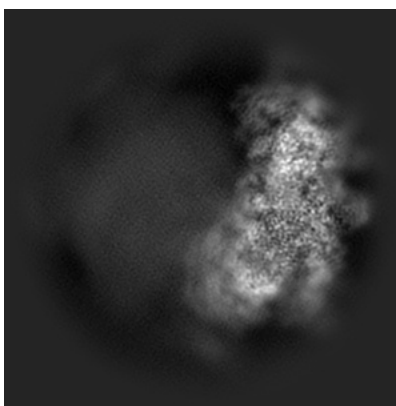
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

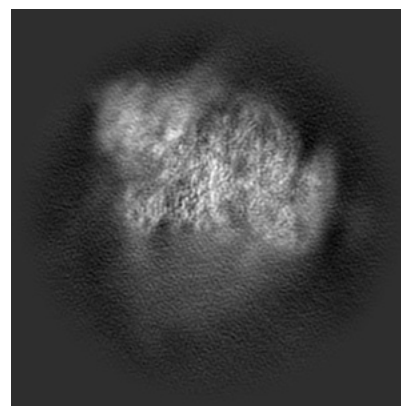
6.1.1 Primary map



X

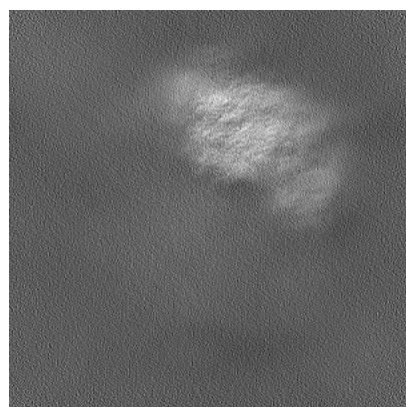


Y

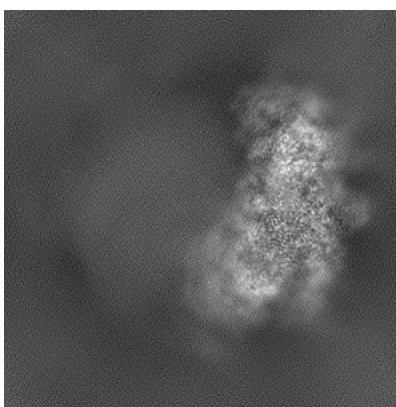


Z

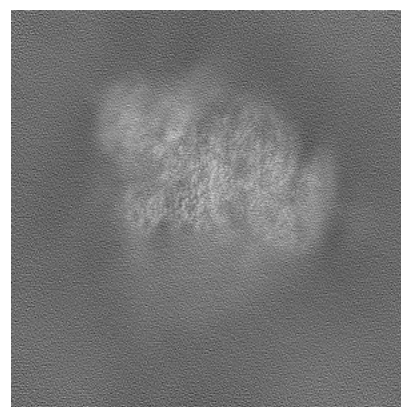
6.1.2 Raw map



X



Y

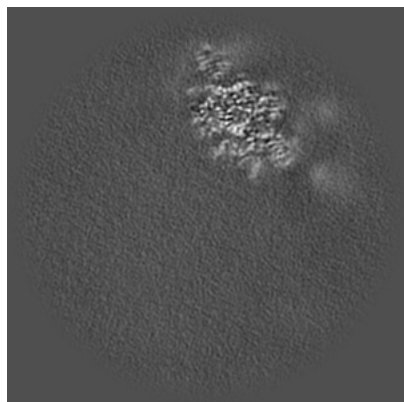


Z

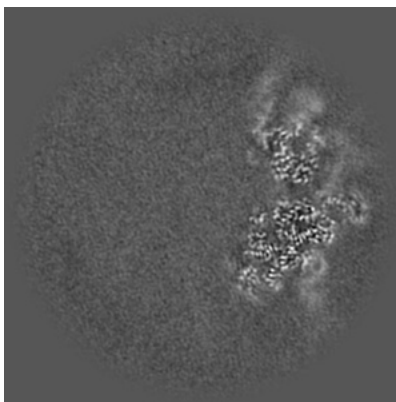
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

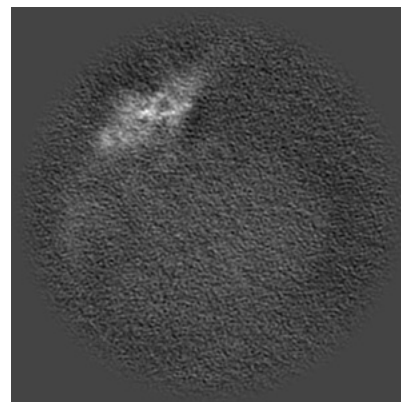
6.2.1 Primary map



X Index: 200

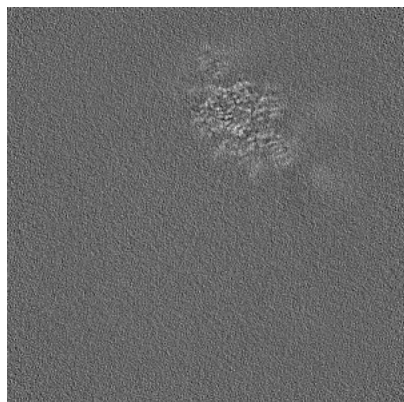


Y Index: 200

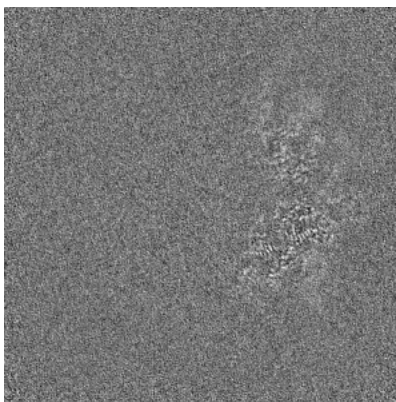


Z Index: 200

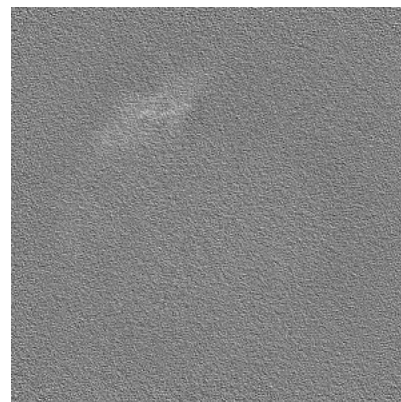
6.2.2 Raw map



X Index: 200



Y Index: 200

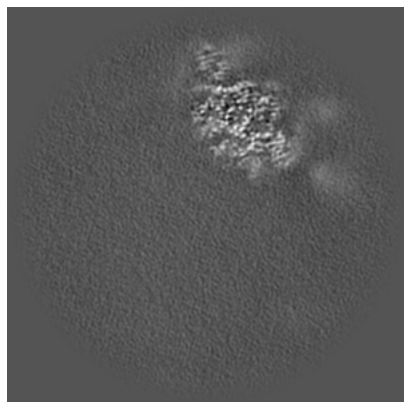


Z Index: 200

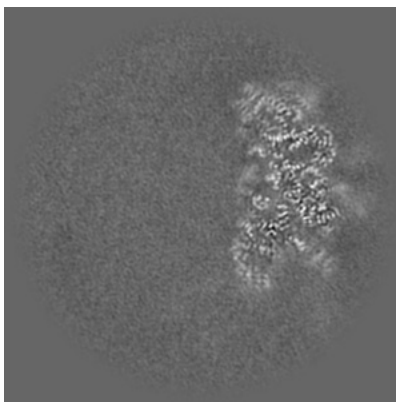
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

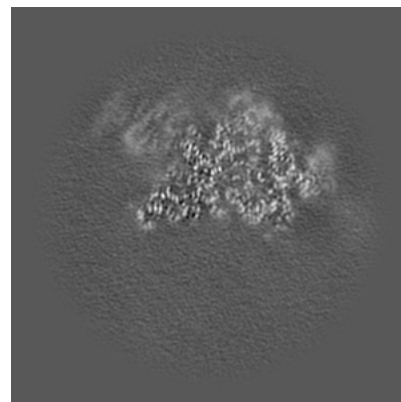
6.3.1 Primary map



X Index: 201

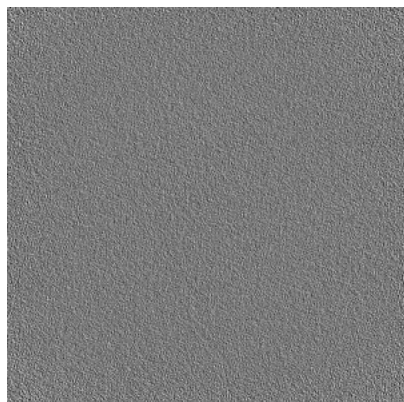


Y Index: 226

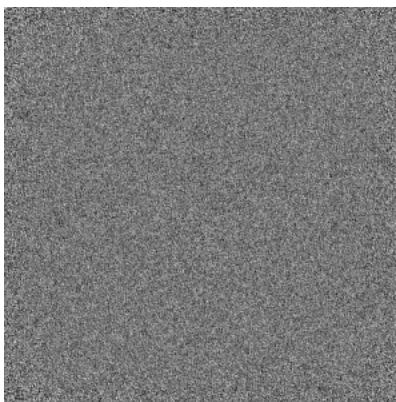


Z Index: 277

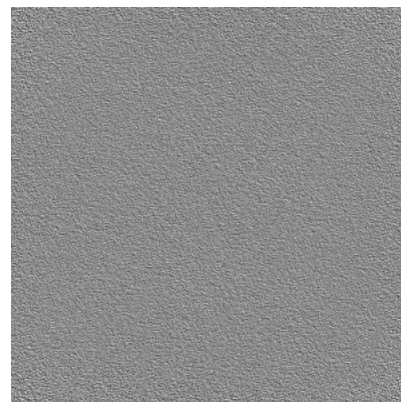
6.3.2 Raw map



X Index: 0



Y Index: 0

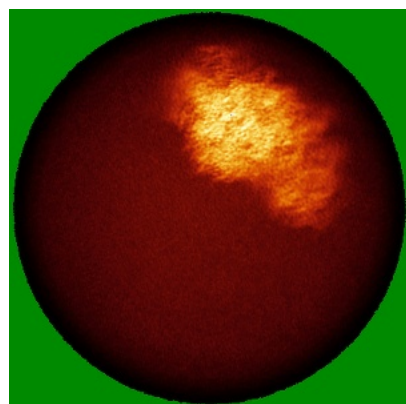


Z Index: 0

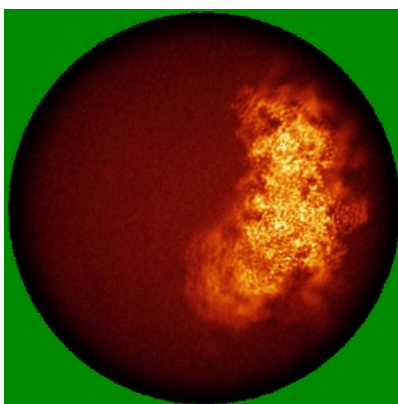
The images above show the largest variance slices of the map in three orthogonal directions.

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

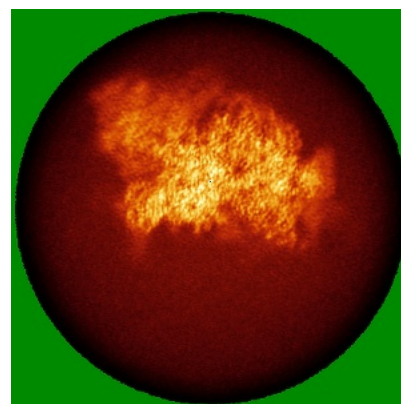
6.4.1 Primary map



X

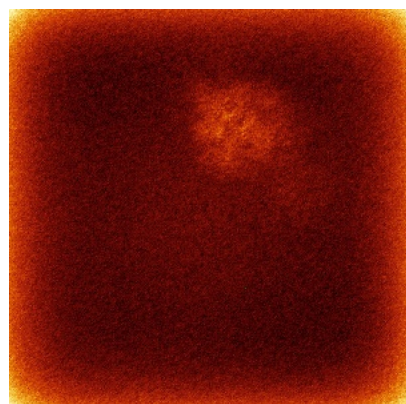


Y

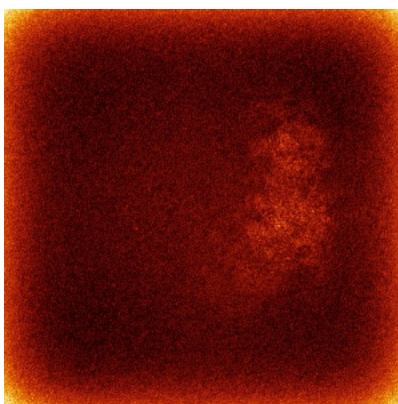


Z

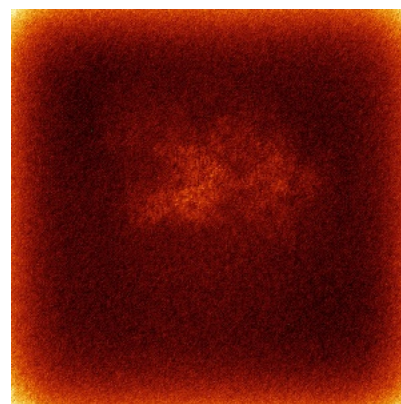
6.4.2 Raw map



X



Y

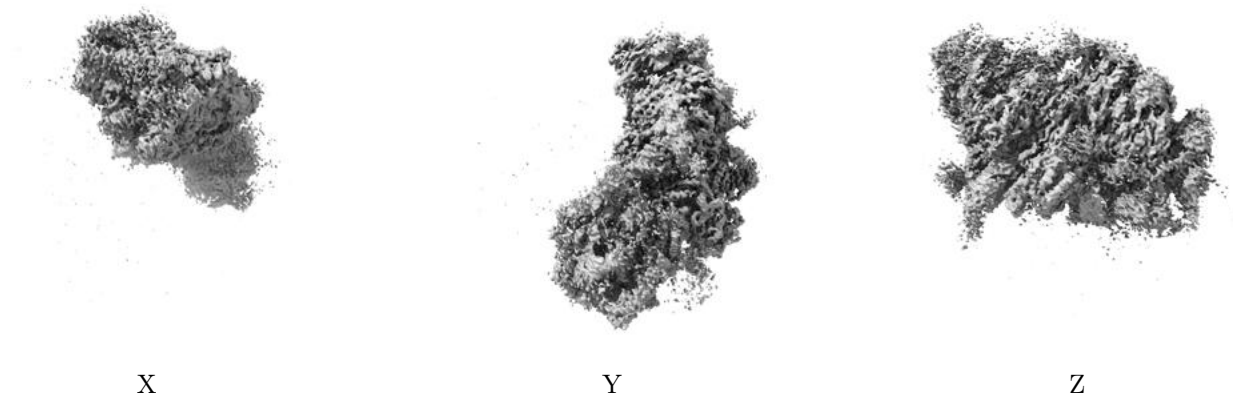


Z

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

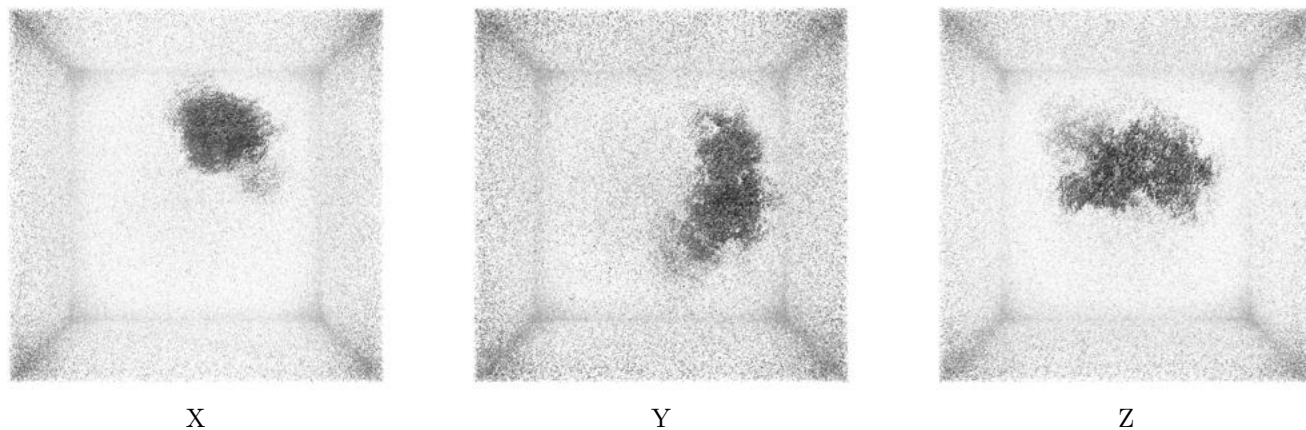
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.43. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

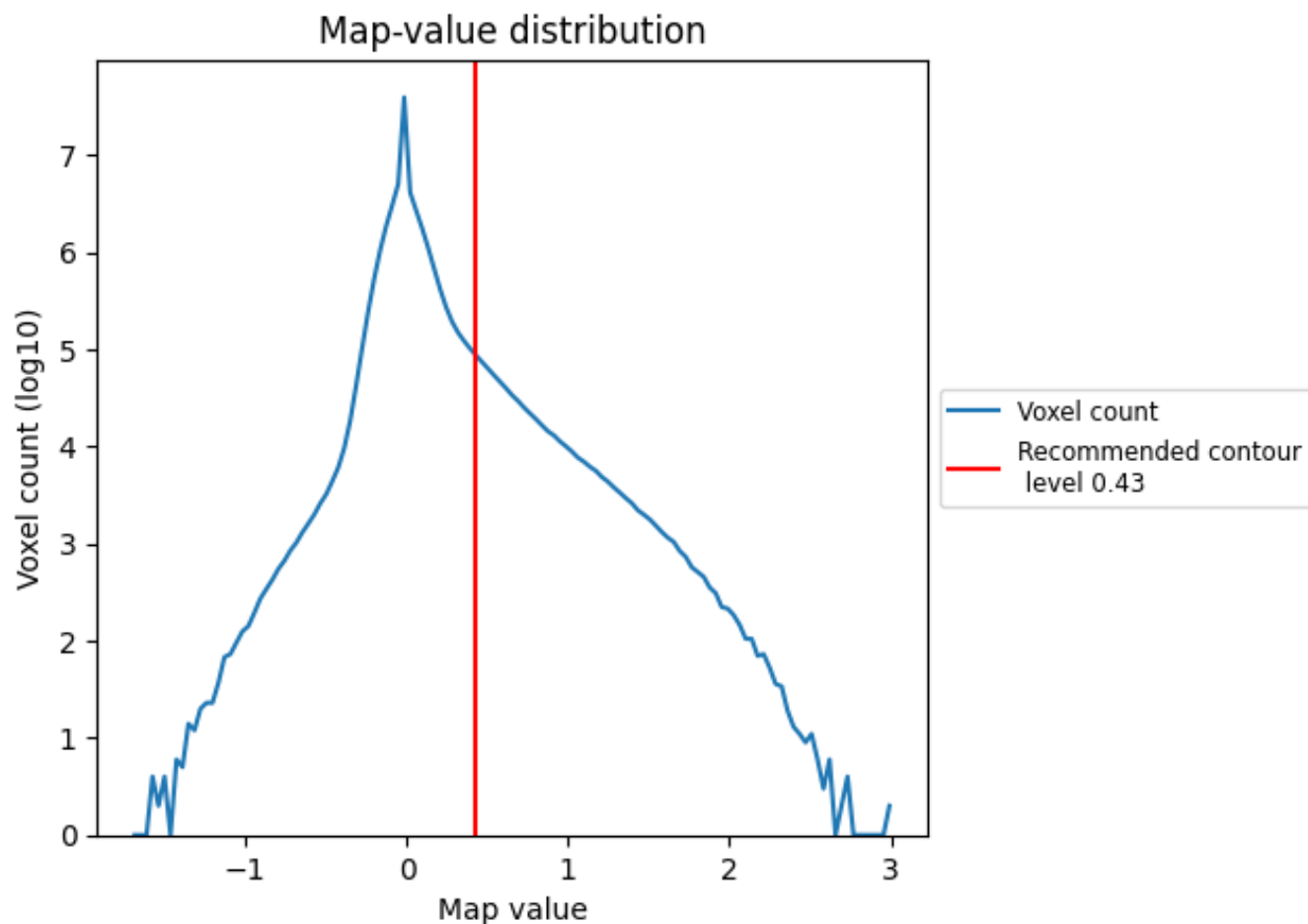
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

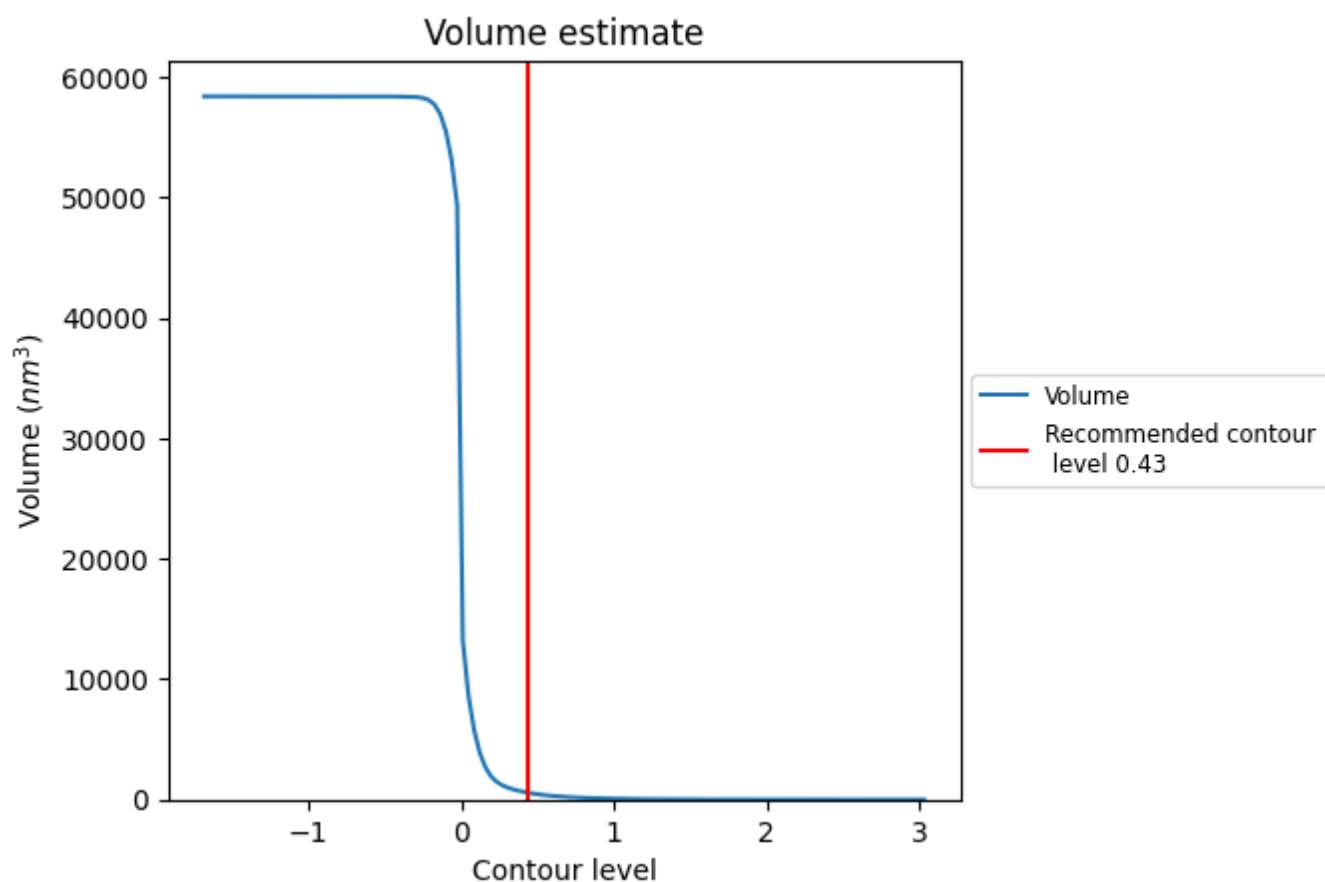
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

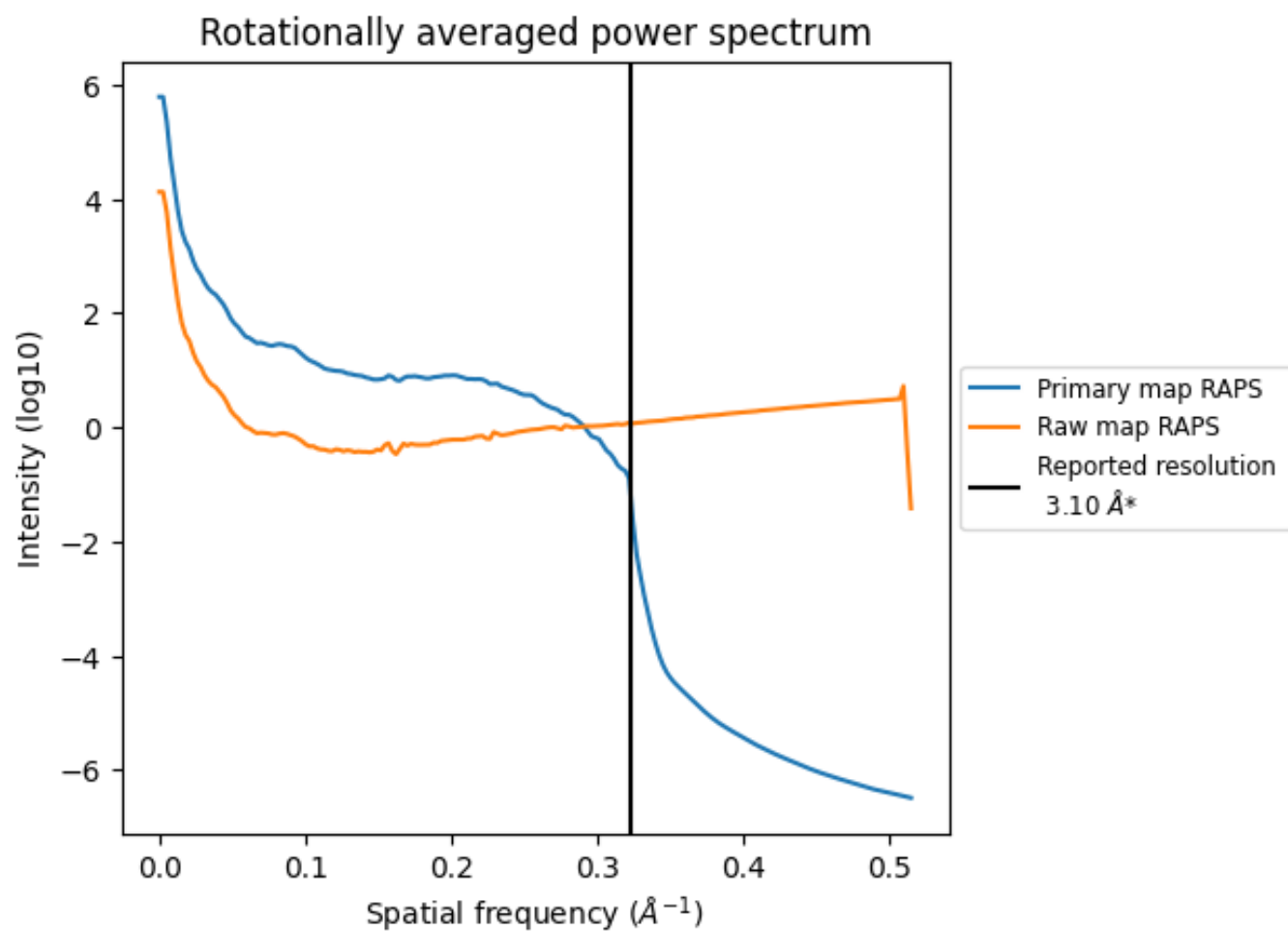
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 586 nm³; this corresponds to an approximate mass of 529 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 ⓘ

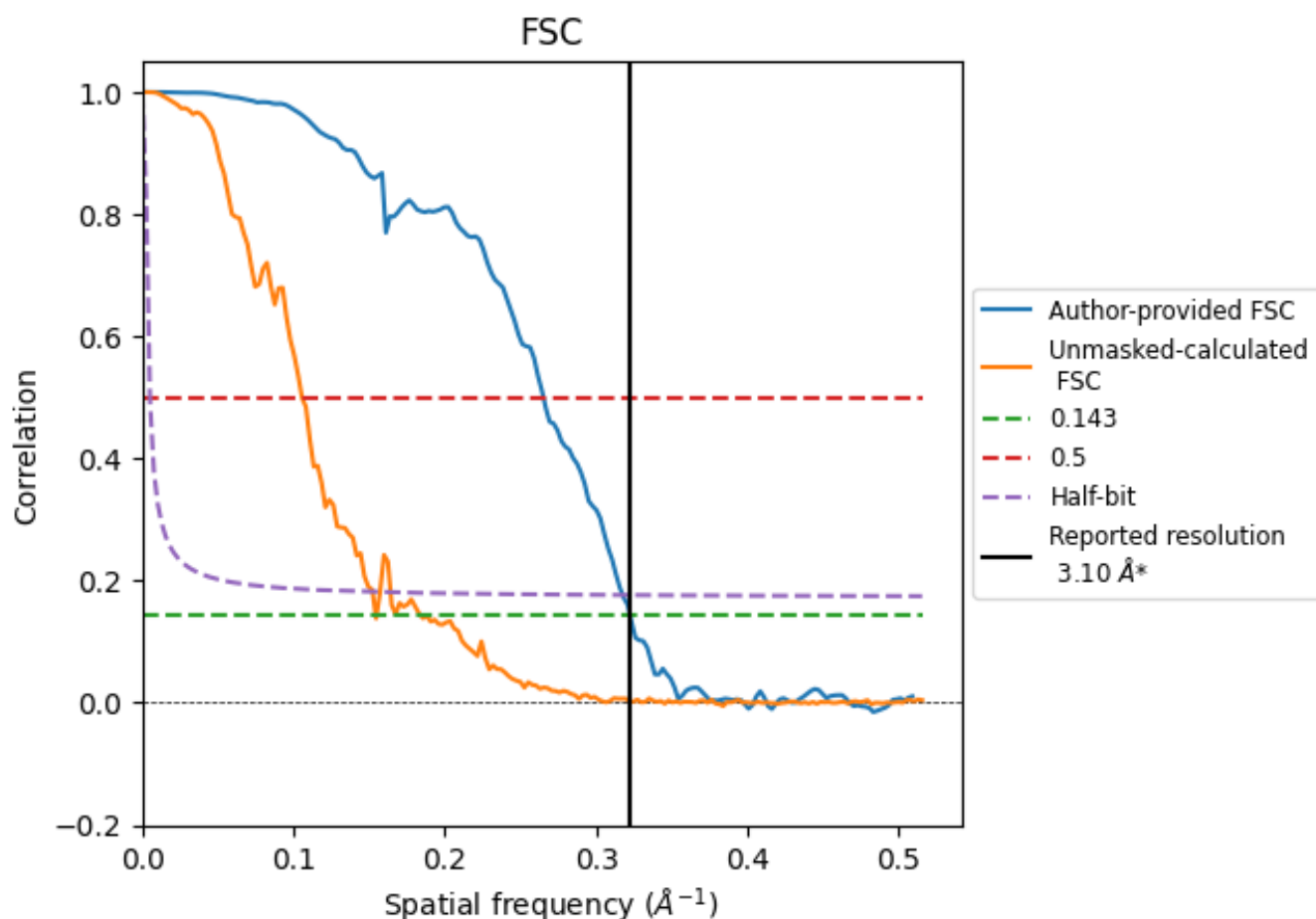


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

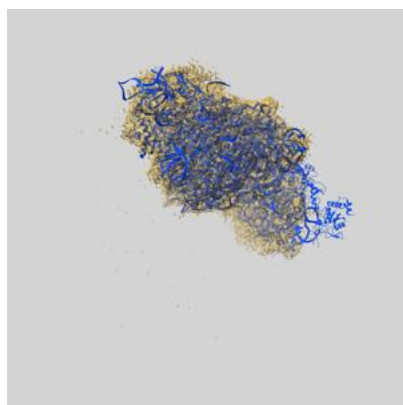
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.10	3.77	3.15
Unmasked-calculated*	6.48	9.47	6.57

*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 6.48 differs from the reported value 3.1 by more than 10 %

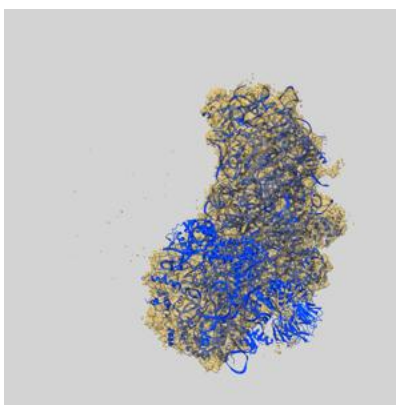
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45307 and PDB model 9C8K. Per-residue inclusion information can be found in section [3](#) on page [12](#).

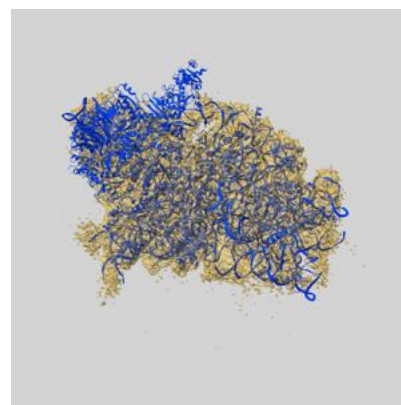
9.1 Map-model overlay [i](#)



X



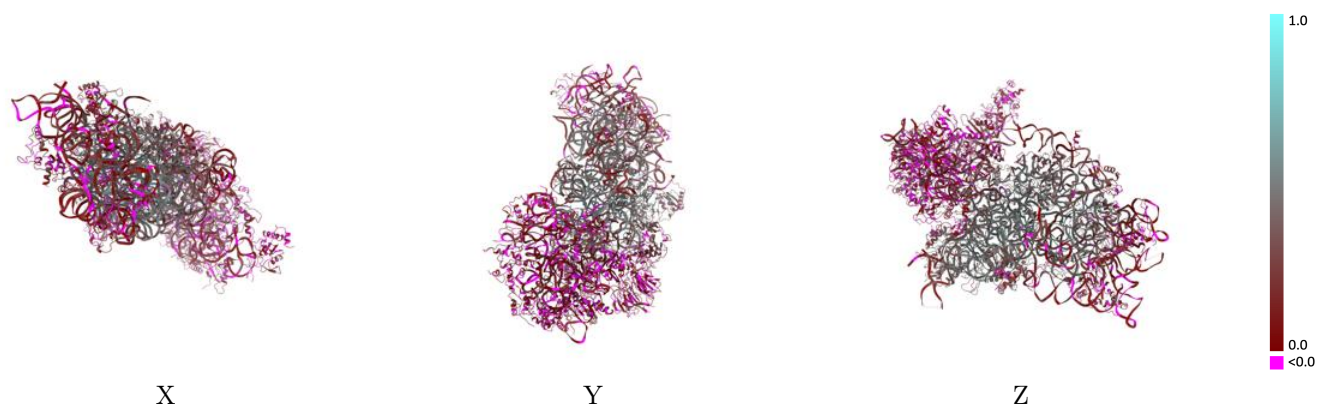
Y



Z

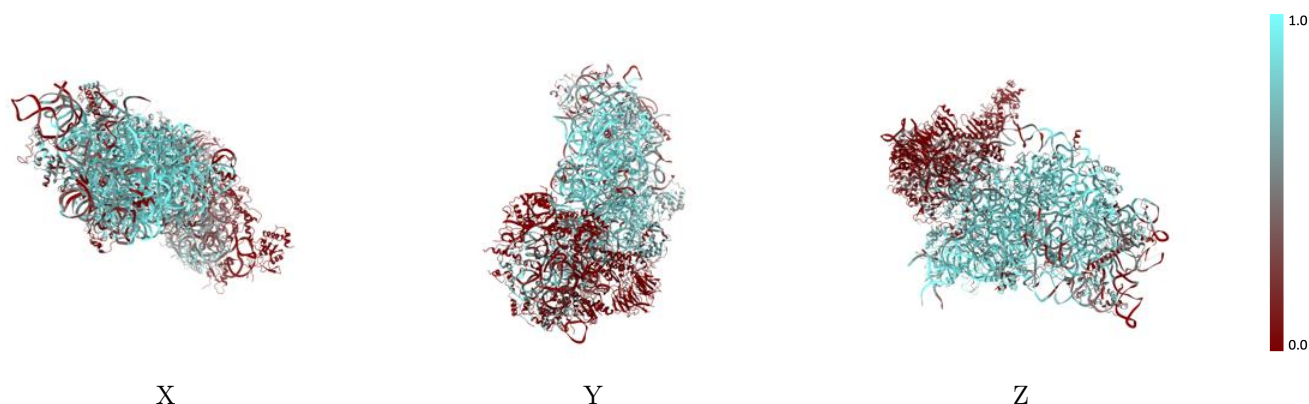
The images above show the 3D surface view of the map at the recommended contour level 0.43 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



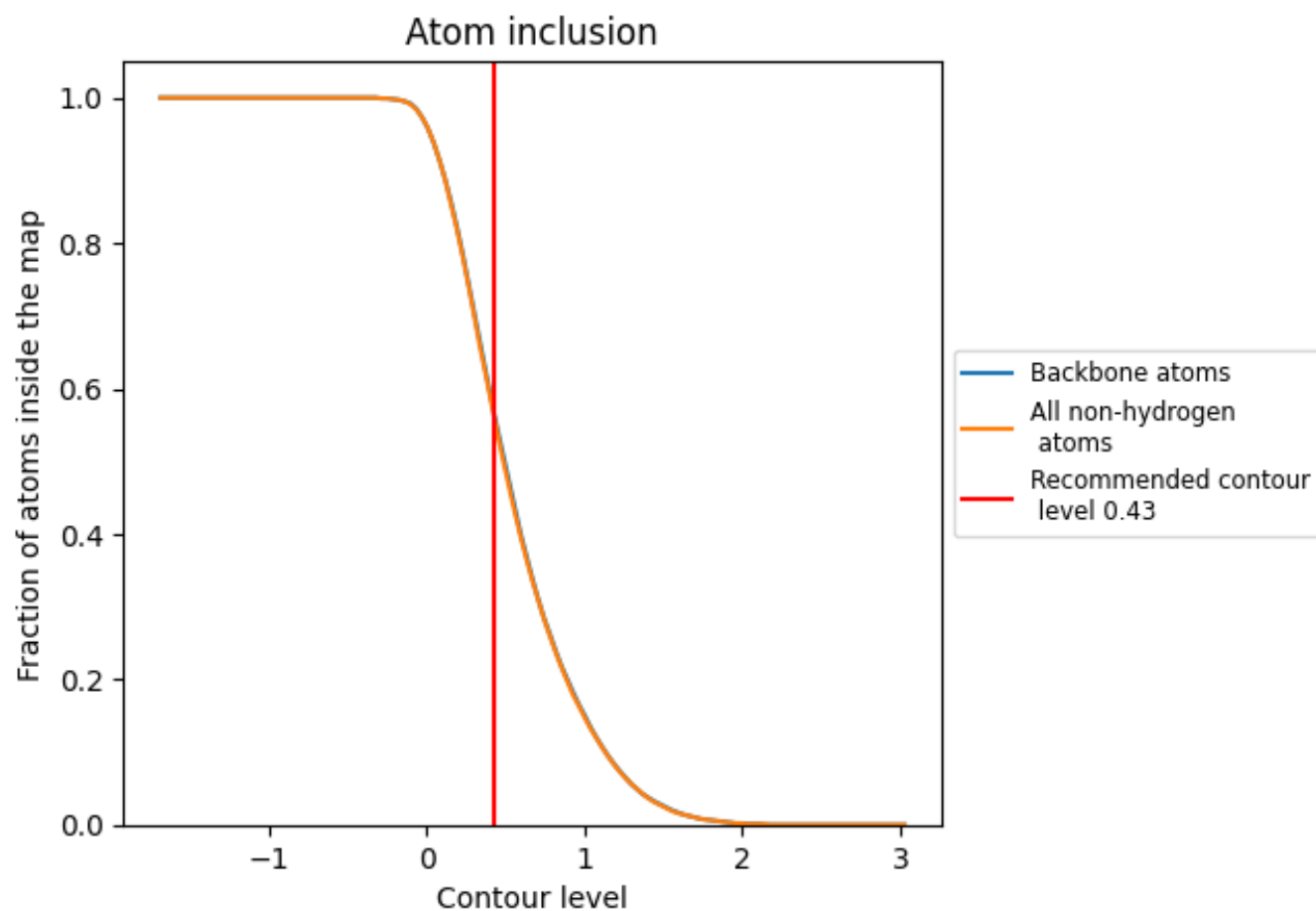
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.43).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 56% 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 (0.43) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5610	 0.2560
1	 0.6570	 0.2800
2	 0.7180	 0.1940
A	 0.5930	 0.2380
B	 0.8190	 0.4000
C	 0.7400	 0.4020
D	 0.0700	 0.1280
E	 0.8180	 0.4050
F	 0.3000	 0.0800
G	 0.3060	 0.0770
H	 0.5820	 0.2850
I	 0.5310	 0.1780
J	 0.7140	 0.3400
K	 0.0370	 0.0900
L	 0.6560	 0.3760
M	 0.0000	 0.0720
N	 0.8100	 0.4510
O	 0.7160	 0.3500
P	 0.3050	 0.1080
Q	 0.1900	 0.1120
R	 0.1010	 0.0830
S	 0.4720	 0.1330
T	 0.3280	 0.0930
U	 0.0320	 0.0800
V	 0.6830	 0.3720
W	 0.8470	 0.4820
X	 0.6800	 0.4350
Y	 0.5520	 0.2210
Z	 0.2630	 0.1080
a	 0.6630	 0.3930
b	 0.8010	 0.4010
c	 0.1910	 0.0890
d	 0.2020	 0.0940
e	 0.4290	 0.2600
f	 0.0920	 0.0660
g	 0.0080	 0.0990

