



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 08:51 PM UTC

PDB ID : 6ID1 / pdb_00006id1
EMDB ID : EMD-9647
Title : Cryo-EM structure of a human intron lariat spliceosome after Prp43 loaded (ILS2 complex) at 2.9 angstrom resolution
Authors : Zhang, X.; Zhan, X.; Yan, C.; Shi, Y.
Deposited on : 2018-09-07
Resolution : 2.86 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

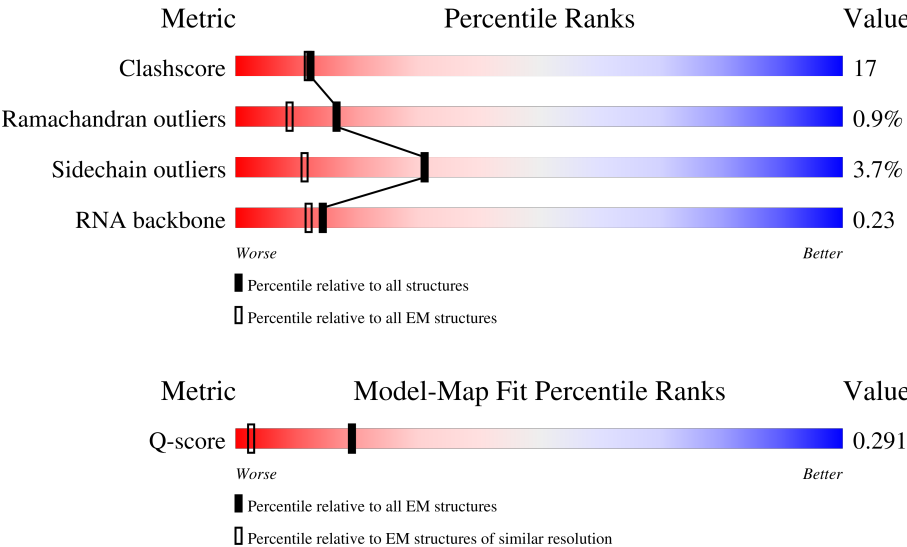
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 Å.

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



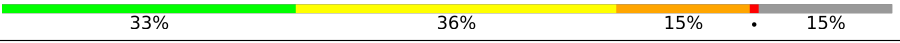
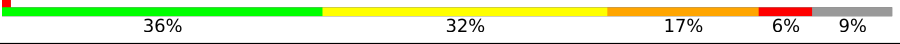
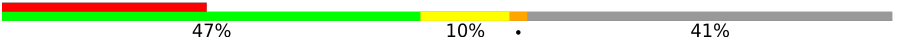
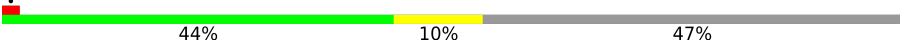
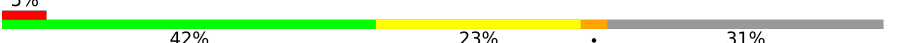
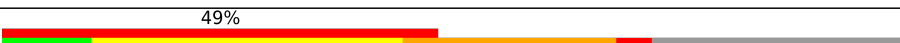
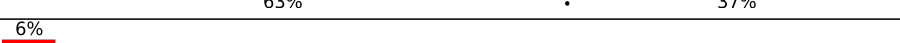
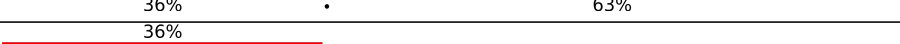
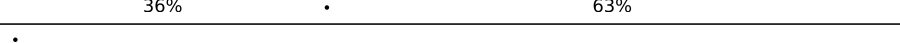
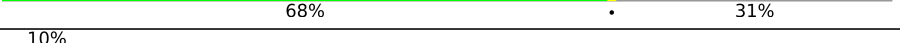
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

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

Mol	Chain	Length	Quality of chain
1	A	2335	69% 14% 15%
2	B	117	24% 26% 33% 16%
3	C	972	70% 20% 9%

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Mol	Chain	Length	Quality of chain
4	E	357	
5	F	107	
6	J	848	
7	L	802	
8	M	243	
9	N	144	
10	O	420	
11	P	229	
12	R	536	
13	S	166	
14	T	514	
15	W	579	
16	G	272	
17	H	188	
18	U	894	
19	a	126	
19	h	126	
20	b	231	
20	i	231	
21	c	119	
21	j	119	
22	d	118	
22	k	118	
23	f	86	
23	m	86	

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Mol	Chain	Length	Quality of chain
24	e	92	
24	l	92	
25	g	76	
25	n	76	
26	q	504	
26	r	504	
26	s	504	
26	t	504	
27	K	225	
28	I	855	
29	Q	1485	
30	y	301	
31	o	255	
32	p	225	
33	V	795	

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

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

2 Entry composition

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

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

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

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

- Molecule 2 is a RNA chain called U5snRNA.

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

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

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

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

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

- Molecule 5 is a RNA chain called U6snRNA.

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

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

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

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

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

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

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

- Molecule 9 is a protein called Protein BUD31 homolog.

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

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

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

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

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

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

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

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

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

- Molecule 14 is a protein called Pleiotropic regulator 1.

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

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

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

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

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

- Molecule 17 is a RNA chain called U2snRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 29 is a protein called RNA helicase aquarius.

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

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

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

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

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

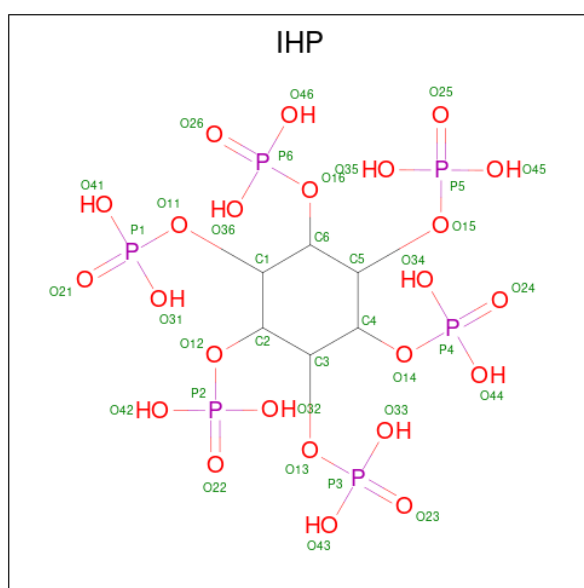
- Molecule 32 is a protein called U2 small nuclear ribonucleoprotein B'.

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

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

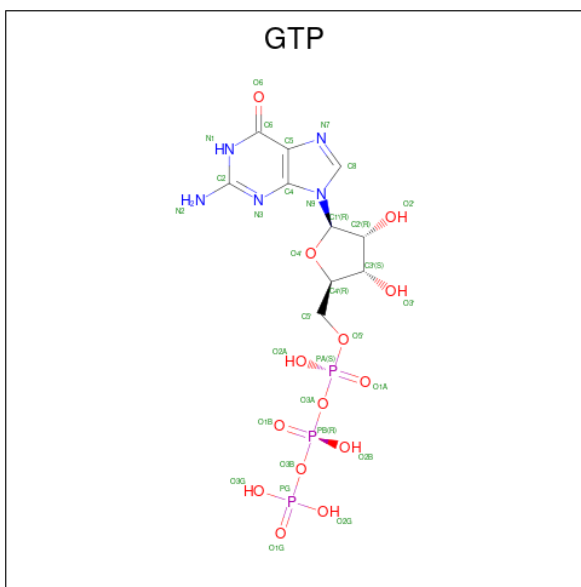
Mol	Chain	Residues	Atoms				AltConf	Trace
33	V	663	Total	C	N	O	0	0
			3285	1959	663	663		

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



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

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



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

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

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

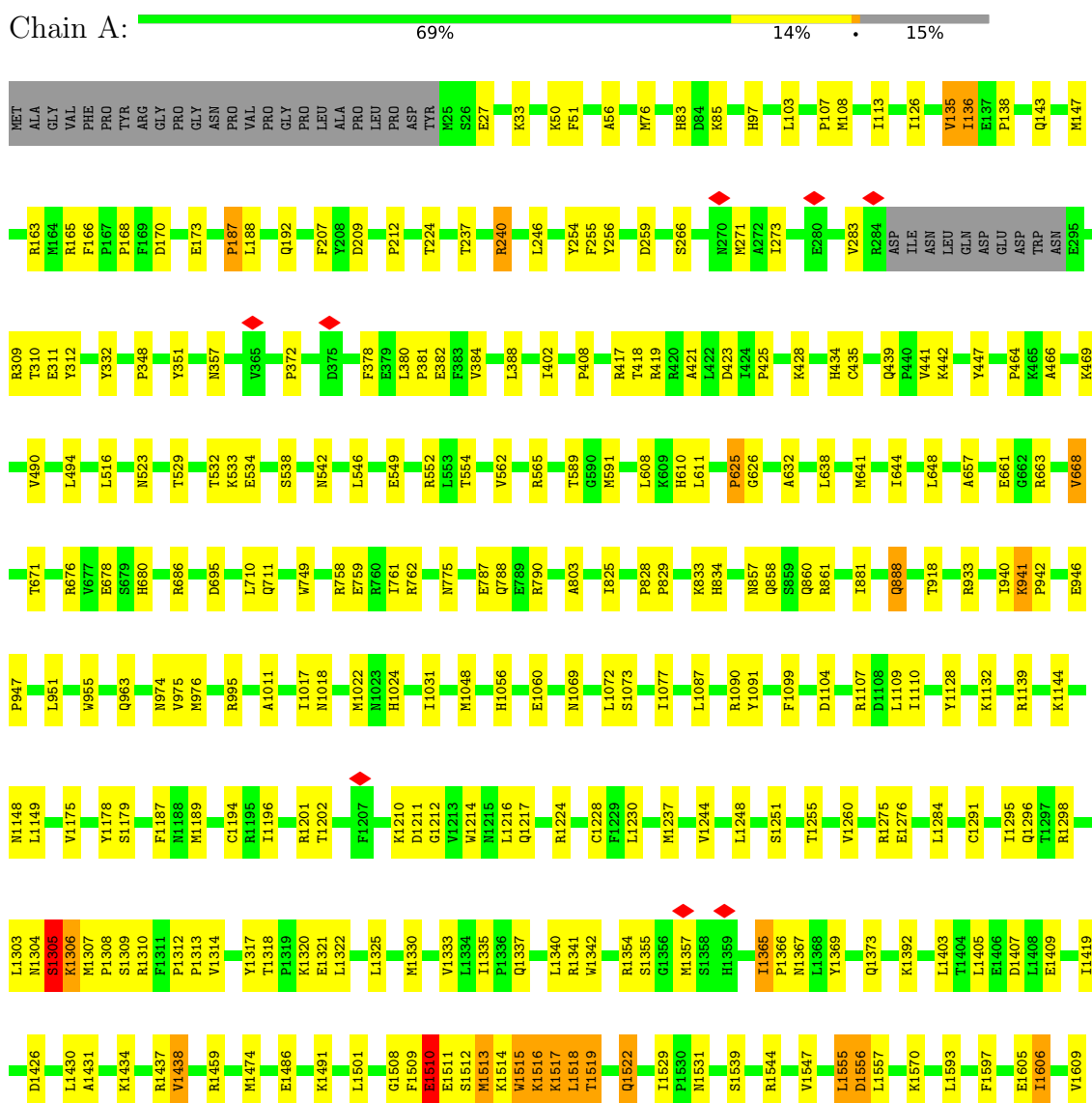
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

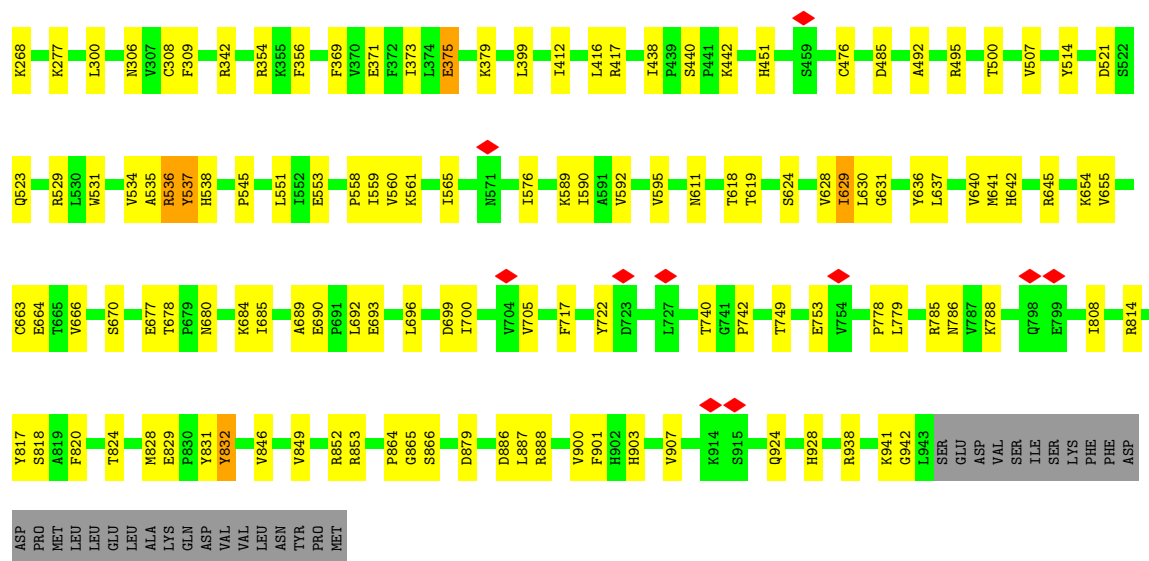
Mol	Chain	Residues	Atoms		AltConf
37	N	3	Total	Zn	0
			3	3	
37	O	3	Total	Zn	0
			3	3	
37	U	1	Total	Zn	0
			1	1	

3 Residue-property plots

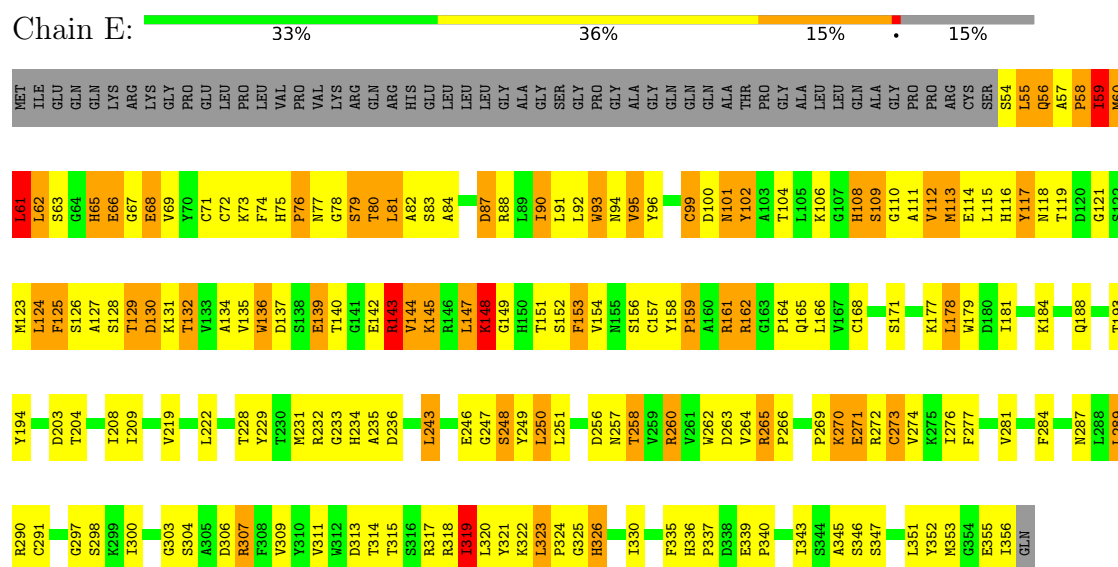
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

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

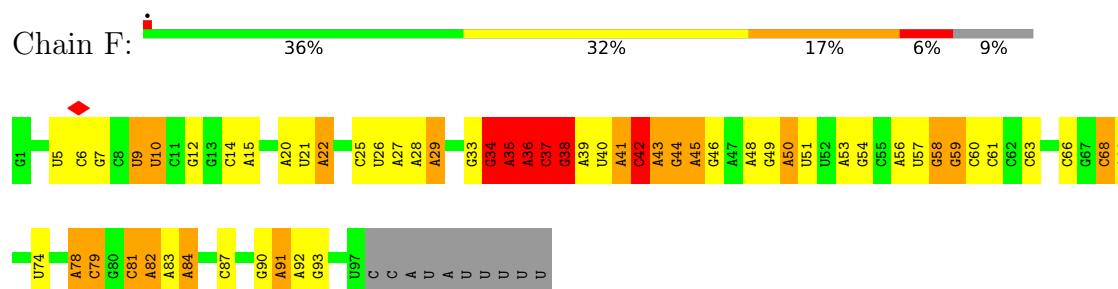




- Molecule 4: U5 small nuclear ribonucleoprotein 40 kDa protein

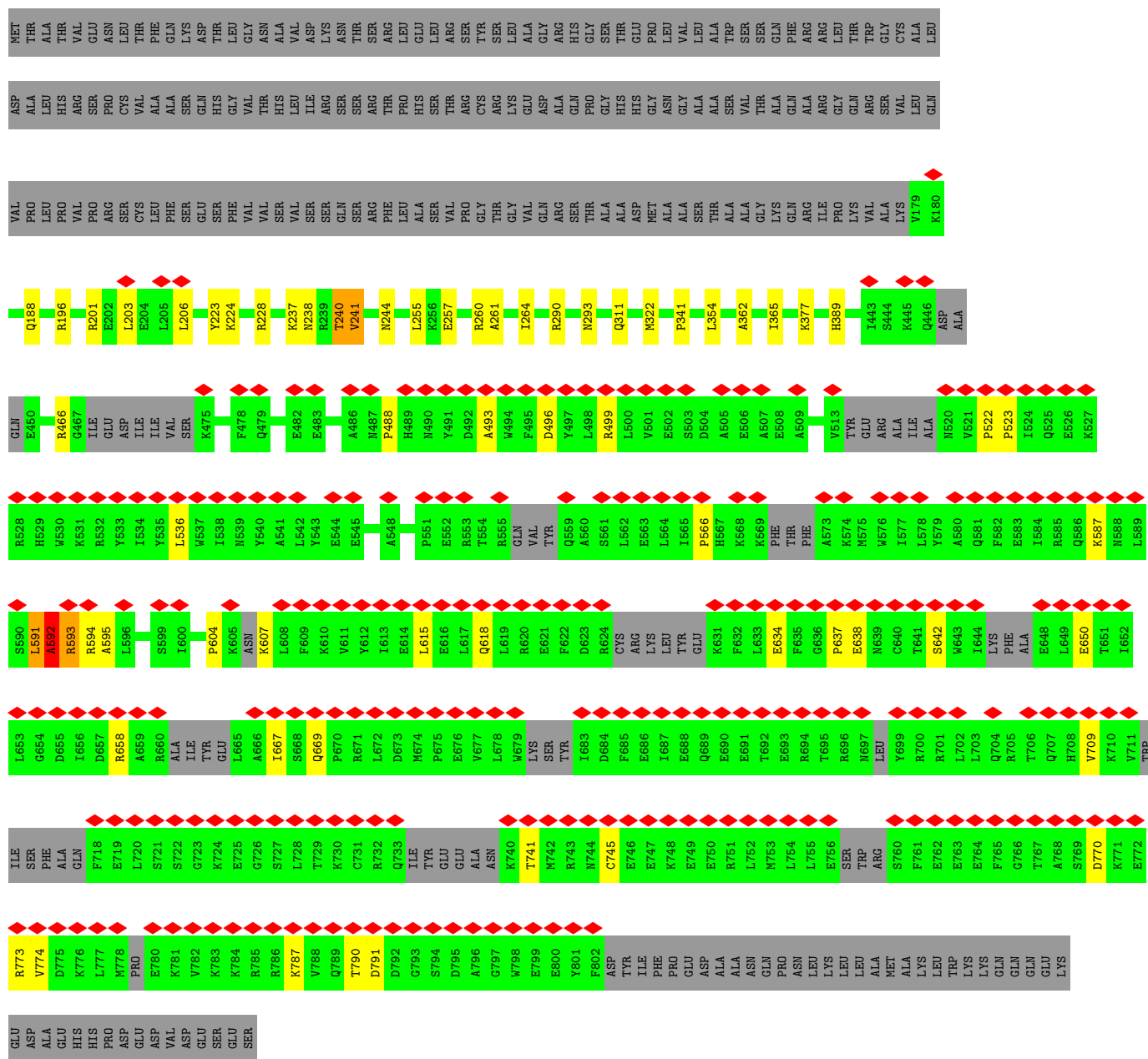


- Molecule 5: U6snRNA

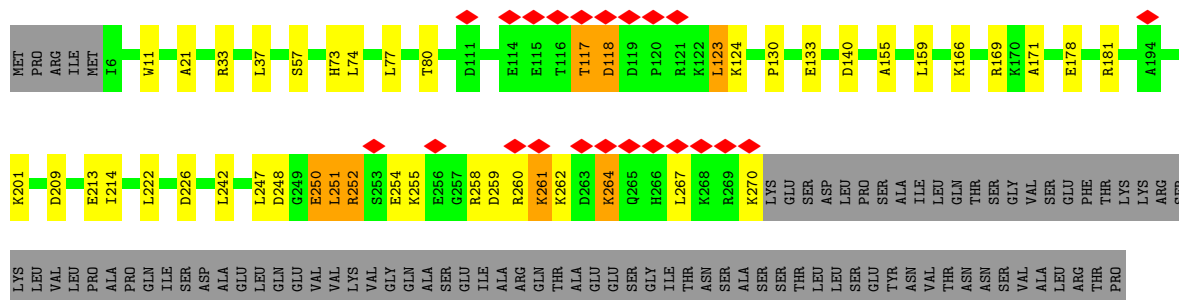


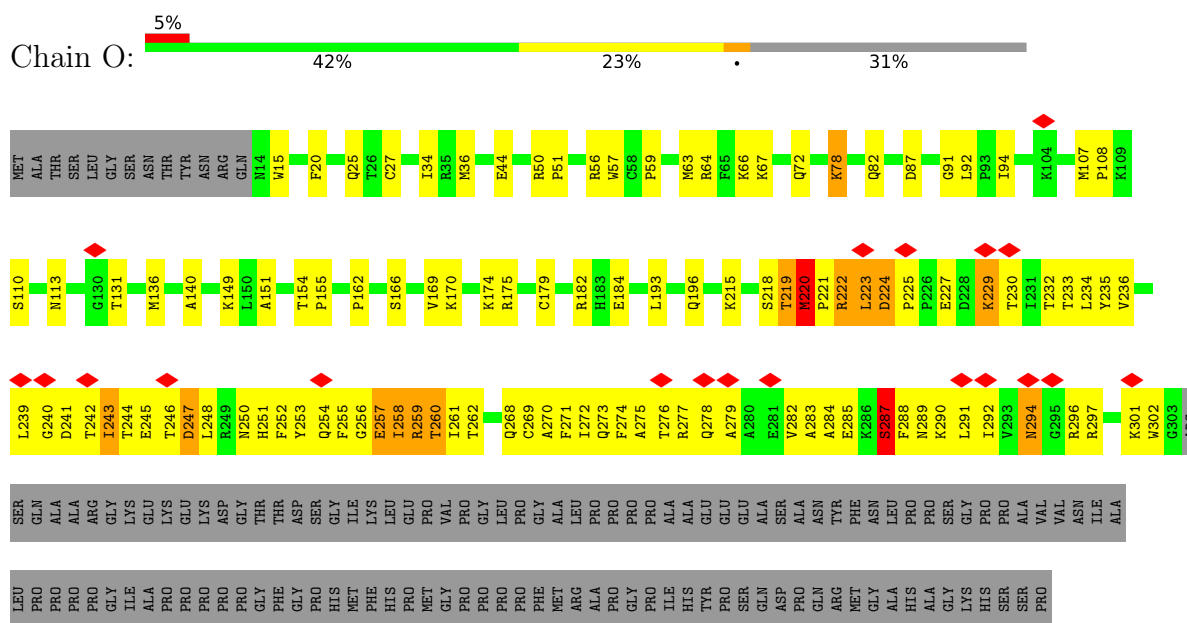
- Molecule 6: Crooked neck-like protein 1



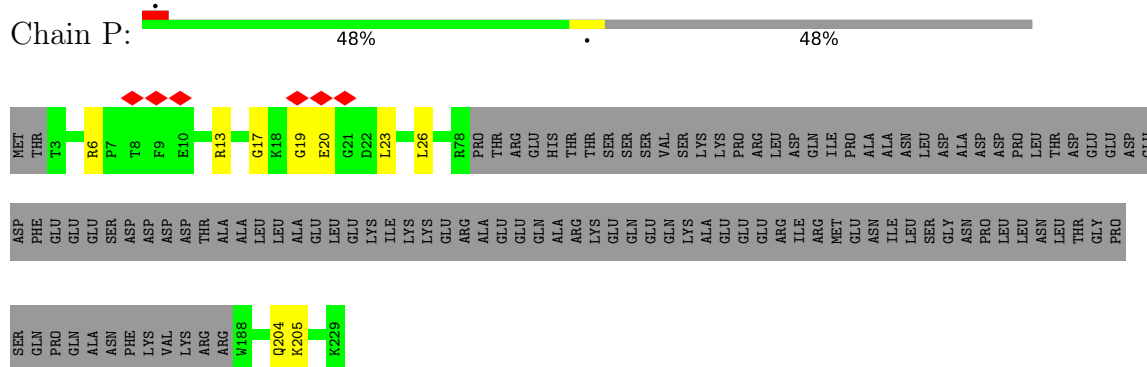


● Molecule 7: Cell division cycle 5-like protein

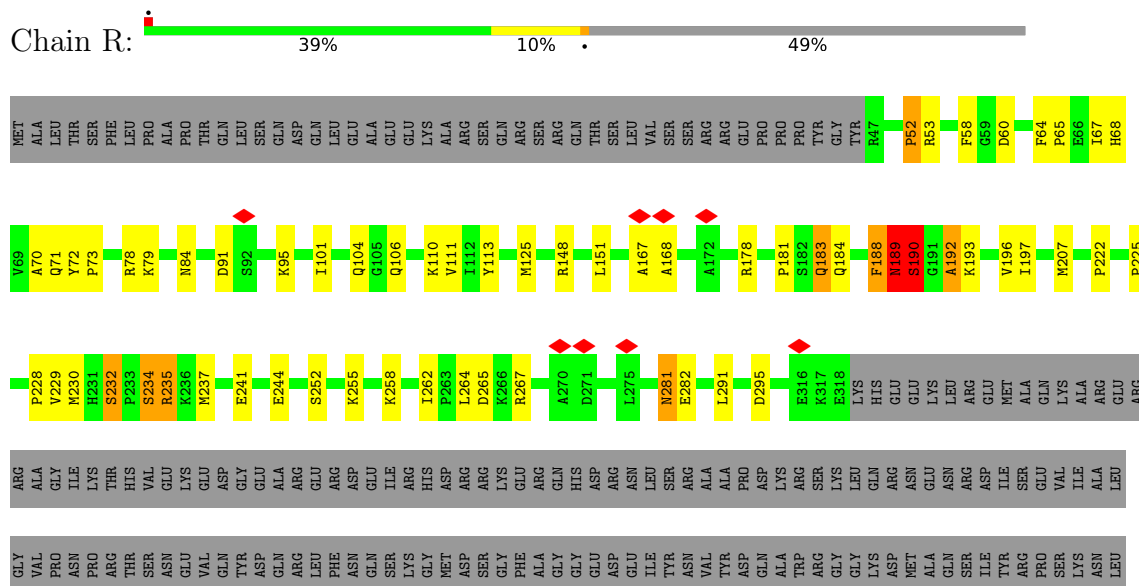




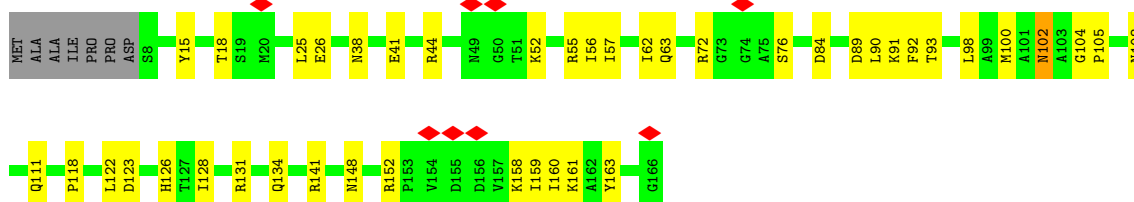
• Molecule 11: Spliceosome-associated protein CWC15 homolog



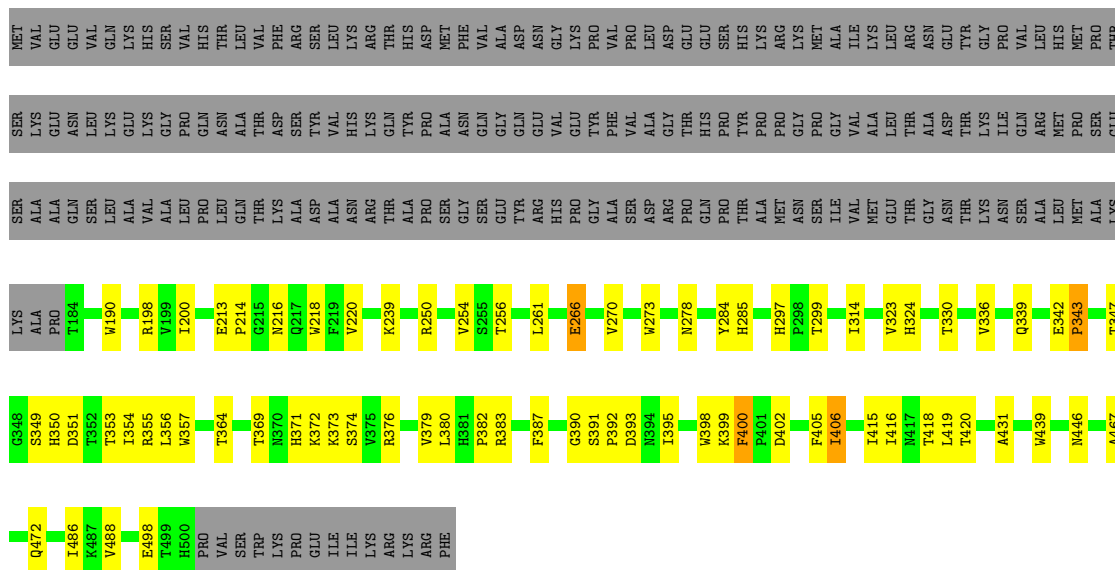
• Molecule 12: SNW domain-containing protein 1



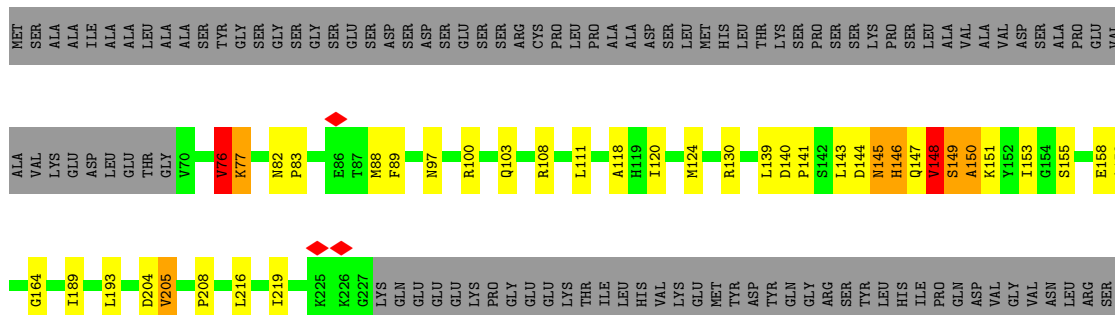
- Molecule 13: Peptidyl-prolyl cis-trans isomerase-like 1



- Molecule 14: Pleiotropic regulator 1

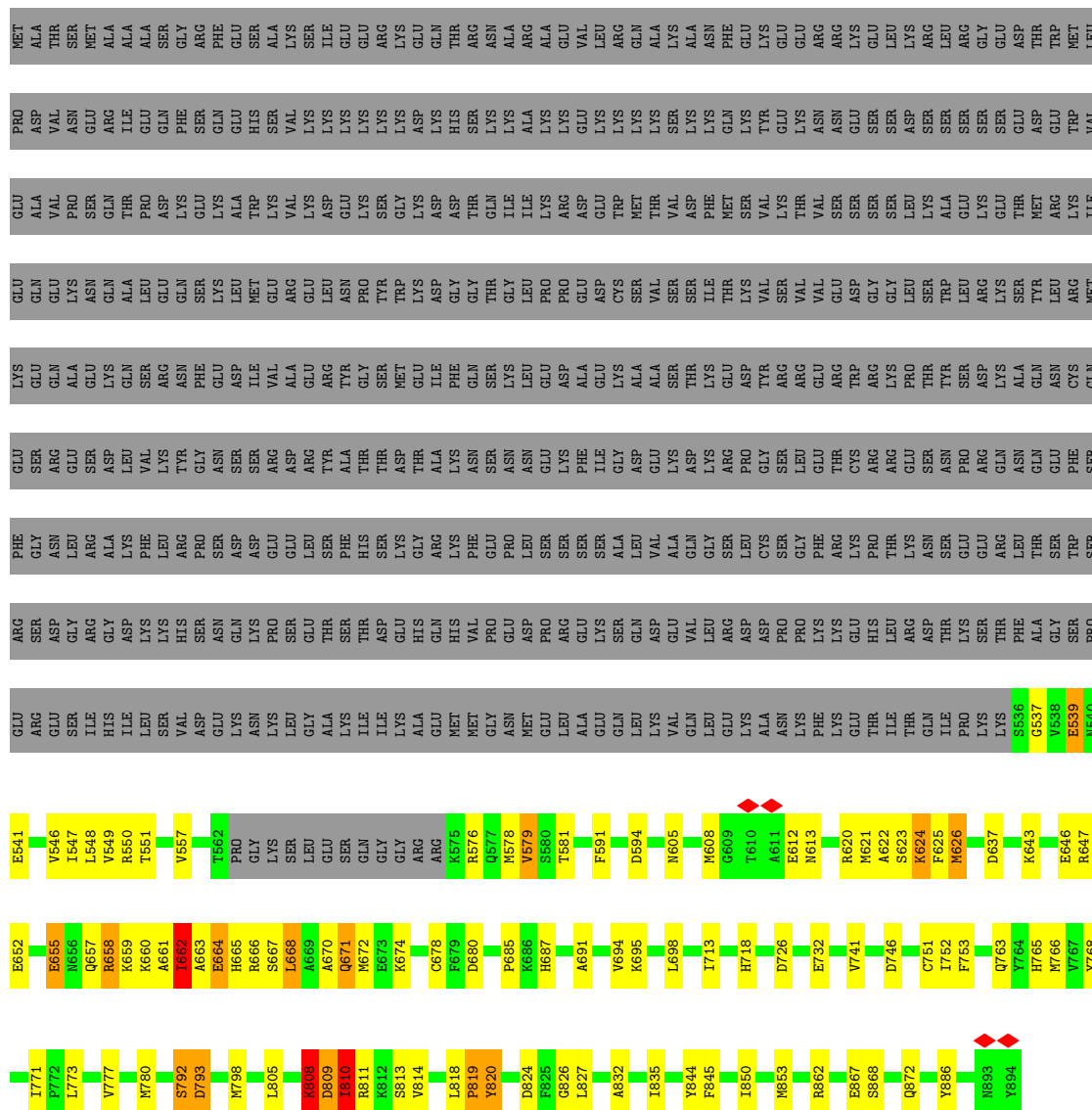


- Molecule 15: Pre-mRNA-processing factor 17



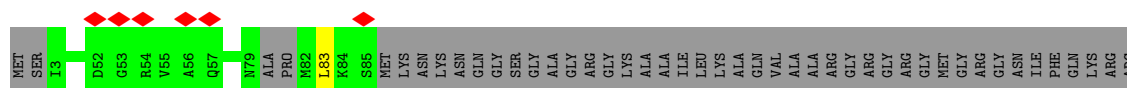
WORLDWIDE
PDB
PROTEIN DATA BANK

Chain U:  28% 9% 61%



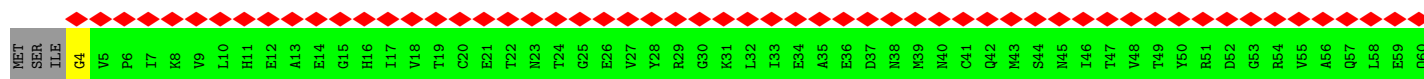
• Molecule 19: Small nuclear ribonucleoprotein Sm D3

Chain a:  5% 63% 36%

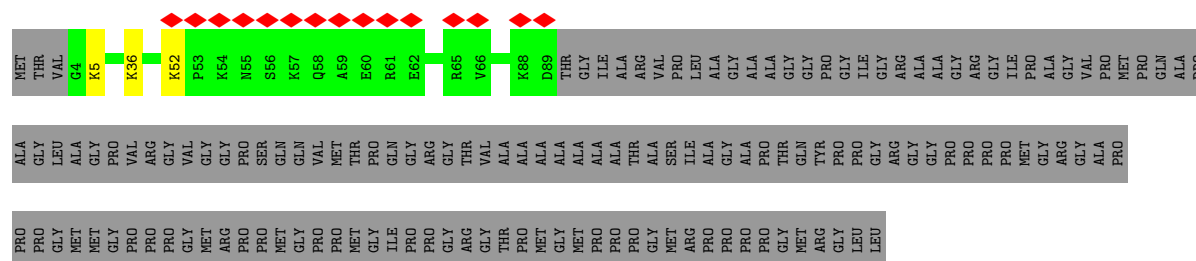


• Molecule 19: Small nuclear ribonucleoprotein Sm D3

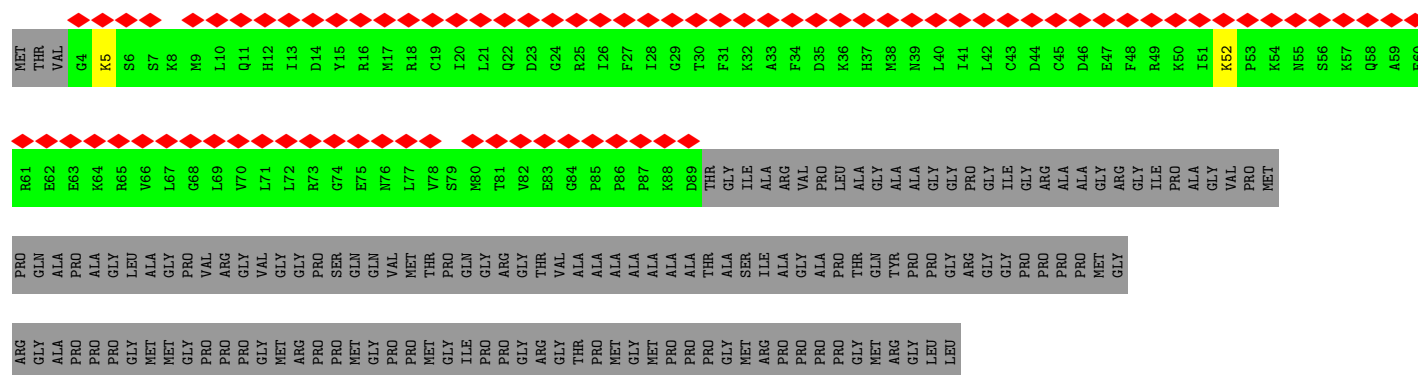
Chain h:  63% 63% 37%



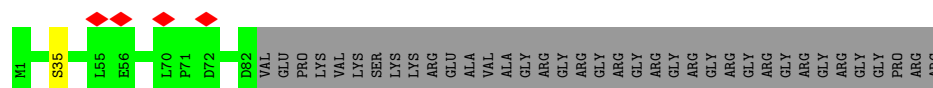
- Molecule 20: Small nuclear ribonucleoprotein-associated protein.



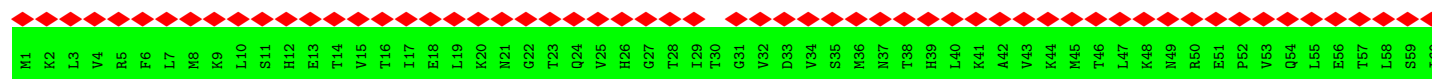
- Molecule 20: Small nuclear ribonucleoprotein-associated protein.

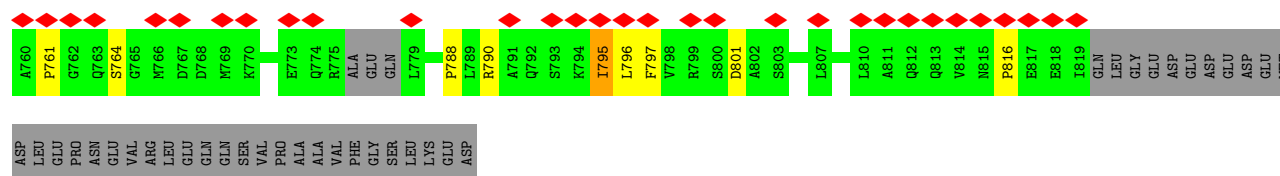


- Molecule 21: Small nuclear ribonucleoprotein Sm D1

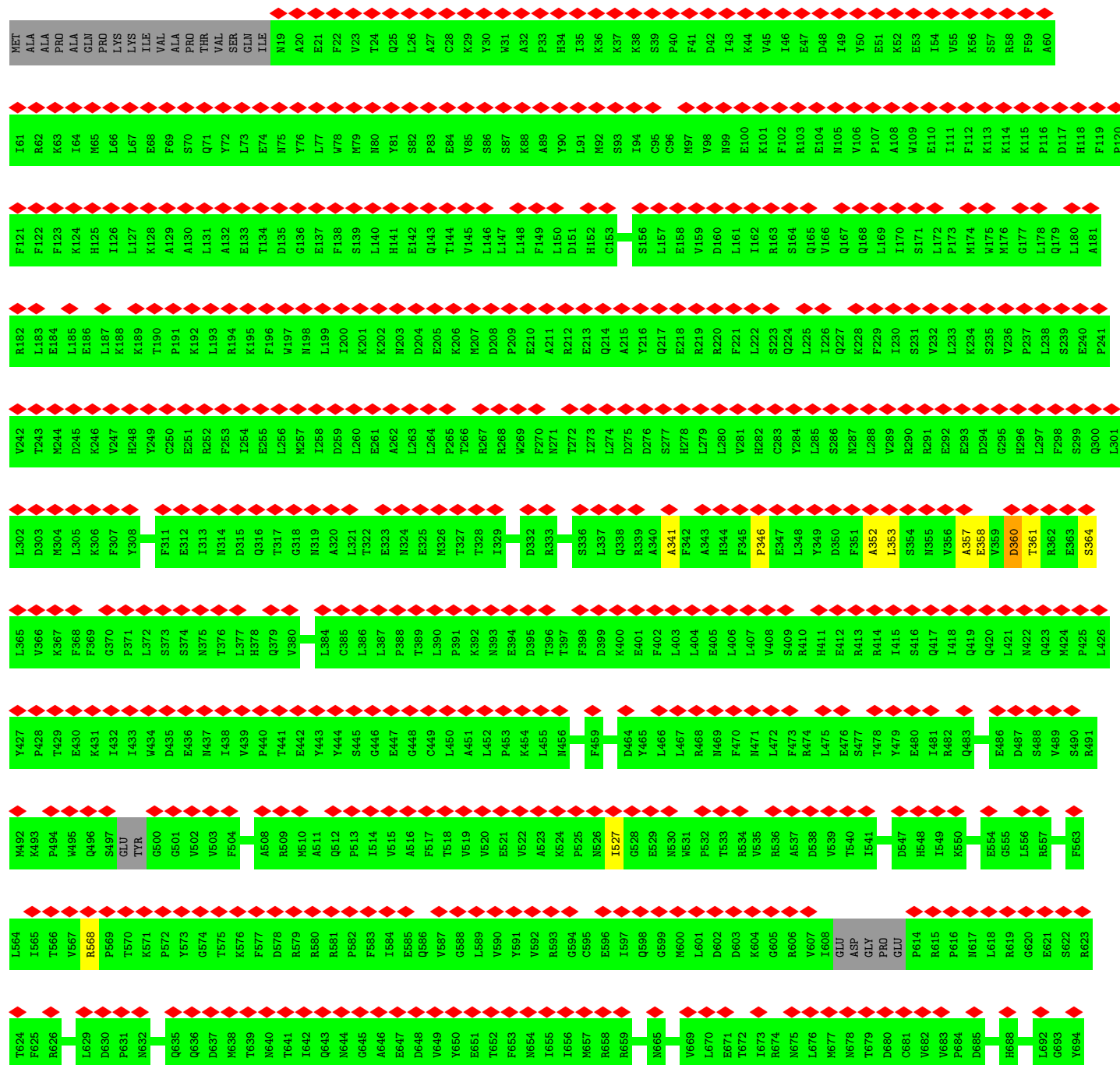
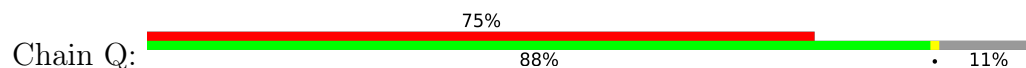


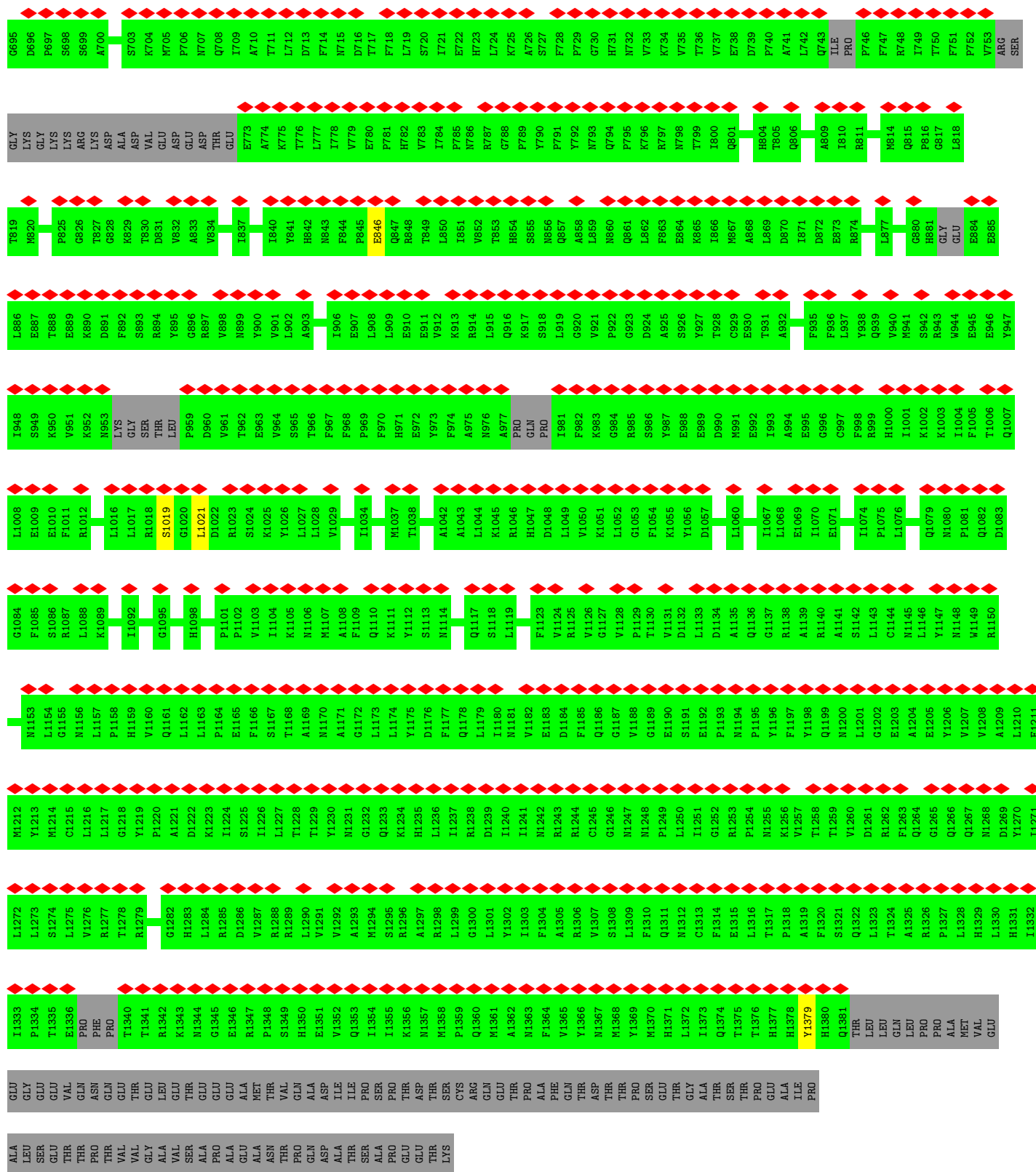
- Molecule 21: Small nuclear ribonucleoprotein Sm D1





• Molecule 29: RNA helicase aquarius





• Molecule 30: Peptidyl-prolyl cis-trans isomerase E



Chain V:



TYR
SER
GLN
TYR

4 Experimental information

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.31	2/16926 (0.0%)	0.72	23/22947 (0.1%)
2	B	0.38	1/2296 (0.0%)	0.54	0/3569
3	C	0.29	1/7181 (0.0%)	0.78	5/9758 (0.1%)
4	E	0.56	0/2420	0.98	11/3281 (0.3%)
5	F	0.42	4/2323 (0.2%)	0.71	8/3619 (0.2%)
6	J	0.40	1/3863 (0.0%)	0.85	14/5250 (0.3%)
7	L	0.43	4/3401 (0.1%)	0.85	12/4570 (0.3%)
8	M	0.22	0/1119	0.59	0/1497
9	N	0.94	3/1210 (0.2%)	0.85	1/1622 (0.1%)
10	O	0.42	0/2390	0.84	5/3227 (0.2%)
11	P	0.26	0/1000	0.66	0/1330
12	R	0.32	0/2186	0.87	13/2937 (0.4%)
13	S	0.24	0/1268	0.66	2/1714 (0.1%)
14	T	0.37	0/2562	0.77	3/3492 (0.1%)
15	W	0.27	0/1306	0.79	4/1760 (0.2%)
16	G	0.81	9/1327 (0.7%)	1.38	28/2053 (1.4%)
17	H	0.56	11/3214 (0.3%)	0.83	6/4989 (0.1%)
18	U	0.35	0/2928	0.89	14/3928 (0.4%)
19	a	0.78	0/397	1.00	0/549
19	h	0.77	0/391	0.99	0/540
20	b	0.85	0/423	1.14	3/587 (0.5%)
20	i	0.84	0/423	1.15	3/587 (0.5%)
21	c	0.88	0/405	1.12	0/563
21	j	0.87	0/405	1.11	0/563
22	d	1.13	0/479	1.25	1/666 (0.2%)
22	k	1.15	0/420	1.24	1/583 (0.2%)
23	f	1.20	0/360	1.26	0/497
23	m	1.21	1/360 (0.3%)	1.24	0/497
24	e	1.04	0/390	1.24	1/542 (0.2%)
24	l	1.03	0/390	1.24	1/542 (0.2%)
25	g	0.86	0/362	1.09	1/501 (0.2%)
25	n	0.83	0/327	1.08	1/451 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	q	0.63	0/658	0.97	3/919 (0.3%)
26	r	0.58	0/653	1.05	5/912 (0.5%)
26	s	0.51	0/334	0.91	0/466
26	t	0.55	0/334	0.82	0/466
27	K	0.86	7/982 (0.7%)	1.07	6/1318 (0.5%)
28	I	0.52	0/2858	1.17	38/3948 (1.0%)
29	Q	0.38	0/6545	0.87	4/9115 (0.0%)
30	y	0.51	0/389	1.32	4/540 (0.7%)
31	o	0.97	0/803	2.25	43/1119 (3.8%)
32	p	0.95	0/463	1.88	7/643 (1.1%)
33	V	1.10	3/3284 (0.1%)	1.20	10/4578 (0.2%)
All	All	0.53	47/81755 (0.1%)	0.91	281/113235 (0.2%)

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

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

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	K	106	CYS	CB-SG	-11.60	1.43	1.81
9	N	101	CYS	CB-SG	-7.96	1.54	1.81
27	K	186	VAL	CA-CB	-7.31	1.44	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	G	4	A	O5'-C5'	7.30	1.53	1.42
5	F	34	G	O3'-P	7.26	1.72	1.61
2	B	103	G	C1'-N9	-7.13	1.37	1.48
17	H	58	U	C1'-N1	7.08	1.59	1.48
17	H	60	U	C1'-N1	7.06	1.59	1.48
5	F	35	A	O5'-C5'	7.00	1.52	1.42
16	G	137	C	C1'-N1	6.92	1.57	1.47
27	K	40	THR	CB-OG1	6.82	1.54	1.43
16	G	149	G	C1'-N9	-6.80	1.36	1.47
17	H	184	C	C1'-N1	6.62	1.58	1.48
17	H	151	C	C1'-N1	6.58	1.58	1.48
5	F	42	C	C3'-O3'	6.33	1.51	1.42
17	H	43	U	C1'-N1	6.31	1.56	1.47
17	H	39	U	C1'-N1	6.26	1.56	1.47
16	G	136	U	C1'-N1	6.26	1.56	1.47
17	H	41	U	C1'-N1	6.26	1.56	1.47
17	H	37	U	C1'-N1	6.22	1.56	1.47
16	G	139	U	C1'-N1	6.21	1.56	1.47
17	H	32	U	C1'-N1	6.20	1.56	1.47
9	N	137	CYS	CB-SG	-5.88	1.61	1.81
1	A	1307	MET	C-N	5.84	1.41	1.33
1	A	1539	SER	C-N	5.82	1.38	1.33
16	G	145	U	O3'-P	5.77	1.69	1.61
16	G	141	C	C1'-N1	5.71	1.56	1.47
17	H	40	C	C1'-N1	5.66	1.55	1.47
16	G	4	A	C5'-C4'	5.61	1.59	1.51
33	V	583	CYS	C-O	5.60	1.29	1.24
27	K	173	THR	CB-OG1	5.48	1.52	1.43
27	K	183	SER	CB-OG	5.43	1.53	1.42
7	L	726	SER	CB-OG	5.36	1.52	1.42
9	N	119	CYS	CB-SG	-5.35	1.63	1.81
7	L	793	LEU	CA-CB	-5.33	1.44	1.53
17	H	110	A	C1'-N9	-5.29	1.40	1.48
7	L	705	THR	CB-OG1	5.29	1.52	1.43
27	K	187	SER	CB-OG	5.20	1.52	1.42
27	K	190	SER	CB-OG	5.17	1.52	1.42
23	m	14	LEU	CA-C	5.14	1.59	1.52
6	J	592	ALA	CA-C	5.09	1.59	1.52
16	G	146	C	O3'-P	-5.08	1.53	1.61
33	V	691	LYS	N-CA	5.07	1.52	1.46
5	F	35	A	C3'-O3'	5.05	1.49	1.42
7	L	696	LEU	CB-CG	-5.05	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	375	GLU	C-N	5.04	1.40	1.34
33	V	720	GLN	CA-C	5.00	1.58	1.52

All (281) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	35	A	C4'-C3'-O3'	13.62	133.43	113.00
16	G	3	A	N9-C1'-C2'	11.80	131.71	114.00
16	G	148	U	C4'-C3'-O3'	-11.58	95.63	113.00
28	I	388	PHE	N-CA-C	10.79	122.79	111.14
30	y	16	GLU	N-CA-C	10.72	122.97	111.28
16	G	144	A	C2'-C3'-O3'	10.46	125.19	109.50
12	R	188	PHE	N-CA-C	10.37	122.34	111.14
5	F	42	C	C2'-C3'-O3'	10.10	128.85	113.70
16	G	145	U	C2'-C3'-O3'	10.08	124.62	109.50
16	G	145	U	O4'-C4'-C3'	-9.95	96.15	106.10
6	J	594	ARG	N-CA-C	-9.79	100.75	112.89
16	G	4	A	O4'-C1'-N9	9.73	123.10	108.50
1	A	1510	GLU	N-CA-C	-9.72	95.16	109.15
10	O	287	SER	N-CA-C	9.71	121.94	111.36
16	G	143	U	N1-C1'-C2'	9.66	126.49	112.00
28	I	327	LEU	N-CA-C	-9.17	101.28	111.28
10	O	224	ASP	CA-C-N	8.99	129.64	120.38
10	O	224	ASP	C-N-CA	8.99	129.64	120.38
16	G	8	C	N1-C1'-C2'	8.98	127.47	114.00
16	G	7	G	O4'-C4'-C3'	-8.92	95.08	104.00
27	K	90	PRO	CA-CB-CG	8.81	121.25	104.50
26	r	46	PRO	N-CA-CB	8.63	111.04	103.27
17	H	59	A	O3'-P-O5'	-8.62	91.08	104.00
17	H	57	A	O3'-P-O5'	-8.57	91.14	104.00
17	H	56	A	O3'-P-O5'	-8.56	91.16	104.00
3	C	167	TYR	N-CA-C	8.54	120.59	111.28
16	G	148	U	C2'-C3'-O3'	8.52	126.48	113.70
17	H	58	U	O3'-P-O5'	-8.52	91.22	104.00
18	U	810	ILE	N-CA-C	8.49	119.28	110.62
31	o	5	THR	N-CA-CB	-8.48	98.33	111.05
26	q	46	PRO	N-CA-CB	8.46	111.21	103.34
15	W	146	HIS	N-CA-C	-8.43	97.31	109.96
18	U	808	LYS	N-CA-C	8.38	120.50	111.36
6	J	593	ARG	N-CA-C	-8.29	101.29	111.40
29	Q	360	ASP	N-CA-C	8.11	120.12	111.28
28	I	237	SER	N-CA-C	8.06	120.06	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	G	142	U	N1-C1'-C2'	8.05	126.07	114.00
31	o	16	THR	CA-C-O	-8.02	111.78	120.36
31	o	99	SER	N-CA-C	7.95	122.75	112.26
30	y	15	GLU	N-CA-C	7.93	119.92	111.28
31	o	47	ILE	N-CA-CB	7.90	123.05	111.52
12	R	234	SER	N-CA-C	7.62	121.90	111.39
31	o	117	TYR	CA-C-O	7.61	128.38	120.40
29	Q	1379	TYR	N-CA-C	7.59	122.63	112.30
27	K	90	PRO	N-CA-CB	7.57	111.20	103.25
7	L	563	PRO	N-CA-CB	7.53	110.39	103.08
28	I	385	VAL	N-CA-C	7.52	117.64	110.42
26	r	64	LYS	CA-C-N	-7.43	114.24	119.66
26	r	64	LYS	C-N-CA	-7.43	114.24	119.66
26	q	60	PRO	N-CA-CB	7.37	110.99	103.25
18	U	662	ILE	N-CA-C	7.30	118.07	110.62
27	K	78	PRO	N-CA-CB	7.29	110.90	103.25
6	J	522	PRO	N-CA-CB	7.28	110.14	103.08
1	A	1305	SER	CA-C-N	7.18	135.25	121.54
1	A	1305	SER	C-N-CA	7.18	135.25	121.54
17	H	33	G	C1'-C2'-O2'	7.17	122.56	111.80
31	o	71	VAL	CA-C-N	7.17	131.57	120.75
31	o	71	VAL	C-N-CA	7.17	131.57	120.75
28	I	588	PRO	N-CA-CB	7.17	110.03	103.08
28	I	353	ASN	CA-C-N	7.10	126.93	119.05
28	I	353	ASN	C-N-CA	7.10	126.93	119.05
16	G	4	A	O4'-C1'-C2'	-7.09	100.51	107.60
1	A	1091	TYR	N-CA-C	-7.06	101.43	110.53
15	W	150	ALA	N-CA-C	7.05	119.58	108.79
10	O	220	MET	CA-C-N	6.95	126.92	119.76
10	O	220	MET	C-N-CA	6.95	126.92	119.76
28	I	589	PRO	N-CA-CB	6.93	110.88	103.39
28	I	354	PRO	N-CA-C	6.89	123.11	113.53
31	o	4	LEU	N-CA-C	-6.89	97.99	108.67
31	o	121	LEU	CA-C-O	6.88	128.88	121.44
28	I	236	GLN	N-CA-C	6.88	118.78	111.28
16	G	4	A	C2'-C3'-O3'	-6.85	103.43	113.70
18	U	623	SER	N-CA-C	6.84	119.36	110.53
32	p	53	PHE	CA-C-O	-6.84	112.79	120.32
7	L	594	PRO	N-CA-CB	6.84	110.43	103.25
28	I	475	PRO	N-CA-CB	6.83	110.76	103.52
28	I	160	PRO	N-CA-CB	6.83	110.42	103.25
26	r	19	PRO	N-CA-CB	6.80	110.37	102.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	q	19	PRO	N-CA-CB	6.78	110.36	103.25
5	F	36	A	O4'-C1'-C2'	-6.76	100.84	107.60
6	J	488	PRO	N-CA-CB	6.74	110.33	103.25
31	o	58	ASP	N-CA-CB	-6.73	100.60	111.24
5	F	38	G	C2'-C3'-O3'	-6.72	103.62	113.70
28	I	162	PRO	N-CA-CB	6.68	110.61	103.52
12	R	192	ALA	N-CA-C	6.68	119.88	109.52
7	L	558	PRO	N-CA-CB	6.66	110.58	103.52
18	U	819	PRO	N-CA-C	6.65	122.98	113.47
16	G	3	A	O4'-C4'-C3'	-6.64	99.46	106.10
18	U	792	SER	CA-C-N	6.63	134.21	121.54
18	U	792	SER	C-N-CA	6.63	134.21	121.54
28	I	580	PHE	N-CA-C	6.63	119.02	109.14
6	J	523	PRO	N-CA-CB	6.62	110.54	103.52
7	L	620	PRO	N-CA-CB	6.62	110.20	103.25
28	I	722	GLU	N-CA-C	6.59	118.47	111.28
16	G	3	A	O3'-P-O5'	6.52	113.78	104.00
1	A	1304	ASN	CA-C-N	6.49	133.94	121.54
1	A	1304	ASN	C-N-CA	6.49	133.94	121.54
6	J	637	PRO	N-CA-CB	6.49	110.40	103.52
28	I	518	PRO	N-CA-CB	6.48	110.39	103.52
1	A	941	LYS	N-CA-C	6.47	124.11	109.81
28	I	816	PRO	N-CA-CB	6.47	110.38	103.52
26	r	60	PRO	N-CA-CB	6.44	110.01	103.25
16	G	4	A	P-O5'-C5'	6.43	130.55	120.90
27	K	40	THR	CA-CB-OG1	6.42	119.23	109.60
4	E	323	LEU	CA-C-N	6.42	127.86	119.84
4	E	323	LEU	C-N-CA	6.42	127.86	119.84
1	A	1303	LEU	CA-C-N	6.42	133.80	121.54
1	A	1303	LEU	C-N-CA	6.42	133.80	121.54
5	F	37	C	O4'-C4'-C3'	-6.38	97.62	104.00
28	I	788	PRO	N-CA-CB	6.38	110.59	103.44
28	I	177	PRO	N-CA-CB	6.37	110.58	103.44
7	L	546	PRO	N-CA-CB	6.36	110.56	103.44
16	G	4	A	C5'-C4'-O4'	6.34	119.32	109.80
31	o	87	LEU	CA-C-N	6.34	126.25	119.28
31	o	87	LEU	C-N-CA	6.34	126.25	119.28
31	o	40	THR	CA-C-N	6.33	131.58	122.40
31	o	40	THR	C-N-CA	6.33	131.58	122.40
4	E	148	LYS	N-CA-C	6.30	120.03	107.62
30	y	17	VAL	N-CA-C	6.29	118.69	109.63
7	L	564	PRO	N-CA-CB	6.28	110.17	103.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	G	4	A	C5'-C4'-C3'	6.22	125.33	116.00
14	T	266	GLU	CA-C-N	6.19	129.41	120.38
14	T	266	GLU	C-N-CA	6.19	129.41	120.38
3	C	113	VAL	N-CA-C	6.16	117.27	107.98
6	J	669	GLN	CA-C-N	6.12	125.85	119.05
6	J	669	GLN	C-N-CA	6.12	125.85	119.05
7	L	548	PRO	N-CA-CB	6.11	110.28	103.44
1	A	1652	MET	CA-C-N	6.10	133.19	121.54
1	A	1652	MET	C-N-CA	6.10	133.19	121.54
14	T	400	PHE	N-CA-C	6.10	123.28	109.81
31	o	73	ASN	N-CA-C	6.07	119.73	111.17
6	J	566	PRO	N-CA-CB	6.07	110.23	103.44
28	I	761	PRO	N-CA-CB	6.07	109.94	103.39
28	I	282	ALA	N-CA-C	6.06	117.89	111.28
12	R	190	SER	N-CA-C	-6.03	97.96	110.80
7	L	753	GLU	N-CA-C	-6.01	104.36	111.03
32	p	46	MET	N-CA-C	-5.98	104.67	111.07
31	o	75	ARG	N-CA-CB	-5.96	102.70	111.51
31	o	79	ILE	CA-C-N	5.95	125.75	120.10
31	o	79	ILE	C-N-CA	5.95	125.75	120.10
28	I	625	PRO	N-CA-CB	5.94	109.86	103.33
33	V	596	VAL	CA-C-N	-5.94	113.85	119.85
33	V	596	VAL	C-N-CA	-5.94	113.85	119.85
16	G	143	U	C1'-C2'-O2'	-5.93	99.50	108.40
1	A	441	VAL	CA-C-N	5.92	128.53	120.54
1	A	441	VAL	C-N-CA	5.92	128.53	120.54
25	n	67	ILE	CB-CA-C	-5.91	104.85	111.23
33	V	372	GLU	N-CA-C	-5.87	101.79	110.48
31	o	27	ARG	CB-CA-C	-5.86	98.77	109.54
33	V	713	VAL	N-CA-C	5.84	116.30	110.23
28	I	352	GLN	N-CA-C	5.83	118.39	111.33
13	S	105	PRO	CA-C-N	5.83	130.67	122.46
13	S	105	PRO	C-N-CA	5.83	130.67	122.46
31	o	50	SER	CA-C-O	5.82	127.71	121.55
31	o	113	LYS	N-CA-C	5.81	118.36	111.33
25	g	67	ILE	CB-CA-C	-5.81	104.96	111.23
5	F	38	G	N9-C1'-C2'	5.80	120.70	112.00
16	G	7	G	O4'-C1'-C2'	-5.79	101.81	107.60
5	F	36	A	C4'-C3'-O3'	5.78	121.67	113.00
12	R	125	MET	CA-C-N	5.77	129.48	120.82
12	R	125	MET	C-N-CA	5.77	129.48	120.82
27	K	107	VAL	CA-CB-CG1	5.76	120.20	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	117	THR	CA-C-N	5.74	132.51	121.54
7	L	117	THR	C-N-CA	5.74	132.51	121.54
4	E	144	VAL	N-CA-C	5.72	121.24	109.34
28	I	484	LEU	N-CA-C	5.71	118.48	109.39
31	o	149	LYS	CB-CA-C	-5.71	101.94	110.16
33	V	359	GLN	N-CA-C	5.70	119.31	112.93
4	E	258	THR	N-CA-C	5.68	118.75	108.69
4	E	76	PRO	N-CA-C	-5.67	105.64	113.53
12	R	189	ASN	CA-C-N	5.67	132.37	121.54
12	R	189	ASN	C-N-CA	5.67	132.37	121.54
1	A	1556	ASP	N-CA-C	5.66	117.14	110.97
15	W	76	VAL	CA-C-N	5.66	132.35	121.54
15	W	76	VAL	C-N-CA	5.66	132.35	121.54
16	G	8	C	O4'-C4'-C3'	-5.66	100.44	106.10
31	o	71	VAL	O-C-N	-5.66	115.50	122.57
1	A	464	PRO	N-CA-C	5.64	121.26	113.98
33	V	170	ILE	CB-CA-C	-5.62	108.40	114.35
28	I	402	ALA	N-CA-C	5.60	117.47	111.36
28	I	252	THR	N-CA-C	5.60	117.39	111.28
31	o	27	ARG	CA-C-N	5.59	128.55	120.11
31	o	27	ARG	C-N-CA	5.59	128.55	120.11
9	N	19	GLU	N-CA-C	5.58	122.14	109.81
31	o	159	GLU	N-CA-C	-5.57	104.83	111.69
16	G	146	C	C4'-C3'-O3'	-5.55	101.07	109.40
20	i	52	LYS	CA-C-N	-5.54	114.22	119.76
20	i	52	LYS	C-N-CA	-5.54	114.22	119.76
28	I	322	GLU	N-CA-C	-5.52	105.36	111.71
20	b	52	LYS	CA-C-N	-5.51	114.25	119.76
20	b	52	LYS	C-N-CA	-5.51	114.25	119.76
7	L	57	SER	N-CA-C	-5.49	106.43	114.39
6	J	593	ARG	CA-C-N	-5.49	111.54	121.14
6	J	593	ARG	C-N-CA	-5.49	111.54	121.14
3	C	87	GLN	CA-CB-CG	5.49	125.07	114.10
20	i	5	LYS	N-CA-C	5.48	118.18	111.82
1	A	1649	LYS	N-CA-C	5.48	115.25	108.19
31	o	34	ILE	CA-C-O	-5.47	114.28	120.74
31	o	16	THR	O-C-N	5.47	129.46	123.22
4	E	68	GLU	CA-C-N	5.46	126.79	121.65
4	E	68	GLU	C-N-CA	5.46	126.79	121.65
16	G	4	A	O5'-C5'-C4'	5.46	119.69	111.50
16	G	9	C	C2'-C3'-O3'	-5.46	105.50	113.70
16	G	142	U	C3'-C2'-C1'	-5.46	96.04	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1653	ASP	CA-C-N	5.46	131.96	121.54
1	A	1653	ASP	C-N-CA	5.46	131.96	121.54
16	G	142	U	C4'-C3'-C2'	-5.45	97.15	102.60
4	E	60	MET	CB-CA-C	-5.44	109.32	115.79
18	U	820	TYR	CA-CB-CG	5.42	123.67	113.90
28	I	235	VAL	N-CA-C	5.41	116.14	110.62
33	V	707	THR	N-CA-C	5.41	119.73	113.18
18	U	793	ASP	CA-C-N	5.41	130.00	121.56
18	U	793	ASP	C-N-CA	5.41	130.00	121.56
31	o	125	VAL	CA-C-N	5.41	128.07	120.28
31	o	125	VAL	C-N-CA	5.41	128.07	120.28
31	o	32	PRO	CA-C-N	5.40	130.50	122.99
31	o	32	PRO	C-N-CA	5.40	130.50	122.99
12	R	222	PRO	O-C-N	5.38	123.68	121.15
31	o	40	THR	N-CA-C	-5.37	106.23	112.89
30	y	73	PHE	N-CA-C	-5.37	105.51	111.36
12	R	91	ASP	CA-C-N	5.37	128.25	120.79
12	R	91	ASP	C-N-CA	5.37	128.25	120.79
3	C	84	GLU	N-CA-C	5.36	117.20	110.24
20	b	5	LYS	N-CA-C	5.35	118.03	111.82
6	J	594	ARG	CA-C-N	-5.32	111.39	121.54
6	J	594	ARG	C-N-CA	-5.32	111.39	121.54
31	o	33	VAL	N-CA-CB	-5.32	103.76	111.52
32	p	20	LYS	N-CA-C	5.29	117.46	111.11
32	p	6	ASN	N-CA-CB	-5.29	101.70	111.53
3	C	143	THR	N-CA-C	5.27	116.83	111.14
31	o	88	PRO	CB-CA-C	-5.26	104.01	112.21
31	o	146	ASP	CA-C-N	5.25	130.01	122.40
31	o	146	ASP	C-N-CA	5.25	130.01	122.40
16	G	142	U	O4'-C4'-C3'	-5.23	100.87	106.10
33	V	379	GLU	N-CA-C	5.22	119.94	111.37
4	E	281	VAL	N-CA-C	5.21	115.81	108.36
27	K	146	ILE	CA-CB-CG1	5.21	119.25	110.40
1	A	187	PRO	CA-C-N	5.20	131.46	121.54
1	A	187	PRO	C-N-CA	5.20	131.46	121.54
1	A	283	VAL	N-CA-C	-5.19	107.77	113.43
6	J	592	ALA	N-CA-C	5.19	121.86	110.80
28	I	755	THR	N-CA-C	5.19	116.94	111.28
7	L	774	VAL	CA-CB-CG2	5.18	119.21	110.40
28	I	281	GLU	CA-C-N	5.18	127.22	120.28
28	I	281	GLU	C-N-CA	5.18	127.22	120.28
28	I	386	ASP	CA-C-N	-5.18	114.93	120.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	I	386	ASP	C-N-CA	-5.18	114.93	120.47
32	p	48	MET	N-CA-C	5.18	119.60	113.28
32	p	51	GLN	N-CA-C	5.17	117.54	109.52
17	H	171	U	C2'-C3'-O3'	-5.17	105.95	113.70
32	p	83	TYR	CA-C-O	-5.15	115.18	121.05
31	o	90	LEU	O-C-N	5.15	129.44	122.59
18	U	541	GLU	CA-C-N	5.14	131.37	121.54
18	U	541	GLU	C-N-CA	5.14	131.37	121.54
12	R	167	ALA	CA-C-N	5.14	131.35	121.54
12	R	167	ALA	C-N-CA	5.14	131.35	121.54
16	G	5	G	N9-C1'-C2'	5.14	119.71	112.00
4	E	95	VAL	N-CA-C	5.13	115.90	110.72
33	V	713	VAL	CA-C-N	-5.13	112.91	122.09
33	V	713	VAL	C-N-CA	-5.13	112.91	122.09
29	Q	568	ARG	CA-C-N	5.12	125.12	119.90
29	Q	568	ARG	C-N-CA	5.12	125.12	119.90
22	k	99	MET	N-CA-C	5.12	116.85	108.76
31	o	90	LEU	CA-C-O	-5.09	113.22	120.51
24	e	85	THR	N-CA-C	-5.09	105.91	112.68
18	U	612	GLU	CA-C-N	5.08	131.23	121.54
18	U	612	GLU	C-N-CA	5.08	131.23	121.54
28	I	550	TRP	CA-C-N	5.07	124.68	119.05
28	I	550	TRP	C-N-CA	5.07	124.68	119.05
31	o	139	VAL	CA-C-N	5.07	124.73	119.56
31	o	139	VAL	C-N-CA	5.07	124.73	119.56
31	o	28	GLY	N-CA-C	5.06	120.87	113.48
31	o	83	LEU	N-CA-C	5.05	117.44	111.33
22	d	99	MET	N-CA-C	5.05	116.74	108.76
5	F	35	A	C3'-C2'-O2'	5.03	118.25	110.70
28	I	403	LYS	N-CA-C	5.03	116.49	108.79
24	l	85	THR	N-CA-C	-5.03	106.00	112.68
28	I	393	LYS	CA-C-N	5.01	124.61	119.05
28	I	393	LYS	C-N-CA	5.01	124.61	119.05
1	A	1196	ILE	CA-C-N	5.00	129.26	122.56
1	A	1196	ILE	C-N-CA	5.00	129.26	122.56

There are no chirality outliers.

All (37) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	PRO	Peptide
1	A	1305	SER	Peptide

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

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16477	0	16462	298	0
2	B	2060	0	1044	109	0
3	C	7022	0	7046	175	0
4	E	2366	0	2303	428	0
5	F	2075	0	1048	126	0
6	J	3817	0	2912	47	0
7	L	3369	0	2929	168	0
8	M	1098	0	1082	21	0
9	N	1184	0	1189	15	0
10	O	2340	0	2316	197	0
11	P	985	0	965	6	0
12	R	2165	0	2214	75	0
13	S	1236	0	1210	31	0
14	T	2496	0	2446	47	0
15	W	1276	0	1221	67	0
16	G	1201	0	609	240	0
17	H	2884	0	1461	303	0
18	U	2864	0	2814	152	0
19	a	399	0	173	1	0
19	h	393	0	170	4	0
20	b	424	0	179	1	0
20	i	424	0	179	0	0
21	c	406	0	170	1	0
21	j	406	0	170	1	0
22	d	480	0	200	6	0
22	k	422	0	175	4	0
23	f	361	0	158	4	0
23	m	361	0	158	1	0
24	e	391	0	163	3	0
24	l	391	0	163	2	0
25	g	363	0	160	1	0
25	n	329	0	138	1	0
26	q	659	0	296	15	0
26	r	654	0	294	17	0
26	s	335	0	168	9	0
26	t	335	0	168	8	0
27	K	980	0	741	177	0
28	I	2875	0	1374	89	0
29	Q	6554	0	2828	24	0
30	y	390	0	190	11	0
31	o	804	0	350	2	0
32	p	464	0	205	17	0
33	V	3285	0	1442	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	A	36	0	6	2	0
35	C	32	0	12	9	0
36	C	1	0	0	0	0
36	F	6	0	0	0	0
37	N	3	0	0	0	0
37	O	3	0	0	0	0
37	U	1	0	0	0	0
All	All	79882	0	61701	2401	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (2401) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:155:PRO:HG3	12:R:188:PHE:CD1	1.21	1.62
16:G:120:G:H2'	29:Q:1019:SER:CB	1.24	1.60
6:J:658:ARG:HA	6:J:667:ILE:CB	1.39	1.53
6:J:496:ASP:CB	6:J:536:LEU:H	1.23	1.51
10:O:260:THR:HG23	10:O:273:GLN:CB	1.32	1.50
17:H:34:U:C5'	18:U:662:ILE:HG12	1.44	1.44
18:U:626:MET:HE2	18:U:643:LYS:NZ	1.19	1.41
27:K:19:PHE:CE1	27:K:175:GLY:HA3	1.58	1.39
16:G:134:U:H2'	16:G:135:G:C8	1.56	1.39
27:K:19:PHE:CZ	27:K:175:GLY:HA3	1.58	1.38
10:O:155:PRO:CG	12:R:188:PHE:CD1	2.08	1.37
7:L:713:MET:HB2	27:K:124:LEU:CD2	1.55	1.36
10:O:155:PRO:CG	12:R:188:PHE:HD1	1.35	1.36
4:E:74:PHE:HA	4:E:81:LEU:CD2	1.52	1.36
4:E:84:ALA:CB	4:E:90:ILE:HD13	1.54	1.35
4:E:65:HIS:ND1	4:E:69:VAL:HG22	1.40	1.35
16:G:147:C:P	18:U:659:LYS:HD3	1.65	1.33
4:E:307:ARG:NH1	15:W:143:LEU:HD13	1.42	1.33
28:I:200:LEU:CB	28:I:207:GLU:CB	2.08	1.31
7:L:703:MET:CG	27:K:113:GLN:CG	2.06	1.31
28:I:756:VAL:CB	28:I:764:SER:CB	2.09	1.31
1:A:534:GLU:HG3	5:F:38:G:OP1	1.28	1.30
15:W:150:ALA:O	15:W:151:LYS:HD2	1.23	1.29
16:G:120:G:C2'	29:Q:1019:SER:CB	2.08	1.29
27:K:131:GLY:O	27:K:135:TRP:HB2	1.23	1.29
17:H:54:U:H2'	17:H:55:U:C6	1.67	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:587:LYS:CB	6:J:593:ARG:CB	2.12	1.27
4:E:336:HIS:ND1	4:E:337:PRO:HD2	1.51	1.26
16:G:122:U:C1'	30:y:75:ARG:CB	2.14	1.25
28:I:365:ALA:HA	28:I:372:ARG:CB	1.65	1.25
4:E:74:PHE:CA	4:E:81:LEU:HD21	1.66	1.25
26:r:61:ILE:O	27:K:138:TYR:HB3	1.31	1.24
1:A:1946:ASN:CG	1:A:1986:LEU:HD23	1.60	1.24
4:E:82:ALA:CB	4:E:92:LEU:CD2	2.16	1.24
4:E:90:ILE:CD1	4:E:112:VAL:HG11	1.68	1.24
17:H:35:A:H5'	18:U:658:ARG:NH2	1.49	1.23
26:q:22:ASN:CB	26:r:55:ILE:HA	1.68	1.23
15:W:147:GLN:O	15:W:148:VAL:HG12	1.35	1.23
28:I:408:ASN:CB	29:Q:353:LEU:CB	2.17	1.23
26:t:72:PRO:HA	27:K:81:LEU:CB	1.67	1.22
4:E:82:ALA:HB2	4:E:92:LEU:CD2	1.69	1.22
28:I:172:PHE:CB	28:I:199:ARG:CB	2.18	1.22
2:B:8:G:H8	2:B:75:G:N1	1.37	1.22
4:E:88:ARG:HG2	4:E:110:GLY:O	1.34	1.22
16:G:147:C:OP1	18:U:659:LYS:HD3	1.37	1.22
4:E:321:TYR:OH	4:E:356:ILE:HG23	1.36	1.21
5:F:42:C:O2'	5:F:43:A:H5'	1.37	1.21
16:G:152:C:H2'	16:G:153:C:C6	1.74	1.21
3:C:157:ILE:HG23	3:C:158:ARG:HG2	1.23	1.20
17:H:153:A:H2'	17:H:154:C:C5'	1.72	1.20
17:H:165:A:C4	32:p:53:PHE:CB	2.25	1.19
4:E:131:LYS:HG2	4:E:152:SER:O	1.40	1.19
7:L:732:MET:CG	26:q:65:PRO:CB	2.20	1.19
4:E:65:HIS:CE1	4:E:69:VAL:HG22	1.78	1.18
27:K:19:PHE:CE2	27:K:172:LEU:HA	1.78	1.18
10:O:283:ALA:O	10:O:287:SER:HB3	1.43	1.18
4:E:76:PRO:CG	4:E:121:GLY:HA3	1.75	1.17
17:H:34:U:P	18:U:662:ILE:HD13	1.83	1.17
10:O:260:THR:CG2	10:O:273:GLN:CB	2.21	1.17
28:I:790:ARG:CB	28:I:801:ASP:CB	2.23	1.17
4:E:84:ALA:HB1	4:E:90:ILE:HD13	1.24	1.17
4:E:65:HIS:ND1	4:E:69:VAL:CG2	2.07	1.16
16:G:147:C:OP1	18:U:659:LYS:CD	1.93	1.16
5:F:43:A:H1'	16:G:4:A:N6	1.58	1.16
17:H:35:A:C5'	18:U:658:ARG:HH21	1.58	1.16
27:K:18:TYR:CD1	27:K:168:LYS:HG2	1.81	1.15
17:H:153:A:H2'	17:H:154:C:H5'	1.18	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:83:A:H2'	17:H:84:C:H6	1.10	1.14
4:E:131:LYS:HG2	4:E:152:SER:C	1.72	1.14
17:H:7:U:C4	17:H:8:C:N4	2.16	1.14
16:G:150:U:H6	16:G:150:U:H5''	1.13	1.13
4:E:76:PRO:HG2	4:E:121:GLY:CA	1.77	1.13
6:J:773:ARG:CB	6:J:790:THR:CB	2.26	1.13
28:I:374:ILE:CB	29:Q:357:ALA:CB	2.25	1.12
6:J:496:ASP:CB	6:J:536:LEU:N	2.09	1.12
7:L:707:ALA:HB2	27:K:117:GLN:OE1	1.44	1.12
17:H:34:U:H5''	18:U:662:ILE:CG1	1.77	1.12
4:E:62:LEU:HB2	4:E:351:LEU:HB2	1.26	1.12
27:K:19:PHE:CZ	27:K:175:GLY:CA	2.31	1.12
1:A:466:ALA:HA	2:B:20:G:N2	1.63	1.12
28:I:374:ILE:CB	29:Q:357:ALA:HB2	1.80	1.12
1:A:466:ALA:CA	2:B:20:G:H21	1.61	1.11
5:F:44:G:N2	16:G:3:A:N6	1.98	1.11
7:L:710:ALA:CB	27:K:120:ARG:HD3	1.79	1.11
16:G:152:C:C2	16:G:153:C:C5	2.38	1.11
7:L:710:ALA:HB1	27:K:120:ARG:HD3	1.14	1.11
7:L:780:ARG:HB2	27:K:188:LEU:HD21	1.26	1.11
4:E:307:ARG:NH1	15:W:143:LEU:CD1	2.13	1.11
10:O:260:THR:HG23	10:O:273:GLN:HB3	1.28	1.11
4:E:129:THR:HG22	4:E:153:PHE:HD2	1.06	1.11
4:E:59:ILE:HD12	15:W:82:ASN:HD21	1.12	1.10
6:J:658:ARG:CA	6:J:667:ILE:CB	2.29	1.10
4:E:84:ALA:HB2	4:E:90:ILE:HG23	1.22	1.10
4:E:90:ILE:HD11	4:E:112:VAL:HG11	1.30	1.10
7:L:731:LEU:HB2	27:K:142:LEU:HD23	1.26	1.10
4:E:108:HIS:ND1	4:E:128:SER:HB2	1.64	1.10
17:H:83:A:H2'	17:H:84:C:C6	1.85	1.10
18:U:626:MET:CE	18:U:643:LYS:NZ	2.15	1.09
4:E:82:ALA:HB2	4:E:92:LEU:HD22	1.20	1.09
17:H:27:U:O2'	17:H:28:C:H5'	1.51	1.09
1:A:1517:LYS:CD	1:A:1522:GLN:HG2	1.82	1.08
17:H:69:U:H2'	17:H:70:C:C6	1.88	1.08
4:E:75:HIS:HB2	4:E:80:THR:O	1.53	1.08
16:G:145:U:C6	16:G:145:U:H5'	1.89	1.08
17:H:154:C:O2'	17:H:155:C:H5'	1.52	1.08
18:U:626:MET:CE	18:U:643:LYS:HZ1	1.65	1.08
2:B:77:G:N7	2:B:80:U:C5	2.22	1.08
4:E:307:ARG:HH12	15:W:143:LEU:CD1	1.66	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:37:C:H2'	5:F:38:G:H5'	1.30	1.07
7:L:710:ALA:HA	27:K:124:LEU:CD2	1.84	1.07
7:L:713:MET:HB3	27:K:124:LEU:HG	1.30	1.07
15:W:147:GLN:O	15:W:148:VAL:CG1	2.02	1.07
1:A:1517:LYS:HD2	1:A:1522:GLN:CG	1.82	1.07
5:F:43:A:C1'	16:G:4:A:H61	1.68	1.07
7:L:762:ALA:HB1	27:K:14:ASP:OD1	1.51	1.07
17:H:182:U:O2'	17:H:183:G:H5'	1.54	1.06
17:H:93:A:O2'	17:H:94:A:H5'	1.55	1.06
7:L:780:ARG:CB	27:K:188:LEU:HD21	1.86	1.06
16:G:5:G:C4	16:G:6:A:C8	2.44	1.06
1:A:51:PHE:CZ	4:E:66:GLU:CG	2.38	1.05
4:E:55:LEU:HG	4:E:96:TYR:OH	1.56	1.05
5:F:37:C:C2'	5:F:38:G:H5'	1.85	1.05
17:H:165:A:N3	32:p:53:PHE:CB	2.19	1.05
17:H:179:C:H2'	17:H:180:G:H8	1.20	1.05
10:O:223:LEU:HG	10:O:285:GLU:HA	1.10	1.05
4:E:82:ALA:CB	4:E:92:LEU:HD23	1.86	1.05
4:E:84:ALA:HB2	4:E:90:ILE:HD13	1.38	1.05
3:C:166:CYS:SG	3:C:536:ARG:NE	2.28	1.05
4:E:95:VAL:HG13	4:E:353:MET:HE1	1.34	1.05
10:O:155:PRO:CA	12:R:188:PHE:HE1	1.69	1.05
17:H:69:U:O2'	17:H:70:C:H5'	1.57	1.05
17:H:153:A:C2'	17:H:154:C:H5'	1.85	1.05
4:E:298:SER:C	4:E:314:THR:HB	1.82	1.04
28:I:465:ARG:CB	28:I:543:ARG:NH2	2.20	1.04
4:E:65:HIS:CD2	4:E:91:LEU:HD11	1.92	1.04
4:E:94:ASN:O	4:E:99:CYS:HA	1.56	1.04
4:E:125:PHE:CE2	4:E:159:PRO:HB3	1.93	1.04
5:F:44:G:C2	16:G:3:A:N6	2.26	1.04
10:O:260:THR:HG23	10:O:273:GLN:HB2	1.08	1.04
17:H:92:U:H2'	17:H:93:A:H8	1.20	1.04
4:E:54:SER:CB	4:E:355:GLU:CD	2.31	1.04
4:E:266:PRO:HG2	7:L:785:GLN:HB2	1.39	1.04
17:H:69:U:H2'	17:H:70:C:H6	1.19	1.03
1:A:1946:ASN:CG	1:A:1986:LEU:CD2	2.31	1.03
3:C:165:LEU:O	3:C:169:ASP:HB3	1.57	1.03
10:O:155:PRO:N	12:R:188:PHE:HE1	1.54	1.03
7:L:713:MET:HB2	27:K:124:LEU:HD23	1.35	1.03
10:O:256:GLY:HA2	12:R:70:ALA:CB	1.89	1.03
28:I:343:LEU:CB	29:Q:527:ILE:CB	2.37	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:134:U:C2'	16:G:135:G:C8	2.40	1.03
2:B:75:G:C5	2:B:76:A:N7	2.26	1.02
18:U:548:LEU:HD22	18:U:661:ALA:CB	1.87	1.02
4:E:108:HIS:CE1	4:E:128:SER:HB2	1.93	1.02
4:E:129:THR:HG22	4:E:153:PHE:CD2	1.94	1.02
10:O:260:THR:CG2	10:O:273:GLN:HB3	1.87	1.02
10:O:245:GLU:OE2	10:O:261:ILE:HG21	1.59	1.01
16:G:6:A:C6	16:G:7:G:C5	2.48	1.01
17:H:34:U:C5'	18:U:662:ILE:CG1	2.34	1.01
4:E:54:SER:HB2	4:E:355:GLU:CD	1.85	1.01
5:F:92:A:C2	5:F:93:G:C5	2.48	1.01
17:H:108:G:H2'	17:H:109:C:C6	1.94	1.01
4:E:54:SER:CB	4:E:355:GLU:OE2	2.09	1.01
4:E:108:HIS:CE1	4:E:128:SER:CB	2.43	1.01
17:H:109:C:H4'	22:k:47:ARG:CB	1.89	1.01
1:A:466:ALA:HA	2:B:20:G:H21	0.84	1.01
27:K:19:PHE:CE1	27:K:175:GLY:CA	2.44	1.01
1:A:51:PHE:HZ	4:E:66:GLU:HG3	1.25	1.00
7:L:710:ALA:HA	27:K:124:LEU:HD23	1.40	1.00
10:O:229:LYS:HG3	10:O:277:ARG:NH1	1.75	1.00
17:H:34:U:OP1	18:U:662:ILE:HD13	1.57	1.00
1:A:1946:ASN:CB	1:A:1986:LEU:HD23	1.91	1.00
28:I:343:LEU:CA	29:Q:527:ILE:CB	2.40	1.00
4:E:65:HIS:CD2	4:E:91:LEU:CD1	2.44	1.00
7:L:713:MET:HB2	27:K:124:LEU:HD21	1.44	0.99
1:A:1514:LYS:HZ3	1:A:1529:ILE:HD11	1.27	0.99
7:L:767:LEU:HD21	27:K:177:LYS:HB2	1.41	0.99
10:O:229:LYS:CD	10:O:277:ARG:HH12	1.76	0.99
16:G:144:A:H5''	16:G:144:A:N3	1.78	0.99
7:L:718:LYS:CG	26:r:66:PRO:CB	2.39	0.99
1:A:51:PHE:CZ	4:E:66:GLU:HB3	1.98	0.99
7:L:707:ALA:HB2	27:K:117:GLN:CD	1.88	0.99
10:O:223:LEU:CG	10:O:285:GLU:HA	1.93	0.99
4:E:125:PHE:HE2	4:E:159:PRO:CB	1.76	0.99
7:L:767:LEU:CD2	27:K:177:LYS:HB2	1.92	0.98
4:E:84:ALA:CB	4:E:90:ILE:CD1	2.41	0.98
10:O:155:PRO:N	12:R:188:PHE:CE1	2.31	0.98
10:O:234:LEU:HD11	10:O:274:PHE:CE2	1.98	0.98
10:O:155:PRO:HG3	12:R:188:PHE:CE1	1.99	0.98
4:E:321:TYR:OH	4:E:356:ILE:CG2	2.12	0.98
6:J:773:ARG:CB	6:J:787:LYS:HA	1.93	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:A:H4'	2:B:68:C:C4	2.00	0.97
10:O:234:LEU:HD11	10:O:274:PHE:CZ	1.99	0.97
2:B:77:G:N7	2:B:80:U:H5	1.59	0.97
7:L:692:LEU:CB	27:K:107:VAL:HG11	1.94	0.97
17:H:83:A:O2'	17:H:84:C:H5'	1.63	0.97
27:K:131:GLY:O	27:K:135:TRP:CB	2.13	0.97
7:L:731:LEU:CB	27:K:142:LEU:HD23	1.95	0.97
7:L:710:ALA:HB1	27:K:120:ARG:CD	1.94	0.97
16:G:150:U:H5''	16:G:150:U:C6	2.00	0.97
16:G:152:C:H3'	16:G:153:C:C5	2.00	0.97
17:H:54:U:H2'	17:H:55:U:H6	1.03	0.97
10:O:149:LYS:HE3	10:O:290:LYS:HZ2	1.29	0.97
1:A:1514:LYS:NZ	1:A:1529:ILE:HD11	1.80	0.96
7:L:713:MET:CB	27:K:124:LEU:CD2	2.43	0.96
28:I:176:SER:CB	28:I:196:ALA:HB1	1.95	0.96
1:A:1827:TRP:HH2	1:A:1837:ALA:HB2	1.29	0.96
10:O:220:MET:HG2	10:O:221:PRO:HD2	1.45	0.96
7:L:713:MET:CB	27:K:124:LEU:HG	1.95	0.96
16:G:152:C:C2'	16:G:153:C:C5	2.49	0.96
4:E:119:THR:CG2	4:E:161:ARG:HB3	1.96	0.96
10:O:223:LEU:HD13	10:O:223:LEU:H	1.30	0.95
16:G:152:C:C4	16:G:153:C:N4	2.34	0.95
28:I:374:ILE:CB	29:Q:357:ALA:HB3	1.95	0.95
10:O:155:PRO:CG	12:R:188:PHE:CE1	2.49	0.95
3:C:538:HIS:HE1	3:C:551:LEU:CD1	1.79	0.95
17:H:56:A:N6	17:H:92:U:C4	2.34	0.95
26:s:112:ALA:O	27:K:15:ALA:CB	2.14	0.95
1:A:1518:LEU:O	1:A:1519:THR:OG1	1.85	0.95
4:E:298:SER:HA	4:E:314:THR:HG21	1.47	0.95
7:L:759:GLU:OE1	27:K:17:PRO:HD2	1.65	0.95
4:E:78:GLY:HA3	4:E:336:HIS:HE1	1.31	0.95
5:F:36:A:N1	16:G:10:U:N3	2.15	0.95
10:O:245:GLU:OE2	10:O:261:ILE:CG2	2.14	0.95
17:H:83:A:C4	17:H:84:C:C5	2.55	0.95
7:L:764:PRO:O	7:L:765:ARG:CG	2.14	0.94
16:G:148:U:H6	16:G:148:U:H5'	1.30	0.94
16:G:148:U:N3	17:H:30:A:C2	2.36	0.94
12:R:232:SEP:HB3	14:T:372:LYS:HE3	1.48	0.94
16:G:27:U:O2'	16:G:28:A:O5'	1.86	0.94
17:H:27:U:C2'	17:H:28:C:H5'	1.96	0.94
17:H:147:G:C6	17:H:148:C:N4	2.36	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:626:MET:HE2	18:U:643:LYS:HZ2	1.25	0.94
1:A:1518:LEU:O	1:A:1519:THR:CB	2.16	0.94
10:O:259:ARG:CG	10:O:274:PHE:C	2.40	0.94
16:G:120:G:H2'	29:Q:1019:SER:CA	1.97	0.94
4:E:118:ASN:HD22	4:E:119:THR:H	1.10	0.94
7:L:780:ARG:HB2	27:K:188:LEU:CD2	1.97	0.94
4:E:59:ILE:HD12	15:W:82:ASN:ND2	1.83	0.93
17:H:93:A:C2'	17:H:94:A:H5'	1.97	0.93
17:H:35:A:C5'	18:U:658:ARG:NH2	2.23	0.93
26:q:22:ASN:CB	26:r:55:ILE:CA	2.46	0.93
4:E:119:THR:CG2	4:E:161:ARG:CB	2.47	0.93
4:E:298:SER:HA	4:E:314:THR:CG2	1.99	0.93
5:F:42:C:HO2'	5:F:43:A:H5'	1.28	0.93
3:C:142:LYS:HG2	3:C:228:PHE:HD2	1.34	0.93
7:L:731:LEU:HB2	27:K:142:LEU:CD2	1.99	0.93
10:O:229:LYS:CG	10:O:277:ARG:HH12	1.82	0.93
17:H:163:G:O6	32:p:50:GLY:HA3	1.68	0.93
5:F:36:A:C2	16:G:10:U:O2	2.22	0.93
17:H:56:A:N6	17:H:92:U:N3	2.17	0.93
29:Q:358:GLU:O	29:Q:364:SER:CB	2.16	0.93
10:O:260:THR:N	10:O:273:GLN:HB3	1.83	0.92
16:G:152:C:H2'	16:G:153:C:C5	2.03	0.92
4:E:99:CYS:SG	4:E:353:MET:SD	2.67	0.92
4:E:307:ARG:HH11	15:W:143:LEU:HD22	1.33	0.92
17:H:57:A:N6	17:H:91:U:H3	1.68	0.92
7:L:699:ASN:HA	27:K:114:LEU:HB2	1.50	0.92
16:G:152:C:C5	16:G:153:C:N4	2.37	0.92
26:t:72:PRO:CA	27:K:81:LEU:CB	2.46	0.92
10:O:259:ARG:HG2	10:O:275:ALA:N	1.84	0.92
2:B:75:G:C6	2:B:76:A:N7	2.37	0.92
4:E:271:GLU:OE2	4:E:273:CYS:SG	2.28	0.92
6:J:604:PRO:HA	6:J:607:LYS:N	1.83	0.92
4:E:66:GLU:CA	4:E:87:ASP:OD2	2.18	0.92
4:E:95:VAL:HG13	4:E:353:MET:CE	1.99	0.92
7:L:710:ALA:O	27:K:124:LEU:HD21	1.69	0.92
16:G:152:C:H2'	16:G:153:C:H6	1.32	0.92
7:L:767:LEU:HD22	27:K:177:LYS:CB	2.00	0.92
2:B:93:U:O2	22:d:104:ASP:CB	2.18	0.91
5:F:38:G:C2	5:F:39:A:C5	2.58	0.91
5:F:44:G:N1	16:G:2:U:C5	2.38	0.91
4:E:298:SER:O	4:E:314:THR:HB	1.70	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:732:MET:N	27:K:142:LEU:HD21	1.86	0.91
17:H:102:U:O2	19:h:4:GLY:N	2.04	0.91
18:U:811:ARG:HH11	18:U:811:ARG:HG3	1.36	0.91
10:O:253:TYR:CE1	13:S:93:THR:OG1	2.24	0.91
17:H:34:U:O2'	17:H:35:A:C8	2.23	0.91
4:E:78:GLY:HA3	4:E:336:HIS:CE1	2.05	0.91
17:H:172:C:O2'	17:H:173:C:H5'	1.71	0.91
17:H:106:G:N2	17:H:107:A:C2	2.39	0.91
16:G:146:C:OP1	18:U:658:ARG:HD2	1.68	0.91
16:G:134:U:H2'	16:G:135:G:N7	1.84	0.90
10:O:155:PRO:CD	12:R:188:PHE:CE1	2.53	0.90
10:O:223:LEU:HG	10:O:285:GLU:CA	2.00	0.90
17:H:179:C:H2'	17:H:180:G:C8	2.05	0.90
3:C:142:LYS:HG2	3:C:228:PHE:CD2	2.05	0.90
17:H:179:C:O2'	17:H:180:G:H5'	1.69	0.90
4:E:65:HIS:HD2	4:E:91:LEU:HD11	1.30	0.90
16:G:146:C:H1'	16:G:147:C:C6	2.07	0.90
1:A:534:GLU:CG	5:F:38:G:OP1	2.16	0.90
4:E:82:ALA:HB1	4:E:92:LEU:CD2	1.97	0.90
4:E:325:GLY:O	4:E:352:TYR:CE2	2.25	0.90
17:H:92:U:H2'	17:H:93:A:C8	2.05	0.90
7:L:731:LEU:CB	27:K:142:LEU:CD2	2.50	0.90
17:H:35:A:H5'	18:U:658:ARG:HH21	1.37	0.90
17:H:108:G:H4'	22:k:104:ASP:CB	2.02	0.90
27:K:19:PHE:CE2	27:K:172:LEU:CA	2.55	0.90
4:E:76:PRO:HG2	4:E:121:GLY:HA3	0.91	0.89
4:E:125:PHE:HE2	4:E:159:PRO:HB3	1.27	0.89
2:B:70:A:N3	2:B:70:A:H5''	1.87	0.89
4:E:92:LEU:O	4:E:101:ASN:HA	1.72	0.89
28:I:465:ARG:CB	28:I:543:ARG:HH22	1.79	0.89
10:O:256:GLY:HA2	12:R:70:ALA:HB3	1.52	0.89
16:G:6:A:H2'	16:G:7:G:C1'	2.02	0.89
3:C:158:ARG:HA	3:C:158:ARG:NH2	1.88	0.89
18:U:666:ARG:HH21	18:U:666:ARG:HG2	1.36	0.89
27:K:135:TRP:O	27:K:136:LYS:CG	2.21	0.89
5:F:44:G:N1	16:G:2:U:C4	2.41	0.89
10:O:234:LEU:O	10:O:271:PHE:HA	1.72	0.89
16:G:122:U:C2'	30:y:75:ARG:CB	2.50	0.89
4:E:124:LEU:HD12	4:E:125:PHE:N	1.86	0.89
10:O:259:ARG:H	10:O:274:PHE:HA	1.34	0.89
16:G:27:U:C2'	16:G:28:A:O5'	2.19	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:PHE:CZ	4:E:66:GLU:CB	2.57	0.88
7:L:767:LEU:HD22	27:K:177:LYS:HB3	1.55	0.88
16:G:152:C:C2'	16:G:153:C:C6	2.55	0.88
17:H:182:U:H2'	17:H:183:G:H8	1.36	0.88
5:F:44:G:C6	16:G:2:U:C5	2.61	0.88
15:W:150:ALA:O	15:W:151:LYS:CD	2.18	0.88
16:G:21:A:H4'	16:G:22:C:OP1	1.71	0.88
17:H:150:U:H2'	17:H:151:C:H6	1.37	0.88
26:r:61:ILE:O	27:K:138:TYR:CB	2.20	0.88
10:O:260:THR:HG23	10:O:273:GLN:CG	2.03	0.88
16:G:147:C:P	18:U:659:LYS:CD	2.59	0.88
28:I:520:ILE:O	28:I:524:TYR:N	2.06	0.88
1:A:51:PHE:CZ	4:E:66:GLU:HG3	2.04	0.88
4:E:54:SER:HB3	4:E:355:GLU:OE2	1.72	0.88
16:G:2:U:N3	18:U:625:PHE:CD2	2.41	0.88
17:H:147:G:C2	17:H:148:C:C4	2.62	0.88
1:A:1522:GLN:HA	1:A:1522:GLN:NE2	1.87	0.88
2:B:8:G:C8	2:B:75:G:N1	2.26	0.88
3:C:690:GLU:O	3:C:788:LYS:HB3	1.74	0.88
7:L:732:MET:CB	26:q:65:PRO:CB	2.52	0.88
10:O:259:ARG:HG2	10:O:274:PHE:C	1.98	0.88
16:G:144:A:H5''	16:G:144:A:C4	2.09	0.88
4:E:336:HIS:ND1	4:E:337:PRO:CD	2.37	0.87
15:W:147:GLN:C	15:W:148:VAL:CG1	2.44	0.87
17:H:163:G:C6	32:p:49:ARG:O	2.27	0.87
4:E:307:ARG:HH12	15:W:143:LEU:HD13	0.74	0.87
10:O:253:TYR:HE1	13:S:93:THR:OG1	1.57	0.87
28:I:343:LEU:HA	29:Q:527:ILE:CB	2.02	0.87
10:O:155:PRO:CD	12:R:188:PHE:CD1	2.57	0.87
16:G:146:C:O2'	16:G:147:C:C6	2.27	0.87
4:E:131:LYS:HA	4:E:154:VAL:HG23	1.56	0.87
5:F:36:A:N1	16:G:10:U:C2	2.43	0.87
16:G:148:U:O2	16:G:149:G:N2	2.08	0.87
27:K:19:PHE:HE2	27:K:172:LEU:HA	1.36	0.87
4:E:62:LEU:CB	4:E:351:LEU:HB2	2.04	0.87
4:E:326:HIS:HD2	4:E:330:ILE:HG12	1.38	0.87
7:L:727:ARG:O	7:L:731:LEU:HD23	1.73	0.87
3:C:160:ARG:NH1	3:C:160:ARG:O	2.08	0.87
17:H:8:C:H2'	17:H:9:U:C6	2.10	0.86
17:H:33:G:O3'	18:U:662:ILE:HD13	1.73	0.86
7:L:731:LEU:HB3	27:K:142:LEU:HG	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:PHE:HZ	4:E:66:GLU:CG	1.79	0.86
4:E:90:ILE:HD11	4:E:112:VAL:CG1	2.05	0.86
4:E:257:ASN:HB2	15:W:149:SER:CB	2.05	0.86
16:G:5:G:N3	16:G:6:A:N7	2.22	0.86
5:F:44:G:N2	16:G:3:A:C6	2.43	0.86
18:U:548:LEU:HD22	18:U:661:ALA:HB2	1.57	0.86
17:H:98:G:O2'	17:H:99:A:H5'	1.76	0.86
17:H:151:C:H2'	17:H:152:G:C8	2.11	0.86
16:G:6:A:C5	16:G:7:G:N7	2.44	0.86
28:I:520:ILE:O	28:I:524:TYR:CB	2.23	0.86
16:G:152:C:C3'	16:G:153:C:C5	2.58	0.86
4:E:62:LEU:HD13	4:E:93:TRP:CD2	2.11	0.85
4:E:131:LYS:CG	4:E:152:SER:O	2.23	0.85
7:L:724:TYR:CG	27:K:135:TRP:CG	2.64	0.85
16:G:152:C:C3'	16:G:153:C:H5	1.89	0.85
4:E:257:ASN:HB2	15:W:149:SER:HB3	1.58	0.85
7:L:252:ARG:HG2	7:L:252:ARG:HH11	1.41	0.85
16:G:152:C:C2	16:G:153:C:C4	2.63	0.85
18:U:668:LEU:HD12	18:U:668:LEU:O	1.77	0.85
7:L:767:LEU:CD2	27:K:177:LYS:CB	2.53	0.85
4:E:93:TRP:HA	4:E:101:ASN:HA	1.58	0.85
4:E:116:HIS:O	4:E:124:LEU:HD13	1.76	0.85
4:E:54:SER:HA	4:E:355:GLU:OE2	1.76	0.85
7:L:710:ALA:CB	27:K:120:ARG:CD	2.55	0.84
10:O:260:THR:H	10:O:273:GLN:HB3	1.41	0.84
16:G:6:A:H2'	16:G:7:G:H1'	1.58	0.84
4:E:307:ARG:HH11	15:W:143:LEU:CD2	1.90	0.84
4:E:84:ALA:HB2	4:E:90:ILE:CD1	2.02	0.84
10:O:155:PRO:CA	12:R:188:PHE:CE1	2.58	0.84
17:H:74:U:H2'	17:H:75:A:H8	1.40	0.84
1:A:50:LYS:HB2	4:E:88:ARG:HH12	1.42	0.84
17:H:8:C:H2'	17:H:9:U:H6	1.41	0.84
4:E:115:LEU:HD22	4:E:126:SER:HB3	1.60	0.84
17:H:55:U:C4	17:H:93:A:N6	2.46	0.84
26:r:127:ALA:C	26:s:127:ALA:HB1	2.03	0.84
4:E:54:SER:CA	4:E:355:GLU:OE2	2.25	0.84
7:L:710:ALA:O	27:K:124:LEU:CD2	2.26	0.84
10:O:149:LYS:HE3	10:O:290:LYS:NZ	1.92	0.84
16:G:134:U:H4'	16:G:135:G:OP1	1.78	0.84
16:G:146:C:O2'	16:G:147:C:O5'	1.94	0.84
17:H:7:U:C4	17:H:8:C:C4	2.65	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:692:LEU:HB3	27:K:107:VAL:CB	2.08	0.83
16:G:144:A:N7	18:U:624:LYS:NZ	2.25	0.83
4:E:108:HIS:ND1	4:E:128:SER:CB	2.42	0.83
5:F:35:A:O2'	5:F:36:A:OP1	1.95	0.83
16:G:148:U:N3	17:H:30:A:H2	1.77	0.83
17:H:164:C:O2	32:p:84:ALA:HA	1.79	0.83
4:E:108:HIS:CE1	4:E:128:SER:HB3	2.11	0.83
28:I:521:VAL:O	28:I:527:PHE:CB	2.27	0.83
4:E:116:HIS:CE1	4:E:158:TYR:CD1	2.67	0.82
4:E:162:ARG:NH2	4:E:203:ASP:O	2.12	0.82
7:L:713:MET:CB	27:K:124:LEU:CG	2.57	0.82
17:H:165:A:C2	32:p:53:PHE:CB	2.62	0.82
17:H:166:G:N2	17:H:166:G:OP2	2.11	0.82
4:E:66:GLU:N	4:E:87:ASP:OD2	2.11	0.82
10:O:283:ALA:O	10:O:287:SER:CB	2.26	0.82
7:L:699:ASN:CG	27:K:114:LEU:HB3	2.05	0.82
16:G:6:A:C6	16:G:7:G:C6	2.67	0.82
4:E:129:THR:CG2	4:E:153:PHE:HD2	1.91	0.82
4:E:266:PRO:HG2	7:L:785:GLN:CB	2.09	0.82
10:O:234:LEU:CD1	10:O:274:PHE:CZ	2.61	0.82
10:O:235:TYR:HD2	10:O:301:LYS:HB2	1.44	0.82
15:W:146:HIS:O	15:W:148:VAL:HG13	1.80	0.82
28:I:749:SER:O	28:I:753:THR:N	2.13	0.82
4:E:66:GLU:CB	4:E:87:ASP:OD2	2.28	0.82
4:E:88:ARG:CG	4:E:110:GLY:O	2.24	0.82
5:F:44:G:C8	16:G:1:G:N2	2.48	0.82
10:O:259:ARG:HG3	10:O:274:PHE:C	2.05	0.82
27:K:19:PHE:CD2	27:K:172:LEU:HA	2.13	0.82
4:E:78:GLY:CA	4:E:336:HIS:HE1	1.93	0.81
7:L:692:LEU:CA	27:K:107:VAL:HG11	2.10	0.81
7:L:743:GLU:CG	26:q:60:PRO:HA	2.09	0.81
16:G:150:U:H6	16:G:150:U:C5'	1.92	0.81
27:K:19:PHE:HE2	27:K:172:LEU:CA	1.92	0.81
4:E:84:ALA:HB2	4:E:90:ILE:CG2	2.07	0.81
4:E:243:LEU:CD1	4:E:247:GLY:HA2	2.10	0.81
5:F:37:C:H2'	5:F:38:G:C5'	2.10	0.81
10:O:259:ARG:HB2	10:O:273:GLN:C	2.05	0.81
4:E:59:ILE:CD1	15:W:82:ASN:HD21	1.92	0.81
10:O:260:THR:O	10:O:273:GLN:N	2.13	0.81
17:H:151:C:H2'	17:H:152:G:H8	1.45	0.81
4:E:59:ILE:CD1	15:W:82:ASN:ND2	2.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:692:LEU:HB3	27:K:107:VAL:CG1	2.10	0.81
12:R:184:GLN:HE21	12:R:184:GLN:HA	1.46	0.81
1:A:1946:ASN:HD22	1:A:1949:ARG:HB3	1.44	0.81
4:E:118:ASN:HD22	4:E:119:THR:N	1.79	0.81
10:O:260:THR:CG2	10:O:273:GLN:CG	2.58	0.81
17:H:33:G:O5'	18:U:666:ARG:NE	2.14	0.81
17:H:105:G:H2'	17:H:106:G:H5''	1.61	0.81
4:E:57:ALA:O	4:E:355:GLU:CB	2.29	0.81
10:O:149:LYS:HZ1	10:O:290:LYS:CG	1.93	0.81
17:H:165:A:H2'	32:p:41:VAL:CB	2.11	0.81
4:E:78:GLY:CA	4:E:336:HIS:CE1	2.64	0.80
4:E:83:SER:O	4:E:91:LEU:N	2.14	0.80
16:G:125:C:OP2	16:G:125:C:H4'	1.78	0.80
17:H:154:C:H2'	17:H:155:C:C6	2.16	0.80
4:E:116:HIS:CE1	4:E:158:TYR:CE1	2.69	0.80
17:H:34:U:H5''	18:U:662:ILE:HG12	0.81	0.80
27:K:19:PHE:CZ	27:K:175:GLY:C	2.59	0.80
4:E:269:PRO:O	4:E:270:LYS:HB3	1.81	0.80
16:G:148:U:H3	17:H:30:A:H2	1.25	0.80
17:H:153:A:H2'	17:H:154:C:H5''	1.62	0.80
5:F:92:A:N1	5:F:93:G:C6	2.50	0.80
16:G:152:C:H3'	16:G:153:C:H5	1.41	0.80
16:G:5:G:C4	16:G:6:A:N7	2.49	0.80
27:K:125:GLU:O	27:K:129:GLN:HB2	1.81	0.80
7:L:763:ILE:CB	7:L:764:PRO:HD2	2.12	0.80
17:H:79:G:H2'	17:H:80:A:H8	1.46	0.80
17:H:172:C:H2'	17:H:173:C:C6	2.17	0.80
2:B:77:G:O6	2:B:80:U:C4	2.35	0.79
5:F:90:G:N2	17:H:8:C:O2	2.15	0.79
16:G:148:U:C2	17:H:30:A:H2	1.98	0.79
2:B:8:G:C8	2:B:75:G:C6	2.69	0.79
2:B:46:U:O4	2:B:47:A:N6	2.16	0.79
10:O:224:ASP:O	10:O:302:TRP:NE1	2.15	0.79
4:E:111:ALA:O	4:E:113:MET:N	2.15	0.79
28:I:463:PRO:O	28:I:464:ALA:HB2	1.82	0.79
16:G:152:C:N1	16:G:153:C:C5	2.49	0.79
2:B:75:G:C5	2:B:76:A:C8	2.71	0.79
7:L:699:ASN:CG	27:K:111:MET:HA	2.06	0.79
17:H:108:G:OP1	21:j:63:ASN:CB	2.31	0.79
4:E:65:HIS:CD2	4:E:91:LEU:HD12	2.17	0.79
4:E:115:LEU:CD2	4:E:126:SER:HB3	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:149:GLY:O	4:E:177:LYS:NZ	2.16	0.79
17:H:54:U:C2'	17:H:55:U:H6	1.92	0.79
4:E:109:SER:C	4:E:130:ASP:OD2	2.26	0.79
10:O:229:LYS:HD2	10:O:277:ARG:HH12	1.47	0.79
17:H:172:C:H2'	17:H:173:C:H6	1.46	0.78
28:I:325:VAL:O	28:I:328:GLU:CB	2.31	0.78
17:H:101:U:H5''	17:H:102:U:H5'	1.64	0.78
4:E:123:MET:HB3	4:E:125:PHE:HE1	1.47	0.78
4:E:125:PHE:CE2	4:E:159:PRO:CB	2.60	0.78
10:O:229:LYS:HD2	10:O:277:ARG:NH1	1.99	0.78
16:G:7:G:H2'	16:G:7:G:N3	1.97	0.78
17:H:153:A:C2'	17:H:154:C:C5'	2.52	0.78
4:E:266:PRO:CG	7:L:785:GLN:HB2	2.12	0.78
7:L:763:ILE:CB	7:L:764:PRO:CD	2.61	0.78
16:G:148:U:H5'	16:G:148:U:C6	2.18	0.78
1:A:888:GLN:N	1:A:888:GLN:HE21	1.81	0.78
1:A:1517:LYS:HB2	1:A:1517:LYS:NZ	1.98	0.78
4:E:69:VAL:CG1	4:E:345:ALA:HB1	2.14	0.78
28:I:545:ILE:HG12	28:I:546:SER:N	1.97	0.78
17:H:147:G:C4	17:H:148:C:C5	2.72	0.78
4:E:118:ASN:ND2	4:E:119:THR:H	1.81	0.77
7:L:713:MET:HB2	27:K:124:LEU:CG	2.15	0.77
17:H:7:U:O4	17:H:8:C:N4	2.16	0.77
2:B:35:U:C5'	2:B:35:U:H6	1.98	0.77
7:L:714:GLU:HG2	26:r:66:PRO:O	1.83	0.77
17:H:33:G:O3'	18:U:662:ILE:CD1	2.32	0.77
17:H:34:U:P	18:U:662:ILE:CD1	2.72	0.77
4:E:66:GLU:C	4:E:87:ASP:OD2	2.27	0.77
4:E:84:ALA:CB	4:E:90:ILE:HG23	2.11	0.77
16:G:9:C:H2'	16:G:10:U:C6	2.20	0.77
4:E:326:HIS:CE1	4:E:352:TYR:HD2	2.02	0.77
7:L:710:ALA:CA	27:K:124:LEU:CD2	2.61	0.77
17:H:150:U:H2'	17:H:151:C:C6	2.17	0.77
7:L:692:LEU:HB3	27:K:107:VAL:HG11	1.66	0.77
7:L:710:ALA:HA	27:K:124:LEU:HD22	1.66	0.77
15:W:147:GLN:C	15:W:148:VAL:HG13	2.08	0.77
17:H:83:A:C6	17:H:84:C:N4	2.52	0.77
17:H:183:G:H2'	17:H:184:C:H6	1.49	0.77
4:E:55:LEU:CG	4:E:96:TYR:OH	2.32	0.77
17:H:154:C:HO2'	17:H:155:C:H5'	1.50	0.77
17:H:69:U:C2	17:H:70:C:C5	2.73	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1827:TRP:CH2	1:A:1837:ALA:HB2	2.18	0.77
10:O:256:GLY:HA2	12:R:70:ALA:HB2	1.67	0.76
5:F:36:A:C5'	5:F:36:A:H8	1.99	0.76
17:H:165:A:N3	32:p:41:VAL:CB	2.47	0.76
16:G:9:C:O2'	16:G:10:U:O4'	2.03	0.76
2:B:75:G:N7	2:B:76:A:N7	2.33	0.76
16:G:151:C:O2'	16:G:152:C:H5''	1.84	0.76
7:L:692:LEU:O	27:K:107:VAL:HG13	1.84	0.76
10:O:229:LYS:CG	10:O:277:ARG:NH1	2.43	0.76
28:I:465:ARG:CB	28:I:543:ARG:CZ	2.64	0.76
4:E:108:HIS:HD2	4:E:136:TRP:HH2	1.33	0.76
17:H:177:A:H5''	17:H:178:A:OP1	1.84	0.76
4:E:147:LEU:N	4:E:147:LEU:HD23	2.01	0.76
4:E:165:GLN:O	4:E:166:LEU:HD23	1.85	0.76
28:I:545:ILE:C	28:I:547:LEU:H	1.92	0.76
5:F:42:C:O2'	5:F:43:A:C5'	2.28	0.75
5:F:38:G:N3	5:F:39:A:C8	2.54	0.75
7:L:759:GLU:OE1	27:K:171:GLN:NE2	2.19	0.75
18:U:655:GLU:HA	18:U:658:ARG:HG2	1.67	0.75
4:E:82:ALA:CA	4:E:92:LEU:HD23	2.16	0.75
3:C:115:GLU:OE1	3:C:189:VAL:HG23	1.85	0.75
5:F:36:A:N1	16:G:10:U:O2	2.20	0.75
16:G:120:G:C2'	29:Q:1019:SER:CA	2.59	0.75
26:q:8:SER:O	26:q:9:ASN:CB	2.34	0.75
27:K:19:PHE:CD1	27:K:175:GLY:HA3	2.19	0.75
1:A:532:THR:HB	16:G:3:A:O5'	1.85	0.75
2:B:8:G:N7	2:B:75:G:O6	2.18	0.75
4:E:78:GLY:O	4:E:336:HIS:CE1	2.39	0.75
27:K:19:PHE:CE2	27:K:175:GLY:HA3	2.18	0.75
2:B:94:U:OP2	23:f:67:ASN:CB	2.35	0.75
5:F:42:C:H2'	5:F:43:A:C8	2.21	0.75
10:O:149:LYS:CE	10:O:290:LYS:HZ2	2.00	0.75
1:A:417:ARG:NH2	2:B:59:G:OP1	2.20	0.75
3:C:160:ARG:HH11	3:C:160:ARG:HG3	1.52	0.75
7:L:759:GLU:HG2	27:K:167:ARG:HD2	1.68	0.75
3:C:538:HIS:CE1	3:C:551:LEU:CD1	2.67	0.75
6:J:642:SER:CB	6:J:650:GLU:HA	2.17	0.74
7:L:731:LEU:HB3	27:K:142:LEU:CG	2.15	0.74
17:H:93:A:O2'	17:H:94:A:C5'	2.33	0.74
1:A:51:PHE:CE1	4:E:66:GLU:HB3	2.22	0.74
2:B:8:G:C8	2:B:75:G:O6	2.40	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:77:G:O6	2:B:80:U:O4	2.05	0.74
18:U:548:LEU:CD2	18:U:661:ALA:HB1	2.18	0.74
5:F:44:G:C2	16:G:2:U:C4	2.75	0.74
7:L:692:LEU:HA	27:K:107:VAL:HG11	1.69	0.74
16:G:6:A:C4	16:G:7:G:C8	2.75	0.74
17:H:80:A:H2'	17:H:81:G:H8	1.51	0.74
17:H:93:A:H2'	17:H:94:A:H5'	1.67	0.74
18:U:548:LEU:CD2	18:U:661:ALA:CB	2.65	0.74
27:K:19:PHE:HE2	27:K:172:LEU:C	1.95	0.74
10:O:220:MET:HG2	10:O:221:PRO:CD	2.16	0.74
18:U:550:ARG:CB	18:U:660:LYS:HD3	2.17	0.74
1:A:1836:LEU:HD11	18:U:549:VAL:HG11	1.70	0.74
4:E:75:HIS:CD2	4:E:80:THR:HG22	2.22	0.74
5:F:37:C:C3'	5:F:38:G:H5'	2.17	0.74
18:U:548:LEU:HD22	18:U:661:ALA:HB1	1.69	0.74
26:t:90:PHE:CB	27:K:111:MET:O	2.35	0.74
27:K:130:HIS:O	27:K:134:ALA:HB3	1.86	0.74
2:B:81:U:O2'	2:B:82:A:OP2	2.04	0.74
4:E:119:THR:CG2	4:E:161:ARG:HB2	2.16	0.74
4:E:231:MET:HB3	4:E:262:TRP:CZ3	2.22	0.74
26:s:112:ALA:O	27:K:15:ALA:HB3	1.88	0.74
4:E:251:LEU:HG	4:E:291:CYS:SG	2.28	0.74
10:O:234:LEU:CD1	10:O:274:PHE:HZ	2.01	0.74
4:E:119:THR:HG21	4:E:161:ARG:HB2	1.68	0.74
6:J:493:ALA:HB1	6:J:499:ARG:CB	2.18	0.74
3:C:832:TYR:HE1	3:C:901:PHE:HB2	1.51	0.74
4:E:162:ARG:NH2	4:E:204:THR:HA	2.01	0.74
10:O:260:THR:CG2	10:O:273:GLN:HB2	2.03	0.74
7:L:707:ALA:CB	27:K:117:GLN:OE1	2.32	0.74
4:E:265:ARG:H	4:E:272:ARG:NH2	1.86	0.73
1:A:1517:LYS:HB2	1:A:1517:LYS:HZ3	1.54	0.73
4:E:266:PRO:HB3	7:L:788:TYR:HB3	1.70	0.73
7:L:713:MET:HB3	27:K:124:LEU:CG	2.14	0.73
17:H:147:G:N3	17:H:148:C:C5	2.56	0.73
28:I:720:ILE:O	28:I:721:LYS:CB	2.34	0.73
3:C:147:ASP:OD2	3:C:164:ASP:HB3	1.87	0.73
27:K:19:PHE:HD2	27:K:171:GLN:C	1.96	0.73
3:C:139:HIS:HA	35:C:1500:GTP:O3B	1.89	0.73
27:K:18:TYR:CD1	27:K:168:LYS:CG	2.68	0.73
27:K:123:ASN:O	27:K:127:MET:N	2.20	0.73
5:F:44:G:C8	16:G:1:G:C2	2.76	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:114:A:H2'	17:H:115:G:H8	1.53	0.73
2:B:9:G:H2'	2:B:9:G:N3	2.04	0.73
5:F:43:A:H1'	16:G:4:A:H61	0.73	0.73
18:U:811:ARG:HG3	18:U:811:ARG:NH1	1.99	0.73
4:E:257:ASN:OD1	15:W:149:SER:CB	2.37	0.73
7:L:752:PHE:HA	7:L:755:LEU:HB2	1.71	0.73
3:C:160:ARG:NH1	3:C:160:ARG:HG3	2.03	0.73
4:E:75:HIS:CB	4:E:80:THR:O	2.35	0.72
4:E:277:PHE:HE2	4:E:300:ILE:CD1	2.01	0.72
16:G:122:U:O2'	30:y:76:THR:N	2.22	0.72
5:F:41:A:H61	16:G:6:A:H61	1.35	0.72
7:L:759:GLU:OE1	27:K:17:PRO:CD	2.36	0.72
16:G:152:C:N3	16:G:153:C:C4	2.57	0.72
4:E:115:LEU:HD22	4:E:126:SER:CB	2.18	0.72
16:G:2:U:C4	18:U:625:PHE:HD2	2.07	0.72
1:A:942:PRO:HB2	1:A:1438:VAL:HG22	1.70	0.72
6:J:223:TYR:OH	7:L:248:ASP:CG	2.31	0.72
17:H:55:U:O4	17:H:93:A:N6	2.22	0.72
4:E:78:GLY:C	4:E:336:HIS:CE1	2.67	0.72
4:E:243:LEU:HD11	4:E:247:GLY:HA2	1.71	0.72
4:E:248:SER:HB2	4:E:249:TYR:CD1	2.24	0.72
10:O:258:ILE:HG22	10:O:274:PHE:CD1	2.24	0.72
16:G:2:U:N3	18:U:625:PHE:HD2	1.85	0.72
16:G:146:C:H1'	16:G:147:C:N1	2.03	0.72
4:E:119:THR:HG22	4:E:161:ARG:HB3	1.71	0.72
1:A:1522:GLN:HA	1:A:1522:GLN:HE21	1.52	0.72
4:E:69:VAL:HG12	4:E:345:ALA:HB1	1.72	0.72
10:O:155:PRO:HA	12:R:188:PHE:HE1	1.54	0.72
10:O:252:PHE:O	10:O:255:PHE:HD2	1.73	0.72
2:B:8:G:H8	2:B:75:G:C6	2.04	0.72
17:H:182:U:HO2'	17:H:183:G:H5'	1.53	0.72
28:I:545:ILE:O	28:I:547:LEU:N	2.22	0.72
4:E:108:HIS:HD2	4:E:136:TRP:CH2	2.07	0.72
10:O:243:ILE:HG22	10:O:294:ASN:OD1	1.89	0.72
17:H:34:U:H5'	18:U:662:ILE:HG12	1.67	0.72
17:H:98:G:O2'	17:H:99:A:C5'	2.38	0.72
17:H:160:A:O2'	17:H:161:U:H5'	1.90	0.72
5:F:38:G:H2'	5:F:39:A:H8	1.54	0.71
1:A:1802:PRO:HG2	1:A:1824:THR:CG2	2.19	0.71
10:O:223:LEU:HD13	10:O:223:LEU:N	2.05	0.71
27:K:115:GLU:HA	27:K:115:GLU:OE2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:92:LEU:O	4:E:101:ASN:CA	2.37	0.71
16:G:6:A:N6	16:G:7:G:C6	2.59	0.71
17:H:182:U:H2'	17:H:183:G:C8	2.23	0.71
1:A:1927:ILE:HG22	1:A:1931:THR:HB	1.73	0.71
2:B:96:A:C6	2:B:97:G:C5	2.78	0.71
4:E:266:PRO:CB	7:L:788:TYR:HB3	2.20	0.71
10:O:224:ASP:HB3	10:O:225:PRO:HD2	1.72	0.71
10:O:258:ILE:HG22	10:O:274:PHE:HD1	1.55	0.71
16:G:120:G:C2'	29:Q:1019:SER:N	2.54	0.71
5:F:40:U:C4	5:F:41:A:N6	2.59	0.71
16:G:122:U:O2'	30:y:75:ARG:CB	2.38	0.71
2:B:77:G:C5	2:B:80:U:H5	2.08	0.71
17:H:54:U:C2'	17:H:55:U:C6	2.63	0.71
28:I:172:PHE:CB	28:I:199:ARG:C	2.64	0.71
3:C:139:HIS:HB3	35:C:1500:GTP:O3G	1.90	0.71
17:H:33:G:OP1	18:U:666:ARG:NH1	2.23	0.71
17:H:154:C:O2'	17:H:155:C:C5'	2.34	0.71
5:F:92:A:C2	5:F:93:G:C4	2.78	0.71
12:R:232:SEP:HB3	14:T:372:LYS:CE	2.18	0.71
2:B:77:G:C5	2:B:80:U:C5	2.79	0.70
4:E:63:SER:O	4:E:93:TRP:HZ3	1.73	0.70
4:E:124:LEU:O	4:E:136:TRP:HD1	1.73	0.70
3:C:158:ARG:HA	3:C:158:ARG:HH21	1.54	0.70
10:O:234:LEU:HD11	10:O:274:PHE:HE2	1.56	0.70
10:O:260:THR:CA	10:O:273:GLN:HB3	2.21	0.70
16:G:6:A:C5	16:G:7:G:C8	2.80	0.70
16:G:5:G:C2	16:G:6:A:C5	2.78	0.70
28:I:365:ALA:CA	28:I:372:ARG:CB	2.59	0.70
7:L:703:MET:HA	27:K:117:GLN:HG3	1.71	0.70
16:G:147:C:OP2	18:U:659:LYS:HD3	1.90	0.70
16:G:148:U:H6	16:G:148:U:C5'	2.01	0.70
17:H:109:C:O2'	17:H:110:A:H5'	1.91	0.70
4:E:114:GLU:HG3	4:E:156:SER:OG	1.90	0.70
7:L:731:LEU:HB3	27:K:142:LEU:CD2	2.20	0.70
27:K:17:PRO:HG3	27:K:167:ARG:NH1	2.07	0.70
4:E:55:LEU:HG	4:E:96:TYR:HH	1.52	0.70
28:I:742:ALA:O	28:I:746:LEU:N	2.24	0.70
1:A:1811:ASN:HD22	1:A:1816:GLN:HB3	1.57	0.70
4:E:71:CYS:SG	4:E:115:LEU:HB2	2.31	0.70
16:G:6:A:N9	16:G:7:G:C8	2.60	0.70
17:H:147:G:N1	17:H:148:C:C4	2.60	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:604:PRO:CA	6:J:607:LYS:N	2.54	0.70
10:O:288:PHE:CD1	10:O:289:ASN:OD1	2.45	0.70
28:I:585:ASP:O	28:I:588:PRO:N	2.25	0.70
5:F:92:A:N1	5:F:93:G:C5	2.60	0.70
26:t:71:ILE:CB	27:K:70:PHE:CB	2.70	0.70
4:E:115:LEU:CD2	4:E:126:SER:CB	2.70	0.69
6:J:223:TYR:HH	7:L:248:ASP:CG	1.99	0.69
10:O:259:ARG:HG3	10:O:274:PHE:O	1.92	0.69
4:E:277:PHE:HE2	4:E:300:ILE:HD13	1.56	0.69
5:F:34:G:C4	5:F:35:A:C8	2.80	0.69
5:F:81:C:H6	5:F:81:C:C5'	2.04	0.69
16:G:27:U:H2'	16:G:28:A:O5'	1.91	0.69
16:G:120:G:C1'	29:Q:1019:SER:CB	2.70	0.69
17:H:34:U:O2'	17:H:35:A:H8	1.75	0.69
17:H:179:C:C2	17:H:180:G:N7	2.60	0.69
1:A:1509:PHE:HZ	1:A:1513:MET:HE2	1.56	0.69
4:E:67:GLY:N	4:E:87:ASP:OD2	2.25	0.69
4:E:82:ALA:HA	4:E:92:LEU:HD23	1.73	0.69
10:O:149:LYS:HZ1	10:O:290:LYS:HG3	1.56	0.69
10:O:223:LEU:N	10:O:223:LEU:HD22	2.06	0.69
18:U:550:ARG:HB2	18:U:660:LYS:HD3	1.75	0.69
4:E:287:ASN:O	4:E:289:LEU:HD23	1.92	0.69
5:F:81:C:H6	5:F:81:C:H5''	1.55	0.69
2:B:93:U:H1'	22:d:104:ASP:CB	2.22	0.69
4:E:108:HIS:HE1	4:E:128:SER:CB	2.04	0.69
4:E:257:ASN:CB	15:W:149:SER:HB3	2.21	0.69
17:H:83:A:C2	17:H:84:C:C4	2.81	0.69
1:A:1513:MET:HE1	18:U:622:ALA:HB3	1.73	0.69
17:H:80:A:C2'	17:H:81:G:H5'	2.23	0.69
17:H:113:G:C2'	17:H:114:A:H5'	2.22	0.69
7:L:692:LEU:CB	27:K:107:VAL:CG1	2.67	0.69
16:G:145:U:H5'	16:G:145:U:N1	2.06	0.69
4:E:62:LEU:HD13	4:E:93:TRP:CE3	2.27	0.69
6:J:592:ALA:H	6:J:595:ALA:HB3	1.56	0.69
10:O:149:LYS:CE	10:O:290:LYS:NZ	2.53	0.69
10:O:262:THR:HB	10:O:271:PHE:HB2	1.75	0.69
16:G:146:C:H3'	16:G:146:C:P	2.33	0.69
1:A:1946:ASN:ND2	1:A:1986:LEU:CD2	2.54	0.69
4:E:54:SER:HB2	4:E:355:GLU:OE1	1.91	0.69
4:E:209:ILE:HG21	4:E:250:LEU:CD1	2.23	0.69
4:E:313:ASP:HA	4:E:320:LEU:HD11	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:3:A:O2'	16:G:4:A:OP2	2.11	0.69
17:H:147:G:C2	17:H:148:C:C5	2.81	0.69
27:K:17:PRO:HG3	27:K:167:ARG:HH12	1.58	0.69
1:A:51:PHE:CZ	4:E:66:GLU:HG2	2.27	0.69
7:L:762:ALA:CB	27:K:14:ASP:OD1	2.37	0.69
3:C:139:HIS:HB2	35:C:1500:GTP:H5''	1.75	0.68
7:L:780:ARG:HB3	27:K:188:LEU:HD21	1.75	0.68
12:R:189:ASN:HD22	12:R:189:ASN:C	2.01	0.68
5:F:44:G:C6	16:G:2:U:C4	2.81	0.68
2:B:77:G:N7	2:B:80:U:C4	2.61	0.68
4:E:119:THR:HG23	4:E:161:ARG:HB3	1.73	0.68
4:E:132:THR:OG1	4:E:148:LYS:HG2	1.94	0.68
16:G:22:C:H1'	16:G:23:U:OP1	1.93	0.68
16:G:147:C:H5'	18:U:659:LYS:NZ	2.09	0.68
5:F:82:A:H5''	5:F:82:A:H8	1.58	0.68
18:U:655:GLU:O	18:U:658:ARG:HG3	1.94	0.68
30:y:69:GLU:HA	30:y:76:THR:HA	1.76	0.68
7:L:699:ASN:CA	27:K:114:LEU:HB2	2.24	0.68
18:U:626:MET:HE2	18:U:643:LYS:CE	2.22	0.68
27:K:18:TYR:CG	27:K:168:LYS:HG2	2.27	0.68
4:E:62:LEU:CD1	4:E:93:TRP:CD2	2.77	0.68
1:A:113:ILE:HG21	9:N:6:ARG:HE	1.58	0.68
2:B:35:U:H6	2:B:35:U:H5''	1.57	0.68
1:A:1210:LYS:HG3	1:A:1212:GLY:H	1.59	0.67
4:E:111:ALA:HB3	4:E:129:THR:OG1	1.93	0.67
17:H:57:A:N6	17:H:91:U:N3	2.35	0.67
2:B:23:C:O2'	2:B:24:G:H3'	1.93	0.67
16:G:22:C:C1'	16:G:23:U:OP1	2.41	0.67
17:H:147:G:N1	17:H:148:C:N4	2.42	0.67
1:A:1836:LEU:HD11	18:U:549:VAL:CG1	2.24	0.67
4:E:55:LEU:O	4:E:57:ALA:N	2.27	0.67
17:H:54:U:C4	17:H:93:A:N6	2.62	0.67
1:A:1836:LEU:CD1	18:U:549:VAL:HG11	2.23	0.67
4:E:54:SER:HB3	4:E:355:GLU:CD	2.10	0.67
5:F:44:G:C8	16:G:1:G:N1	2.63	0.67
7:L:692:LEU:CA	27:K:107:VAL:CG1	2.72	0.67
5:F:36:A:H2	16:G:10:U:O2	1.71	0.67
16:G:148:U:H3'	16:G:149:G:H5''	1.76	0.67
4:E:61:LEU:HD13	4:E:352:TYR:CE1	2.30	0.67
4:E:82:ALA:HB1	4:E:92:LEU:HD21	1.74	0.67
4:E:125:PHE:CD2	4:E:159:PRO:HB3	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:153:A:C3'	17:H:154:C:H5'	2.24	0.67
28:I:790:ARG:CB	28:I:797:PHE:O	2.43	0.67
4:E:246:GLU:HB2	4:E:248:SER:OG	1.95	0.67
7:L:252:ARG:HG2	7:L:252:ARG:NH1	2.10	0.67
28:I:403:LYS:O	28:I:405:TYR:N	2.27	0.67
28:I:463:PRO:O	28:I:464:ALA:CB	2.42	0.67
10:O:149:LYS:NZ	10:O:290:LYS:NZ	2.43	0.67
4:E:266:PRO:HG2	7:L:785:GLN:CA	2.25	0.67
1:A:1605:GLU:HB3	1:A:1637:TRP:HE1	1.58	0.66
4:E:264:VAL:HA	4:E:272:ARG:HH21	1.58	0.66
10:O:292:ILE:HG12	10:O:297:ARG:HA	1.77	0.66
4:E:130:ASP:C	4:E:131:LYS:HG3	2.19	0.66
4:E:264:VAL:HA	4:E:272:ARG:NH2	2.10	0.66
16:G:119:G:O2'	29:Q:1021:LEU:CB	2.43	0.66
17:H:147:G:H2'	17:H:148:C:C6	2.31	0.66
17:H:183:G:H2'	17:H:184:C:C6	2.30	0.66
2:B:92:U:O4	20:b:36:LYS:O	2.14	0.66
4:E:298:SER:O	4:E:314:THR:N	2.27	0.66
10:O:247:ASP:N	10:O:247:ASP:OD1	2.25	0.66
27:K:128:SER:O	27:K:132:CYS:N	2.25	0.66
4:E:58:PRO:HD2	4:E:59:ILE:H	1.61	0.66
4:E:250:LEU:HD23	4:E:250:LEU:O	1.93	0.66
13:S:56:ILE:HG12	13:S:62:ILE:HG23	1.78	0.66
1:A:1809:ILE:HB	1:A:1818:PHE:HB2	1.76	0.66
7:L:267:LEU:HD23	7:L:267:LEU:C	2.21	0.66
2:B:96:A:O2'	2:B:97:G:H5'	1.95	0.66
5:F:34:G:H2'	5:F:35:A:O5'	1.96	0.66
2:B:96:A:C6	2:B:97:G:C6	2.84	0.66
5:F:82:A:H62	12:R:258:LYS:NZ	1.94	0.66
7:L:759:GLU:CG	27:K:171:GLN:HE22	2.08	0.66
27:K:19:PHE:HD2	27:K:172:LEU:N	1.94	0.66
28:I:790:ARG:CB	28:I:801:ASP:CA	2.74	0.66
4:E:54:SER:CB	4:E:355:GLU:OE1	2.43	0.66
17:H:83:A:O2'	17:H:84:C:C5'	2.42	0.66
14:T:216:ASN:HD21	14:T:472:GLN:H	1.44	0.65
27:K:119:VAL:O	27:K:123:ASN:N	2.27	0.65
1:A:1832:ARG:HA	1:A:1832:ARG:NE	2.08	0.65
14:T:261:LEU:HB3	14:T:273:TRP:HB2	1.78	0.65
7:L:692:LEU:HA	27:K:107:VAL:CG1	2.27	0.65
10:O:240:GLY:HA3	10:O:296:ARG:HH12	1.60	0.65
4:E:139:GLU:HG3	4:E:140:THR:HG23	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:321:TYR:CE1	4:E:356:ILE:HD13	2.31	0.65
7:L:706:GLU:HB2	27:K:117:GLN:HB3	1.77	0.65
10:O:220:MET:CG	10:O:221:PRO:HD2	2.24	0.65
4:E:124:LEU:HD12	4:E:124:LEU:C	2.21	0.65
28:I:545:ILE:C	28:I:547:LEU:N	2.52	0.65
7:L:759:GLU:CG	27:K:167:ARG:HD2	2.26	0.65
2:B:8:G:H8	2:B:75:G:H1	0.71	0.65
1:A:1836:LEU:CD2	18:U:547:ILE:HG21	2.27	0.65
16:G:6:A:C5	16:G:7:G:C5	2.84	0.65
17:H:8:C:O2'	17:H:9:U:H5'	1.96	0.65
26:r:128:ARG:N	26:s:127:ALA:HB1	2.12	0.65
29:Q:341:ALA:HB1	29:Q:352:ALA:HB2	1.79	0.65
1:A:1214:TRP:HB2	1:A:1228:CYS:HB3	1.78	0.65
4:E:234:HIS:HA	4:E:256:ASP:OD2	1.96	0.65
7:L:242:LEU:HD21	7:L:247:LEU:HD21	1.79	0.65
1:A:1802:PRO:HG2	1:A:1824:THR:HG21	1.77	0.65
4:E:125:PHE:HE2	4:E:159:PRO:HB2	1.61	0.65
7:L:201:LYS:HB2	16:G:8:C:OP1	1.97	0.65
17:H:7:U:N3	17:H:8:C:C4	2.65	0.65
17:H:43:U:O2'	17:H:44:U:C5	2.47	0.65
17:H:80:A:C2	17:H:81:G:C5	2.84	0.65
1:A:888:GLN:OE1	7:L:130:PRO:HG3	1.97	0.64
4:E:326:HIS:CD2	4:E:330:ILE:HG12	2.28	0.64
10:O:259:ARG:CG	10:O:275:ALA:N	2.55	0.64
16:G:148:U:O2	17:H:30:A:H2	1.79	0.64
1:A:1518:LEU:HD21	17:H:29:A:N6	2.13	0.64
4:E:74:PHE:HA	4:E:81:LEU:HD21	0.70	0.64
4:E:74:PHE:CA	4:E:81:LEU:CD2	2.45	0.64
27:K:18:TYR:CG	27:K:168:LYS:HA	2.32	0.64
7:L:696:LEU:HA	27:K:110:SER:OG	1.96	0.64
16:G:6:A:N7	16:G:7:G:N7	2.45	0.64
16:G:22:C:H1'	16:G:23:U:P	2.38	0.64
17:H:7:U:C5	17:H:8:C:N4	2.64	0.64
17:H:165:A:C2'	32:p:41:VAL:CB	2.75	0.64
27:K:19:PHE:CD2	27:K:171:GLN:C	2.75	0.64
5:F:36:A:C8	5:F:36:A:H3'	2.32	0.64
12:R:193:LYS:CB	15:W:145:ASN:HD21	2.10	0.64
3:C:114:TYR:CZ	19:a:83:LEU:CB	2.81	0.64
3:C:137:HIS:CD2	3:C:236:MET:HB3	2.32	0.64
4:E:73:LYS:O	4:E:81:LEU:HD22	1.98	0.64
5:F:36:A:C8	5:F:36:A:C3'	2.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:221:PRO:HA	10:O:222:ARG:NH2	2.12	0.64
27:K:19:PHE:CD2	27:K:172:LEU:CA	2.80	0.64
1:A:1946:ASN:ND2	1:A:1949:ARG:HB3	2.11	0.64
3:C:136:GLY:HA3	3:C:142:LYS:HZ3	1.63	0.64
4:E:307:ARG:NH1	15:W:143:LEU:HD22	2.08	0.64
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.80	0.64
1:A:1831:LYS:O	1:A:1831:LYS:NZ	2.24	0.64
4:E:92:LEU:O	4:E:101:ASN:CB	2.46	0.64
18:U:668:LEU:HD12	18:U:668:LEU:C	2.22	0.64
1:A:1662:ILE:HA	1:A:1701:VAL:O	1.98	0.64
3:C:160:ARG:HH11	3:C:160:ARG:C	2.04	0.64
3:C:832:TYR:CD1	3:C:900:VAL:O	2.51	0.64
4:E:307:ARG:NH1	15:W:143:LEU:CD2	2.61	0.64
4:E:326:HIS:CE1	4:E:352:TYR:CD2	2.85	0.64
6:J:223:TYR:OH	7:L:248:ASP:OD2	2.16	0.64
17:H:27:U:O2'	17:H:28:C:C5'	2.39	0.64
1:A:1518:LEU:O	1:A:1519:THR:HB	1.97	0.63
1:A:1570:LYS:HE2	18:U:637:ASP:HB3	1.80	0.63
1:A:1839:TRP:NE1	18:U:557:VAL:O	2.31	0.63
3:C:112:THR:HG23	3:C:115:GLU:HG3	1.80	0.63
10:O:149:LYS:NZ	10:O:290:LYS:CG	2.61	0.63
10:O:276:THR:HG23	10:O:279:ALA:H	1.62	0.63
4:E:90:ILE:HD12	4:E:112:VAL:HG11	1.75	0.63
4:E:108:HIS:CD2	4:E:136:TRP:CH2	2.86	0.63
4:E:131:LYS:HD3	4:E:151:THR:C	2.23	0.63
12:R:184:GLN:HA	12:R:184:GLN:NE2	2.13	0.63
12:R:234:SER:O	12:R:235:ARG:C	2.42	0.63
17:H:80:A:N3	17:H:81:G:C8	2.66	0.63
18:U:666:ARG:HG2	18:U:666:ARG:NH2	2.09	0.63
1:A:761:ILE:HD12	1:A:775:ASN:HD22	1.62	0.63
1:A:940:ILE:HD12	1:A:1090:ARG:HH21	1.62	0.63
3:C:832:TYR:CE1	3:C:901:PHE:HB2	2.33	0.63
4:E:82:ALA:HB1	4:E:92:LEU:HD23	1.71	0.63
16:G:145:U:H1'	16:G:146:C:H5'	1.81	0.63
17:H:163:G:N1	32:p:49:ARG:O	2.29	0.63
1:A:50:LYS:HB2	4:E:88:ARG:NH1	2.12	0.63
16:G:5:G:N2	16:G:6:A:H62	1.97	0.63
2:B:37:G:N2	2:B:45:C:O2	2.26	0.63
10:O:87:ASP:HB3	10:O:91:GLY:H	1.64	0.63
17:H:74:U:H2'	17:H:75:A:C8	2.28	0.63
17:H:83:A:C2	17:H:84:C:N3	2.66	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:57:ALA:O	4:E:355:GLU:HB3	1.99	0.63
4:E:284:PHE:O	15:W:124:MET:HE2	1.99	0.63
15:W:97:ASN:HD21	15:W:100:ARG:HH21	1.47	0.63
16:G:152:C:C4	16:G:153:C:C4	2.86	0.63
26:r:8:SER:O	26:r:9:ASN:CB	2.47	0.63
4:E:134:ALA:HB1	4:E:143:ARG:HD2	1.80	0.62
10:O:149:LYS:HZ1	10:O:290:LYS:NZ	1.96	0.62
10:O:149:LYS:NZ	10:O:290:LYS:HG3	2.14	0.62
17:H:102:U:C2	19:h:4:GLY:N	2.66	0.62
2:B:74:U:O4	2:B:76:A:N6	2.32	0.62
4:E:178:LEU:HD11	4:E:222:LEU:CD2	2.29	0.62
28:I:484:LEU:O	28:I:485:LYS:C	2.43	0.62
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.80	0.62
4:E:178:LEU:HD21	4:E:208:ILE:CD1	2.29	0.62
4:E:178:LEU:CD1	4:E:222:LEU:CD2	2.77	0.62
5:F:36:A:H8	5:F:36:A:O5'	1.81	0.62
10:O:27:CYS:SG	10:O:66:LYS:NZ	2.72	0.62
16:G:146:C:C1'	16:G:147:C:C6	2.80	0.62
17:H:8:C:O2'	17:H:9:U:C5'	2.47	0.62
17:H:83:A:C6	17:H:84:C:C4	2.86	0.62
1:A:1928:SER:OG	1:A:1930:TYR:CD1	2.52	0.62
2:B:88:A:H61	23:f:40:MET:CB	2.12	0.62
5:F:45:A:C2	18:U:625:PHE:CE1	2.88	0.62
10:O:149:LYS:HZ1	10:O:290:LYS:CE	2.12	0.62
4:E:298:SER:O	4:E:314:THR:CB	2.44	0.62
9:N:139:CYS:SG	9:N:140:ARG:N	2.72	0.62
16:G:147:C:H5'	18:U:659:LYS:HZ1	1.64	0.62
16:G:152:C:C2'	16:G:153:C:H5	2.00	0.62
1:A:1515:TRP:CE3	1:A:1515:TRP:HA	2.34	0.62
1:A:1515:TRP:HA	1:A:1515:TRP:HE3	1.64	0.62
3:C:618:THR:HB	3:C:630:LEU:HB2	1.81	0.62
4:E:235:ALA:HB3	4:E:256:ASP:HB2	1.82	0.62
7:L:764:PRO:O	7:L:765:ARG:CB	2.48	0.62
17:H:163:G:O6	32:p:50:GLY:CA	2.47	0.62
10:O:239:LEU:O	10:O:243:ILE:HD11	2.00	0.62
16:G:6:A:C8	16:G:7:G:C8	2.88	0.62
1:A:888:GLN:OE1	7:L:130:PRO:CG	2.48	0.62
26:s:112:ALA:O	27:K:15:ALA:HB1	1.99	0.62
18:U:662:ILE:C	18:U:662:ILE:HD12	2.25	0.61
4:E:153:PHE:O	4:E:171:SER:HB2	2.00	0.61
10:O:235:TYR:HD1	10:O:271:PHE:HE1	1.46	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:272:ILE:CG2	10:O:274:PHE:CE1	2.83	0.61
17:H:30:A:O2'	17:H:31:G:C8	2.52	0.61
17:H:83:A:C2	17:H:84:C:C2	2.88	0.61
17:H:112:G:H2'	17:H:113:G:H8	1.65	0.61
26:q:22:ASN:CB	26:r:55:ILE:CB	2.78	0.61
28:I:526:MET:HE2	28:I:526:MET:O	2.00	0.61
1:A:1342:TRP:HB2	1:A:1486:GLU:HG3	1.81	0.61
4:E:69:VAL:HG12	4:E:69:VAL:O	2.00	0.61
17:H:98:G:H5''	17:H:104:U:P	2.40	0.61
6:J:741:THR:O	6:J:745:CYS:CB	2.48	0.61
3:C:141:GLY:N	35:C:1500:GTP:O2B	2.34	0.61
7:L:713:MET:CB	27:K:124:LEU:HD21	2.21	0.61
10:O:155:PRO:HD3	12:R:188:PHE:CD1	2.35	0.61
14:T:350:HIS:HA	14:T:374:SER:HB2	1.82	0.61
16:G:3:A:H1'	16:G:4:A:O5'	2.00	0.61
16:G:7:G:C2	16:G:8:C:H1'	2.36	0.61
1:A:469:LYS:NZ	2:B:59:G:O6	2.33	0.61
1:A:1941:ARG:O	1:A:1945:VAL:HG22	2.01	0.61
3:C:666:VAL:HG13	3:C:824:THR:HG23	1.83	0.61
4:E:108:HIS:CD2	4:E:136:TRP:HH2	2.17	0.61
4:E:116:HIS:HE1	4:E:158:TYR:CE1	2.17	0.61
16:G:120:G:C1'	29:Q:1019:SER:CA	2.78	0.61
28:I:399:VAL:O	28:I:399:VAL:HG13	2.00	0.61
1:A:1946:ASN:CG	1:A:1986:LEU:CG	2.73	0.61
7:L:710:ALA:CA	27:K:124:LEU:HD22	2.26	0.61
7:L:759:GLU:OE2	7:L:759:GLU:HA	2.01	0.61
16:G:120:G:H2'	29:Q:1019:SER:N	2.14	0.61
17:H:69:U:H2'	17:H:70:C:C5	2.35	0.61
18:U:814:VAL:HG11	18:U:820:TYR:HB3	1.83	0.61
1:A:1892:PRO:HD3	1:A:1941:ARG:HH21	1.66	0.61
3:C:160:ARG:O	3:C:160:ARG:HG3	1.99	0.61
4:E:93:TRP:HA	4:E:101:ASN:CA	2.30	0.61
2:B:71:C:H6	2:B:71:C:H5''	1.66	0.61
7:L:784:LEU:CB	27:K:195:ILE:CB	2.78	0.61
2:B:103:G:O2'	2:B:104:C:H5'	2.00	0.61
4:E:58:PRO:CD	4:E:59:ILE:H	2.14	0.61
4:E:325:GLY:O	4:E:352:TYR:HE2	1.83	0.61
5:F:36:A:C8	5:F:36:A:C4'	2.84	0.61
17:H:154:C:H2'	17:H:155:C:H6	1.65	0.61
28:I:795:ILE:O	28:I:795:ILE:HG22	1.99	0.61
3:C:160:ARG:HH11	3:C:160:ARG:CG	2.14	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:259:ARG:N	10:O:273:GLN:O	2.34	0.60
1:A:788:GLN:HG2	1:A:1024:HIS:HB3	1.83	0.60
1:A:1508:GLY:O	1:A:1511:GLU:HG3	2.01	0.60
10:O:234:LEU:HD11	10:O:274:PHE:HZ	1.59	0.60
17:H:147:G:H2'	17:H:148:C:H6	1.65	0.60
18:U:620:ARG:NH2	18:U:643:LYS:O	2.34	0.60
30:y:13:LEU:CB	30:y:48:GLY:O	2.48	0.60
1:A:1516:LYS:NZ	1:A:1516:LYS:HA	2.16	0.60
4:E:233:GLY:O	4:E:260:ARG:NH2	2.33	0.60
7:L:707:ALA:HB2	27:K:117:GLN:NE2	2.16	0.60
7:L:781:GLU:HG2	27:K:191:LYS:CG	2.30	0.60
10:O:235:TYR:CD2	10:O:301:LYS:HB2	2.33	0.60
18:U:579:VAL:HG22	18:U:646:GLU:HB2	1.83	0.60
2:B:87:A:N7	22:d:61:ARG:CB	2.64	0.60
4:E:298:SER:CA	4:E:314:THR:HB	2.31	0.60
10:O:72:GLN:OE1	10:O:82:GLN:NE2	2.34	0.60
17:H:34:U:OP1	18:U:662:ILE:CD1	2.44	0.60
28:I:285:THR:CB	28:I:288:THR:CB	2.79	0.60
1:A:663:ARG:HH22	5:F:63:C:H3'	1.66	0.60
7:L:267:LEU:HD23	7:L:267:LEU:O	2.01	0.60
7:L:732:MET:HA	26:q:65:PRO:CB	2.31	0.60
16:G:146:C:H3'	16:G:146:C:OP2	2.01	0.60
7:L:259:ASP:CG	8:M:199:ARG:NH2	2.59	0.60
7:L:692:LEU:CG	27:K:107:VAL:HG11	2.31	0.60
10:O:221:PRO:HB2	10:O:289:ASN:ND2	2.17	0.60
16:G:147:C:OP2	18:U:659:LYS:HB2	2.01	0.60
18:U:868:SER:HB2	18:U:872:GLN:H	1.66	0.60
28:I:405:TYR:O	28:I:409:GLY:N	2.34	0.60
3:C:137:HIS:HA	3:C:238:ASN:HB3	1.83	0.60
4:E:61:LEU:HD13	4:E:352:TYR:CD1	2.37	0.60
16:G:120:G:O2'	29:Q:1019:SER:N	2.35	0.60
17:H:58:U:O4	17:H:90:A:N1	2.34	0.60
17:H:162:U:C2	32:p:13:ASN:CB	2.85	0.60
1:A:1144:LYS:HE2	1:A:1148:ASN:HD21	1.66	0.60
3:C:113:VAL:HG23	3:C:113:VAL:O	2.00	0.60
10:O:234:LEU:CD1	10:O:274:PHE:CE2	2.82	0.60
17:H:93:A:C2'	17:H:94:A:C5'	2.79	0.60
27:K:117:GLN:HA	27:K:117:GLN:HE21	1.66	0.60
1:A:695:ASP:OD2	14:T:376:ARG:NH2	2.35	0.60
1:A:1330:MET:HE1	1:A:1369:TYR:HB2	1.83	0.60
10:O:222:ARG:CZ	10:O:222:ARG:H	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:79:G:H2'	17:H:80:A:C8	2.34	0.60
1:A:1636:LYS:HB2	1:A:1655:THR:HB	1.84	0.59
18:U:626:MET:CE	18:U:643:LYS:HZ2	1.97	0.59
2:B:72:U:O5'	2:B:72:U:H6	1.86	0.59
3:C:168:THR:HG22	3:C:168:THR:O	2.02	0.59
4:E:313:ASP:HB2	4:E:320:LEU:HD21	1.82	0.59
16:G:26:U:H2'	16:G:27:U:H5''	1.82	0.59
4:E:66:GLU:HB2	4:E:87:ASP:OD2	2.02	0.59
16:G:6:A:H3'	16:G:7:G:H8	1.65	0.59
3:C:538:HIS:HE1	3:C:551:LEU:HD11	1.62	0.59
5:F:45:A:N3	18:U:625:PHE:CE1	2.69	0.59
5:F:82:A:H5''	5:F:82:A:C8	2.37	0.59
10:O:251:HIS:CE1	10:O:291:LEU:HD11	2.38	0.59
14:T:314:ILE:HD12	14:T:324:HIS:HB2	1.84	0.59
16:G:5:G:N2	16:G:6:A:N6	2.50	0.59
17:H:113:G:H2'	17:H:114:A:H5'	1.83	0.59
17:H:165:A:C5	32:p:53:PHE:CB	2.84	0.59
4:E:116:HIS:CD2	4:E:157:CYS:O	2.56	0.59
4:E:128:SER:OG	4:E:130:ASP:OD1	2.11	0.59
17:H:7:U:C2	17:H:8:C:C5	2.91	0.59
27:K:128:SER:O	27:K:132:CYS:CB	2.50	0.59
3:C:678:THR:OG1	3:C:680:ASN:O	2.20	0.59
4:E:81:LEU:O	4:E:92:LEU:HA	2.03	0.59
4:E:93:TRP:CZ2	4:E:351:LEU:CD1	2.86	0.59
3:C:210:ASN:HB3	3:C:636:TYR:HB2	1.85	0.59
16:G:2:U:C4	18:U:625:PHE:CD2	2.88	0.59
17:H:97:G:H8	17:H:97:G:OP2	1.84	0.59
1:A:425:PRO:HB2	1:A:428:LYS:HB2	1.84	0.59
2:B:77:G:C6	2:B:80:U:O4	2.56	0.59
18:U:550:ARG:CB	18:U:660:LYS:CD	2.81	0.59
27:K:128:SER:O	27:K:132:CYS:HB2	2.01	0.59
28:I:464:ALA:O	28:I:467:ALA:N	2.35	0.59
12:R:78:ARG:HG3	12:R:79:LYS:HG2	1.83	0.59
3:C:117:ASP:N	3:C:117:ASP:OD1	2.31	0.59
5:F:36:A:C5'	5:F:36:A:C8	2.85	0.59
5:F:78:A:O2'	11:P:6:ARG:NH1	2.35	0.59
5:F:90:G:N1	5:F:91:A:C6	2.70	0.59
10:O:260:THR:CG2	10:O:273:GLN:OE1	2.50	0.59
13:S:18:THR:HG22	13:S:159:ILE:HG12	1.85	0.59
16:G:1:G:O2'	16:G:2:U:OP1	2.17	0.59
16:G:123:U:C1'	30:y:78:ARG:CB	2.81	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:147:C:OP1	18:U:659:LYS:HD2	1.97	0.58
16:G:147:C:H2'	16:G:148:U:H5''	1.85	0.58
17:H:54:U:O2'	17:H:55:U:H5'	2.03	0.58
28:I:465:ARG:CB	28:I:543:ARG:NH1	2.66	0.58
1:A:995:ARG:HG3	12:R:291:LEU:HD13	1.85	0.58
1:A:1631:LEU:HB2	1:A:1660:TYR:HB3	1.86	0.58
4:E:243:LEU:HD12	4:E:247:GLY:HA2	1.85	0.58
17:H:80:A:C4	17:H:81:G:N7	2.71	0.58
17:H:83:A:N3	17:H:84:C:C6	2.71	0.58
17:H:172:C:O2'	17:H:173:C:C5'	2.48	0.58
1:A:1431:ALA:O	1:A:1434:LYS:NZ	2.36	0.58
5:F:84:A:H62	6:J:241:VAL:HG13	1.68	0.58
10:O:15:TRP:HE1	11:P:26:LEU:HB2	1.66	0.58
18:U:550:ARG:HB3	18:U:660:LYS:HD3	1.84	0.58
1:A:348:PRO:HG2	1:A:351:TYR:HB3	1.85	0.58
1:A:1865:ARG:NH1	18:U:726:ASP:OD2	2.36	0.58
3:C:693:GLU:H	3:C:696:LEU:HD12	1.68	0.58
7:L:37:LEU:HD11	7:L:155:ALA:HA	1.84	0.58
10:O:288:PHE:CE1	10:O:289:ASN:OD1	2.56	0.58
12:R:101:ILE:O	12:R:104:GLN:NE2	2.36	0.58
4:E:90:ILE:CD1	4:E:112:VAL:CG1	2.61	0.58
2:B:96:A:N6	2:B:97:G:C6	2.71	0.58
4:E:125:PHE:HB3	4:E:135:VAL:HG22	1.86	0.58
7:L:73:HIS:O	7:L:77:LEU:HB2	2.02	0.58
8:M:166:SER:O	13:S:141:ARG:NH2	2.37	0.58
1:A:33:LYS:NZ	4:E:236:ASP:OD1	2.23	0.58
1:A:857:ASN:OD1	1:A:860:GLN:NE2	2.36	0.58
4:E:65:HIS:ND1	4:E:69:VAL:HG23	2.13	0.58
11:P:13:ARG:HH12	14:T:330:THR:HA	1.69	0.58
18:U:626:MET:HE2	18:U:643:LYS:HZ1	0.75	0.58
2:B:20:G:H4'	2:B:20:G:OP1	2.02	0.58
10:O:240:GLY:HA3	10:O:296:ARG:HH22	1.68	0.58
1:A:1784:ASN:HD22	1:A:1897:LEU:HD12	1.69	0.58
4:E:77:ASN:OD1	4:E:79:SER:OG	2.20	0.58
4:E:257:ASN:CB	15:W:149:SER:CB	2.81	0.58
13:S:92:PHE:H	13:S:123:ASP:HB3	1.69	0.58
2:B:10:U:O2	2:B:67:A:N6	2.37	0.58
3:C:692:LEU:O	3:C:786:ASN:ND2	2.37	0.58
4:E:66:GLU:OE1	4:E:66:GLU:HA	2.04	0.58
4:E:178:LEU:HD21	4:E:208:ILE:HD13	1.85	0.58
17:H:97:G:H2'	17:H:97:G:N3	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:168:THR:OG1	3:C:204:ASP:OD2	2.13	0.57
5:F:49:G:OP1	7:L:33:ARG:NH2	2.36	0.57
5:F:81:C:C5'	5:F:81:C:C6	2.86	0.57
1:A:542:ASN:O	1:A:546:LEU:HB2	2.04	0.57
4:E:119:THR:HG22	4:E:161:ARG:CB	2.31	0.57
6:J:658:ARG:CB	6:J:667:ILE:CB	2.82	0.57
7:L:261:LYS:HE2	7:L:261:LYS:HA	1.84	0.57
10:O:260:THR:HG21	10:O:273:GLN:OE1	2.04	0.57
16:G:147:C:OP1	18:U:659:LYS:CE	2.52	0.57
16:G:152:C:C2'	16:G:153:C:H6	2.09	0.57
4:E:61:LEU:HD12	4:E:351:LEU:O	2.04	0.57
5:F:42:C:H2'	5:F:43:A:H8	1.69	0.57
10:O:233:THR:HA	10:O:272:ILE:O	2.03	0.57
1:A:610:HIS:NE2	34:A:3000:IHP:O33	2.36	0.57
2:B:96:A:C2'	2:B:97:G:H5'	2.34	0.57
2:B:96:A:C5	2:B:97:G:N7	2.73	0.57
16:G:26:U:H2'	16:G:27:U:C5'	2.34	0.57
16:G:146:C:C1'	16:G:147:C:C5	2.87	0.57
17:H:170:C:H2'	32:p:44:LYS:CB	2.35	0.57
4:E:257:ASN:O	4:E:257:ASN:ND2	2.38	0.57
3:C:167:TYR:CD1	3:C:167:TYR:N	2.73	0.57
4:E:75:HIS:H	4:E:81:LEU:HD23	1.69	0.57
4:E:94:ASN:ND2	4:E:100:ASP:O	2.37	0.57
7:L:123:LEU:HD13	7:L:124:LYS:H	1.70	0.57
12:R:178:ARG:HB2	15:W:118:ALA:HB2	1.87	0.57
27:K:19:PHE:CD2	27:K:172:LEU:N	2.72	0.57
27:K:135:TRP:O	27:K:136:LYS:CB	2.52	0.57
1:A:1629:ILE:HG22	1:A:1662:ILE:HG12	1.86	0.57
4:E:102:TYR:N	4:E:102:TYR:CD1	2.73	0.57
5:F:44:G:N7	16:G:1:G:C2	2.72	0.57
7:L:759:GLU:HG3	27:K:171:GLN:HE22	1.70	0.57
8:M:165:ASN:HD22	12:R:95:LYS:HA	1.69	0.57
1:A:1639:VAL:HG12	1:A:1719:PHE:HB3	1.86	0.57
14:T:200:ILE:HB	14:T:486:ILE:HB	1.87	0.57
1:A:1813:ARG:HD3	1:A:1814:THR:HG23	1.86	0.57
5:F:36:A:H8	5:F:36:A:C4'	2.18	0.57
5:F:45:A:C2	18:U:625:PHE:CD1	2.93	0.57
16:G:148:U:C6	16:G:148:U:C5'	2.83	0.57
28:I:749:SER:O	28:I:753:THR:CB	2.53	0.57
1:A:1820:LYS:NZ	1:A:1844:GLU:OE1	2.38	0.57
4:E:136:TRP:CD1	4:E:136:TRP:N	2.73	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:307:ARG:HB3	4:E:326:HIS:O	2.05	0.57
13:S:26:GLU:OE1	13:S:131:ARG:NH1	2.38	0.57
4:E:257:ASN:OD1	15:W:149:SER:CA	2.53	0.56
7:L:710:ALA:C	27:K:124:LEU:CD2	2.78	0.56
10:O:288:PHE:HD1	10:O:289:ASN:OD1	1.87	0.56
16:G:155:U:O2	16:G:155:U:H2'	2.05	0.56
17:H:69:U:O2'	17:H:70:C:C5'	2.44	0.56
1:A:382:GLU:HA	3:C:354:ARG:HH12	1.69	0.56
3:C:154:HIS:CB	3:C:158:ARG:HG3	2.36	0.56
4:E:83:SER:O	4:E:90:ILE:HA	2.05	0.56
4:E:145:LYS:NZ	4:E:184:LYS:HG2	2.20	0.56
4:E:257:ASN:CG	15:W:149:SER:HB3	2.30	0.56
10:O:149:LYS:NZ	10:O:290:LYS:HZ3	2.03	0.56
10:O:261:ILE:O	10:O:261:ILE:HG22	2.05	0.56
27:K:120:ARG:O	27:K:124:LEU:N	2.30	0.56
1:A:388:LEU:HD11	3:C:399:LEU:HD11	1.87	0.56
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.38	0.56
1:A:532:THR:HB	16:G:3:A:C5'	2.34	0.56
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	1.86	0.56
1:A:1513:MET:CE	18:U:622:ALA:HB3	2.36	0.56
3:C:142:LYS:CG	3:C:228:PHE:HD2	2.12	0.56
4:E:93:TRP:N	4:E:93:TRP:CD1	2.73	0.56
5:F:44:G:O2'	16:G:1:G:N2	2.35	0.56
18:U:678:CYS:SG	18:U:718:HIS:CD2	2.98	0.56
1:A:419:ARG:NH2	1:A:423:ASP:O	2.39	0.56
4:E:93:TRP:CZ2	4:E:351:LEU:HD12	2.41	0.56
4:E:298:SER:HA	4:E:314:THR:CB	2.36	0.56
1:A:888:GLN:HE21	1:A:888:GLN:CA	2.16	0.56
5:F:29:A:N6	16:G:17:U:OP2	2.38	0.56
18:U:809:ASP:O	18:U:813:SER:OG	2.13	0.56
1:A:1313:PRO:HG2	1:A:1335:ILE:HG22	1.86	0.56
1:A:1946:ASN:OD1	1:A:1986:LEU:CG	2.54	0.56
2:B:96:A:C4	2:B:97:G:C8	2.93	0.56
5:F:38:G:C2	5:F:39:A:C4	2.93	0.56
10:O:155:PRO:HA	12:R:188:PHE:CE1	2.34	0.56
16:G:22:C:C1'	16:G:23:U:P	2.94	0.56
17:H:55:U:H2'	17:H:56:A:H8	1.70	0.56
17:H:57:A:H2'	17:H:58:U:H6	1.70	0.56
18:U:741:VAL:HG11	18:U:827:LEU:HG	1.88	0.56
26:s:81:GLU:CB	27:K:67:ARG:CB	2.84	0.56
6:J:293:ASN:ND2	7:L:226:ASP:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L:710:ALA:HB2	27:K:120:ARG:HD3	1.82	0.56
18:U:671:GLN:HG3	18:U:763:GLN:O	2.06	0.56
3:C:158:ARG:HD3	3:C:537:TYR:OH	2.05	0.56
5:F:34:G:C5	5:F:35:A:C8	2.94	0.56
7:L:178:GLU:OE2	7:L:181:ARG:NH2	2.39	0.56
10:O:174:LYS:HA	15:W:205:VAL:HG22	1.88	0.56
10:O:252:PHE:O	10:O:255:PHE:CD2	2.57	0.56
17:H:59:A:H2'	17:H:60:U:H6	1.70	0.56
1:A:1941:ARG:O	1:A:1945:VAL:CG2	2.54	0.56
2:B:35:U:C5'	2:B:35:U:C6	2.85	0.56
10:O:258:ILE:CG2	10:O:274:PHE:HD1	2.19	0.56
12:R:193:LYS:HB3	15:W:145:ASN:HD21	1.71	0.56
17:H:165:A:H61	32:p:88:SER:CB	2.19	0.56
18:U:678:CYS:SG	18:U:718:HIS:HD2	2.29	0.56
26:q:58:ALA:HB1	26:r:6:SER:HA	1.87	0.56
27:K:120:ARG:O	27:K:124:LEU:HB2	2.06	0.56
1:A:83:HIS:NE2	16:G:16:G:N7	2.51	0.55
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.89	0.55
4:E:232:ARG:O	4:E:262:TRP:HH2	1.89	0.55
4:E:304:SER:OG	4:E:306:ASP:OD1	2.17	0.55
16:G:140:A:O2'	16:G:141:C:C6	2.59	0.55
1:A:1335:ILE:HG23	1:A:1365:ILE:HD11	1.88	0.55
3:C:134:LEU:HD13	3:C:202:ILE:HG23	1.88	0.55
4:E:75:HIS:HD2	4:E:80:THR:HG22	1.69	0.55
10:O:34:ILE:HB	12:R:197:ILE:HG12	1.89	0.55
16:G:5:G:C4	16:G:6:A:C5	2.94	0.55
17:H:83:A:N3	17:H:84:C:C5	2.74	0.55
1:A:1018:ASN:HA	1:A:1022:MET:O	2.06	0.55
1:A:1928:SER:OG	1:A:1930:TYR:CE1	2.55	0.55
5:F:22:A:H2'	15:W:130:ARG:HH21	1.71	0.55
10:O:260:THR:CB	10:O:273:GLN:HB3	2.36	0.55
12:R:148:ARG:NH2	14:T:299:THR:O	2.40	0.55
17:H:42:G:O2'	17:H:43:U:C6	2.59	0.55
17:H:54:U:H2'	17:H:55:U:C5	2.32	0.55
17:H:106:G:N2	17:H:107:A:N1	2.54	0.55
27:K:19:PHE:H	27:K:171:GLN:HG2	1.70	0.55
5:F:42:C:C2'	5:F:43:A:H5'	2.34	0.55
7:L:745:ALA:HB1	27:K:156:LEU:CG	2.36	0.55
17:H:160:A:H2'	17:H:161:U:C6	2.41	0.55
18:U:662:ILE:HD12	18:U:662:ILE:O	2.07	0.55
4:E:257:ASN:HB2	15:W:149:SER:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:658:ARG:HG3	18:U:659:LYS:N	2.21	0.55
3:C:742:PRO:HG3	3:C:785:ARG:HD2	1.88	0.55
4:E:62:LEU:CD1	4:E:93:TRP:CG	2.90	0.55
4:E:74:PHE:CD2	4:E:336:HIS:HA	2.41	0.55
10:O:284:ALA:O	10:O:288:PHE:N	2.26	0.55
16:G:136:U:O2'	16:G:137:C:C6	2.58	0.55
17:H:10:C:H2'	17:H:11:G:H8	1.72	0.55
3:C:148:CYS:SG	3:C:417:ARG:NH2	2.79	0.55
4:E:82:ALA:HA	4:E:91:LEU:O	2.07	0.55
7:L:258:ARG:O	7:L:261:LYS:HB3	2.06	0.55
10:O:232:THR:HG22	10:O:277:ARG:HA	1.89	0.55
14:T:393:ASP:OD1	14:T:393:ASP:N	2.39	0.55
17:H:39:U:O2'	17:H:40:C:C6	2.59	0.55
6:J:770:ASP:CB	6:J:791:ASP:CB	2.85	0.55
10:O:243:ILE:CG2	10:O:294:ASN:OD1	2.53	0.55
17:H:80:A:O2'	17:H:81:G:H5'	2.07	0.55
1:A:1214:TRP:NE1	1:A:1276:GLU:OE2	2.34	0.55
3:C:523:GLN:HE21	3:C:558:PRO:HG3	1.70	0.55
5:F:37:C:C3'	5:F:38:G:C5'	2.85	0.55
5:F:44:G:N2	16:G:3:A:H62	1.92	0.55
5:F:92:A:C2	5:F:93:G:N7	2.74	0.55
10:O:259:ARG:HB2	10:O:274:PHE:N	2.21	0.55
13:S:52:LYS:HA	13:S:158:LYS:HA	1.89	0.55
17:H:7:U:H2'	17:H:8:C:H5'	1.89	0.55
17:H:80:A:C2	17:H:81:G:N7	2.75	0.55
18:U:550:ARG:HB2	18:U:660:LYS:CD	2.35	0.55
1:A:686:ARG:HH21	1:A:710:LEU:HD13	1.72	0.54
3:C:514:TYR:HB3	3:C:576:ILE:HD11	1.89	0.54
4:E:134:ALA:HB3	4:E:136:TRP:CZ2	2.42	0.54
6:J:618:GLN:O	6:J:634:GLU:CB	2.55	0.54
7:L:721:LEU:HA	7:L:724:TYR:CG	2.41	0.54
10:O:229:LYS:HA	10:O:277:ARG:NH2	2.22	0.54
16:G:3:A:O2'	16:G:4:A:P	2.65	0.54
17:H:34:U:C5'	18:U:662:ILE:CD1	2.84	0.54
17:H:57:A:C4	17:H:58:U:C5	2.95	0.54
17:H:59:A:C4	17:H:60:U:C5	2.95	0.54
27:K:18:TYR:CD2	27:K:168:LYS:HA	2.42	0.54
27:K:130:HIS:O	27:K:134:ALA:CB	2.54	0.54
1:A:1833:LEU:HD11	18:U:718:HIS:HB2	1.89	0.54
1:A:1863:VAL:HG11	1:A:1868:MET:HB2	1.89	0.54
4:E:82:ALA:CB	4:E:92:LEU:HD21	2.27	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:131:THR:O	15:W:108:ARG:NH1	2.36	0.54
17:H:67:C:H2'	17:H:68:G:H8	1.73	0.54
4:E:74:PHE:CE2	4:E:343:ILE:HG12	2.42	0.54
4:E:323:LEU:HD22	15:W:83:PRO:HG2	1.89	0.54
14:T:349:SER:OG	14:T:351:ASP:OD1	2.25	0.54
1:A:1514:LYS:HZ2	1:A:1529:ILE:HD11	1.70	0.54
1:A:1830:GLN:HG2	1:A:1831:LYS:H	1.71	0.54
2:B:100:C:H2'	2:B:101:U:C6	2.42	0.54
9:N:118:ILE:HD12	9:N:132:ILE:HD12	1.89	0.54
10:O:229:LYS:CD	10:O:277:ARG:NH1	2.50	0.54
16:G:138:A:O2'	16:G:139:U:C6	2.59	0.54
16:G:152:C:C3'	16:G:153:C:C6	2.89	0.54
17:H:109:C:C4'	22:k:47:ARG:CB	2.76	0.54
17:H:150:U:C2	17:H:151:C:C5	2.95	0.54
1:A:668:VAL:HB	5:F:68:C:H5''	1.89	0.54
1:A:671:THR:O	1:A:676:ARG:NH2	2.41	0.54
2:B:85:C:OP1	2:B:85:C:H3'	2.07	0.54
3:C:173:THR:OG1	3:C:642:HIS:NE2	2.39	0.54
3:C:538:HIS:CE1	3:C:551:LEU:HD12	2.42	0.54
5:F:92:A:N3	5:F:93:G:C8	2.76	0.54
9:N:28:LYS:HD2	15:W:189:ILE:HG23	1.88	0.54
10:O:234:LEU:HD12	10:O:274:PHE:CZ	2.42	0.54
28:I:585:ASP:O	28:I:586:GLY:C	2.50	0.54
1:A:1614:ILE:HD13	1:A:1626:CYS:HB2	1.90	0.54
4:E:263:ASP:HB3	4:E:274:VAL:HG21	1.90	0.54
10:O:272:ILE:HG21	10:O:274:PHE:CE1	2.43	0.54
16:G:146:C:H1'	16:G:147:C:C5	2.42	0.54
16:G:152:C:O2	16:G:153:C:C6	2.61	0.54
17:H:38:A:O2'	17:H:39:U:C6	2.59	0.54
1:A:1597:PHE:HB3	1:A:1609:VAL:HG11	1.90	0.54
4:E:325:GLY:O	4:E:352:TYR:CZ	2.61	0.54
5:F:90:G:N2	5:F:91:A:C2	2.76	0.54
7:L:732:MET:CA	26:q:65:PRO:CB	2.86	0.54
10:O:260:THR:CG2	10:O:273:GLN:CD	2.81	0.54
17:H:80:A:H2'	17:H:81:G:H5'	1.88	0.54
10:O:236:VAL:O	10:O:269:CYS:HA	2.07	0.54
10:O:294:ASN:O	10:O:296:ARG:HG3	2.07	0.54
16:G:120:G:C1'	29:Q:1019:SER:HA	2.37	0.54
27:K:17:PRO:CG	27:K:167:ARG:NH1	2.71	0.54
27:K:123:ASN:O	27:K:127:MET:HB2	2.07	0.54
1:A:608:LEU:HD13	1:A:632:ALA:HB1	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:ALA:O	1:A:661:GLU:HB2	2.08	0.54
4:E:80:THR:O	4:E:81:LEU:HD23	2.07	0.54
5:F:34:G:C5	5:F:35:A:N7	2.76	0.54
6:J:290:ARG:NH1	8:M:180:ASP:OD1	2.40	0.54
6:J:362:ALA:HA	6:J:365:ILE:HD12	1.89	0.54
17:H:183:G:C4	17:H:184:C:C5	2.95	0.54
18:U:671:GLN:OE1	18:U:671:GLN:HA	2.06	0.54
26:q:22:ASN:CB	26:r:54:ASP:O	2.56	0.54
1:A:881:ILE:HG23	1:A:918:THR:HG23	1.90	0.54
1:A:1757:GLU:HG2	18:U:808:LYS:HE3	1.89	0.54
28:I:797:PHE:O	28:I:801:ASP:CB	2.56	0.54
1:A:143:GLN:NE2	1:A:207:PHE:O	2.34	0.53
1:A:787:GLU:OE2	1:A:790:ARG:NH2	2.38	0.53
3:C:277:LYS:NZ	3:C:864:PRO:O	2.41	0.53
3:C:637:LEU:HA	3:C:640:VAL:HG12	1.90	0.53
4:E:314:THR:HG23	4:E:315:THR:HG23	1.89	0.53
7:L:699:ASN:CG	27:K:114:LEU:CB	2.80	0.53
10:O:259:ARG:CA	10:O:273:GLN:O	2.56	0.53
17:H:31:G:O2'	17:H:32:U:C6	2.59	0.53
26:t:72:PRO:CB	27:K:81:LEU:CB	2.87	0.53
28:I:176:SER:HA	28:I:196:ALA:HB2	1.91	0.53
4:E:136:TRP:CD1	4:E:136:TRP:H	2.26	0.53
10:O:232:THR:OG1	10:O:273:GLN:HG3	2.07	0.53
16:G:123:U:O2'	30:y:78:ARG:CB	2.56	0.53
17:H:83:A:C5	17:H:84:C:C4	2.97	0.53
3:C:561:LYS:NZ	3:C:611:ASN:OD1	2.42	0.53
4:E:78:GLY:C	4:E:336:HIS:HE1	2.08	0.53
12:R:68:HIS:NE2	13:S:89:ASP:O	2.41	0.53
12:R:106:GLN:HG2	12:R:110:LYS:HG2	1.89	0.53
28:I:343:LEU:N	29:Q:527:ILE:CB	2.71	0.53
1:A:1333:VAL:HG13	1:A:1365:ILE:HD13	1.90	0.53
1:A:1609:VAL:HG12	1:A:1631:LEU:HG	1.90	0.53
2:B:74:U:H3	2:B:76:A:H62	1.55	0.53
8:M:198:ARG:NH2	17:H:11:G:N7	2.48	0.53
12:R:196:VAL:HG11	15:W:120:ILE:HD12	1.90	0.53
17:H:36:G:O2'	17:H:37:U:C6	2.59	0.53
18:U:694:VAL:HG12	18:U:695:LYS:HG3	1.91	0.53
1:A:1392:LYS:HD3	1:A:1407:ASP:HB3	1.91	0.53
2:B:72:U:H6	2:B:72:U:P	2.32	0.53
4:E:309:VAL:O	4:E:309:VAL:HG12	2.09	0.53
12:R:64:PHE:O	12:R:71:GLN:NE2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:R:65:PRO:HG2	13:S:90:LEU:HD22	1.91	0.53
16:G:5:G:N9	16:G:6:A:C8	2.76	0.53
1:A:1194:CYS:HB3	1:A:1230:LEU:HD23	1.91	0.53
2:B:68:C:O2	2:B:68:C:H2'	2.09	0.53
10:O:239:LEU:HD12	10:O:243:ILE:HD12	1.90	0.53
13:S:18:THR:HA	13:S:159:ILE:HA	1.91	0.53
18:U:605:ASN:HA	18:U:608:MET:HG2	1.91	0.53
28:I:176:SER:CB	28:I:196:ALA:CB	2.80	0.53
1:A:1405:LEU:O	1:A:1409:GLU:HB2	2.09	0.53
4:E:178:LEU:CD1	4:E:222:LEU:HD22	2.39	0.53
4:E:266:PRO:HB2	7:L:788:TYR:HB3	1.91	0.53
18:U:576:ARG:HH22	18:U:647:ARG:HD3	1.73	0.53
2:B:79:C:O2	2:B:79:C:H2'	2.07	0.53
4:E:323:LEU:N	4:E:323:LEU:HD23	2.24	0.53
6:J:496:ASP:CB	6:J:536:LEU:CB	2.87	0.53
8:M:236:ASN:ND2	8:M:242:ALA:O	2.42	0.53
16:G:152:C:C6	16:G:153:C:N4	2.74	0.53
2:B:67:A:H4'	2:B:68:C:C5	2.43	0.53
4:E:250:LEU:CD2	4:E:262:TRP:HB2	2.38	0.53
6:J:774:VAL:CA	6:J:787:LYS:CB	2.87	0.53
7:L:732:MET:HB3	26:q:65:PRO:CB	2.37	0.53
8:M:237:LEU:HD11	12:R:264:LEU:HB2	1.91	0.53
17:H:33:G:H4'	18:U:662:ILE:HD11	1.91	0.53
17:H:108:G:O2'	17:H:109:C:H5'	2.08	0.53
1:A:136:ILE:HG12	1:A:418:THR:HG22	1.91	0.53
2:B:23:C:HO2'	2:B:24:G:H3'	1.71	0.53
2:B:96:A:N6	2:B:97:G:O6	2.42	0.53
3:C:749:THR:HG23	3:C:753:GLU:HB3	1.91	0.53
3:C:814:ARG:NH1	3:C:818:SER:OG	2.42	0.53
12:R:228:PRO:HB2	12:R:230:MET:HE3	1.90	0.53
14:T:392:PRO:HG3	14:T:415:ILE:HA	1.91	0.53
16:G:141:C:O2'	16:G:142:U:C6	2.61	0.53
17:H:113:G:H2'	17:H:114:A:H8	1.72	0.53
1:A:1835:GLN:HB2	18:U:557:VAL:HG11	1.91	0.52
3:C:592:VAL:HG22	3:C:655:VAL:HG22	1.91	0.52
4:E:93:TRP:CD1	4:E:93:TRP:H	2.27	0.52
5:F:44:G:H21	16:G:3:A:N6	2.01	0.52
10:O:223:LEU:H	10:O:223:LEU:HD22	1.74	0.52
17:H:148:C:H2'	17:H:149:A:C8	2.44	0.52
2:B:44:A:H8	2:B:44:A:O5'	1.92	0.52
4:E:147:LEU:HD12	4:E:179:TRP:CG	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:326:HIS:HE1	4:E:352:TYR:HD2	1.57	0.52
12:R:151:LEU:HD22	14:T:323:VAL:HG11	1.91	0.52
17:H:69:U:HO2'	17:H:70:C:H5'	1.70	0.52
18:U:550:ARG:HB3	18:U:660:LYS:CD	2.39	0.52
2:B:38:C:C5	2:B:39:C:C2	2.97	0.52
2:B:70:A:H2'	2:B:71:C:C6	2.44	0.52
3:C:166:CYS:O	3:C:170:ILE:HG22	2.10	0.52
16:G:2:U:C2	18:U:625:PHE:HB3	2.45	0.52
17:H:114:A:H2'	17:H:115:G:C8	2.40	0.52
17:H:180:G:H2'	17:H:181:G:C8	2.44	0.52
27:K:119:VAL:O	27:K:123:ASN:HB2	2.08	0.52
3:C:167:TYR:CE2	3:C:536:ARG:HB2	2.45	0.52
4:E:56:GLN:HG3	4:E:56:GLN:O	2.09	0.52
4:E:161:ARG:NH1	4:E:203:ASP:OD1	2.42	0.52
5:F:92:A:H2'	5:F:93:G:H8	1.74	0.52
10:O:222:ARG:CZ	10:O:222:ARG:N	2.73	0.52
17:H:70:C:H2'	17:H:71:C:C6	2.44	0.52
18:U:548:LEU:HD21	18:U:661:ALA:HB1	1.91	0.52
1:A:641:MET:HA	1:A:644:ILE:HG22	1.91	0.52
3:C:166:CYS:SG	3:C:536:ARG:CZ	2.97	0.52
4:E:123:MET:HB3	4:E:125:PHE:CE1	2.37	0.52
4:E:162:ARG:CZ	4:E:203:ASP:O	2.57	0.52
4:E:251:LEU:CG	4:E:291:CYS:SG	2.98	0.52
10:O:154:THR:C	12:R:188:PHE:CE1	2.88	0.52
10:O:155:PRO:CB	12:R:188:PHE:CE1	2.92	0.52
4:E:284:PHE:HZ	15:W:120:ILE:HD13	1.74	0.52
6:J:591:LEU:O	6:J:592:ALA:HB3	2.09	0.52
17:H:89:U:H2'	17:H:90:A:H8	1.75	0.52
17:H:179:C:O2	17:H:180:G:C8	2.63	0.52
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.42	0.52
7:L:731:LEU:C	27:K:142:LEU:HD21	2.34	0.52
10:O:223:LEU:H	10:O:223:LEU:CD1	1.98	0.52
16:G:22:C:O4'	16:G:23:U:OP1	2.28	0.52
17:H:71:C:H2'	17:H:72:U:C6	2.45	0.52
18:U:546:VAL:HG23	18:U:546:VAL:O	2.08	0.52
27:K:19:PHE:HB2	27:K:171:GLN:CG	2.39	0.52
28:I:337:LEU:O	28:I:338:ILE:C	2.53	0.52
3:C:139:HIS:HB2	35:C:1500:GTP:C5'	2.40	0.52
7:L:759:GLU:HB2	27:K:167:ARG:CD	2.40	0.52
16:G:7:G:N3	16:G:7:G:C2'	2.69	0.52
17:H:179:C:C2	17:H:180:G:C8	2.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:765:HIS:HD2	18:U:766:MET:O	1.93	0.52
17:H:89:U:H2'	17:H:90:A:C8	2.44	0.52
28:I:795:ILE:N	28:I:795:ILE:CD1	2.73	0.52
1:A:388:LEU:O	3:C:379:LYS:NZ	2.39	0.52
1:A:1179:SER:O	1:A:1201:ARG:NH2	2.40	0.52
1:A:1833:LEU:CD1	18:U:718:HIS:HB2	2.40	0.52
3:C:829:GLU:HB2	3:C:907:VAL:HG22	1.92	0.52
4:E:116:HIS:HE1	4:E:158:TYR:HE1	1.58	0.52
7:L:251:LEU:HB2	7:L:254:GLU:HB3	1.92	0.52
7:L:759:GLU:HG2	27:K:167:ARG:CD	2.39	0.52
15:W:150:ALA:C	15:W:151:LYS:HD2	2.21	0.52
16:G:152:C:C1'	16:G:153:C:C5	2.93	0.52
17:H:77:C:H2'	17:H:78:C:C6	2.45	0.52
17:H:83:A:C4	17:H:84:C:C4	2.98	0.52
18:U:662:ILE:HG13	18:U:663:ALA:N	2.24	0.52
18:U:666:ARG:NH2	18:U:666:ARG:CG	2.73	0.52
1:A:1946:ASN:OD1	1:A:1986:LEU:HB3	2.09	0.51
3:C:476:CYS:HB2	3:C:565:ILE:HB	1.92	0.51
4:E:101:ASN:HD22	4:E:101:ASN:N	2.06	0.51
10:O:257:GLU:HG2	10:O:257:GLU:O	2.09	0.51
12:R:193:LYS:HB2	15:W:145:ASN:HD21	1.73	0.51
17:H:34:U:H5'	18:U:662:ILE:CD1	2.41	0.51
17:H:83:A:C5	17:H:84:C:C5	2.98	0.51
33:V:370:LYS:N	33:V:372:GLU:O	2.44	0.51
2:B:99:C:H2'	2:B:100:C:C6	2.45	0.51
3:C:221:ILE:O	3:C:495:ARG:NH1	2.43	0.51
3:C:670:SER:HB2	3:C:689:ALA:H	1.74	0.51
4:E:65:HIS:NE2	4:E:91:LEU:HD12	2.26	0.51
4:E:300:ILE:O	4:E:311:VAL:HA	2.09	0.51
5:F:44:G:O6	16:G:2:U:C5	2.63	0.51
5:F:82:A:N6	12:R:258:LYS:NZ	2.57	0.51
10:O:250:ASN:HD21	13:S:91:LYS:HE3	1.74	0.51
17:H:40:C:O2'	17:H:41:U:C6	2.59	0.51
17:H:67:C:H2'	17:H:68:G:C8	2.45	0.51
1:A:1699:THR:HA	1:A:1717:ASN:HD22	1.76	0.51
1:A:1782:ASP:HB3	1:A:1841:THR:HG21	1.92	0.51
3:C:158:ARG:HB3	3:C:158:ARG:CZ	2.41	0.51
4:E:277:PHE:HE2	4:E:300:ILE:HD12	1.75	0.51
4:E:277:PHE:CE2	4:E:300:ILE:CD1	2.88	0.51
4:E:277:PHE:CE2	4:E:300:ILE:HD13	2.41	0.51
10:O:258:ILE:CG2	10:O:274:PHE:CD1	2.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:134:U:C2'	16:G:135:G:H8	2.13	0.51
17:H:81:G:H2'	17:H:82:G:C8	2.45	0.51
17:H:111:G:O3'	17:H:112:G:O4'	2.28	0.51
26:t:90:PHE:CB	27:K:111:MET:C	2.83	0.51
28:I:729:SER:O	28:I:732:ALA:HB3	2.09	0.51
2:B:77:G:C6	2:B:80:U:C4	2.98	0.51
3:C:308:CYS:SG	3:C:309:PHE:N	2.84	0.51
4:E:265:ARG:H	4:E:272:ARG:HH21	1.57	0.51
5:F:34:G:H2'	5:F:35:A:H8	1.74	0.51
17:H:153:A:C3'	17:H:154:C:C5'	2.85	0.51
26:q:127:ALA:HB1	26:t:127:ALA:HB1	1.93	0.51
1:A:435:CYS:SG	1:A:439:GLN:NE2	2.67	0.51
3:C:832:TYR:HD1	3:C:900:VAL:O	1.93	0.51
4:E:93:TRP:CZ2	4:E:351:LEU:HD11	2.46	0.51
4:E:115:LEU:CD2	4:E:126:SER:HB2	2.41	0.51
16:G:6:A:N6	16:G:7:G:O6	2.43	0.51
1:A:1296:GLN:NE2	1:A:1317:TYR:OH	2.43	0.51
4:E:80:THR:HG23	4:E:81:LEU:N	2.24	0.51
7:L:259:ASP:CB	8:M:199:ARG:NH2	2.74	0.51
7:L:731:LEU:HD11	27:K:143:VAL:HG12	1.93	0.51
10:O:136:MET:O	10:O:140:ALA:HB2	2.11	0.51
10:O:235:TYR:CD1	10:O:271:PHE:HE1	2.29	0.51
16:G:5:G:N3	16:G:6:A:C5	2.77	0.51
17:H:71:C:O5'	17:H:71:C:H6	1.94	0.51
17:H:72:U:H2'	17:H:73:C:C6	2.45	0.51
17:H:88:A:H2'	17:H:89:U:C6	2.46	0.51
17:H:168:A:N3	17:H:168:A:H2'	2.25	0.51
4:E:209:ILE:HG21	4:E:250:LEU:HD13	1.92	0.51
6:J:228:ARG:NH2	6:J:257:GLU:OE1	2.43	0.51
16:G:6:A:H3'	16:G:7:G:C8	2.45	0.51
16:G:143:U:H6	16:G:143:U:C5'	2.23	0.51
1:A:1832:ARG:NH1	18:U:680:ASP:OD2	2.44	0.51
4:E:62:LEU:HB3	4:E:351:LEU:HD12	1.93	0.51
4:E:114:GLU:O	4:E:127:ALA:N	2.40	0.51
4:E:355:GLU:N	15:W:82:ASN:OD1	2.33	0.51
7:L:759:GLU:CD	27:K:171:GLN:HE22	2.18	0.51
17:H:7:U:C2'	17:H:8:C:H5'	2.41	0.51
1:A:271:MET:HE1	1:A:311:GLU:HA	1.93	0.51
1:A:947:PRO:HA	1:A:1437:ARG:HH22	1.76	0.51
12:R:262:ILE:HB	12:R:267:ARG:HH21	1.75	0.51
16:G:123:U:O4'	30:y:12:GLY:HA3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:134:U:C3'	16:G:135:G:H8	2.24	0.51
17:H:106:G:N2	17:H:107:A:C6	2.79	0.51
1:A:1017:ILE:HD11	1:A:1031:ILE:HD11	1.93	0.51
3:C:529:ARG:H	3:C:553:GLU:HB3	1.74	0.51
5:F:38:G:N3	5:F:39:A:N7	2.58	0.51
17:H:83:A:N1	17:H:84:C:C4	2.79	0.51
17:H:90:A:H2'	17:H:91:U:C6	2.45	0.51
18:U:621:MET:HA	18:U:626:MET:SD	2.51	0.51
18:U:753:PHE:HB2	18:U:824:ASP:HB2	1.91	0.51
27:K:196:GLU:O	27:K:199:ILE:CG1	2.59	0.51
7:L:696:LEU:HA	27:K:110:SER:CB	2.40	0.50
8:M:178:GLU:OE1	8:M:181:ARG:NH1	2.41	0.50
10:O:234:LEU:HD12	10:O:274:PHE:HZ	1.75	0.50
11:P:17:GLY:N	11:P:20:GLU:OE1	2.41	0.50
16:G:152:C:O2	16:G:153:C:C5	2.63	0.50
17:H:182:U:O2'	17:H:183:G:C5'	2.44	0.50
27:K:188:LEU:C	27:K:188:LEU:HD13	2.36	0.50
28:I:238:LEU:O	28:I:242:ALA:N	2.42	0.50
28:I:464:ALA:O	28:I:465:ARG:C	2.53	0.50
28:I:795:ILE:N	28:I:795:ILE:HD12	2.27	0.50
1:A:163:ARG:HE	1:A:625:PRO:HB3	1.74	0.50
1:A:381:PRO:O	3:C:354:ARG:NH2	2.43	0.50
4:E:322:LYS:HG2	15:W:89:PHE:HE2	1.75	0.50
13:S:63:GLN:NE2	13:S:111:GLN:OE1	2.44	0.50
14:T:343:PRO:HG2	14:T:356:LEU:HD23	1.92	0.50
27:K:134:ALA:O	27:K:136:LYS:N	2.44	0.50
7:L:259:ASP:HB3	8:M:199:ARG:NH2	2.27	0.50
10:O:222:ARG:H	10:O:222:ARG:NE	2.08	0.50
16:G:133:A:O2'	16:G:135:G:OP1	2.20	0.50
1:A:309:ARG:HE	1:A:310:THR:H	1.58	0.50
3:C:157:ILE:CG2	3:C:158:ARG:HG2	2.16	0.50
3:C:938:ARG:HH21	3:C:942:GLY:HA3	1.76	0.50
4:E:178:LEU:N	4:E:178:LEU:HD23	2.26	0.50
17:H:47:U:H5'	17:H:47:U:O2	2.12	0.50
17:H:84:C:H2'	17:H:85:A:C8	2.46	0.50
28:I:264:ASP:O	28:I:268:ARG:CB	2.59	0.50
28:I:315:SER:O	28:I:316:GLU:C	2.54	0.50
2:B:69:A:H3'	2:B:70:A:N3	2.26	0.50
4:E:178:LEU:CD2	4:E:208:ILE:CD1	2.90	0.50
5:F:38:G:C2	5:F:39:A:N7	2.79	0.50
5:F:44:G:O6	16:G:2:U:H5	1.95	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:R:252:SER:OG	12:R:255:LYS:O	2.30	0.50
3:C:166:CYS:HG	3:C:536:ARG:HE	1.47	0.50
3:C:259:LYS:HG2	35:C:1500:GTP:C6	2.47	0.50
4:E:243:LEU:CD1	4:E:247:GLY:CA	2.88	0.50
6:J:615:LEU:CB	6:J:638:GLU:CB	2.89	0.50
7:L:759:GLU:OE1	27:K:171:GLN:CD	2.55	0.50
10:O:229:LYS:HA	10:O:277:ARG:HH22	1.77	0.50
17:H:56:A:C6	17:H:92:U:N3	2.78	0.50
1:A:1946:ASN:OD1	1:A:1986:LEU:CB	2.60	0.50
3:C:137:HIS:O	3:C:207:GLY:O	2.30	0.50
4:E:57:ALA:O	4:E:355:GLU:CG	2.59	0.50
4:E:260:ARG:NH1	4:E:276:ILE:HD11	2.26	0.50
5:F:38:G:O6	16:G:9:C:N3	2.45	0.50
16:G:146:C:O2'	16:G:147:C:H6	1.87	0.50
16:G:152:C:H2'	16:G:152:C:O2	2.10	0.50
17:H:83:A:HO2'	17:H:84:C:H5'	1.72	0.50
24:e:15:VAL:O	25:g:33:GLY:HA3	2.12	0.50
28:I:337:LEU:O	28:I:340:ARG:N	2.45	0.50
1:A:1275:ARG:NH1	1:A:1373:GLN:O	2.42	0.50
2:B:8:G:C2'	2:B:8:G:N3	2.74	0.50
2:B:75:G:O6	2:B:76:A:C5	2.65	0.50
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.93	0.50
3:C:531:TRP:HB2	3:C:551:LEU:HB2	1.94	0.50
4:E:75:HIS:O	4:E:76:PRO:C	2.51	0.50
5:F:78:A:H4'	6:J:237:LYS:HE2	1.94	0.50
6:J:311:GLN:HG3	8:M:131:GLN:HG2	1.93	0.50
7:L:209:ASP:HB2	10:O:113:ASN:HD21	1.76	0.50
16:G:146:C:OP2	16:G:146:C:H2'	2.12	0.50
18:U:662:ILE:O	18:U:666:ARG:HG3	2.12	0.50
1:A:888:GLN:CA	1:A:888:GLN:NE2	2.74	0.50
1:A:1836:LEU:HD21	18:U:547:ILE:HG21	1.94	0.50
3:C:500:THR:HG22	3:C:545:PRO:HA	1.93	0.50
14:T:250:ARG:NH1	14:T:266:GLU:OE2	2.44	0.50
18:U:546:VAL:HG11	18:U:665:HIS:NE2	2.26	0.50
4:E:55:LEU:C	4:E:57:ALA:H	2.20	0.49
4:E:62:LEU:O	4:E:351:LEU:N	2.38	0.49
4:E:134:ALA:HB1	4:E:143:ARG:CD	2.40	0.49
16:G:21:A:H3'	16:G:21:A:P	2.52	0.49
17:H:57:A:N6	17:H:91:U:C2	2.80	0.49
2:B:79:C:C5'	2:B:79:C:C6	2.95	0.49
3:C:849:VAL:HG22	3:C:852:ARG:HH21	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:284:PHE:O	15:W:124:MET:CE	2.59	0.49
12:R:178:ARG:NH1	15:W:141:PRO:O	2.45	0.49
15:W:103:GLN:NE2	15:W:111:LEU:O	2.45	0.49
17:H:34:U:H5'	18:U:662:ILE:CG1	2.35	0.49
1:A:254:TYR:OH	1:A:434:HIS:O	2.30	0.49
6:J:322:MET:O	8:M:181:ARG:NH1	2.45	0.49
14:T:213:GLU:HG3	14:T:218:TRP:CE2	2.47	0.49
16:G:134:U:C3'	16:G:135:G:C8	2.95	0.49
17:H:54:U:C6	17:H:55:U:C5	3.00	0.49
28:I:545:ILE:HG12	28:I:546:SER:H	1.77	0.49
1:A:1104:ASP:OD1	1:A:1107:ARG:NH2	2.46	0.49
1:A:1491:LYS:O	1:A:1710:ASN:ND2	2.46	0.49
3:C:147:ASP:OD2	3:C:164:ASP:CB	2.57	0.49
4:E:57:ALA:O	4:E:355:GLU:HB2	2.09	0.49
4:E:336:HIS:CD2	4:E:339:GLU:OE1	2.66	0.49
6:J:260:ARG:HD3	7:L:214:ILE:HG12	1.95	0.49
17:H:92:U:O2'	17:H:93:A:H5'	2.13	0.49
24:l:15:VAL:O	25:n:33:GLY:HA3	2.12	0.49
2:B:67:A:H4'	2:B:68:C:N4	2.27	0.49
4:E:55:LEU:CD1	4:E:96:TYR:CZ	2.96	0.49
4:E:62:LEU:HB2	4:E:351:LEU:CB	2.19	0.49
4:E:74:PHE:CD2	4:E:335:PHE:C	2.91	0.49
4:E:117:TYR:HE1	4:E:121:GLY:O	1.96	0.49
4:E:229:TYR:CE2	4:E:272:ARG:NH1	2.79	0.49
5:F:14:C:H2'	5:F:15:A:H8	1.77	0.49
6:J:238:ASN:HD22	6:J:244:ASN:HD21	1.61	0.49
12:R:241:GLU:HA	12:R:244:GLU:HG2	1.94	0.49
1:A:1320:LYS:HG2	18:U:798:MET:HG2	1.93	0.49
1:A:1606:ILE:O	1:A:1634:SER:OG	2.30	0.49
3:C:219:LEU:HD13	3:C:245:HIS:HD2	1.77	0.49
3:C:699:ASP:OD2	3:C:722:TYR:OH	2.30	0.49
4:E:276:ILE:C	4:E:277:PHE:CD1	2.91	0.49
13:S:98:LEU:H	13:S:131:ARG:HA	1.77	0.49
14:T:371:HIS:ND1	14:T:391:SER:OG	2.46	0.49
14:T:380:LEU:HG	14:T:400:PHE:HZ	1.76	0.49
17:H:180:G:H2'	17:H:181:G:H8	1.76	0.49
28:I:405:TYR:O	28:I:409:GLY:HA3	2.13	0.49
3:C:154:HIS:HB3	3:C:158:ARG:HG3	1.93	0.49
3:C:641:MET:HE3	3:C:655:VAL:HG21	1.94	0.49
1:A:256:TYR:HE1	1:A:332:TYR:HB2	1.77	0.49
3:C:140:HIS:N	35:C:1500:GTP:O2B	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:58:PRO:O	15:W:82:ASN:OD1	2.30	0.49
4:E:95:VAL:CG1	4:E:353:MET:HE1	2.24	0.49
1:A:546:LEU:HD22	1:A:648:LEU:HD11	1.95	0.49
3:C:154:HIS:HB2	3:C:158:ARG:HG3	1.95	0.49
6:J:354:LEU:HD22	6:J:389:HIS:HE1	1.78	0.49
12:R:192:ALA:HB2	15:W:153:ILE:HD13	1.95	0.49
13:S:41:GLU:OE2	13:S:44:ARG:NH2	2.45	0.49
18:U:539:GLU:HG2	18:U:546:VAL:CG2	2.43	0.49
3:C:174:GLU:HG3	3:C:181:ILE:H	1.77	0.49
7:L:252:ARG:HH11	7:L:252:ARG:CG	2.19	0.49
16:G:7:G:N2	16:G:8:C:H1'	2.28	0.49
27:K:19:PHE:HB2	27:K:171:GLN:HG2	1.95	0.49
1:A:888:GLN:HE21	1:A:888:GLN:H	1.56	0.48
1:A:995:ARG:HH12	12:R:295:ASP:HB2	1.77	0.48
4:E:257:ASN:OD1	15:W:149:SER:HB3	2.13	0.48
6:J:466:ARG:O	28:I:606:TRP:CB	2.61	0.48
8:M:235:GLN:HB3	8:M:239:ARG:HH21	1.76	0.48
9:N:101:CYS:SG	9:N:139:CYS:HB2	2.53	0.48
12:R:228:PRO:HB2	12:R:230:MET:CE	2.43	0.48
16:G:152:C:C1'	16:G:153:C:H5	2.25	0.48
17:H:54:U:N3	17:H:94:A:N6	2.61	0.48
33:V:369:ILE:C	33:V:372:GLU:O	2.56	0.48
1:A:1947:ASN:O	1:A:1950:ALA:N	2.46	0.48
5:F:41:A:N6	16:G:6:A:H61	2.08	0.48
5:F:92:A:H2'	5:F:93:G:C8	2.47	0.48
10:O:222:ARG:N	10:O:222:ARG:NE	2.60	0.48
2:B:78:U:H6	2:B:78:U:H3'	1.79	0.48
3:C:205:THR:HB	3:C:215:VAL:HG22	1.94	0.48
3:C:779:LEU:O	3:C:938:ARG:NH1	2.46	0.48
7:L:267:LEU:C	7:L:267:LEU:CD2	2.85	0.48
12:R:281:ASN:ND2	12:R:282:GLU:OE1	2.47	0.48
18:U:691:ALA:HB3	18:U:698:LEU:H	1.77	0.48
3:C:258:ASN:OD1	3:C:259:LYS:N	2.46	0.48
4:E:131:LYS:CB	4:E:152:SER:O	2.62	0.48
7:L:252:ARG:NH1	7:L:252:ARG:CG	2.77	0.48
7:L:714:GLU:N	27:K:124:LEU:HD21	2.28	0.48
1:A:1201:ARG:HG3	1:A:1202:THR:H	1.78	0.48
2:B:69:A:H3'	2:B:70:A:C2	2.48	0.48
2:B:89:U:O2'	2:B:90:U:O5'	2.30	0.48
3:C:663:CYS:HB2	3:C:828:MET:HB2	1.94	0.48
13:S:84:ASP:OD1	13:S:108:ASN:ND2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:78:C:H2'	17:H:79:G:H8	1.78	0.48
1:A:27:GLU:OE2	4:E:194:TYR:OH	2.32	0.48
2:B:96:A:C2	2:B:97:G:C4	3.02	0.48
3:C:115:GLU:CD	3:C:189:VAL:HG23	2.38	0.48
4:E:314:THR:CG2	4:E:315:THR:HG23	2.44	0.48
17:H:172:C:C2	17:H:173:C:C5	3.01	0.48
1:A:1189:MET:HE3	1:A:1189:MET:HB2	1.78	0.48
3:C:157:ILE:HG13	3:C:158:ARG:H	1.79	0.48
3:C:191:PRO:HA	3:C:197:SER:HA	1.95	0.48
3:C:342:ARG:NH2	3:C:356:PHE:O	2.46	0.48
4:E:145:LYS:HZ1	4:E:184:LYS:HG2	1.79	0.48
9:N:18:ILE:HG21	9:N:70:ILE:HD11	1.96	0.48
17:H:166:G:N3	17:H:166:G:H2'	2.29	0.48
28:I:327:LEU:O	28:I:330:ARG:N	2.46	0.48
1:A:56:ALA:O	9:N:109:ARG:NH1	2.38	0.48
1:A:529:THR:OG1	18:U:581:THR:OG1	2.23	0.48
1:A:825:ILE:HA	1:A:933:ARG:HH12	1.78	0.48
1:A:941:LYS:HB3	1:A:951:LEU:HD11	1.95	0.48
2:B:77:G:C6	2:B:80:U:C5	3.01	0.48
3:C:492:ALA:O	3:C:551:LEU:HA	2.14	0.48
3:C:619:THR:HG22	3:C:629:ILE:HG13	1.95	0.48
4:E:54:SER:HB3	4:E:355:GLU:OE1	2.11	0.48
4:E:74:PHE:CD1	4:E:81:LEU:HD21	2.47	0.48
4:E:231:MET:SD	4:E:262:TRP:CE3	3.07	0.48
7:L:222:LEU:HD12	12:R:84:ASN:HB2	1.96	0.48
17:H:168:A:H3'	17:H:169:C:C6	2.49	0.48
27:K:19:PHE:HE2	27:K:172:LEU:O	1.96	0.48
3:C:104:LEU:HD21	3:C:166:CYS:SG	2.53	0.48
3:C:924:GLN:OE1	3:C:928:HIS:NE2	2.41	0.48
4:E:115:LEU:HD23	4:E:126:SER:CB	2.43	0.48
5:F:35:A:H2'	5:F:35:A:N3	2.29	0.48
5:F:82:A:N6	12:R:258:LYS:HZ1	2.12	0.48
13:S:15:TYR:HB2	13:S:163:TYR:HB2	1.94	0.48
28:I:348:VAL:CB	28:I:357:VAL:HA	2.44	0.48
1:A:1946:ASN:HB2	1:A:1986:LEU:HD23	1.85	0.48
2:B:20:G:O6	2:B:58:U:O2	2.32	0.48
2:B:92:U:C2	21:c:35:SER:CB	2.97	0.48
8:M:230:THR:HB	12:R:265:ASP:HB2	1.95	0.48
14:T:347:THR:HG22	14:T:357:TRP:HE1	1.78	0.48
17:H:56:A:N6	17:H:92:U:H3	2.07	0.48
17:H:57:A:N1	17:H:91:U:O2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:I:712:VAL:O	28:I:713:ARG:C	2.56	0.48
28:I:748:VAL:O	28:I:752:ALA:N	2.40	0.48
1:A:1306:LYS:HD2	1:A:1306:LYS:HA	1.73	0.47
3:C:139:HIS:HB2	35:C:1500:GTP:O3A	2.14	0.47
4:E:162:ARG:HH22	4:E:204:THR:HA	1.76	0.47
5:F:34:G:C2'	5:F:35:A:O5'	2.61	0.47
13:S:25:LEU:HD22	13:S:98:LEU:HD22	1.96	0.47
14:T:373:LYS:HD2	14:T:392:PRO:HB2	1.96	0.47
16:G:148:U:C6	16:G:148:U:C4'	2.97	0.47
17:H:80:A:H2'	17:H:81:G:C8	2.39	0.47
17:H:83:A:C4	17:H:84:C:C6	3.01	0.47
1:A:209:ASP:HB2	1:A:212:PRO:HA	1.95	0.47
3:C:700:ILE:O	3:C:740:THR:OG1	2.31	0.47
3:C:832:TYR:HD1	3:C:901:PHE:HA	1.78	0.47
5:F:44:G:C6	16:G:2:U:H5	2.28	0.47
13:S:55:ARG:HB3	13:S:63:GLN:HB3	1.96	0.47
14:T:418:THR:HG21	14:T:467:ALA:HA	1.95	0.47
17:H:165:A:N6	32:p:88:SER:CB	2.77	0.47
26:q:57:VAL:N	27:K:152:GLU:OE1	2.27	0.47
27:K:18:TYR:CD2	27:K:168:LYS:CA	2.97	0.47
28:I:545:ILE:HG13	28:I:581:GLU:HA	1.94	0.47
1:A:255:PHE:HB3	1:A:259:ASP:HB3	1.95	0.47
1:A:1510:GLU:CD	1:A:1510:GLU:N	2.73	0.47
7:L:731:LEU:CD1	27:K:143:VAL:HG12	2.45	0.47
8:M:221:LYS:NZ	17:H:18:U:OP2	2.47	0.47
12:R:193:LYS:HD2	15:W:145:ASN:ND2	2.30	0.47
13:S:57:ILE:HD13	15:W:97:ASN:HB3	1.96	0.47
14:T:336:VAL:HG23	14:T:347:THR:HB	1.95	0.47
16:G:152:C:N1	16:G:153:C:H5	2.05	0.47
17:H:27:U:HO2'	17:H:28:C:H5'	1.72	0.47
3:C:641:MET:HE2	3:C:645:ARG:HH12	1.79	0.47
4:E:147:LEU:HD23	4:E:147:LEU:H	1.80	0.47
10:O:235:TYR:HD1	10:O:271:PHE:CE1	2.30	0.47
27:K:195:ILE:CG1	27:K:196:GLU:N	2.78	0.47
1:A:51:PHE:CE2	4:E:66:GLU:HG2	2.49	0.47
1:A:1946:ASN:OD1	1:A:1986:LEU:HD23	2.06	0.47
4:E:76:PRO:CG	4:E:121:GLY:CA	2.59	0.47
7:L:250:GLU:CD	7:L:250:GLU:N	2.73	0.47
16:G:143:U:H2'	16:G:145:U:O4	2.14	0.47
16:G:146:C:N1	16:G:147:C:C5	2.82	0.47
1:A:126:ILE:HG21	12:R:207:MET:HE2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.97	0.47
1:A:1832:ARG:NE	1:A:1832:ARG:CA	2.73	0.47
3:C:167:TYR:O	3:C:535:ALA:HB1	2.15	0.47
10:O:240:GLY:HA3	10:O:296:ARG:NH1	2.29	0.47
16:G:21:A:H8	16:G:21:A:O5'	1.97	0.47
28:I:187:LEU:CB	30:y:28:PRO:O	2.62	0.47
28:I:197:ALA:HB1	28:I:211:SER:CB	2.44	0.47
1:A:1306:LYS:HB3	1:A:1308:PRO:HD2	1.96	0.47
1:A:1802:PRO:CG	1:A:1824:THR:CG2	2.91	0.47
1:A:1946:ASN:ND2	1:A:1986:LEU:HG	2.30	0.47
2:B:93:U:H4'	2:B:94:U:H5''	1.97	0.47
4:E:266:PRO:CD	7:L:785:GLN:HB2	2.44	0.47
10:O:64:ARG:HH11	10:O:66:LYS:HG2	1.80	0.47
13:S:122:LEU:HA	13:S:126:HIS:HD2	1.80	0.47
14:T:390:GLY:HA3	14:T:416:ILE:HD11	1.95	0.47
16:G:22:C:C4'	16:G:23:U:OP1	2.63	0.47
17:H:89:U:H6	17:H:89:U:O5'	1.98	0.47
18:U:811:ARG:HH11	18:U:811:ARG:CG	2.14	0.47
28:I:238:LEU:O	28:I:241:ASP:CB	2.63	0.47
28:I:338:ILE:O	28:I:342:PRO:N	2.47	0.47
28:I:520:ILE:O	28:I:524:TYR:CA	2.61	0.47
28:I:521:VAL:O	28:I:527:PHE:N	2.48	0.47
1:A:1509:PHE:CZ	1:A:1513:MET:HE2	2.45	0.47
1:A:1518:LEU:C	1:A:1519:THR:OG1	2.53	0.47
4:E:250:LEU:HD22	4:E:262:TRP:HB2	1.97	0.47
5:F:37:C:H2'	5:F:38:G:C4'	2.44	0.47
12:R:106:GLN:NE2	12:R:225:PRO:HD2	2.29	0.47
14:T:379:VAL:HG21	14:T:420:THR:HA	1.97	0.47
15:W:216:LEU:HA	15:W:219:ILE:HG22	1.97	0.47
16:G:2:U:C6	16:G:2:U:P	3.08	0.47
16:G:2:U:C6	16:G:2:U:O5'	2.68	0.47
1:A:1517:LYS:HD2	1:A:1522:GLN:HG2	0.86	0.47
2:B:75:G:O6	2:B:76:A:N7	2.47	0.47
3:C:589:LYS:HG3	3:C:628:VAL:HG13	1.96	0.47
4:E:117:TYR:CE1	4:E:121:GLY:O	2.68	0.47
4:E:243:LEU:HD11	4:E:247:GLY:CA	2.42	0.47
4:E:257:ASN:CG	15:W:149:SER:CB	2.88	0.47
4:E:263:ASP:OD1	4:E:272:ARG:HB3	2.15	0.47
8:M:135:TYR:O	8:M:139:THR:OG1	2.33	0.47
3:C:224:GLY:HA3	3:C:438:ILE:HD12	1.95	0.47
4:E:116:HIS:CE1	4:E:158:TYR:HD1	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:297:GLY:O	4:E:314:THR:OG1	2.19	0.47
5:F:20:A:H4'	9:N:97:TYR:HE1	1.80	0.47
7:L:751:THR:O	7:L:755:LEU:N	2.38	0.47
14:T:254:VAL:HG22	14:T:261:LEU:HD23	1.97	0.47
27:K:19:PHE:CE2	27:K:175:GLY:CA	2.88	0.47
1:A:1430:LEU:HD21	1:A:1459:ARG:HE	1.80	0.46
1:A:1836:LEU:HD21	18:U:547:ILE:CG2	2.45	0.46
1:A:1836:LEU:HD23	18:U:547:ILE:HG21	1.97	0.46
2:B:8:G:N3	2:B:8:G:H2'	2.30	0.46
3:C:123:MET:HE2	3:C:545:PRO:HD2	1.97	0.46
10:O:259:ARG:C	10:O:273:GLN:O	2.58	0.46
10:O:272:ILE:CG2	10:O:274:PHE:CZ	2.99	0.46
1:A:332:TYR:O	3:C:888:ARG:NH2	2.39	0.46
1:A:1802:PRO:HG2	1:A:1824:THR:HG23	1.98	0.46
3:C:832:TYR:CD1	3:C:901:PHE:HA	2.51	0.46
10:O:36:MET:HB3	10:O:57:TRP:HB3	1.97	0.46
10:O:260:THR:HG22	10:O:273:GLN:CG	2.40	0.46
12:R:237:MET:HE3	12:R:241:GLU:HG3	1.96	0.46
18:U:551:THR:HG22	18:U:664:GLU:OE2	2.15	0.46
18:U:752:ILE:HD12	18:U:773:LEU:HD21	1.97	0.46
18:U:805:LEU:HD11	18:U:832:ALA:HB2	1.95	0.46
31:o:61:PRO:O	31:o:86:ALA:HB1	2.16	0.46
33:V:299:LYS:O	33:V:301:GLN:N	2.48	0.46
3:C:259:LYS:HE3	35:C:1500:GTP:C4	2.50	0.46
3:C:440:SER:O	3:C:442:LYS:N	2.48	0.46
4:E:59:ILE:HD13	15:W:82:ASN:ND2	2.29	0.46
4:E:232:ARG:O	4:E:262:TRP:CH2	2.67	0.46
6:J:774:VAL:HA	6:J:787:LYS:CB	2.45	0.46
16:G:137:C:O2'	16:G:138:A:C8	2.67	0.46
16:G:148:U:C2	17:H:30:A:C2	2.87	0.46
17:H:102:U:H3	19:h:4:GLY:N	2.14	0.46
3:C:135:CYS:HB2	3:C:242:LEU:HD13	1.98	0.46
3:C:692:LEU:HD12	3:C:696:LEU:HB3	1.97	0.46
6:J:261:ALA:HA	6:J:264:ILE:HD12	1.98	0.46
10:O:155:PRO:HD3	12:R:188:PHE:CE1	2.45	0.46
1:A:442:LYS:NZ	34:A:3000:IHP:O45	2.48	0.46
1:A:1237:MET:HG2	1:A:1284:LEU:HD23	1.97	0.46
26:r:3:LEU:CB	27:K:145:MET:CG	2.94	0.46
1:A:378:PHE:HB3	3:C:342:ARG:HH11	1.81	0.46
1:A:1337:GLN:O	1:A:1341:ARG:NH2	2.49	0.46
1:A:1946:ASN:CG	1:A:1986:LEU:HG	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:224:LYS:NZ	6:J:257:GLU:OE2	2.39	0.46
7:L:264:LYS:HE3	7:L:264:LYS:HB2	1.60	0.46
7:L:731:LEU:N	7:L:731:LEU:CD2	2.79	0.46
11:P:19:GLY:HA2	11:P:23:LEU:HD12	1.96	0.46
17:H:59:A:H2'	17:H:60:U:C6	2.50	0.46
33:V:219:TYR:HA	33:V:235:TYR:O	2.16	0.46
1:A:372:PRO:HG2	3:C:342:ARG:HG2	1.98	0.46
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.97	0.46
1:A:1513:MET:CE	18:U:622:ALA:CB	2.94	0.46
1:A:1830:GLN:HG3	1:A:1834:GLY:HA2	1.98	0.46
4:E:125:PHE:N	4:E:125:PHE:CD1	2.82	0.46
4:E:266:PRO:HG2	7:L:785:GLN:C	2.41	0.46
10:O:230:THR:H	10:O:277:ARG:CZ	2.28	0.46
13:S:38:ASN:HD21	13:S:76:SER:HB2	1.81	0.46
13:S:148:ASN:HD21	13:S:152:ARG:HB2	1.81	0.46
17:H:113:G:O2'	17:H:114:A:H5'	2.15	0.46
18:U:537:GLY:HA3	18:U:548:LEU:HD12	1.97	0.46
18:U:626:MET:SD	18:U:643:LYS:HE3	2.56	0.46
18:U:771:ILE:HG21	18:U:850:ILE:HG21	1.97	0.46
26:r:61:ILE:O	27:K:138:TYR:CG	2.69	0.46
1:A:76:MET:O	1:A:85:LYS:NZ	2.38	0.46
1:A:678:GLU:HG2	1:A:749:TRP:HH2	1.81	0.46
1:A:1517:LYS:NZ	1:A:1517:LYS:CB	2.73	0.46
2:B:88:A:N6	23:f:39:TYR:C	2.74	0.46
4:E:276:ILE:C	4:E:277:PHE:HD1	2.23	0.46
7:L:21:ALA:HB1	7:L:159:LEU:HD21	1.97	0.46
7:L:742:ILE:CG1	26:q:57:VAL:CB	2.94	0.46
1:A:402:ILE:HG21	3:C:268:LYS:HD3	1.98	0.46
1:A:1312:PRO:HB2	1:A:1314:VAL:HG12	1.97	0.46
1:A:1833:LEU:HD11	18:U:718:HIS:O	2.16	0.46
2:B:87:A:H2'	2:B:87:A:N3	2.31	0.46
4:E:69:VAL:HG11	4:E:345:ALA:HB1	1.92	0.46
4:E:326:HIS:CD2	4:E:346:SER:HB3	2.50	0.46
1:A:1889:LEU:HG	1:A:2013:GLY:HA3	1.96	0.46
3:C:534:VAL:O	3:C:534:VAL:HG12	2.16	0.46
4:E:321:TYR:CZ	4:E:356:ILE:CG2	2.96	0.46
16:G:2:U:O2	18:U:625:PHE:HB3	2.16	0.46
17:H:73:C:O5'	17:H:73:C:H6	1.99	0.46
18:U:546:VAL:HB	18:U:665:HIS:CE1	2.50	0.46
28:I:238:LEU:O	28:I:241:ASP:N	2.49	0.46
3:C:166:CYS:SG	3:C:536:ARG:NH2	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:55:LEU:CD1	4:E:96:TYR:OH	2.64	0.45
4:E:63:SER:O	4:E:93:TRP:CZ3	2.62	0.45
4:E:260:ARG:CD	4:E:276:ILE:HG12	2.46	0.45
5:F:36:A:N6	16:G:10:U:H3	2.14	0.45
7:L:789:ALA:O	7:L:792:LEU:CG	2.64	0.45
14:T:390:GLY:HA2	14:T:395:ILE:HG12	1.98	0.45
17:H:33:G:P	18:U:666:ARG:HE	2.37	0.45
1:A:1244:VAL:HG11	1:A:1291:CYS:HB3	1.98	0.45
2:B:36:C:C2'	2:B:37:G:H5'	2.45	0.45
4:E:277:PHE:CE2	4:E:300:ILE:HD12	2.52	0.45
10:O:166:SER:O	10:O:170:LYS:NZ	2.43	0.45
14:T:214:PRO:HG3	14:T:256:THR:HG22	1.98	0.45
14:T:395:ILE:HD13	14:T:419:LEU:HD21	1.96	0.45
16:G:23:U:C6	16:G:23:U:H5''	2.51	0.45
16:G:27:U:HO2'	16:G:28:A:C4'	2.29	0.45
17:H:41:U:O2'	17:H:42:G:C8	2.66	0.45
17:H:57:A:H2'	17:H:58:U:C6	2.50	0.45
17:H:172:C:O5'	17:H:172:C:H6	1.98	0.45
1:A:1946:ASN:ND2	1:A:1986:LEU:HD21	2.30	0.45
4:E:339:GLU:HB3	4:E:340:PRO:HD2	1.99	0.45
14:T:387:PHE:HB3	14:T:400:PHE:CZ	2.51	0.45
17:H:33:G:H3'	18:U:666:ARG:CD	2.46	0.45
26:t:90:PHE:CB	27:K:111:MET:CB	2.94	0.45
1:A:466:ALA:CA	2:B:20:G:N2	2.46	0.45
1:A:516:LEU:HD11	1:A:538:SER:HB2	1.99	0.45
10:O:260:THR:HG22	10:O:273:GLN:HG2	1.97	0.45
14:T:270:VAL:HB	14:T:284:TYR:HB2	1.98	0.45
28:I:405:TYR:O	28:I:409:GLY:CA	2.65	0.45
28:I:712:VAL:O	28:I:715:GLY:N	2.49	0.45
2:B:10:U:O2	2:B:69:A:N1	2.50	0.45
2:B:77:G:N7	2:B:80:U:O4	2.49	0.45
4:E:73:LYS:O	4:E:81:LEU:CD2	2.65	0.45
5:F:36:A:H2'	5:F:37:C:C6	2.52	0.45
7:L:74:LEU:HA	7:L:77:LEU:HB3	1.97	0.45
7:L:250:GLU:CD	7:L:250:GLU:H	2.24	0.45
10:O:223:LEU:CD1	10:O:285:GLU:HA	2.44	0.45
15:W:148:VAL:HG21	15:W:151:LYS:HD3	1.98	0.45
16:G:146:C:C6	16:G:147:C:C5	3.05	0.45
17:H:56:A:H2'	17:H:57:A:H8	1.82	0.45
4:E:66:GLU:HB2	4:E:87:ASP:CG	2.41	0.45
4:E:95:VAL:HA	4:E:99:CYS:SG	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:147:LEU:HD12	4:E:179:TRP:CD2	2.51	0.45
5:F:9:U:O2	5:F:10:U:N3	2.49	0.45
5:F:90:G:C6	5:F:91:A:C6	3.04	0.45
6:J:224:LYS:HE2	6:J:255:LEU:HD13	1.98	0.45
10:O:59:PRO:HB2	10:O:63:MET:HG3	1.99	0.45
12:R:229:VAL:O	12:R:230:MET:HB2	2.15	0.45
16:G:27:U:HO2'	16:G:28:A:C5'	2.27	0.45
16:G:145:U:C6	16:G:145:U:OP2	2.70	0.45
2:B:96:A:N1	2:B:97:G:C5	2.84	0.45
3:C:134:LEU:O	3:C:205:THR:OG1	2.31	0.45
4:E:74:PHE:CD1	4:E:81:LEU:CD2	2.99	0.45
4:E:135:VAL:HB	4:E:145:LYS:O	2.17	0.45
4:E:153:PHE:HD1	4:E:153:PHE:H	1.64	0.45
4:E:164:PRO:O	4:E:166:LEU:HG	2.17	0.45
4:E:177:LYS:C	4:E:178:LEU:HD23	2.41	0.45
4:E:228:THR:HG22	4:E:229:TYR:HD1	1.81	0.45
5:F:21:U:H5'	9:N:120:ARG:O	2.16	0.45
10:O:234:LEU:HB2	10:O:272:ILE:HB	1.99	0.45
16:G:139:U:O2'	16:G:140:A:C8	2.67	0.45
17:H:91:U:O5'	17:H:91:U:H6	2.00	0.45
1:A:136:ILE:HG22	1:A:138:PRO:HD2	1.98	0.45
1:A:246:LEU:HD22	1:A:408:PRO:HG2	1.97	0.45
1:A:266:SER:OG	1:A:271:MET:O	2.31	0.45
3:C:166:CYS:O	3:C:170:ILE:CG2	2.65	0.45
4:E:157:CYS:HA	4:E:168:CYS:O	2.17	0.45
10:O:162:PRO:O	10:O:182:ARG:NE	2.46	0.45
10:O:224:ASP:O	10:O:302:TRP:CE2	2.69	0.45
17:H:33:G:H3'	18:U:666:ARG:HD2	1.98	0.45
28:I:526:MET:HE2	28:I:528:LEU:H	1.82	0.45
1:A:1544:ARG:HB2	1:A:1547:VAL:HG12	1.98	0.45
1:A:1835:GLN:CB	18:U:557:VAL:HG11	2.46	0.45
3:C:677:GLU:HB3	3:C:684:LYS:HG2	1.98	0.45
4:E:153:PHE:N	4:E:153:PHE:CD1	2.85	0.45
8:M:210:TYR:HB2	8:M:215:ASN:HB3	1.99	0.45
9:N:70:ILE:HG12	9:N:74:LEU:HD23	1.98	0.45
16:G:5:G:C2	16:G:6:A:C6	3.05	0.45
16:G:120:G:C2'	29:Q:1019:SER:H	2.27	0.45
1:A:1110:ILE:HD11	1:A:1149:LEU:HB2	1.98	0.45
1:A:1128:TYR:OH	1:A:1175:VAL:O	2.34	0.45
2:B:78:U:O2'	2:B:79:C:OP1	2.28	0.45
11:P:23:LEU:HD23	11:P:26:LEU:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:2:U:OP1	16:G:2:U:C6	2.70	0.45
18:U:867:GLU:HB3	18:U:872:GLN:HB3	1.99	0.45
27:K:156:LEU:O	27:K:160:ILE:CG1	2.65	0.45
3:C:108:THR:HG21	3:C:538:HIS:O	2.17	0.44
5:F:29:A:H62	16:G:16:G:H1'	1.82	0.44
5:F:40:U:O4	5:F:41:A:N6	2.50	0.44
10:O:256:GLY:CA	12:R:70:ALA:HB2	2.43	0.44
17:H:58:U:H2'	17:H:59:A:H8	1.82	0.44
18:U:713:ILE:HB	18:U:768:TYR:HB3	1.97	0.44
29:Q:360:ASP:O	29:Q:361:THR:C	2.56	0.44
1:A:758:ARG:HA	1:A:758:ARG:HD2	1.76	0.44
4:E:323:LEU:HD21	15:W:83:PRO:O	2.17	0.44
5:F:38:G:C4	5:F:39:A:N7	2.85	0.44
7:L:706:GLU:O	27:K:121:ILE:CG1	2.65	0.44
15:W:155:SER:OG	15:W:158:GLU:OE1	2.31	0.44
1:A:711:GLN:HE22	17:H:18:U:H3'	1.82	0.44
3:C:853:ARG:NH2	3:C:886:ASP:OD2	2.50	0.44
4:E:57:ALA:HA	4:E:58:PRO:HD3	1.82	0.44
4:E:116:HIS:O	4:E:124:LEU:CD1	2.57	0.44
4:E:131:LYS:CG	4:E:152:SER:C	2.67	0.44
14:T:355:ARG:HH11	14:T:364:THR:HG21	1.81	0.44
27:K:19:PHE:CE2	27:K:172:LEU:C	2.85	0.44
1:A:888:GLN:OE1	7:L:130:PRO:HG2	2.15	0.44
3:C:507:VAL:HG13	3:C:565:ILE:HG23	2.00	0.44
4:E:111:ALA:C	4:E:113:MET:N	2.74	0.44
4:E:115:LEU:HD23	4:E:126:SER:HB2	1.99	0.44
4:E:131:LYS:HD3	4:E:152:SER:N	2.32	0.44
5:F:44:G:C2'	16:G:1:G:H22	2.31	0.44
17:H:83:A:H2'	17:H:84:C:C5	2.44	0.44
27:K:17:PRO:HD2	27:K:171:GLN:OE1	2.16	0.44
27:K:18:TYR:HB2	27:K:171:GLN:OE1	2.17	0.44
27:K:120:ARG:O	27:K:124:LEU:CB	2.66	0.44
28:I:176:SER:HA	28:I:196:ALA:CB	2.47	0.44
30:y:10:VAL:CB	30:y:50:ALA:O	2.65	0.44
1:A:759:GLU:OE2	1:A:762:ARG:NH1	2.43	0.44
1:A:1011:ALA:HB2	7:L:80:THR:HB	1.98	0.44
1:A:1947:ASN:O	1:A:1949:ARG:N	2.50	0.44
2:B:74:U:H6	2:B:74:U:H5''	1.83	0.44
3:C:92:PRO:HA	14:T:278:ASN:HD21	1.83	0.44
4:E:101:ASN:N	4:E:101:ASN:ND2	2.60	0.44
10:O:78:LYS:HD3	10:O:94:ILE:HG21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:21:A:O5'	16:G:21:A:C8	2.70	0.44
1:A:1392:LYS:NZ	1:A:1407:ASP:O	2.45	0.44
2:B:75:G:C6	2:B:76:A:C8	3.03	0.44
4:E:58:PRO:CD	4:E:59:ILE:N	2.79	0.44
4:E:321:TYR:CZ	4:E:356:ILE:HG23	2.40	0.44
5:F:58:G:H2'	5:F:59:G:C8	2.53	0.44
7:L:213:GLU:OE2	10:O:110:SER:OG	2.31	0.44
10:O:250:ASN:O	10:O:253:TYR:CD2	2.71	0.44
15:W:159:ALA:O	15:W:164:GLY:N	2.51	0.44
16:G:154:U:C6	16:G:154:U:O5'	2.70	0.44
17:H:81:G:H2'	17:H:82:G:H8	1.83	0.44
1:A:103:LEU:HD11	1:A:554:THR:HG22	2.00	0.44
1:A:828:PRO:HA	1:A:829:PRO:HD3	1.81	0.44
3:C:167:TYR:HH	3:C:537:TYR:HH	1.55	0.44
5:F:38:G:C4	5:F:39:A:C8	3.06	0.44
5:F:81:C:C6	5:F:81:C:C4'	3.01	0.44
10:O:251:HIS:O	10:O:251:HIS:CD2	2.70	0.44
12:R:113:TYR:OH	14:T:402:ASP:O	2.32	0.44
1:A:1354:ARG:NE	1:A:1357:MET:SD	2.91	0.44
2:B:90:U:OP2	2:B:90:U:H4'	2.17	0.44
4:E:119:THR:HG21	4:E:161:ARG:CB	2.32	0.44
7:L:759:GLU:HG2	27:K:167:ARG:CG	2.48	0.44
16:G:5:G:C5	16:G:6:A:C4	3.06	0.44
17:H:54:U:C6	17:H:55:U:H5	2.36	0.44
17:H:80:A:N3	17:H:81:G:N7	2.66	0.44
17:H:84:C:H2'	17:H:85:A:H8	1.83	0.44
1:A:1340:LEU:HD12	1:A:1355:SER:HB2	1.99	0.44
3:C:250:ARG:HG3	3:C:451:HIS:CD2	2.53	0.44
3:C:631:GLY:HA3	3:C:637:LEU:HD21	2.00	0.44
4:E:145:LYS:HE2	4:E:145:LYS:HA	2.00	0.44
7:L:703:MET:O	7:L:707:ALA:HB3	2.18	0.44
10:O:272:ILE:HG22	10:O:274:PHE:CE1	2.52	0.44
17:H:155:C:H6	17:H:155:C:O5'	2.01	0.44
18:U:694:VAL:N	18:U:732:GLU:OE2	2.50	0.44
28:I:545:ILE:O	28:I:548:PHE:N	2.51	0.44
1:A:163:ARG:HH21	1:A:625:PRO:HB3	1.83	0.43
1:A:680:HIS:NE2	14:T:266:GLU:O	2.37	0.43
1:A:1836:LEU:CD2	18:U:547:ILE:CG2	2.96	0.43
3:C:163:GLN:HE21	3:C:163:GLN:HB2	1.55	0.43
3:C:538:HIS:CE1	3:C:551:LEU:HD11	2.46	0.43
3:C:853:ARG:NH1	3:C:879:ASP:O	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:272:ILE:HG22	10:O:274:PHE:CZ	2.53	0.43
18:U:655:GLU:O	18:U:658:ARG:CG	2.65	0.43
18:U:670:ALA:O	18:U:674:LYS:HG2	2.18	0.43
18:U:819:PRO:HB2	18:U:835:ILE:HB	2.00	0.43
1:A:1255:THR:C	1:A:1531:ASN:HD21	2.27	0.43
3:C:101:LYS:HA	3:C:485:ASP:HB2	1.99	0.43
17:H:166:G:O6	32:p:88:SER:CB	2.66	0.43
26:r:127:ALA:CB	26:s:127:ALA:HB3	2.48	0.43
2:B:68:C:C6	2:B:68:C:OP1	2.70	0.43
2:B:72:U:OP2	2:B:72:U:C6	2.72	0.43
4:E:58:PRO:O	4:E:59:ILE:HB	2.16	0.43
14:T:416:ILE:HA	14:T:431:ALA:HA	1.98	0.43
16:G:154:U:H3'	16:G:154:U:H6	1.84	0.43
28:I:477:GLN:O	28:I:480:VAL:O	2.37	0.43
1:A:533:LYS:HD2	16:G:3:A:O2'	2.17	0.43
1:A:1946:ASN:OD1	1:A:1986:LEU:HG	2.19	0.43
2:B:9:G:N3	2:B:9:G:C2'	2.79	0.43
3:C:230:ASP:OD2	3:C:262:ARG:NH1	2.52	0.43
18:U:805:LEU:HD13	18:U:810:ILE:HG12	1.99	0.43
4:E:75:HIS:H	4:E:81:LEU:CD2	2.30	0.43
4:E:101:ASN:ND2	4:E:101:ASN:H	2.16	0.43
5:F:42:C:C2'	5:F:43:A:C5'	2.95	0.43
5:F:43:A:H8	5:F:43:A:O5'	2.02	0.43
10:O:193:LEU:O	10:O:196:GLN:NE2	2.52	0.43
14:T:382:PRO:HB2	14:T:383:ARG:HD2	1.99	0.43
17:H:82:G:C2'	17:H:83:A:H5'	2.49	0.43
18:U:662:ILE:CD1	18:U:662:ILE:C	2.86	0.43
4:E:260:ARG:HD2	4:E:276:ILE:HG12	2.00	0.43
7:L:166:LYS:HA	7:L:169:ARG:HG2	2.00	0.43
10:O:223:LEU:HA	10:O:288:PHE:CD2	2.53	0.43
10:O:239:LEU:CD1	10:O:243:ILE:HD12	2.49	0.43
3:C:371:GLU:O	3:C:375:GLU:HB3	2.18	0.43
4:E:131:LYS:HD3	4:E:152:SER:CA	2.48	0.43
4:E:147:LEU:N	4:E:147:LEU:CD2	2.73	0.43
10:O:292:ILE:HG23	10:O:296:ARG:C	2.44	0.43
13:S:90:LEU:HB3	13:S:128:ILE:HD12	2.00	0.43
13:S:160:ILE:HG22	13:S:161:LYS:HG3	2.00	0.43
14:T:439:TRP:HD1	14:T:446:ASN:HA	1.83	0.43
18:U:685:PRO:O	18:U:687:HIS:ND1	2.48	0.43
27:K:131:GLY:O	27:K:135:TRP:N	2.46	0.43
1:A:1309:SER:OG	1:A:1310:ARG:N	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:35:U:C6	2:B:35:U:C4'	3.02	0.43
4:E:165:GLN:HG3	4:E:181:ILE:HD11	2.01	0.43
4:E:277:PHE:CD1	4:E:277:PHE:N	2.85	0.43
17:H:80:A:N1	17:H:81:G:C5	2.87	0.43
2:B:89:U:HO2'	2:B:90:U:P	2.42	0.43
3:C:263:LEU:HD23	3:C:267:LEU:HD12	2.00	0.43
3:C:624:SER:HB3	3:C:941:LYS:HA	2.01	0.43
4:E:127:ALA:HB2	4:E:157:CYS:HB3	2.00	0.43
4:E:313:ASP:CB	4:E:320:LEU:HD21	2.48	0.43
10:O:25:GLN:NE2	12:R:181:PRO:HB3	2.34	0.43
10:O:92:LEU:HD11	10:O:151:ALA:HA	2.01	0.43
12:R:52:PRO:HG3	12:R:67:ILE:HG21	2.00	0.43
13:S:102:ASN:ND2	13:S:104:GLY:O	2.51	0.43
14:T:399:LYS:HD2	14:T:406:ILE:HD11	2.01	0.43
16:G:141:C:O2'	16:G:142:U:OP2	2.36	0.43
16:G:145:U:H6	16:G:145:U:H2'	1.61	0.43
17:H:8:C:C2	17:H:9:U:C5	3.07	0.43
17:H:175:G:C6	17:H:176:G:C5	3.07	0.43
17:H:179:C:HO2'	17:H:180:G:H5'	1.78	0.43
3:C:300:LEU:HA	3:C:306:ASN:HD21	1.84	0.43
10:O:182:ARG:NH1	10:O:184:GLU:OE2	2.45	0.43
10:O:220:MET:HE3	10:O:220:MET:HB3	1.60	0.43
13:S:93:THR:HG23	13:S:118:PRO:HB3	2.01	0.43
17:H:112:G:H2'	17:H:113:G:C8	2.50	0.43
26:r:124:VAL:HA	26:s:124:VAL:CB	2.49	0.43
27:K:112:ALA:O	27:K:116:HIS:CG	2.70	0.43
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.52	0.42
3:C:118:PHE:HE2	3:C:122:LEU:HD11	1.84	0.42
17:H:33:G:H2'	17:H:33:G:OP2	2.19	0.42
17:H:83:A:C5	17:H:84:C:N4	2.85	0.42
17:H:98:G:OP1	17:H:98:G:C8	2.72	0.42
27:K:19:PHE:CE1	27:K:175:GLY:C	2.95	0.42
1:A:224:THR:HG23	2:B:12:U:H5''	2.01	0.42
3:C:115:GLU:CD	3:C:189:VAL:CG2	2.92	0.42
4:E:109:SER:CA	4:E:130:ASP:OD2	2.67	0.42
4:E:326:HIS:HD1	4:E:352:TYR:HE2	1.66	0.42
8:M:207:ASP:OD1	8:M:207:ASP:N	2.52	0.42
10:O:149:LYS:NZ	10:O:290:LYS:HG2	2.34	0.42
17:H:108:G:C5	17:H:109:C:N4	2.87	0.42
18:U:751:CYS:HB2	18:U:826:GLY:HA2	2.00	0.42
1:A:1515:TRP:CE3	1:A:1515:TRP:CA	3.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:77:G:C5	2:B:80:U:O4	2.72	0.42
5:F:45:A:C4	18:U:625:PHE:CE1	3.07	0.42
9:N:128:VAL:HG13	9:N:130:ARG:H	1.84	0.42
10:O:221:PRO:HA	10:O:222:ARG:CZ	2.48	0.42
17:H:30:A:O2'	17:H:31:G:H8	1.98	0.42
17:H:80:A:C2	17:H:81:G:C8	3.07	0.42
28:I:455:LEU:C	28:I:457:ARG:H	2.27	0.42
1:A:686:ARG:HE	1:A:710:LEU:HD22	1.83	0.42
3:C:160:ARG:CD	3:C:164:ASP:HB2	2.49	0.42
4:E:119:THR:HG23	4:E:161:ARG:CB	2.37	0.42
5:F:35:A:C2'	5:F:36:A:OP1	2.68	0.42
5:F:38:G:C2	5:F:39:A:C6	3.06	0.42
10:O:155:PRO:CG	12:R:188:PHE:HA	2.49	0.42
10:O:230:THR:H	10:O:277:ARG:NH1	2.17	0.42
10:O:236:VAL:HB	10:O:270:ALA:O	2.19	0.42
13:S:100:MET:HE2	13:S:108:ASN:HB3	2.01	0.42
14:T:198:ARG:HB3	14:T:488:VAL:HB	2.01	0.42
17:H:114:A:N3	17:H:115:G:C8	2.88	0.42
28:I:337:LEU:C	28:I:339:SER:N	2.75	0.42
1:A:833:LYS:HG3	1:A:834:HIS:CD2	2.54	0.42
4:E:178:LEU:HG	4:E:188:GLN:HB2	2.01	0.42
8:M:190:ILE:HG12	8:M:193:ARG:HH22	1.84	0.42
17:H:32:U:O2'	17:H:33:G:OP2	2.37	0.42
17:H:32:U:O2'	17:H:33:G:C8	2.66	0.42
1:A:380:LEU:HD12	1:A:384:VAL:HG21	2.00	0.42
1:A:1314:VAL:O	1:A:1318:THR:OG1	2.28	0.42
1:A:1628:ASP:OD2	1:A:1664:ILE:N	2.45	0.42
3:C:664:GLU:HB3	3:C:820:PHE:HZ	1.83	0.42
12:R:60:ASP:HB2	13:S:134:GLN:HA	2.02	0.42
17:H:169:C:O5'	17:H:169:C:H6	2.03	0.42
18:U:844:TYR:OH	18:U:862:ARG:NH1	2.53	0.42
22:d:68:GLU:HA	22:d:97:SER:O	2.19	0.42
28:I:577:ARG:O	28:I:580:PHE:O	2.37	0.42
1:A:97:HIS:HE1	2:B:56:C:H5''	1.85	0.42
1:A:533:LYS:N	16:G:3:A:H5'	2.34	0.42
2:B:43:U:H3'	2:B:44:A:C8	2.54	0.42
2:B:75:G:C6	2:B:76:A:C5	3.06	0.42
3:C:138:LEU:C	3:C:138:LEU:CD2	2.92	0.42
4:E:75:HIS:N	4:E:81:LEU:CD2	2.82	0.42
4:E:108:HIS:CD2	4:E:136:TRP:CZ2	3.07	0.42
4:E:265:ARG:H	4:E:272:ARG:HH22	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:276:ILE:O	4:E:277:PHE:HD1	2.01	0.42
4:E:307:ARG:NH1	15:W:143:LEU:CG	2.79	0.42
5:F:49:G:H2'	5:F:50:A:H8	1.84	0.42
5:F:91:A:C2	17:H:8:C:O2	2.73	0.42
10:O:251:HIS:CE1	10:O:291:LEU:CD1	3.02	0.42
12:R:184:GLN:NE2	12:R:184:GLN:CA	2.73	0.42
17:H:80:A:C4	17:H:81:G:C8	3.08	0.42
1:A:135:VAL:HG11	1:A:421:ALA:HB2	2.00	0.42
1:A:1211:ASP:OD1	1:A:1211:ASP:N	2.52	0.42
1:A:1802:PRO:CG	1:A:1824:THR:HG23	2.50	0.42
1:A:1836:LEU:HD12	1:A:1836:LEU:HA	1.84	0.42
3:C:87:GLN:HE21	14:T:239:LYS:HG2	1.85	0.42
3:C:136:GLY:N	3:C:142:LYS:HD3	2.35	0.42
4:E:74:PHE:CD2	4:E:336:HIS:CA	3.02	0.42
4:E:234:HIS:ND1	4:E:256:ASP:OD2	2.50	0.42
10:O:50:ARG:HA	10:O:51:PRO:HD3	1.89	0.42
17:H:108:G:C5	17:H:109:C:C4	3.08	0.42
17:H:178:A:N3	17:H:178:A:H2'	2.33	0.42
18:U:777:VAL:HG12	18:U:853:MET:HE2	2.02	0.42
1:A:357:ASN:ND2	3:C:866:SER:O	2.52	0.42
3:C:814:ARG:HA	3:C:817:TYR:HD2	1.84	0.42
5:F:20:A:O2'	9:N:120:ARG:NH2	2.53	0.42
6:J:377:LYS:HE2	6:J:377:LYS:HB3	1.85	0.42
10:O:215:LYS:O	10:O:219:THR:HG23	2.20	0.42
10:O:253:TYR:O	10:O:254:GLN:C	2.63	0.42
13:S:92:PHE:CD2	13:S:122:LEU:HB3	2.55	0.42
14:T:353:THR:HG22	14:T:369:THR:HG22	2.01	0.42
15:W:140:ASP:OD2	15:W:145:ASN:OD1	2.38	0.42
16:G:3:A:H1'	16:G:4:A:P	2.60	0.42
16:G:146:C:P	16:G:146:C:C3'	3.07	0.42
16:G:152:C:C2	16:G:153:C:C6	2.96	0.42
17:H:33:G:O3'	18:U:662:ILE:HD11	2.16	0.42
27:K:19:PHE:CZ	27:K:176:SER:N	2.87	0.42
22:k:68:GLU:HA	22:k:97:SER:O	2.19	0.42
1:A:490:VAL:HG21	1:A:565:ARG:HG3	2.01	0.42
1:A:1069:ASN:ND2	1:A:1073:SER:O	2.53	0.42
1:A:1501:LEU:HD13	1:A:1753:LEU:HD11	2.01	0.42
3:C:104:LEU:HD13	3:C:172:PHE:HE1	1.85	0.42
5:F:91:A:N1	17:H:8:C:C2	2.88	0.42
7:L:259:ASP:CG	8:M:199:ARG:HH21	2.25	0.42
9:N:70:ILE:HG23	9:N:74:LEU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:146:C:H2'	16:G:146:C:H6	1.64	0.42
17:H:7:U:H3'	17:H:8:C:C5	2.55	0.42
17:H:102:U:N3	19:h:4:GLY:N	2.68	0.42
28:I:790:ARG:CB	28:I:801:ASP:HA	2.48	0.42
3:C:171:LEU:HD22	3:C:181:ILE:HD11	2.02	0.41
3:C:514:TYR:HB2	3:C:521:ASP:HB3	2.02	0.41
4:E:83:SER:O	4:E:90:ILE:CA	2.67	0.41
4:E:289:LEU:HD12	4:E:303:GLY:O	2.21	0.41
4:E:323:LEU:HD22	15:W:83:PRO:HD2	2.01	0.41
13:S:72:ARG:NH2	15:W:88:MET:O	2.52	0.41
16:G:120:G:H2'	29:Q:1019:SER:H	1.85	0.41
18:U:810:ILE:H	18:U:810:ILE:HG13	1.49	0.41
1:A:955:TRP:CE2	1:A:1189:MET:HE1	2.55	0.41
2:B:87:A:C5	22:d:61:ARG:CB	3.03	0.41
4:E:178:LEU:CD2	4:E:208:ILE:HD13	2.47	0.41
10:O:253:TYR:CD1	10:O:253:TYR:C	2.98	0.41
14:T:220:VAL:HG11	14:T:261:LEU:HD21	2.01	0.41
16:G:5:G:C8	16:G:6:A:C8	3.07	0.41
16:G:143:U:H6	16:G:143:U:H5''	1.84	0.41
17:H:108:G:H2'	17:H:109:C:C5	2.47	0.41
28:I:526:MET:O	28:I:526:MET:SD	2.79	0.41
1:A:237:THR:HA	1:A:240:ARG:HD3	2.01	0.41
2:B:81:U:HO2'	2:B:82:A:P	2.40	0.41
5:F:92:A:C2	5:F:93:G:C8	3.08	0.41
7:L:759:GLU:HG2	27:K:167:ARG:HG2	2.02	0.41
15:W:77:LYS:HD3	15:W:77:LYS:HA	1.93	0.41
16:G:145:U:OP2	16:G:145:U:C5	2.73	0.41
16:G:153:C:O2	16:G:153:C:H2'	2.19	0.41
17:H:8:C:C2'	17:H:9:U:C6	2.95	0.41
28:I:455:LEU:C	28:I:457:ARG:N	2.78	0.41
1:A:941:LYS:HA	1:A:941:LYS:HD2	1.74	0.41
1:A:1518:LEU:C	1:A:1519:THR:HG1	2.11	0.41
3:C:160:ARG:HD2	3:C:164:ASP:HB2	2.03	0.41
4:E:74:PHE:CD2	4:E:336:HIS:N	2.88	0.41
4:E:243:LEU:HD22	4:E:243:LEU:HA	1.86	0.41
6:J:188:GLN:NE2	7:L:140:ASP:OD1	2.54	0.41
1:A:534:GLU:OE2	5:F:38:G:C5'	2.69	0.41
1:A:946:GLU:O	1:A:1437:ARG:NH2	2.54	0.41
1:A:1321:GLU:HG3	1:A:1322:LEU:HD22	2.02	0.41
1:A:1899:VAL:HB	1:A:1902:PHE:HD2	1.85	0.41
3:C:412:ILE:O	3:C:416:LEU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:75:HIS:O	4:E:78:GLY:N	2.53	0.41
6:J:238:ASN:C	6:J:240:THR:H	2.28	0.41
9:N:57:THR:HG23	9:N:85:ASP:H	1.85	0.41
14:T:297:HIS:NE2	14:T:339:GLN:O	2.54	0.41
16:G:145:U:O3'	18:U:658:ARG:NH1	2.53	0.41
17:H:103:U:C3'	17:H:104:U:H5'	2.51	0.41
17:H:149:A:N6	17:H:183:G:O6	2.53	0.41
1:A:147:MET:HE1	1:A:192:GLN:H	1.85	0.41
1:A:995:ARG:NH1	12:R:291:LEU:O	2.53	0.41
1:A:1260:VAL:HG21	1:A:1325:LEU:HD13	2.03	0.41
2:B:87:A:H5'	2:B:88:A:OP1	2.20	0.41
3:C:136:GLY:HA3	3:C:142:LYS:NZ	2.32	0.41
5:F:79:C:N4	7:L:166:LYS:HD2	2.36	0.41
16:G:126:C:H4'	16:G:127:U:C1'	2.50	0.41
16:G:141:C:O2'	16:G:142:U:C5	2.72	0.41
16:G:147:C:OP2	18:U:659:LYS:CB	2.68	0.41
18:U:548:LEU:HD22	18:U:661:ALA:CA	2.47	0.41
26:r:127:ALA:HB3	26:s:127:ALA:HB3	2.03	0.41
28:I:585:ASP:C	28:I:587:CYS:N	2.78	0.41
1:A:858:GLN:OE1	1:A:861:ARG:NH1	2.54	0.41
1:A:1365:ILE:HG23	1:A:1474:MET:HE1	2.01	0.41
1:A:1663:ASP:HB3	1:A:1702:LEU:HB2	2.02	0.41
1:A:1971:LEU:HB2	1:A:1976:TRP:CE2	2.55	0.41
3:C:369:PHE:O	3:C:373:ILE:HB	2.21	0.41
3:C:590:ILE:HG22	3:C:592:VAL:HG23	2.02	0.41
3:C:831:TYR:HB2	3:C:903:HIS:HB3	2.02	0.41
4:E:284:PHE:HB3	15:W:139:LEU:HD22	2.01	0.41
7:L:710:ALA:O	27:K:124:LEU:HD22	2.16	0.41
12:R:234:SER:O	12:R:235:ARG:O	2.38	0.41
14:T:354:ILE:HD12	14:T:398:TRP:HZ3	1.86	0.41
17:H:147:G:N3	17:H:148:C:C6	2.88	0.41
27:K:19:PHE:CD2	27:K:171:GLN:O	2.73	0.41
1:A:447:TYR:HE1	1:A:611:LEU:HA	1.86	0.41
1:A:549:GLU:HB3	1:A:591:MET:HG2	2.03	0.41
1:A:955:TRP:CD2	1:A:1189:MET:HE1	2.56	0.41
1:A:1426:ASP:OD1	1:A:1426:ASP:N	2.53	0.41
2:B:77:G:C5	2:B:80:U:C4	3.08	0.41
3:C:115:GLU:OE1	3:C:189:VAL:CG2	2.64	0.41
4:E:115:LEU:HD13	4:E:116:HIS:N	2.36	0.41
4:E:128:SER:O	4:E:154:VAL:HB	2.21	0.41
4:E:265:ARG:N	4:E:272:ARG:HH21	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:206:LEU:HD21	7:L:171:ALA:HB1	2.02	0.41
7:L:741:GLN:O	7:L:744:GLN:CG	2.69	0.41
12:R:183:GLN:O	12:R:183:GLN:CG	2.69	0.41
16:G:146:C:HO2'	16:G:147:C:C5'	2.23	0.41
16:G:150:U:C6	16:G:150:U:C4'	3.04	0.41
18:U:591:PHE:N	18:U:594:ASP:OD2	2.54	0.41
18:U:746:ASP:OD2	18:U:886:TYR:OH	2.34	0.41
1:A:103:LEU:HB2	1:A:638:LEU:HD21	2.03	0.41
1:A:1631:LEU:HD13	1:A:1660:TYR:HD2	1.86	0.41
1:A:1946:ASN:ND2	1:A:1986:LEU:CG	2.84	0.41
3:C:142:LYS:O	3:C:145:PHE:HB3	2.21	0.41
3:C:277:LYS:HD2	3:C:865:GLY:HA3	2.03	0.41
3:C:685:ILE:HD11	3:C:808:ILE:HG23	2.01	0.41
3:C:832:TYR:CD1	3:C:900:VAL:C	2.99	0.41
4:E:81:LEU:HD22	4:E:81:LEU:HA	1.86	0.41
4:E:88:ARG:HD2	4:E:110:GLY:N	2.36	0.41
4:E:161:ARG:HG2	4:E:161:ARG:HH11	1.86	0.41
4:E:284:PHE:CE2	15:W:120:ILE:HG23	2.56	0.41
4:E:319:ILE:H	4:E:319:ILE:HG12	1.66	0.41
10:O:136:MET:O	10:O:140:ALA:CB	2.69	0.41
10:O:241:ASP:CG	10:O:268:GLN:HE21	2.28	0.41
12:R:58:PHE:HZ	12:R:71:GLN:HG3	1.86	0.41
12:R:72:TYR:HA	12:R:73:PRO:HD3	1.95	0.41
17:H:7:U:N3	17:H:8:C:C5	2.89	0.41
17:H:78:C:H2'	17:H:79:G:C8	2.56	0.41
17:H:112:G:O5'	17:H:112:G:H8	2.04	0.41
27:K:18:TYR:CB	27:K:168:LYS:HA	2.51	0.41
27:K:92:PRO:O	27:K:93:SER:C	2.64	0.41
31:o:160:LYS:O	31:o:161:MET:C	2.63	0.41
1:A:1132:LYS:HA	1:A:1139:ARG:HH12	1.85	0.41
1:A:1217:GLN:HA	1:A:1224:ARG:HA	2.02	0.41
4:E:219:VAL:HB	4:E:229:TYR:HB2	2.02	0.41
15:W:144:ASP:OD1	15:W:144:ASP:N	2.51	0.41
17:H:59:A:C6	17:H:60:U:C4	3.09	0.41
1:A:552:ARG:NH1	1:A:589:THR:O	2.54	0.40
1:A:1519:THR:O	1:A:1522:GLN:HB2	2.21	0.40
1:A:1876:LEU:HD12	1:A:1884:ILE:HD11	2.02	0.40
1:A:1947:ASN:O	1:A:1948:ASP:C	2.64	0.40
3:C:230:ASP:HB3	3:C:233:GLU:HB2	2.03	0.40
3:C:705:VAL:HG22	3:C:717:PHE:HE2	1.87	0.40
4:E:74:PHE:HE1	4:E:95:VAL:HG21	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:137:ASP:OD1	4:E:137:ASP:N	2.53	0.40
6:J:201:ARG:HB3	6:J:203:LEU:HD23	2.03	0.40
10:O:169:VAL:HA	15:W:216:LEU:HD13	2.03	0.40
10:O:221:PRO:CB	10:O:289:ASN:ND2	2.82	0.40
14:T:190:TRP:HE1	14:T:498:GLU:HB3	1.86	0.40
16:G:146:C:OP2	16:G:146:C:C3'	2.68	0.40
17:H:55:U:H2'	17:H:56:A:C8	2.53	0.40
17:H:168:A:H5'	17:H:169:C:H5	1.87	0.40
27:K:19:PHE:HB2	27:K:171:GLN:HB3	2.03	0.40
27:K:134:ALA:O	27:K:137:VAL:N	2.40	0.40
28:I:616:TYR:O	28:I:618:ARG:N	2.54	0.40
1:A:1048:MET:HE3	1:A:1048:MET:HB2	1.86	0.40
1:A:1513:MET:HE1	18:U:622:ALA:CB	2.48	0.40
1:A:1838:LYS:HG3	1:A:1868:MET:SD	2.62	0.40
1:A:1954:LEU:HD21	1:A:1983:LEU:HD11	2.02	0.40
2:B:95:G:C5	24:e:36:TYR:O	2.74	0.40
3:C:101:LYS:NZ	3:C:106:GLU:OE1	2.39	0.40
3:C:216:THR:HG22	3:C:220:ARG:HH12	1.86	0.40
3:C:778:PRO:HB3	3:C:817:TYR:HD1	1.85	0.40
5:F:49:G:H2'	5:F:50:A:C8	2.56	0.40
6:J:223:TYR:OH	7:L:248:ASP:OD1	2.39	0.40
16:G:5:G:C2	16:G:6:A:N6	2.89	0.40
16:G:146:C:C2'	16:G:147:C:C6	3.03	0.40
17:H:37:U:O2'	17:H:38:A:C8	2.67	0.40
22:d:62:HIS:O	22:d:103:GLY:HA3	2.21	0.40
28:I:606:TRP:O	28:I:609:ALA:HB3	2.21	0.40
23:m:5:LEU:O	24:l:49:GLY:HA3	2.21	0.40
1:A:170:ASP:HB3	1:A:173:GLU:HG3	2.03	0.40
1:A:963:GLN:HG3	1:A:1077:ILE:HG23	2.03	0.40
1:A:1248:LEU:O	1:A:1298:ARG:NH1	2.45	0.40
1:A:1403:LEU:HB3	18:U:780:MET:HE1	2.02	0.40
1:A:1556:ASP:OD1	1:A:1557:LEU:N	2.48	0.40
1:A:1781:ASP:HB3	1:A:1808:PHE:HB3	2.03	0.40
3:C:595:VAL:HG22	3:C:654:LYS:HG3	2.03	0.40
4:E:57:ALA:O	4:E:355:GLU:HG3	2.20	0.40
6:J:493:ALA:CB	6:J:499:ARG:CB	2.96	0.40
7:L:699:ASN:CB	27:K:114:LEU:HB2	2.51	0.40
9:N:37:HIS:HA	9:N:40:LYS:HE2	2.03	0.40
10:O:278:GLN:O	10:O:282:VAL:HG23	2.22	0.40
12:R:106:GLN:OE1	12:R:225:PRO:HG2	2.22	0.40
16:G:146:C:O2'	16:G:147:C:C5'	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:149:A:C2'	17:H:150:U:H5'	2.51	0.40
28:I:559:THR:CB	28:I:570:GLY:HA3	2.51	0.40
33:V:191:THR:HA	33:V:236:MET:O	2.21	0.40
1:A:165:ARG:NH2	1:A:168:PRO:O	2.55	0.40
1:A:312:TYR:OH	3:C:886:ASP:OD2	2.36	0.40
1:A:668:VAL:O	14:T:285:HIS:NE2	2.47	0.40
1:A:1615:HIS:HA	1:A:1616:PRO:HD3	1.97	0.40
1:A:1862:ILE:HG12	1:A:1885:LYS:HB3	2.02	0.40
2:B:67:A:O5'	2:B:68:C:N4	2.55	0.40
3:C:227:LEU:HD21	3:C:239:THR:HG23	2.03	0.40
4:E:68:GLU:HG2	4:E:347:SER:HB2	2.03	0.40
4:E:118:ASN:ND2	4:E:119:THR:N	2.53	0.40
4:E:162:ARG:HH21	4:E:204:THR:HA	1.82	0.40
5:F:34:G:C6	5:F:35:A:C5	3.10	0.40
7:L:11:TRP:HE1	7:L:133:GLU:HG3	1.85	0.40
10:O:175:ARG:HB2	10:O:179:CYS:HB2	2.04	0.40
16:G:9:C:C2'	16:G:10:U:C6	3.00	0.40
17:H:57:A:C6	17:H:58:U:C4	3.10	0.40
17:H:91:U:C2'	17:H:92:U:H5'	2.51	0.40
18:U:680:ASP:OD1	18:U:680:ASP:N	2.54	0.40
23:f:5:LEU:O	24:e:49:GLY:HA3	2.22	0.40
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.90	0.40
4:E:55:LEU:C	4:E:57:ALA:N	2.76	0.40
4:E:90:ILE:HD13	4:E:112:VAL:HG11	1.86	0.40
4:E:124:LEU:C	4:E:124:LEU:CD1	2.85	0.40
4:E:248:SER:HB2	4:E:249:TYR:HD1	1.78	0.40
4:E:260:ARG:CZ	4:E:276:ILE:HD11	2.51	0.40
5:F:44:G:C6	16:G:2:U:O4	2.75	0.40
5:F:44:G:N7	16:G:1:G:N1	2.69	0.40
5:F:57:U:H2'	5:F:58:G:C8	2.55	0.40
6:J:196:ARG:HA	8:M:208:ILE:HD11	2.04	0.40
7:L:696:LEU:HA	27:K:110:SER:HB2	2.02	0.40
7:L:696:LEU:CA	27:K:110:SER:OG	2.67	0.40
10:O:44:GLU:HA	10:O:51:PRO:HA	2.04	0.40
10:O:56:ARG:HD2	10:O:67:LYS:HE2	2.04	0.40
10:O:107:MET:HA	10:O:108:PRO:HD3	1.98	0.40
10:O:223:LEU:HB3	10:O:288:PHE:HB2	2.02	0.40
17:H:153:A:H3'	17:H:154:C:H5'	1.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1977/2335 (85%)	1799 (91%)	160 (8%)	18 (1%)	14	28
3	C	886/972 (91%)	799 (90%)	84 (10%)	3 (0%)	36	54
4	E	301/357 (84%)	268 (89%)	22 (7%)	11 (4%)	2	5
6	J	536/848 (63%)	495 (92%)	37 (7%)	4 (1%)	18	35
7	L	459/802 (57%)	421 (92%)	33 (7%)	5 (1%)	11	24
8	M	128/243 (53%)	115 (90%)	13 (10%)	0	100	100
9	N	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
10	O	288/420 (69%)	262 (91%)	24 (8%)	2 (1%)	18	35
11	P	114/229 (50%)	96 (84%)	17 (15%)	1 (1%)	14	28
12	R	268/536 (50%)	234 (87%)	30 (11%)	4 (2%)	8	18
13	S	157/166 (95%)	141 (90%)	16 (10%)	0	100	100
14	T	315/514 (61%)	297 (94%)	16 (5%)	2 (1%)	21	38
15	W	156/579 (27%)	134 (86%)	18 (12%)	4 (3%)	4	9
18	U	343/894 (38%)	289 (84%)	49 (14%)	5 (2%)	8	18
19	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
19	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
20	b	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
20	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
21	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
21	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
22	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
22	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
23	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
23	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
24	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
25	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
25	n	63/76 (83%)	61 (97%)	2 (3%)	0	100	100
26	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	3	7
26	r	129/504 (26%)	119 (92%)	8 (6%)	2 (2%)	7	17
26	s	65/504 (13%)	62 (95%)	2 (3%)	1 (2%)	8	18
26	t	65/504 (13%)	64 (98%)	0	1 (2%)	8	18
27	K	144/225 (64%)	130 (90%)	7 (5%)	7 (5%)	1	3
28	I	538/855 (63%)	501 (93%)	25 (5%)	12 (2%)	5	12
29	Q	1304/1485 (88%)	1278 (98%)	25 (2%)	1 (0%)	48	68
30	y	77/301 (26%)	74 (96%)	3 (4%)	0	100	100
31	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	21
32	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
33	V	661/795 (83%)	614 (93%)	40 (6%)	7 (1%)	11	24
All	All	10524/16892 (62%)	9733 (92%)	695 (7%)	96 (1%)	16	28

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1306	LYS
1	A	1519	THR
1	A	1639	VAL
1	A	1653	ASP
1	A	1948	ASP
4	E	56	GLN
4	E	58	PRO
4	E	59	ILE
4	E	112	VAL
4	E	193	THR
7	L	118	ASP
10	O	259	ARG
12	R	190	SER
18	U	613	ASN
18	U	793	ASP
26	q	59	HIS
26	q	60	PRO
26	s	71	ILE

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Mol	Chain	Res	Type
26	t	69	THR
27	K	78	PRO
27	K	90	PRO
27	K	136	LYS
28	I	239	ASN
28	I	404	PHE
28	I	424	VAL
28	I	464	ALA
28	I	721	LYS
33	V	376	LEU
1	A	136	ILE
1	A	626	GLY
1	A	803	ALA
1	A	1305	SER
1	A	1367	ASN
1	A	1654	SER
6	J	592	ALA
6	J	709	VAL
7	L	765	ARG
12	R	52	PRO
14	T	406	ILE
18	U	579	VAL
26	q	9	ASN
26	r	9	ASN
27	K	135	TRP
27	K	172	LEU
28	I	546	SER
28	I	618	ARG
28	I	634	ILE
29	Q	346	PRO
31	o	160	LYS
33	V	422	ASN
33	V	490	TYR
1	A	625	PRO
1	A	1366	PRO
3	C	94	ILE
11	P	205	LYS
12	R	53	ARG
12	R	235	ARG
26	q	19	PRO
28	I	601	GLN
33	V	300	PHE

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Mol	Chain	Res	Type
33	V	395	GLN
1	A	187	PRO
1	A	1251	SER
1	A	1419	ILE
3	C	138	LEU
3	C	163	GLN
4	E	61	LEU
4	E	143	ARG
4	E	159	PRO
4	E	162	ARG
4	E	324	PRO
7	L	585	TYR
15	W	148	VAL
18	U	845	PHE
27	K	65	ILE
28	I	617	GLU
31	o	32	PRO
1	A	1365	ILE
6	J	241	VAL
6	J	341	PRO
10	O	20	PHE
15	W	77	LYS
15	W	205	VAL
15	W	208	PRO
18	U	792	SER
28	I	796	LEU
1	A	108	MET
7	L	763	ILE
7	L	764	PRO
14	T	343	PRO
27	K	17	PRO
28	I	321	GLU
33	V	184	PRO
4	E	319	ILE
33	V	369	ILE
26	r	60	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1792/2108 (85%)	1761 (98%)	31 (2%)	53	75
3	C	787/866 (91%)	771 (98%)	16 (2%)	48	71
4	E	259/300 (86%)	204 (79%)	55 (21%)	1	1
6	J	242/751 (32%)	241 (100%)	1 (0%)	84	92
7	L	248/709 (35%)	233 (94%)	15 (6%)	17	36
8	M	117/209 (56%)	116 (99%)	1 (1%)	70	84
9	N	130/130 (100%)	128 (98%)	2 (2%)	57	77
10	O	259/361 (72%)	240 (93%)	19 (7%)	13	27
11	P	104/203 (51%)	104 (100%)	0	100	100
12	R	227/457 (50%)	222 (98%)	5 (2%)	45	69
13	S	129/134 (96%)	128 (99%)	1 (1%)	73	86
14	T	273/441 (62%)	273 (100%)	0	100	100
15	W	135/502 (27%)	130 (96%)	5 (4%)	30	55
18	U	313/806 (39%)	297 (95%)	16 (5%)	21	43
27	K	54/196 (28%)	41 (76%)	13 (24%)	1	0
28	I	12/749 (2%)	5 (42%)	7 (58%)	0	0
All	All	5081/8922 (57%)	4894 (96%)	187 (4%)	31	55

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	188	LEU
1	A	240	ARG
1	A	273	ILE
1	A	668	VAL
1	A	888	GLN
1	A	1109	LEU
1	A	1216	LEU
1	A	1295	ILE
1	A	1438	VAL
1	A	1510	GLU
1	A	1512	SER
1	A	1513	MET
1	A	1515	TRP
1	A	1516	LYS

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Mol	Chain	Res	Type
1	A	1517	LYS
1	A	1518	LEU
1	A	1522	GLN
1	A	1555	LEU
1	A	1593	LEU
1	A	1649	LYS
1	A	1825	SER
1	A	1826	VAL
1	A	1831	LYS
1	A	1832	ARG
1	A	1833	LEU
1	A	1835	GLN
1	A	1836	LEU
1	A	1838	LYS
1	A	1927	ILE
1	A	1945	VAL
1	A	1946	ASN
3	C	115	GLU
3	C	116	MET
3	C	117	ASP
3	C	128	LEU
3	C	135	CYS
3	C	138	LEU
3	C	139	HIS
3	C	160	ARG
3	C	161	TYR
3	C	163	GLN
3	C	190	LEU
3	C	221	ILE
3	C	536	ARG
3	C	537	TYR
3	C	629	ILE
3	C	832	TYR
4	E	55	LEU
4	E	59	ILE
4	E	60	MET
4	E	61	LEU
4	E	62	LEU
4	E	65	HIS
4	E	66	GLU
4	E	72	CYS
4	E	79	SER

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Mol	Chain	Res	Type
4	E	80	THR
4	E	81	LEU
4	E	87	ASP
4	E	90	ILE
4	E	93	TRP
4	E	99	CYS
4	E	101	ASN
4	E	102	TYR
4	E	104	THR
4	E	106	LYS
4	E	108	HIS
4	E	109	SER
4	E	113	MET
4	E	117	TYR
4	E	124	LEU
4	E	125	PHE
4	E	129	THR
4	E	130	ASP
4	E	132	THR
4	E	136	TRP
4	E	139	GLU
4	E	142	GLU
4	E	143	ARG
4	E	144	VAL
4	E	145	LYS
4	E	147	LEU
4	E	148	LYS
4	E	153	PHE
4	E	161	ARG
4	E	178	LEU
4	E	243	LEU
4	E	248	SER
4	E	250	LEU
4	E	258	THR
4	E	260	ARG
4	E	265	ARG
4	E	270	LYS
4	E	271	GLU
4	E	273	CYS
4	E	289	LEU
4	E	290	ARG
4	E	307	ARG

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Mol	Chain	Res	Type
4	E	317	ARG
4	E	318	ARG
4	E	319	ILE
4	E	326	HIS
6	J	591	LEU
7	L	123	LEU
7	L	250	GLU
7	L	251	LEU
7	L	252	ARG
7	L	255	LYS
7	L	260	ARG
7	L	261	LYS
7	L	262	LYS
7	L	264	LYS
7	L	270	LYS
7	L	731	LEU
7	L	733	LYS
7	L	755	LEU
7	L	761	SER
7	L	781	GLU
8	M	212	ASN
9	N	49	ILE
9	N	60	ILE
10	O	78	LYS
10	O	218	SER
10	O	219	THR
10	O	220	MET
10	O	222	ARG
10	O	223	LEU
10	O	227	GLU
10	O	229	LYS
10	O	242	THR
10	O	243	ILE
10	O	244	THR
10	O	246	THR
10	O	247	ASP
10	O	248	LEU
10	O	257	GLU
10	O	258	ILE
10	O	260	THR
10	O	287	SER
10	O	294	ASN

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Mol	Chain	Res	Type
12	R	111	VAL
12	R	183	GLN
12	R	189	ASN
12	R	190	SER
12	R	281	ASN
13	S	102	ASN
15	W	76	VAL
15	W	145	ASN
15	W	148	VAL
15	W	149	SER
15	W	193	LEU
18	U	539	GLU
18	U	624	LYS
18	U	626	MET
18	U	652	GLU
18	U	655	GLU
18	U	657	GLN
18	U	658	ARG
18	U	662	ILE
18	U	664	GLU
18	U	667	SER
18	U	668	LEU
18	U	671	GLN
18	U	672	MET
18	U	808	LYS
18	U	809	ASP
18	U	810	ILE
27	K	38	GLU
27	K	90	PRO
27	K	115	GLU
27	K	117	GLN
27	K	119	VAL
27	K	120	ARG
27	K	126	LEU
27	K	130	HIS
27	K	147	GLU
27	K	161	GLN
27	K	168	LYS
27	K	171	GLN
27	K	173	THR
28	I	384	THR
28	I	385	VAL

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Mol	Chain	Res	Type
28	I	399	VAL
28	I	486	VAL
28	I	526	MET
28	I	545	ILE
28	I	795	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (112) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	HIS
1	A	328	HIS
1	A	361	HIS
1	A	368	GLN
1	A	675	GLN
1	A	723	ASN
1	A	775	ASN
1	A	860	GLN
1	A	884	HIS
1	A	888	GLN
1	A	1023	ASN
1	A	1042	GLN
1	A	1124	ASN
1	A	1148	ASN
1	A	1188	ASN
1	A	1238	GLN
1	A	1241	HIS
1	A	1293	ASN
1	A	1296	GLN
1	A	1337	GLN
1	A	1363	GLN
1	A	1373	GLN
1	A	1487	HIS
1	A	1522	GLN
1	A	1527	ASN
1	A	1531	ASN
1	A	1580	HIS
1	A	1658	GLN
1	A	1784	ASN
1	A	1811	ASN
1	A	1816	GLN
1	A	1835	GLN
1	A	1894	GLN

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Mol	Chain	Res	Type
1	A	1918	ASN
1	A	1946	ASN
3	C	60	HIS
3	C	87	GLN
3	C	154	HIS
3	C	163	GLN
3	C	175	GLN
3	C	238	ASN
3	C	245	HIS
3	C	437	HIS
3	C	451	HIS
3	C	513	ASN
3	C	523	GLN
3	C	538	HIS
3	C	627	HIS
3	C	837	GLN
4	E	101	ASN
4	E	108	HIS
4	E	116	HIS
4	E	118	ASN
4	E	165	GLN
4	E	188	GLN
4	E	225	ASN
6	J	244	ASN
6	J	250	GLN
6	J	275	ASN
6	J	311	GLN
6	J	331	GLN
6	J	344	GLN
6	J	347	HIS
6	J	389	HIS
6	J	394	HIS
6	J	410	HIS
7	L	13	ASN
7	L	30	GLN
7	L	233	GLN
7	L	244	GLN
8	M	134	GLN
8	M	136	HIS
8	M	172	HIS
8	M	212	ASN
9	N	87	ASN

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Mol	Chain	Res	Type
9	N	99	ASN
9	N	116	ASN
9	N	136	HIS
10	O	79	ASN
10	O	113	ASN
10	O	254	GLN
10	O	268	GLN
11	P	75	ASN
11	P	212	ASN
12	R	133	GLN
12	R	184	GLN
12	R	203	GLN
12	R	276	GLN
12	R	279	HIS
12	R	281	ASN
12	R	307	GLN
13	S	10	GLN
13	S	38	ASN
13	S	102	ASN
13	S	108	ASN
14	T	216	ASN
14	T	217	GLN
14	T	324	HIS
14	T	407	GLN
14	T	446	ASN
15	W	102	GLN
15	W	103	GLN
15	W	128	GLN
15	W	145	ASN
18	U	605	ASN
18	U	615	ASN
18	U	702	ASN
18	U	717	GLN
18	U	718	HIS
18	U	757	ASN
18	U	765	HIS
18	U	828	HIS

5.3.3 RNA ⓘ

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	G	67/272 (24%)	55 (82%)	14 (20%)
17	H	129/188 (68%)	53 (41%)	2 (1%)
2	B	97/117 (82%)	57 (58%)	4 (4%)
5	F	96/107 (89%)	43 (44%)	7 (7%)
All	All	389/684 (56%)	208 (53%)	27 (6%)

All (208) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	8	G
2	B	9	G
2	B	10	U
2	B	11	U
2	B	12	U
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G
2	B	25	C
2	B	26	A
2	B	27	U
2	B	28	A
2	B	33	U
2	B	34	U
2	B	35	U
2	B	36	C
2	B	37	G
2	B	38	C
2	B	39	C
2	B	40	U
2	B	45	C
2	B	47	A
2	B	48	A
2	B	52	U
2	B	53	U
2	B	67	A
2	B	68	C
2	B	69	A
2	B	70	A

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Mol	Chain	Res	Type
2	B	71	C
2	B	72	U
2	B	73	C
2	B	74	U
2	B	75	G
2	B	76	A
2	B	77	G
2	B	78	U
2	B	79	C
2	B	80	U
2	B	81	U
2	B	82	A
2	B	83	A
2	B	84	C
2	B	85	C
2	B	86	C
2	B	87	A
2	B	88	A
2	B	89	U
2	B	90	U
2	B	91	U
2	B	92	U
2	B	94	U
2	B	95	G
2	B	96	A
5	F	5	U
5	F	6	C
5	F	7	G
5	F	9	U
5	F	10	U
5	F	12	G
5	F	22	A
5	F	25	C
5	F	26	U
5	F	27	A
5	F	28	A
5	F	29	A
5	F	33	G
5	F	34	G
5	F	35	A
5	F	36	A
5	F	37	C

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Mol	Chain	Res	Type
5	F	41	A
5	F	42	C
5	F	43	A
5	F	44	G
5	F	45	A
5	F	46	G
5	F	48	A
5	F	51	U
5	F	53	A
5	F	54	G
5	F	56	A
5	F	59	G
5	F	60	C
5	F	61	C
5	F	66	C
5	F	68	C
5	F	69	A
5	F	74	U
5	F	78	A
5	F	79	C
5	F	81	C
5	F	82	A
5	F	83	A
5	F	84	A
5	F	87	C
5	F	91	A
16	G	2	U
16	G	3	A
16	G	4	A
16	G	6	A
16	G	7	G
16	G	8	C
16	G	9	C
16	G	11	A
16	G	12	G
16	G	17	U
16	G	20	A
16	G	21	A
16	G	22	C
16	G	23	U
16	G	24	G
16	G	25	G

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Mol	Chain	Res	Type
16	G	26	U
16	G	27	U
16	G	28	A
16	G	29	C
16	G	30	C
16	G	119	G
16	G	120	G
16	G	121	G
16	G	122	U
16	G	123	U
16	G	125	C
16	G	127	U
16	G	128	U
16	G	129	G
16	G	130	A
16	G	131	U
16	G	132	G
16	G	133	A
16	G	134	U
16	G	135	G
16	G	136	U
16	G	137	C
16	G	138	A
16	G	139	U
16	G	140	A
16	G	141	C
16	G	142	U
16	G	143	U
16	G	144	A
16	G	145	U
16	G	146	C
16	G	147	C
16	G	148	U
16	G	149	G
16	G	150	U
16	G	151	C
16	G	152	C
16	G	154	U
16	G	155	U
17	H	8	C
17	H	14	C
17	H	15	U

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Mol	Chain	Res	Type
17	H	16	U
17	H	19	G
17	H	20	G
17	H	24	A
17	H	28	C
17	H	29	A
17	H	30	A
17	H	31	G
17	H	32	U
17	H	33	G
17	H	34	U
17	H	35	A
17	H	36	G
17	H	37	U
17	H	38	A
17	H	39	U
17	H	40	C
17	H	41	U
17	H	42	G
17	H	43	U
17	H	44	U
17	H	45	C
17	H	46	U
17	H	47	U
17	H	69	U
17	H	74	U
17	H	79	G
17	H	81	G
17	H	83	A
17	H	92	U
17	H	94	A
17	H	98	G
17	H	106	G
17	H	107	A
17	H	109	C
17	H	112	G
17	H	114	A
17	H	150	U
17	H	154	C
17	H	157	G
17	H	164	C
17	H	165	A

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Mol	Chain	Res	Type
17	H	166	G
17	H	167	U
17	H	168	A
17	H	169	C
17	H	177	A
17	H	178	A
17	H	179	C
17	H	182	U

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	78	U
2	B	79	C
2	B	92	U
2	B	95	G
5	F	5	U
5	F	33	G
5	F	35	A
5	F	50	A
5	F	58	G
5	F	81	C
5	F	82	A
16	G	1	G
16	G	2	U
16	G	3	A
16	G	7	G
16	G	8	C
16	G	16	G
16	G	21	A
16	G	22	C
16	G	134	U
16	G	142	U
16	G	143	U
16	G	144	A
16	G	145	U
16	G	150	U
17	H	7	U
17	H	28	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
12	SEP	R	224	12	8,9,10	0.86	0	7,12,14	1.05	0
12	SEP	R	232	12	8,9,10	1.01	0	7,12,14	2.04	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	SEP	R	224	12	-	0/6/8/10	-
12	SEP	R	232	12	-	2/6/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

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

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 2 short contacts:

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
35	GTP	C	1500	36	33,34,34	1.14	4 (12%)	50,54,54	1.71	7 (14%)
34	IHP	A	3000	-	36,36,36	0.72	0	60,60,60	0.99	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	GTP	C	1500	36	-	4/22/38/38	0/3/3/3
34	IHP	A	3000	-	-	0/30/54/54	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	C	1500	GTP	C6-N1	-2.89	1.33	1.38
35	C	1500	GTP	C5-C4	2.68	1.46	1.38
35	C	1500	GTP	C5-N7	-2.40	1.34	1.39
35	C	1500	GTP	C4-N9	-2.06	1.32	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	C	1500	GTP	C5-C4-N3	-6.08	118.72	128.39
35	C	1500	GTP	C2-N3-C4	4.97	120.87	112.30
35	C	1500	GTP	N9-C4-N3	4.65	135.25	125.95
35	C	1500	GTP	C6-C5-N7	3.16	136.03	130.29
35	C	1500	GTP	O6-C6-C5	-2.56	119.78	126.53
35	C	1500	GTP	C4-C5-N7	-2.36	106.92	110.67
35	C	1500	GTP	C5-C6-N1	2.12	118.65	113.25

There are no chirality outliers.

All (4) torsion outliers are listed below:

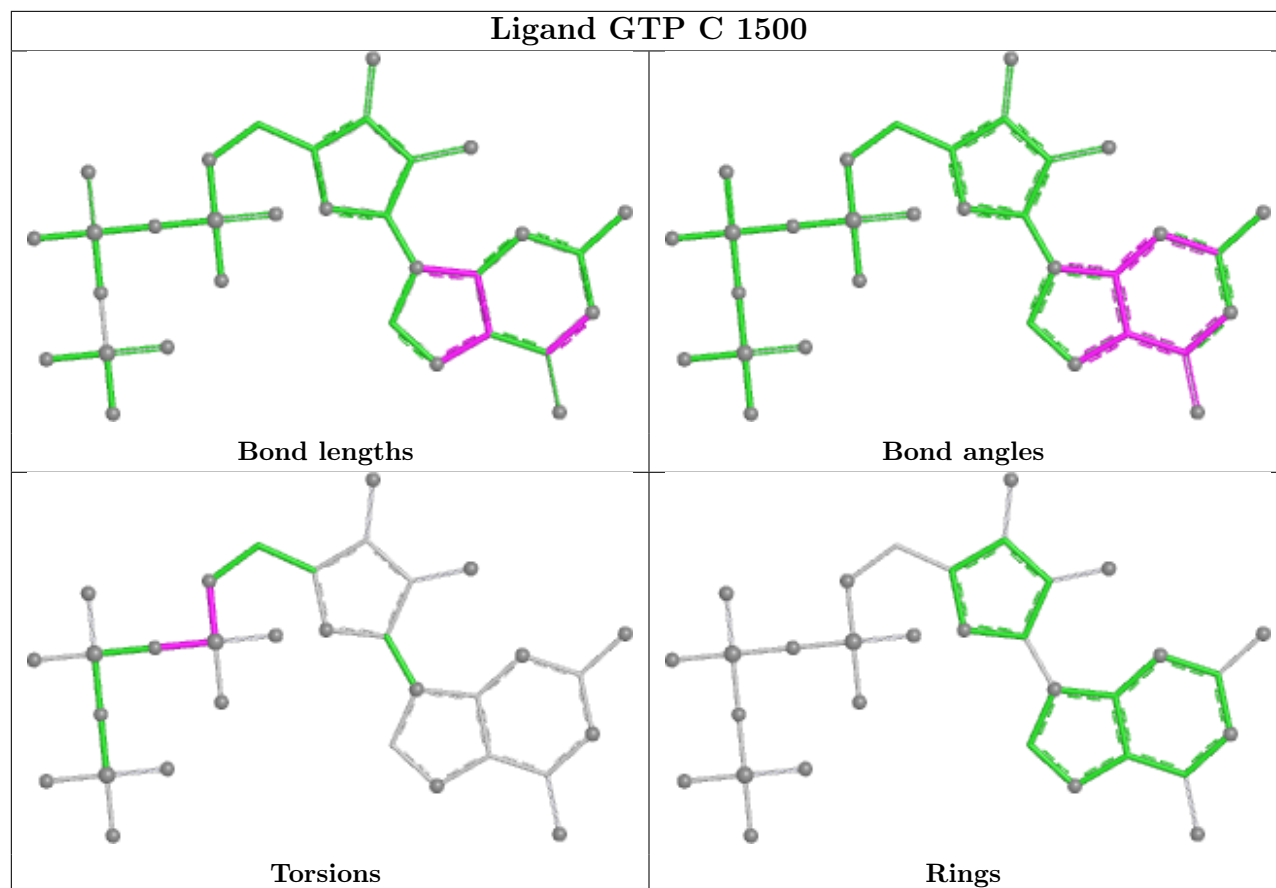
Mol	Chain	Res	Type	Atoms
35	C	1500	GTP	C5'-O5'-PA-O1A
35	C	1500	GTP	C5'-O5'-PA-O2A
35	C	1500	GTP	C5'-O5'-PA-O3A
35	C	1500	GTP	PB-O3A-PA-O2A

There are no ring outliers.

2 monomers are involved in 11 short contacts:

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

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

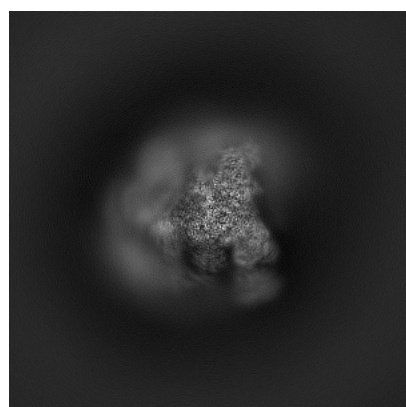
6 Map visualisation [i](#)

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

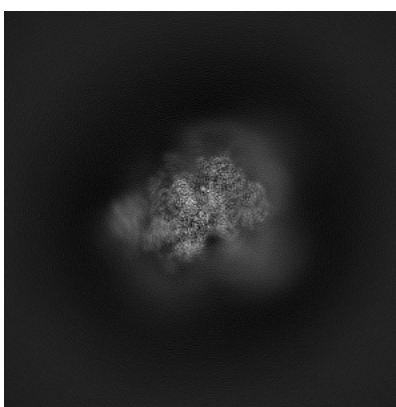
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

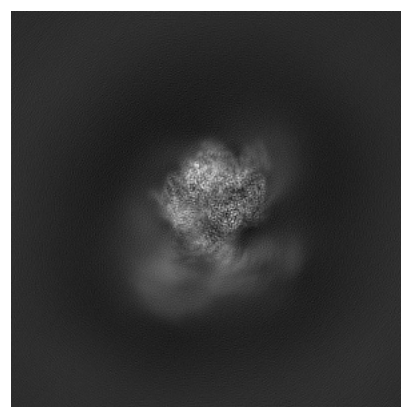
6.1.1 Primary map



X



Y

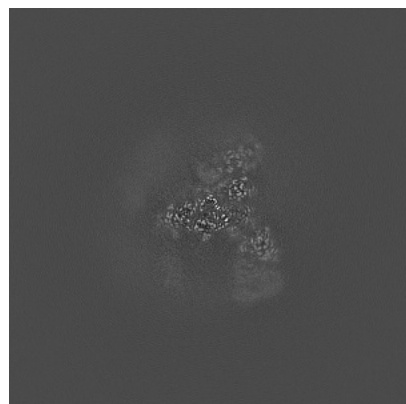


Z

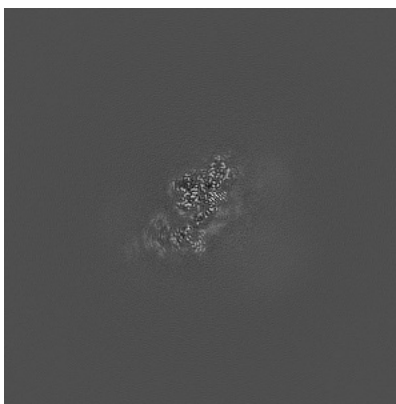
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

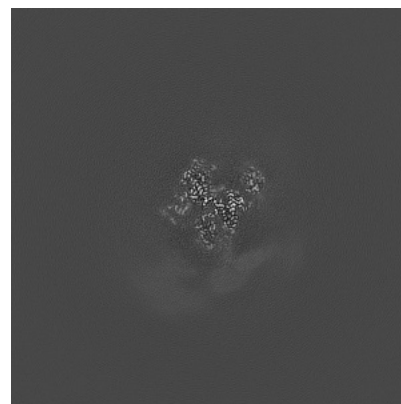
6.2.1 Primary map



X Index: 200



Y Index: 200

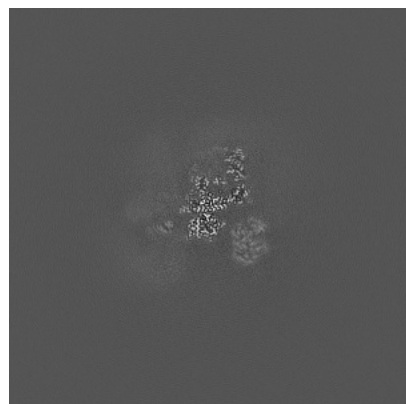


Z Index: 200

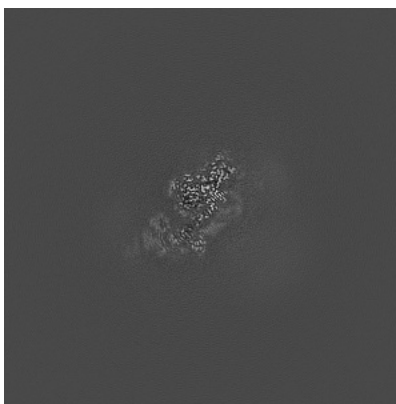
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

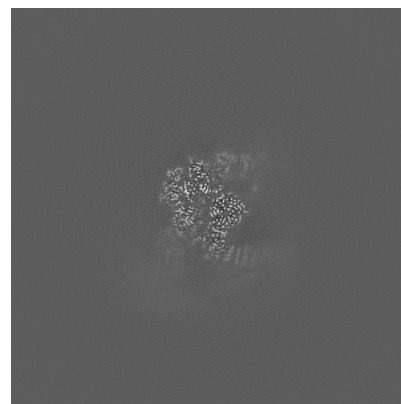
6.3.1 Primary map



X Index: 221



Y Index: 201

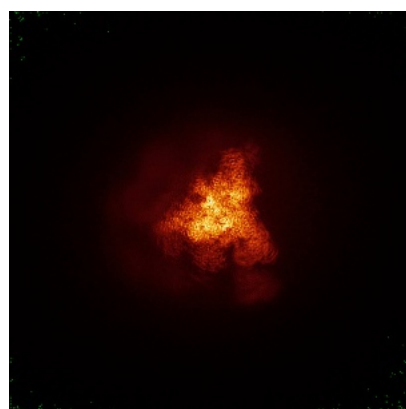


Z Index: 185

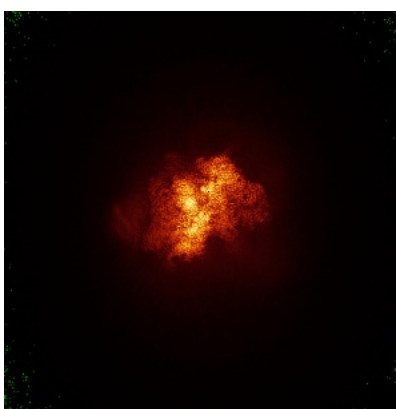
The images above show the largest variance slices of the map in three orthogonal directions.

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

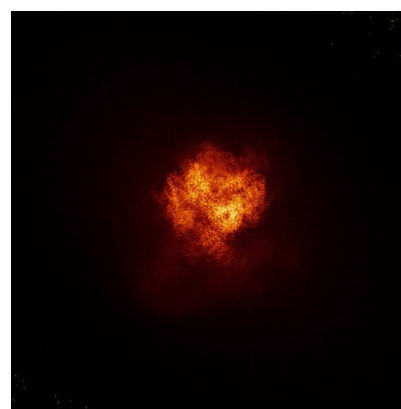
6.4.1 Primary map



X



Y

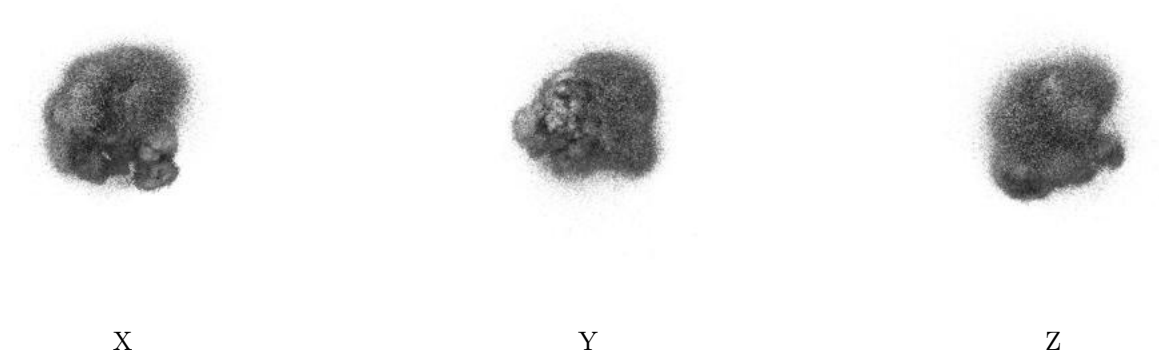


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

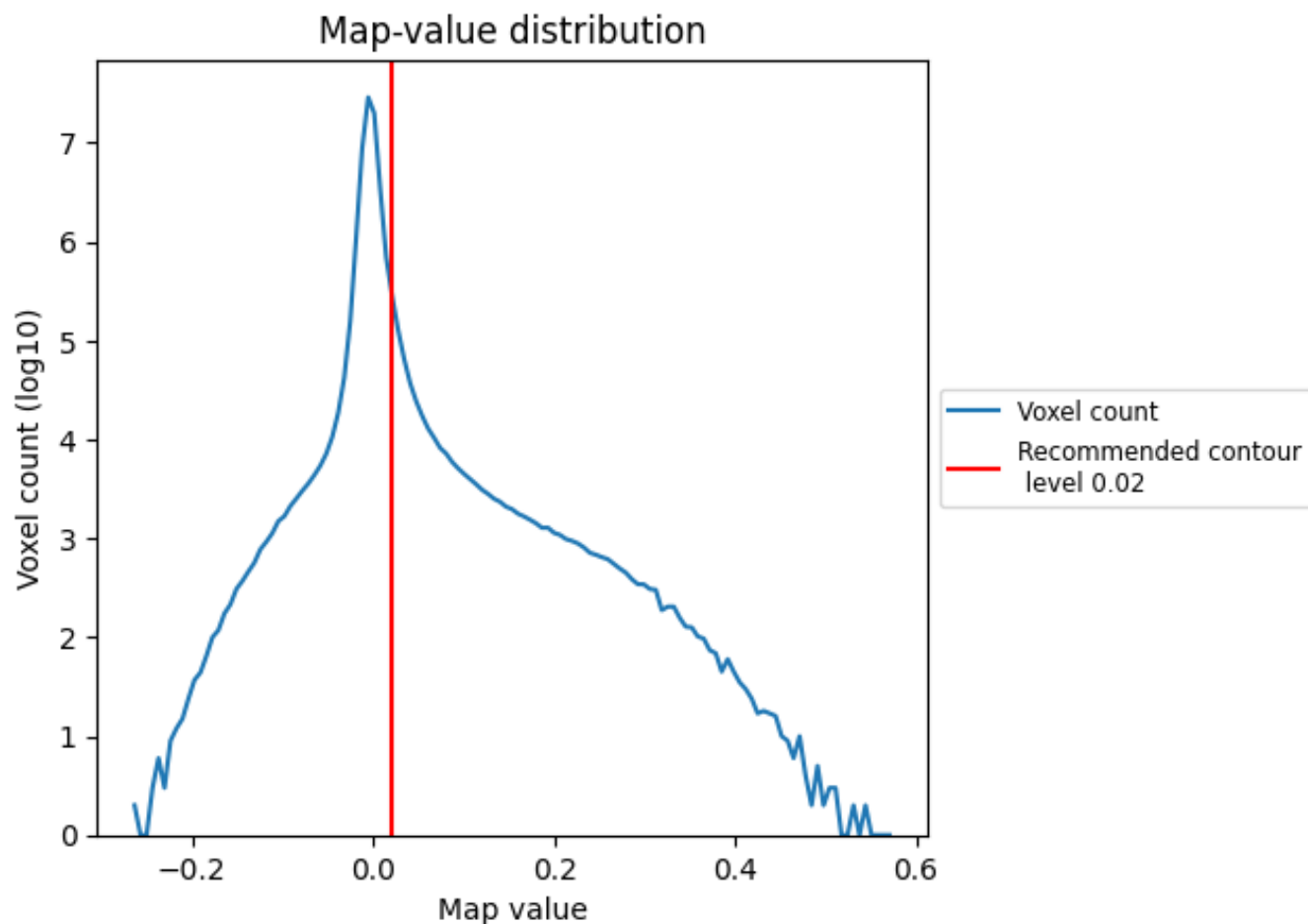
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

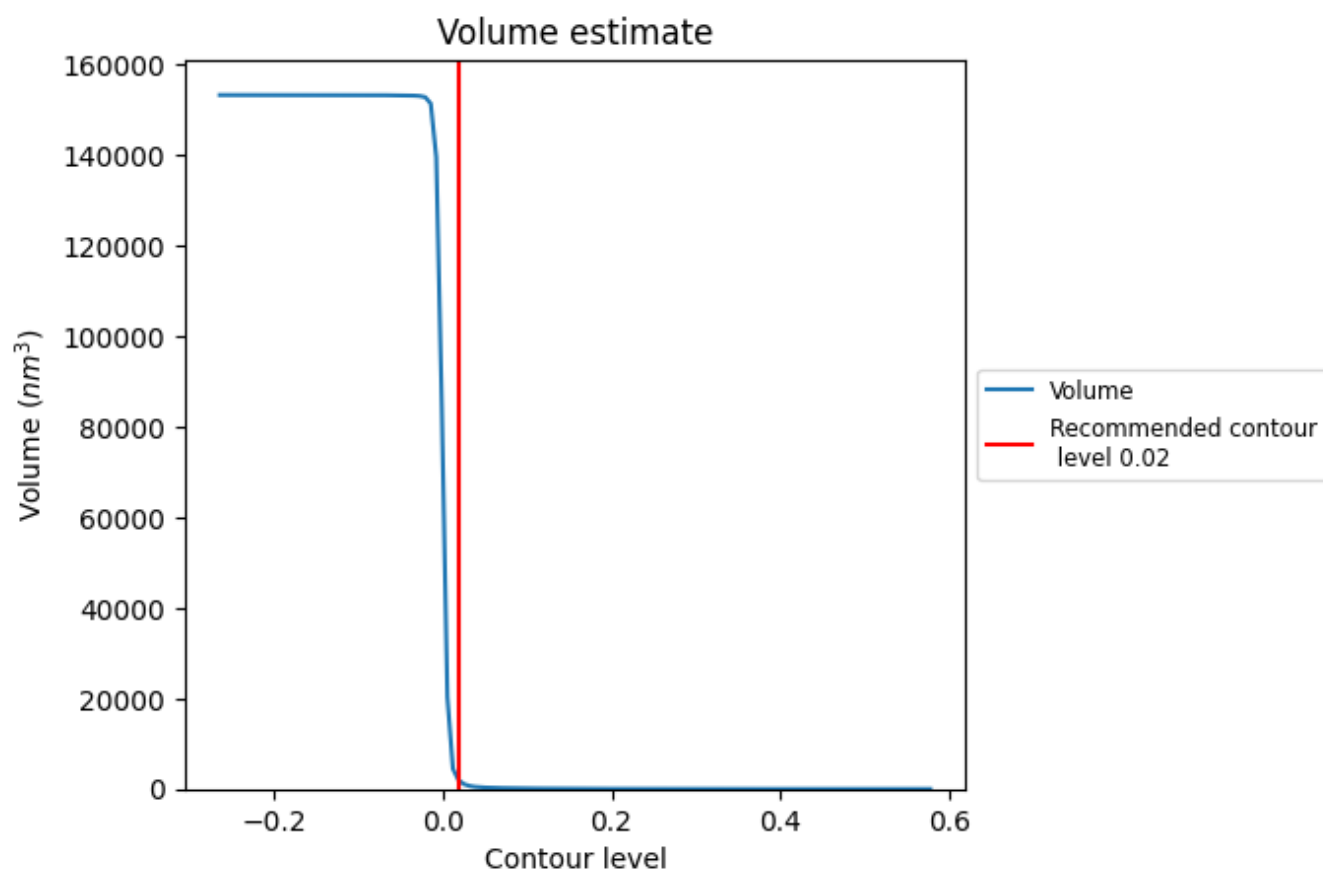
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

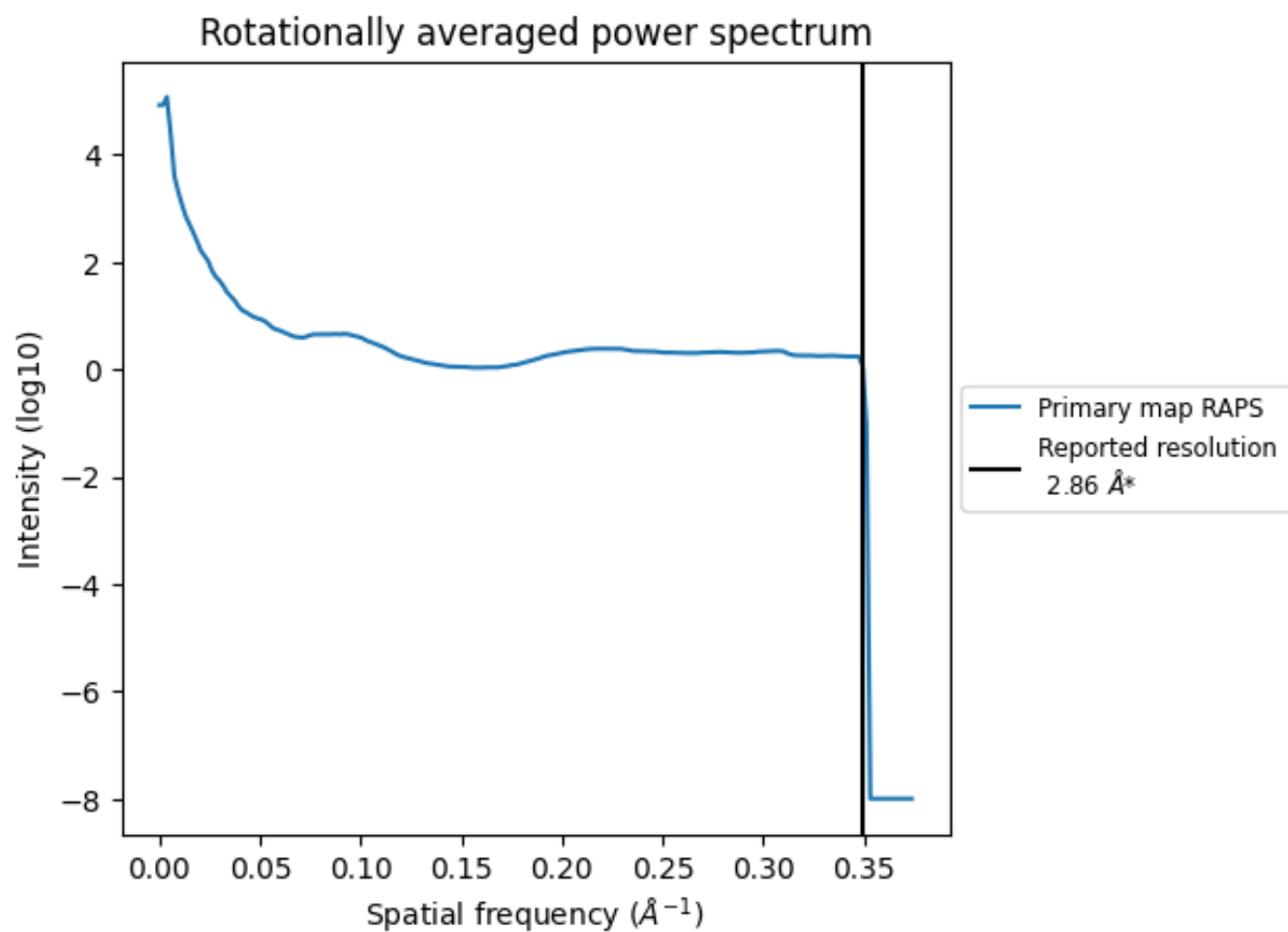
7.2 Volume estimate [i](#)



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

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

7.3 Rotationally averaged power spectrum ⓘ



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

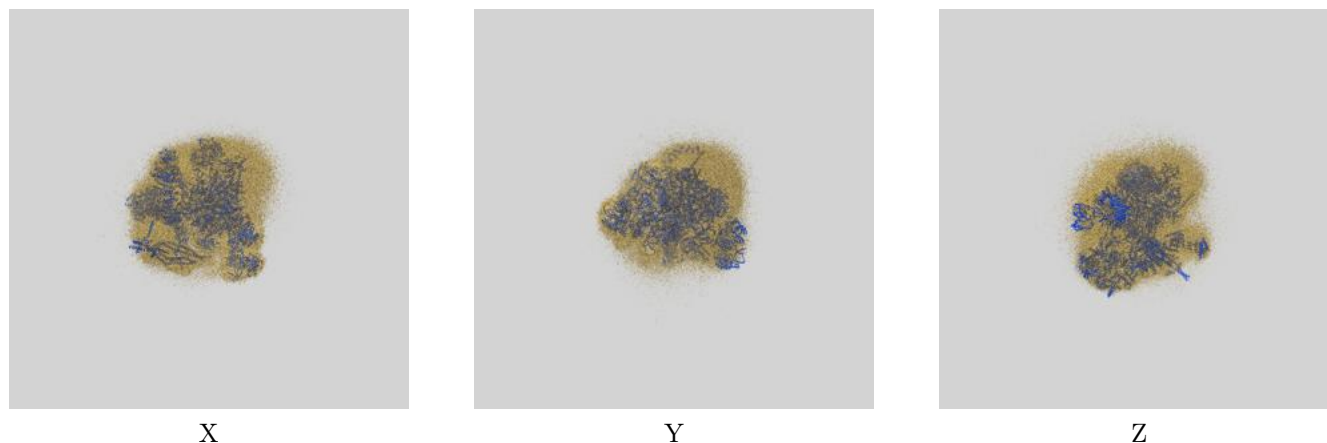
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

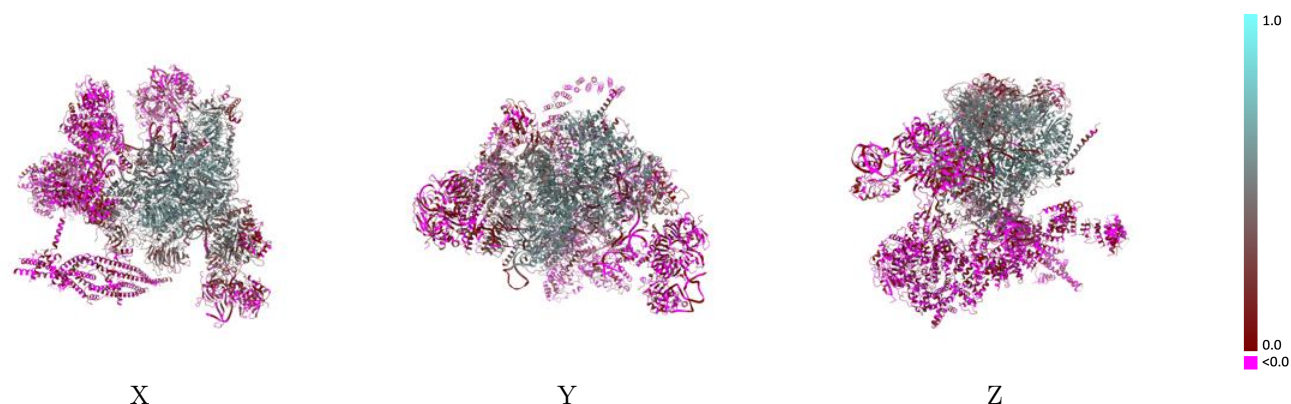
This section contains information regarding the fit between EMDB map EMD-9647 and PDB model 6ID1. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



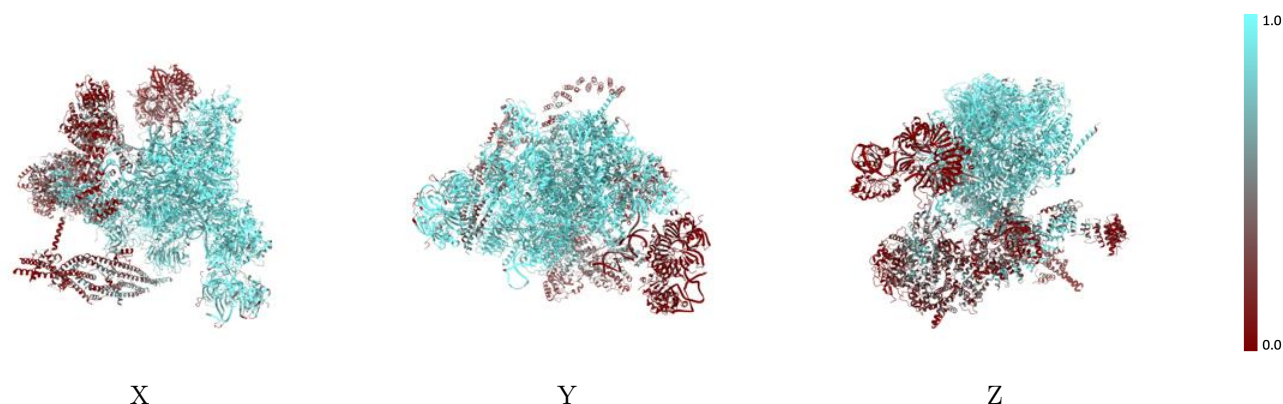
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



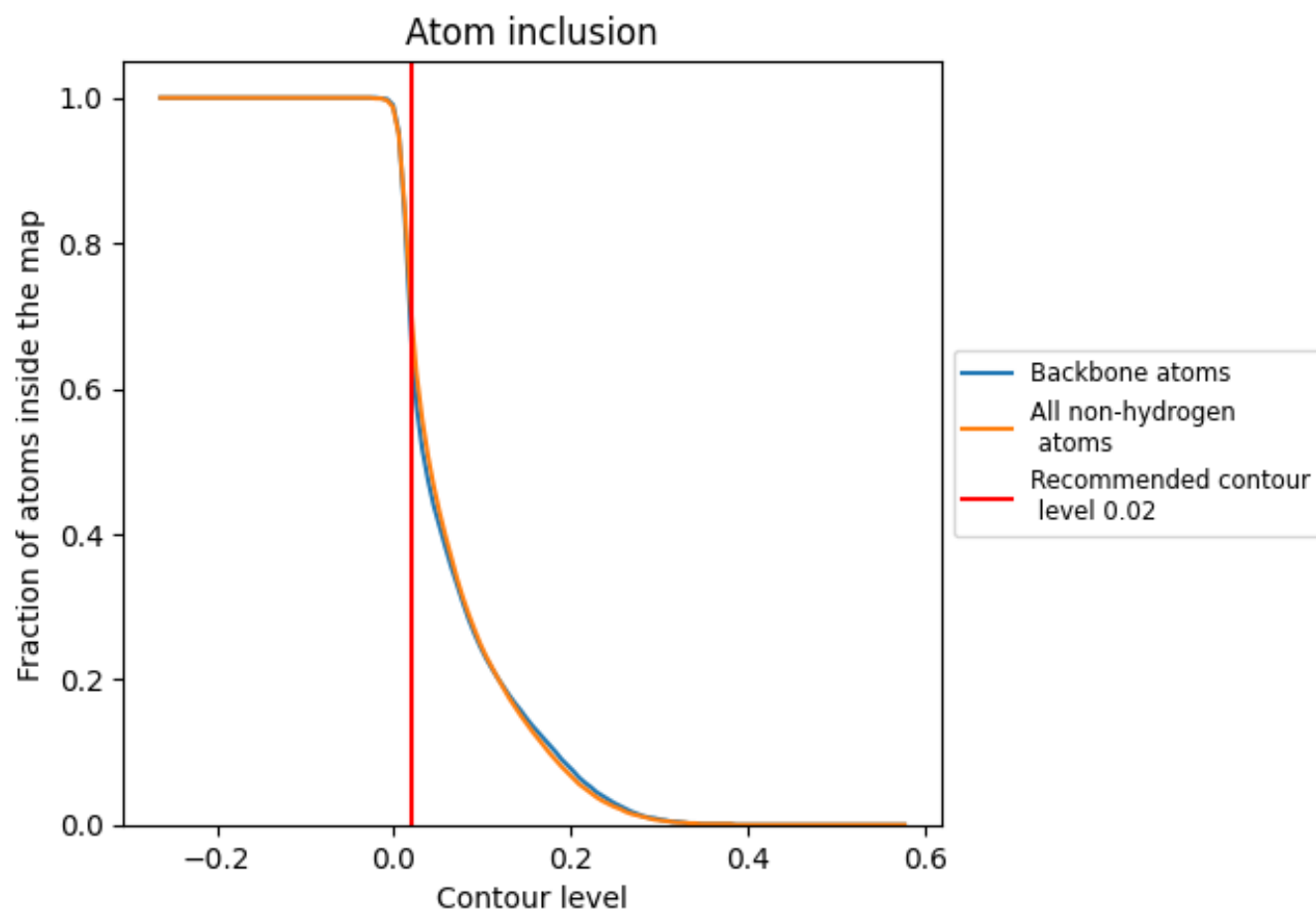
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion ⓘ



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

9.5 Map-model fit summary

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

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



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