



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 12:31 PM UTC

PDB ID : 6J6Q / pdb_00006j6q
EMDB ID : EMD-0692
Title : Cryo-EM structure of the yeast B*-b2 complex at an average resolution of 3.7 angstrom
Authors : Wan, R.; Bai, R.; Yan, C.; Lei, J.; Shi, Y.
Deposited on : 2019-01-15
Resolution : 3.70 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

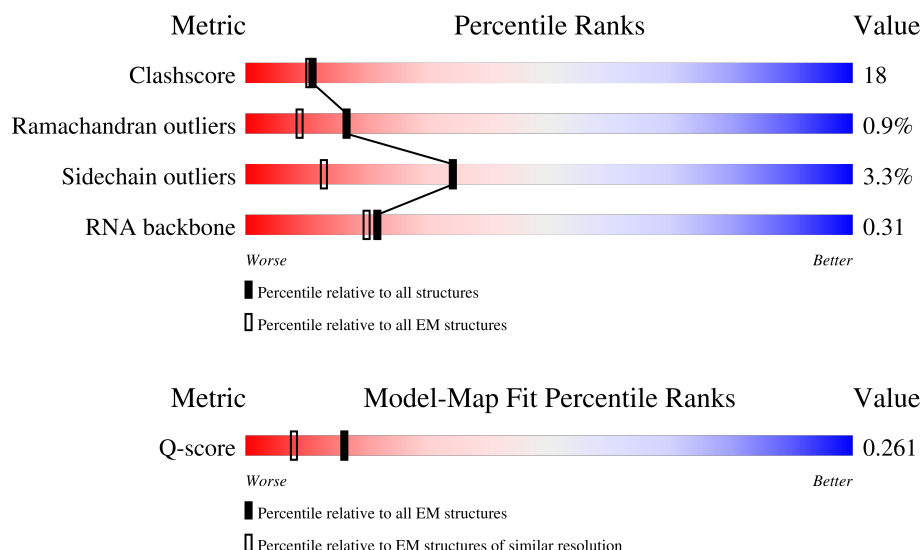
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



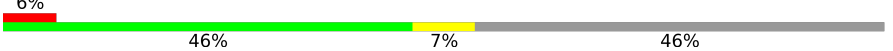
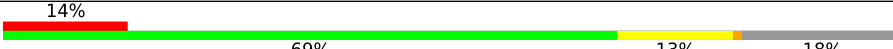
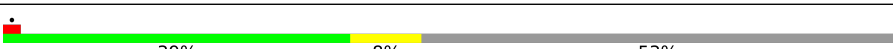
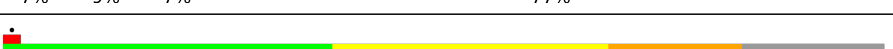
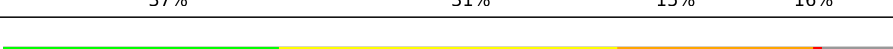
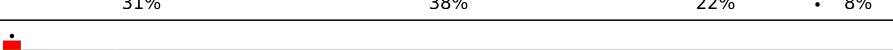
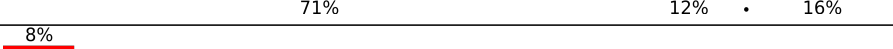
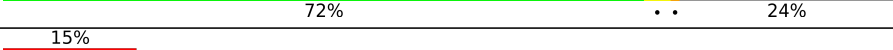
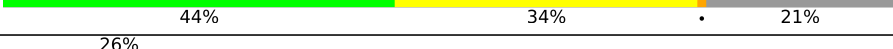
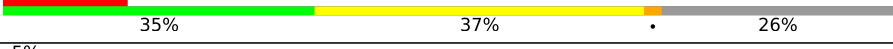
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	2413	
2	C	1008	
3	J	135	

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Mol	Chain	Length	Quality of chain
4	O	451	
5	P	379	
6	Q	364	
7	R	339	
8	S	175	
9	T	157	
10	Z	577	
11	c	590	
12	d	687	
13	I	215	
14	n	455	
15	H	235	
16	B	246	
17	D	214	
18	E	112	
19	L	1175	
20	v	859	
21	a	111	
22	b	238	
23	t	175	
24	i	94	
24	u	94	
25	m	146	
25	z	146	
26	j	77	

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Mol	Chain	Length	Quality of chain
26	x	77	
27	h	86	
27	w	86	
28	e	110	
28	g	110	
29	k	196	
29	s	196	
30	l	101	
30	y	101	
31	o	503	
31	p	503	
31	q	503	
31	r	503	
32	F	278	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 80535 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-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1913	Total	C	N	O	S	0	0
			15793	10154	2714	2868	57		

- Molecule 2 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	920	Total	C	N	O	S	0	0
			7348	4733	1223	1362	30		

- Molecule 3 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	27	Total	C	N	O	0	0
			190	112	38	40		

- Molecule 4 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	357	Total	C	N	O	S	0	0
			2810	1777	493	530	10		

- Molecule 5 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	205	Total	C	N	O	S	0	0
			1608	1003	294	304	7		

- Molecule 6 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	292	Total	C	N	O	S	0	0
			2301	1461	399	426	15		

- Molecule 7 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 8 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	70	Total	C	N	O	S	0	0
			567	355	113	98	1		

- Molecule 9 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	T	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Z	447	Total	C	N	O	S	0	0
			3651	2343	602	688	18		

- Molecule 11 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	436	Total	C	N	O	S	0	0
			2978	1843	552	575	8		

- Molecule 12 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	566	Total	C	N	O	S	0	0
			3881	2433	707	732	9		

- Molecule 13 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 14 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	n	299	Total	C	N	O	P	S	0	0
			1894	1175	340	372	1	6		

- Molecule 15 is a protein called Pre-mRNA-splicing factor ISY1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	95	Total	C	N	O	S	0	0
			810	506	152	151	1		

- Molecule 16 is a RNA chain called UBC4 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B	57	Total	C	N	O	P	0	0
			1206	542	209	398	57		

- Molecule 17 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	179	Total	C	N	O	P	0	0
			3795	1699	660	1258	178		

- Molecule 18 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	E	103	Total	C	N	O	P	0	0
			2192	982	391	716	103		

- Molecule 19 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	210	Total	C	N	O	P	0	0
			4425	1981	739	1495	210		

- Molecule 20 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	722	Total	C	N	O	S	0	0
			4625	2893	825	895	12		

- Molecule 21 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	84	Total	C	N	O	0	0
			416	248	84	84		

- Molecule 22 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	b	169	Total	C	N	O	0	0
			841	503	169	169		

- Molecule 23 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	156	Total	C	N	O	S	0	0
			926	585	160	180	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	74	Total	C	N	O	S	0	0
			526	346	87	90	3		
24	i	74	Total	C	N	O	S	0	0
			541	358	90	90	3		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	m	119	Total	C	N	O	S	0	0
			917	575	163	176	3		
25	z	108	Total	C	N	O	S	0	0
			824	521	142	158	3		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	75	Total	C	N	O	S	0	0
			552	350	98	103	1		
26	x	75	Total	C	N	O	S	0	0
			552	350	98	103	1		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	68	Total	C	N	O	S	0	0
			518	337	96	84	1		
27	w	68	Total	C	N	O	S	0	0
			518	337	96	84	1		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	101	Total	C	N	O	S	0	0
			785	504	149	128	4		
28	e	101	Total	C	N	O	S	0	0
			785	504	149	128	4		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	100	Total	C	N	O	S	0	0
			809	514	150	142	3		
29	s	93	Total	C	N	O	S	0	0
			749	476	138	132	3		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	83	Total	C	N	O	S	0	0
			641	408	111	120	2		
30	y	81	Total	C	N	O	S	0	0
			616	394	107	113	2		

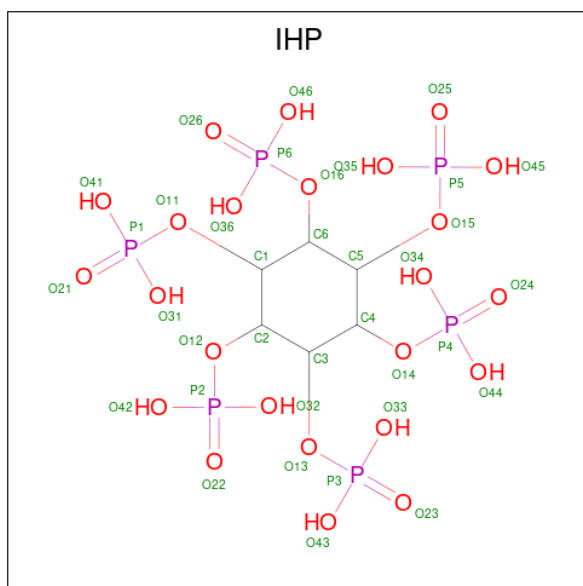
- Molecule 31 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		
31	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
31	q	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
31	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		

- Molecule 32 is a protein called Splicing factor YJU2.

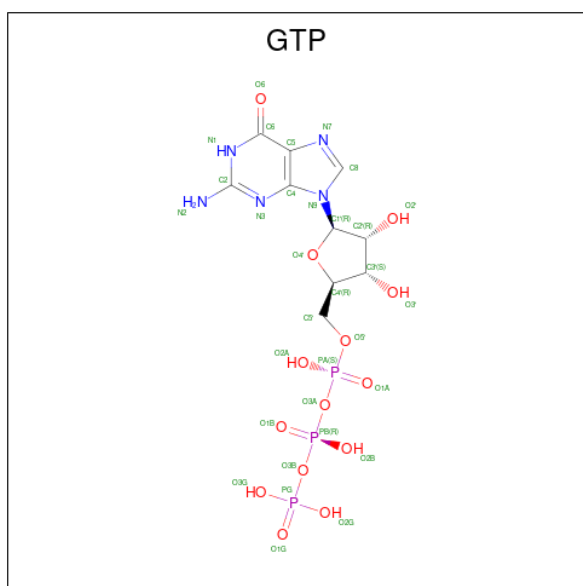
Mol	Chain	Residues	Atoms					AltConf	Trace
32	F	161	Total	C	N	O	S	0	0
			1316	817	240	248	11		

- Molecule 33 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $\text{C}_6\text{H}_{18}\text{O}_{24}\text{P}_6$).



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

- Molecule 34 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	C	1	Total	Mg	0
			1	1	
35	B	1	Total	Mg	0
			1	1	
35	E	4	Total	Mg	0
			4	4	

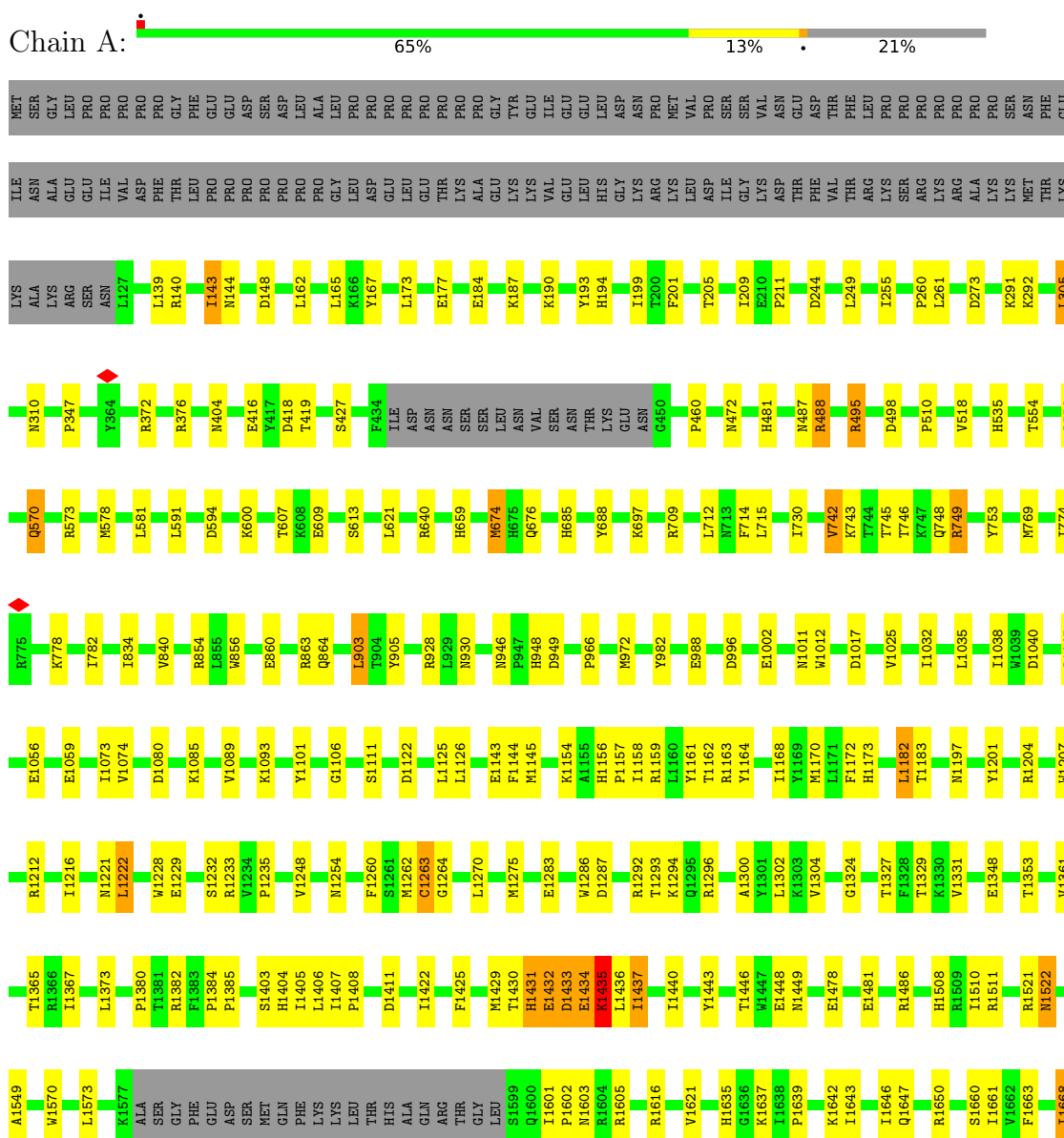
- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

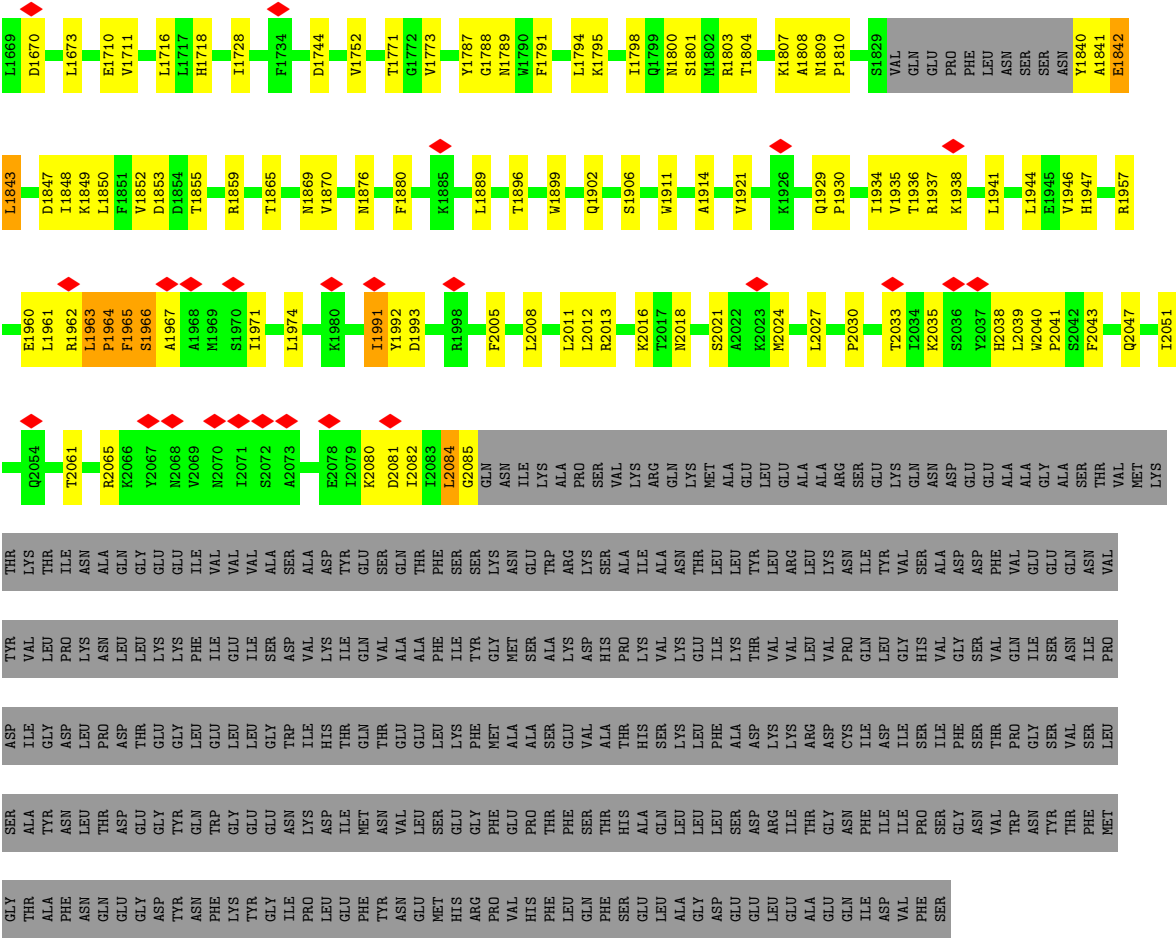
Mol	Chain	Residues	Atoms		AltConf
36	Q	2	Total	Zn	0
			2	2	
36	R	1	Total	Zn	0
			1	1	
36	T	3	Total	Zn	0
			3	3	
36	F	1	Total	Zn	0
			1	1	

3 Residue-property plots

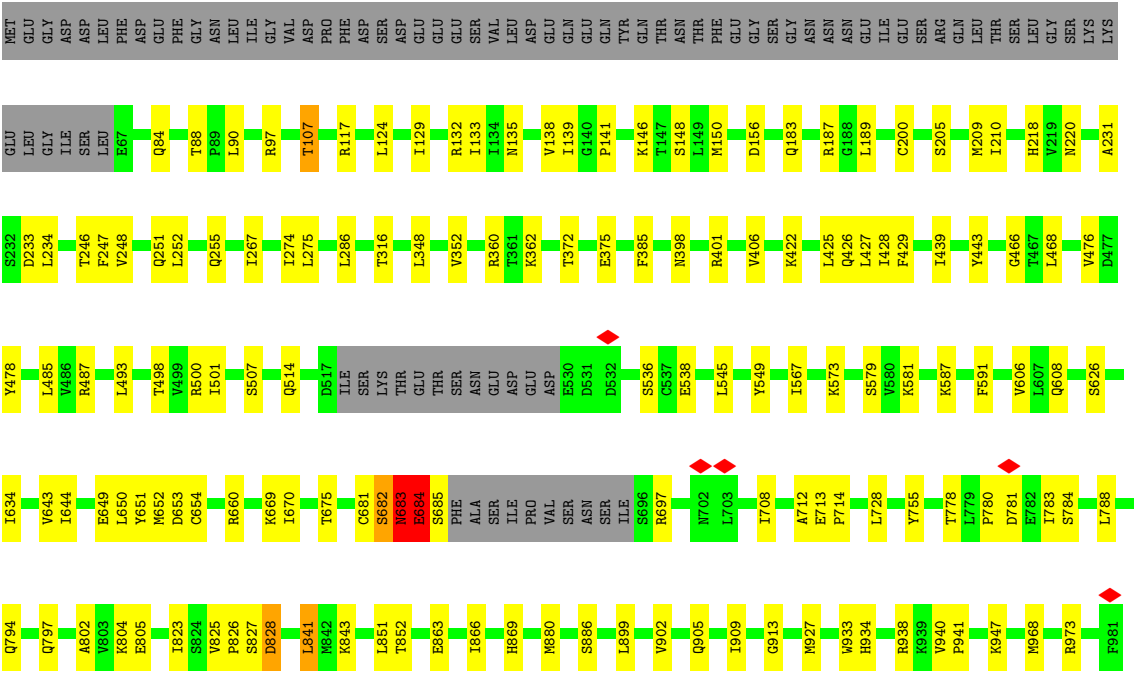
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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-splicing factor 8

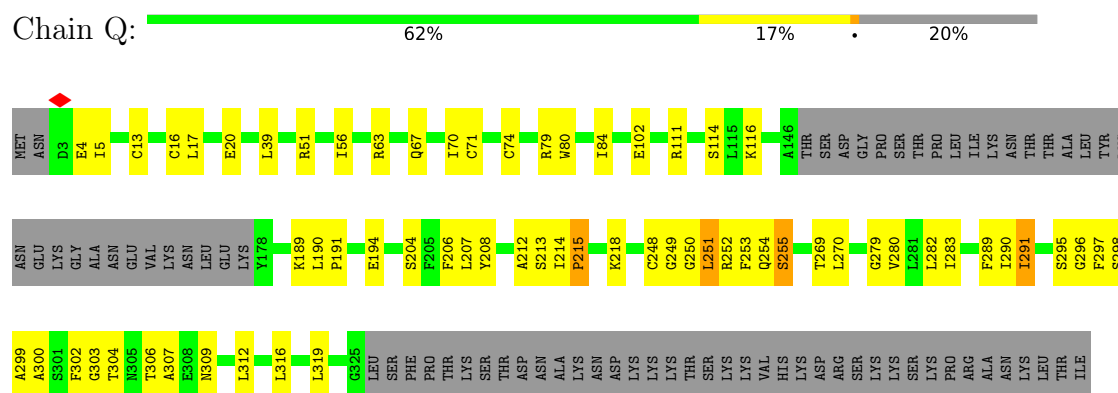




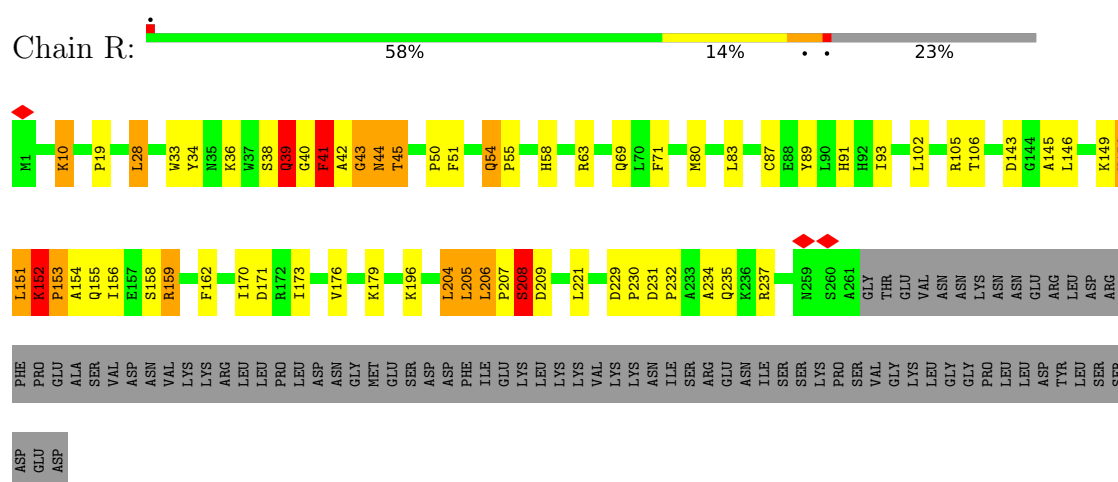
● Molecule 2: Pre-mRNA-splicing factor SNU114



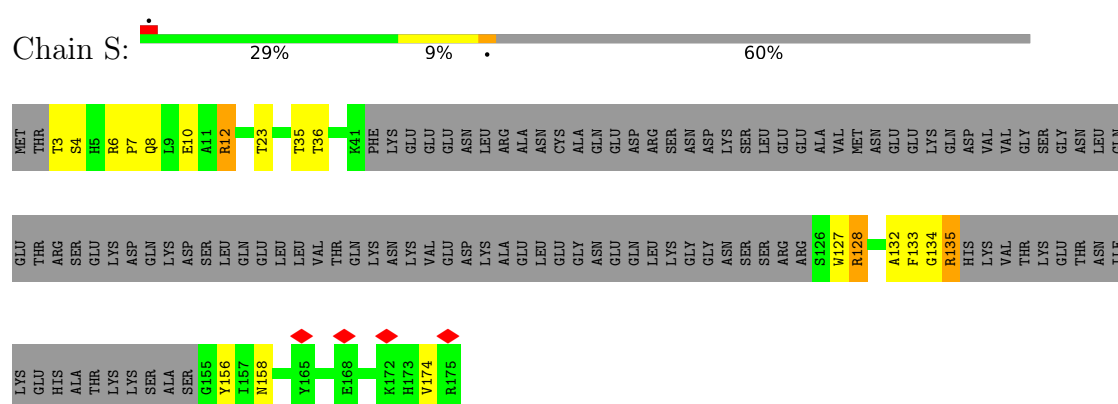
- Molecule 6: Pre-mRNA-splicing factor SLT11



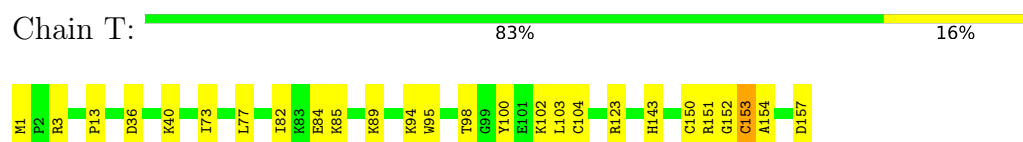
- Molecule 7: Pre-mRNA-splicing factor CWC2



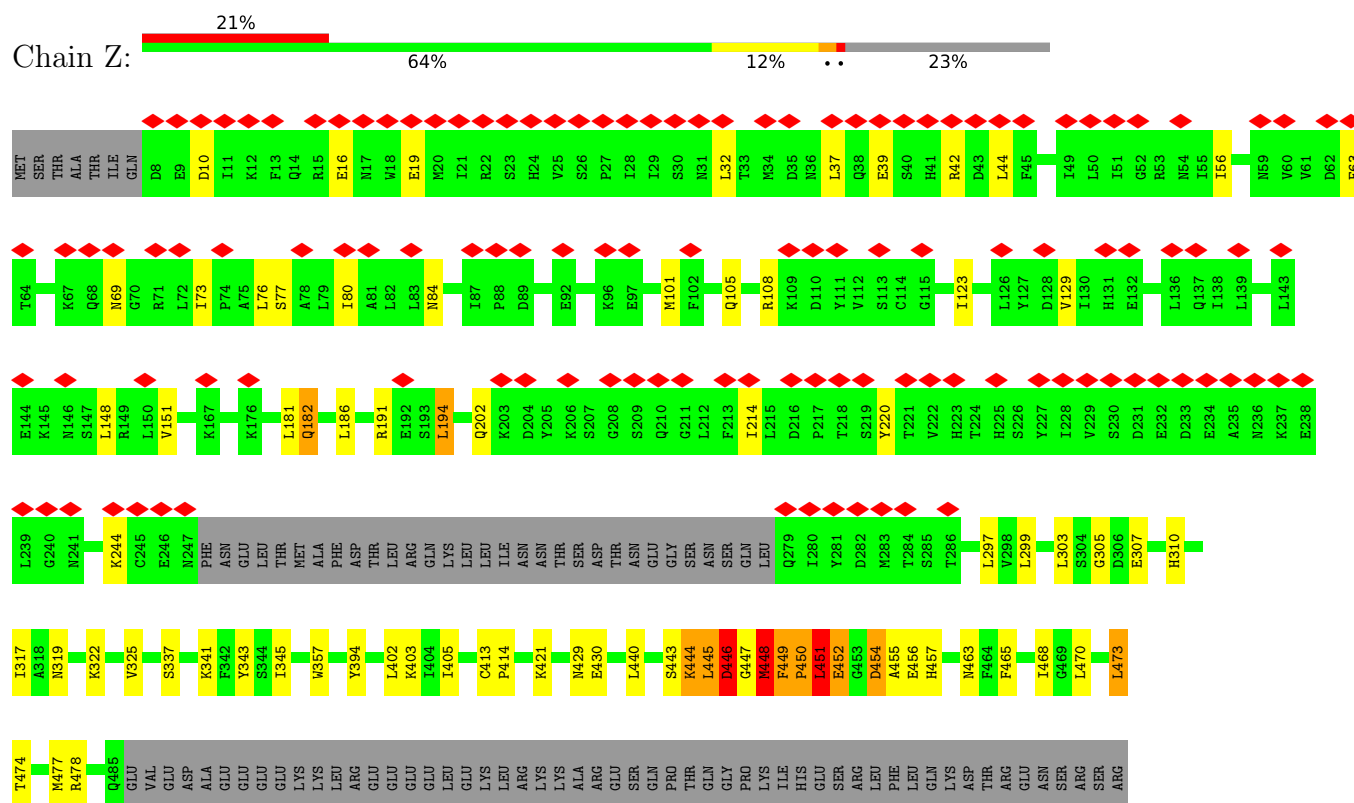
- Molecule 8: Pre-mRNA-splicing factor CWC15



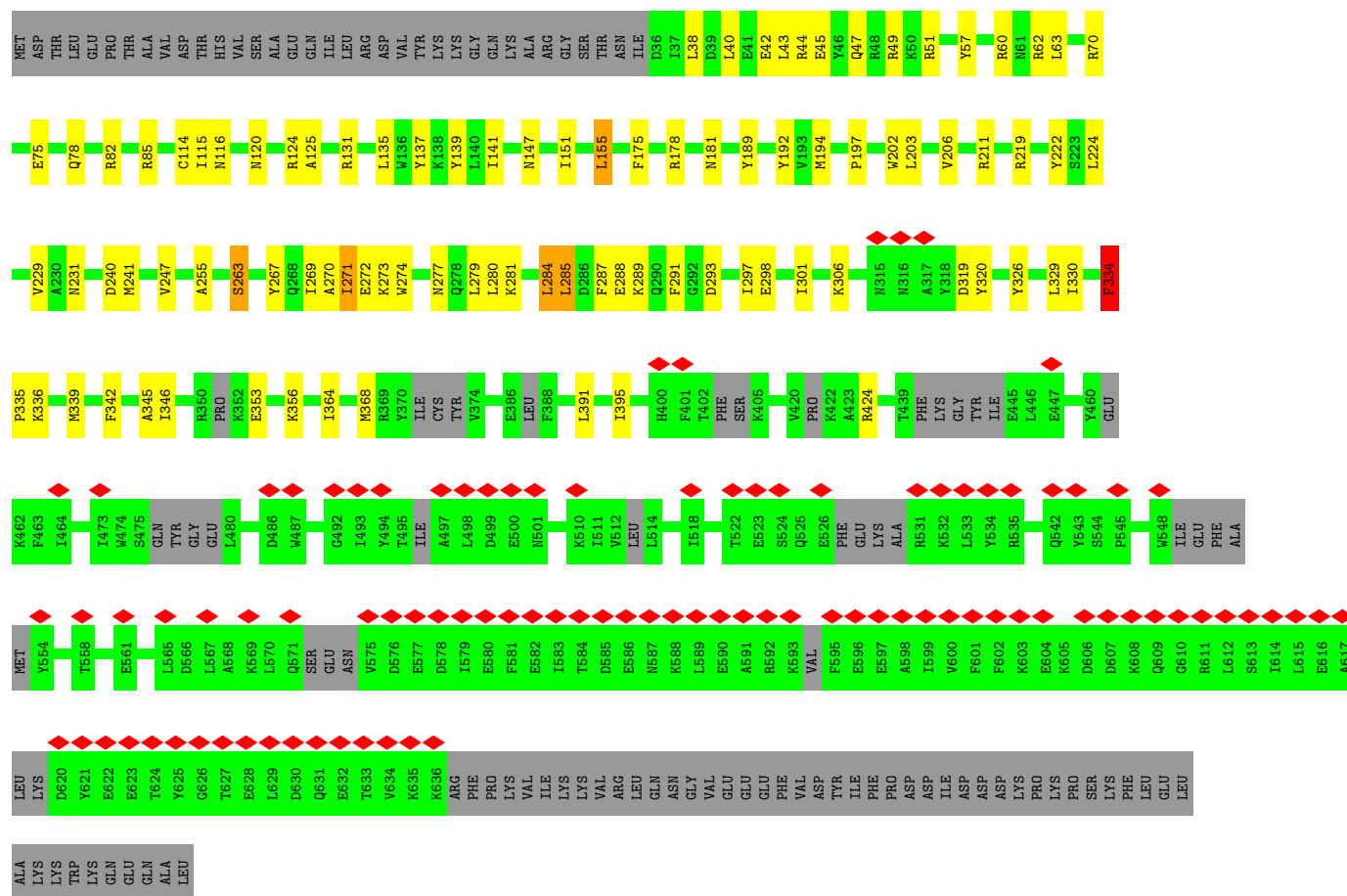
- Molecule 9: Pre-mRNA-splicing factor BUD31



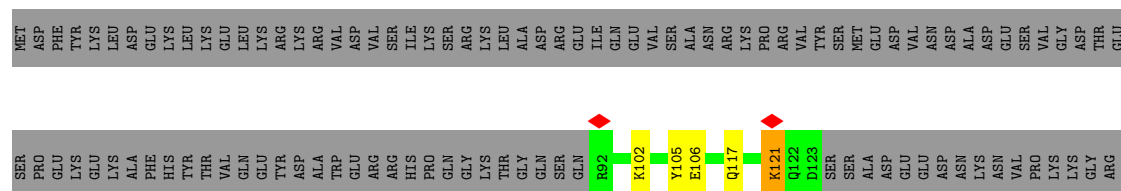
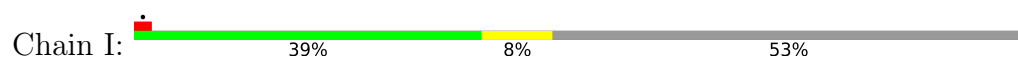
• Molecule 10: Pre-mRNA-splicing factor CWC22

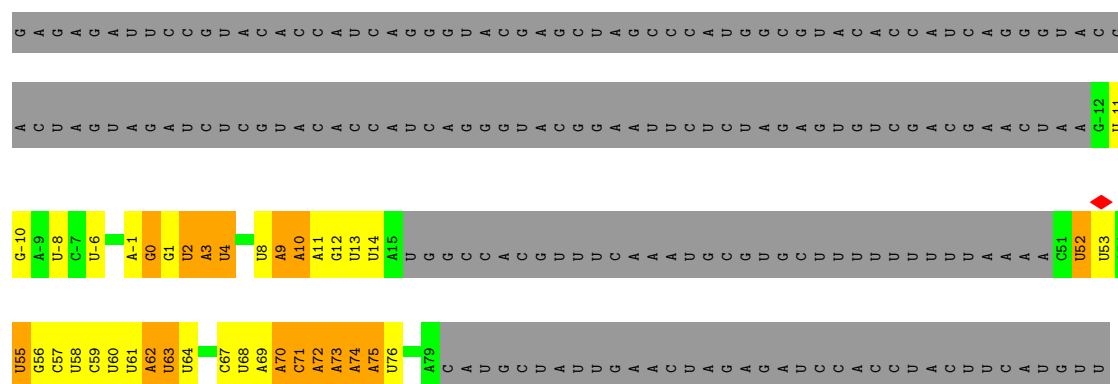


- Molecule 12: Pre-mRNA-splicing factor CLF1

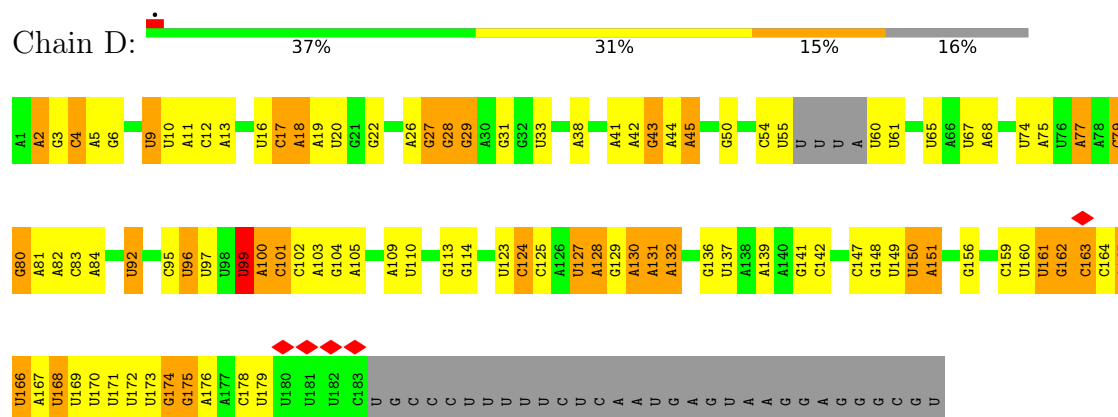


- Molecule 13: Pre-mRNA-splicing factor SYF2

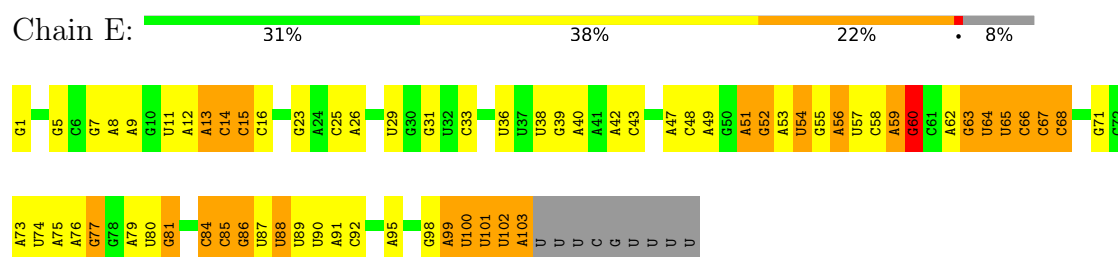




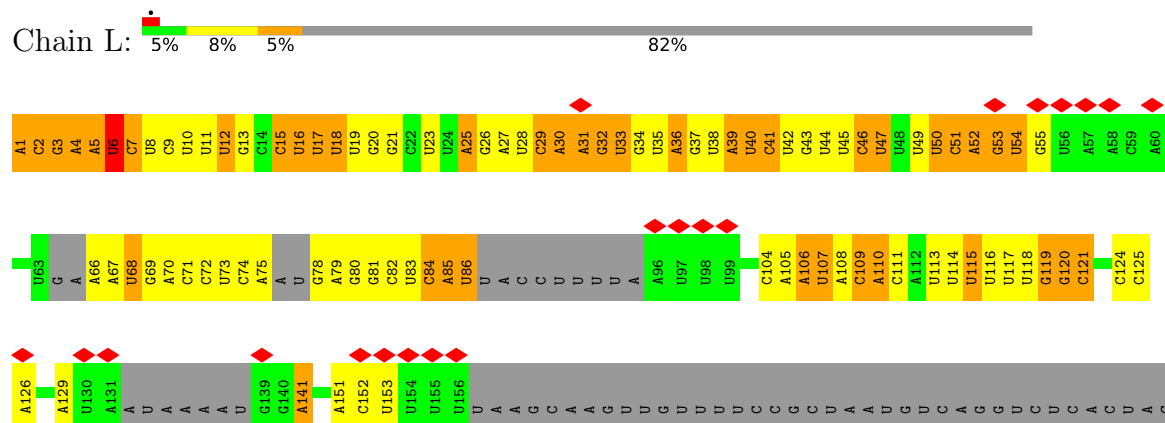
• Molecule 17: U5 snRNA

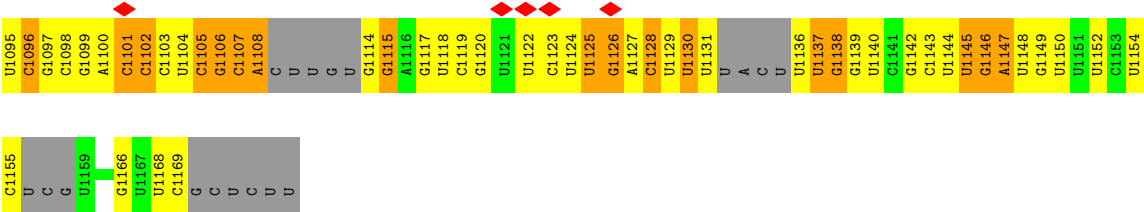
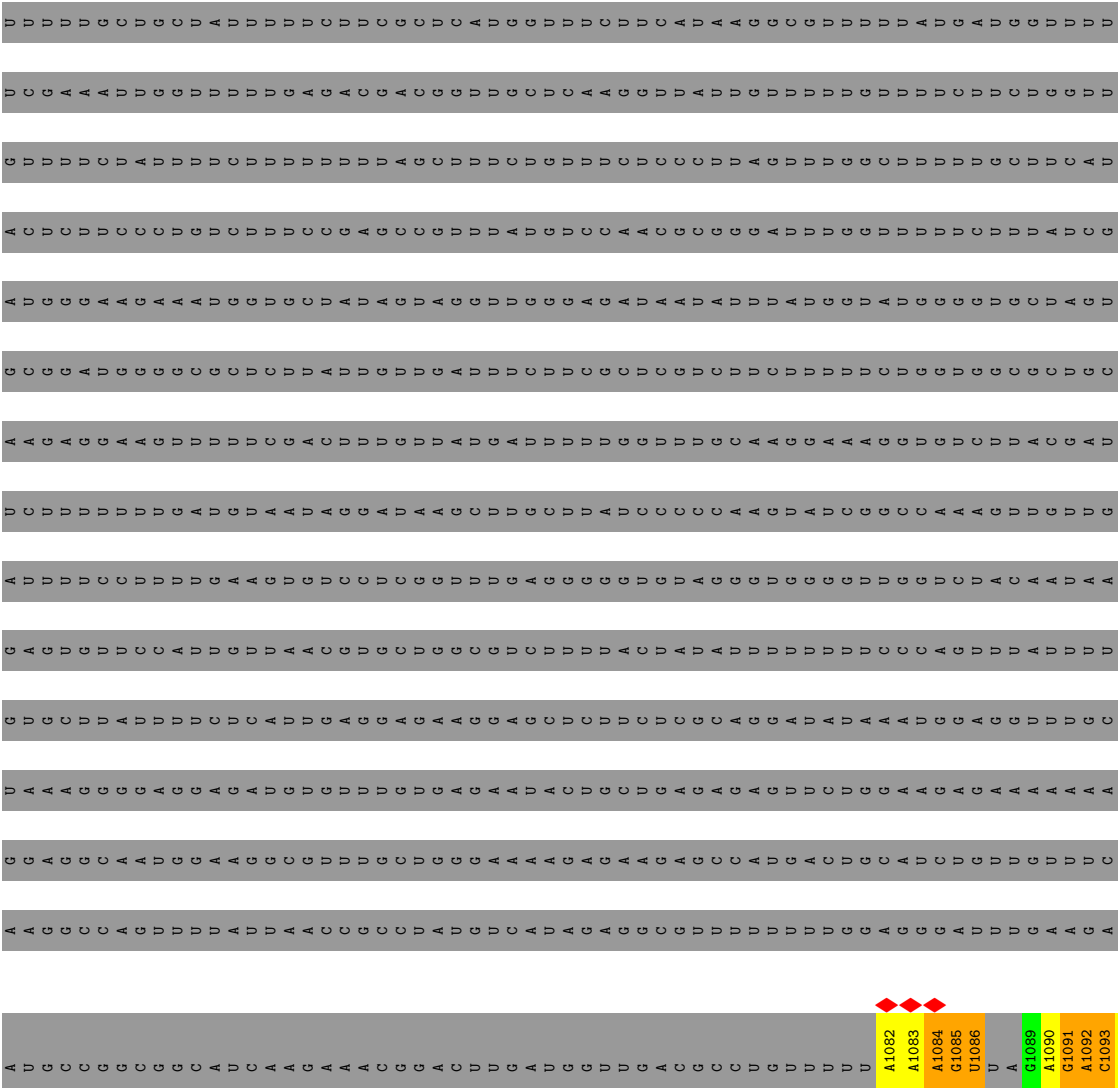


• Molecule 18: U6 snRNA

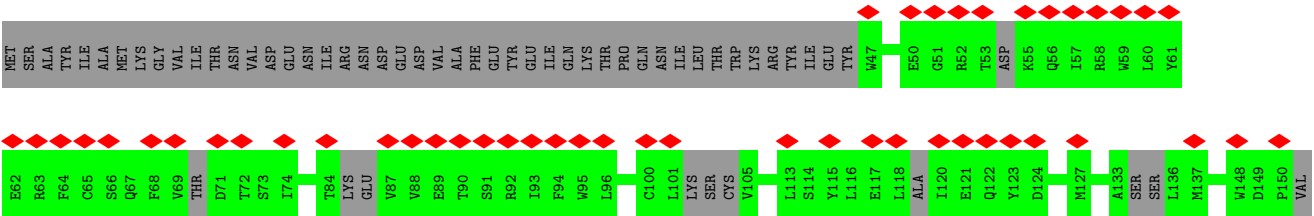


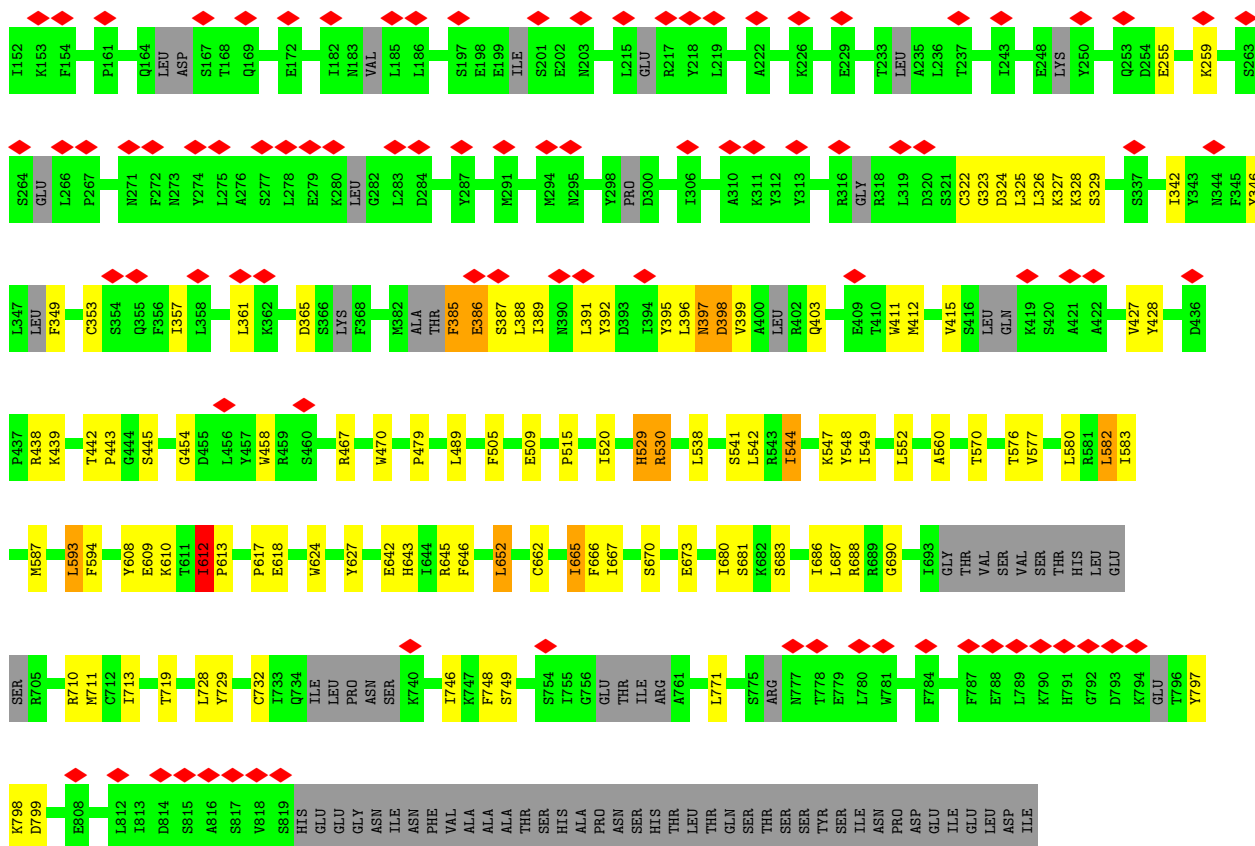
• Molecule 19: U2 snRNA



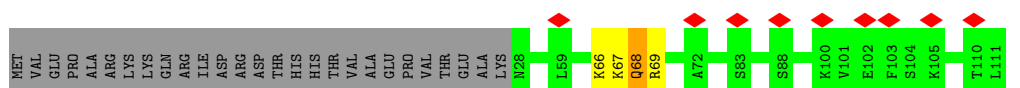


● Molecule 20: Pre-mRNA-splicing factor SYF1





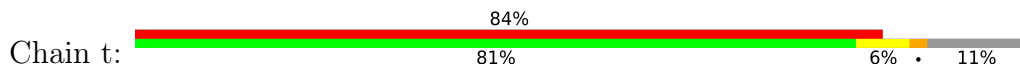
- Molecule 21: U2 small nuclear ribonucleoprotein B''

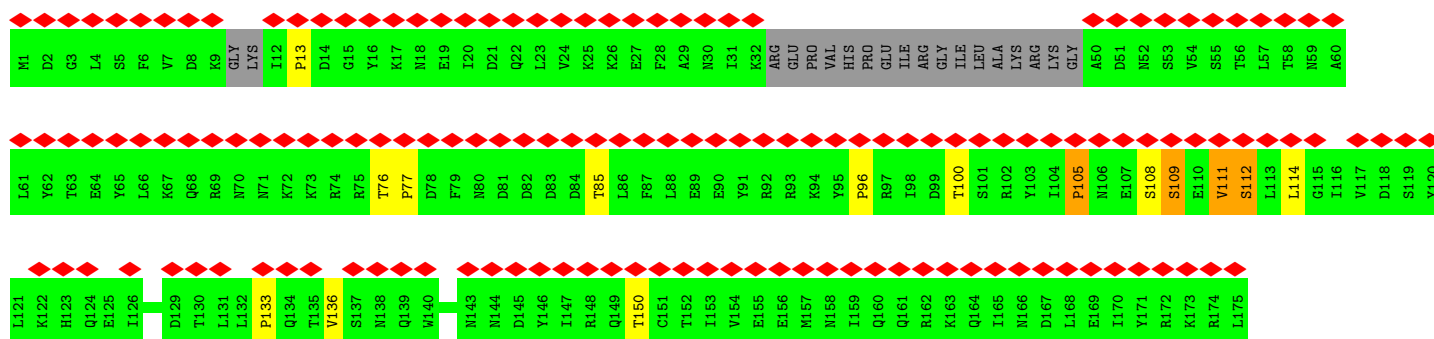


- Molecule 22: U2 small nuclear ribonucleoprotein A'

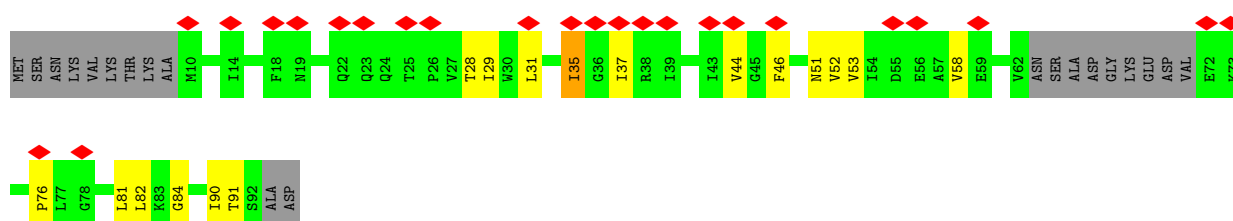


- Molecule 23: Pre-mRNA-splicing factor SNT309

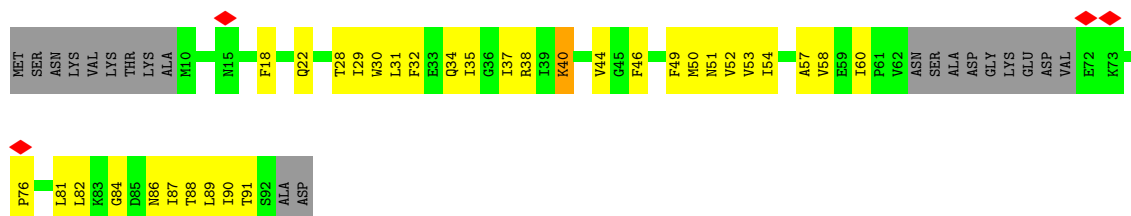




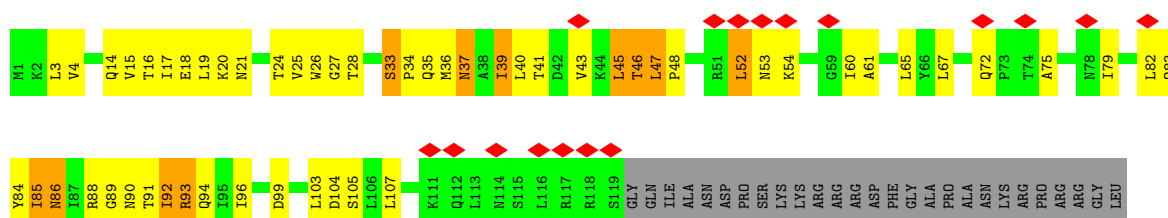
• Molecule 24: Small nuclear ribonucleoprotein E



• Molecule 24: Small nuclear ribonucleoprotein E

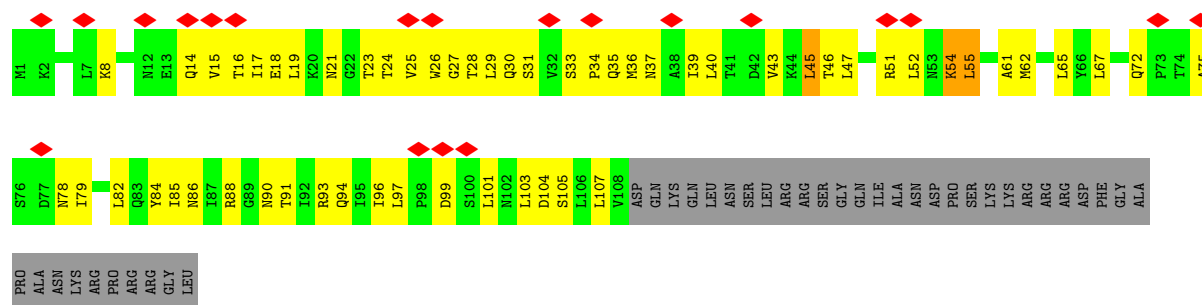


• Molecule 25: Small nuclear ribonucleoprotein Sm D1

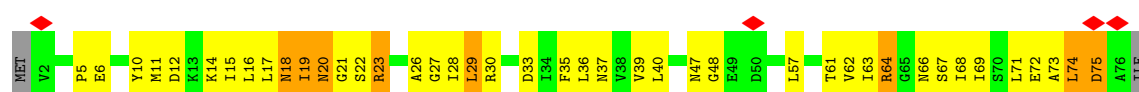
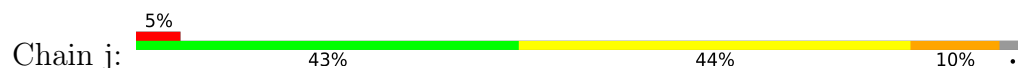


• Molecule 25: Small nuclear ribonucleoprotein Sm D1

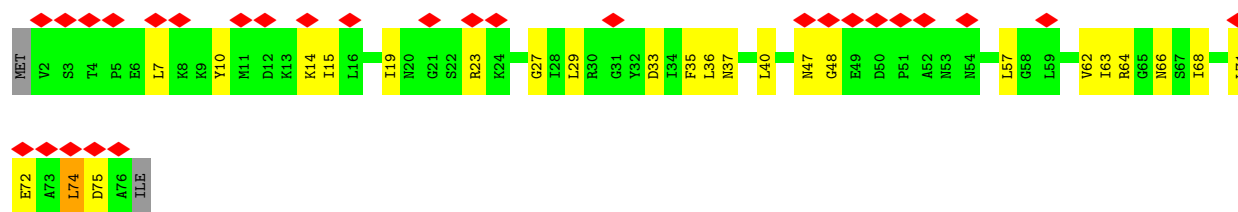




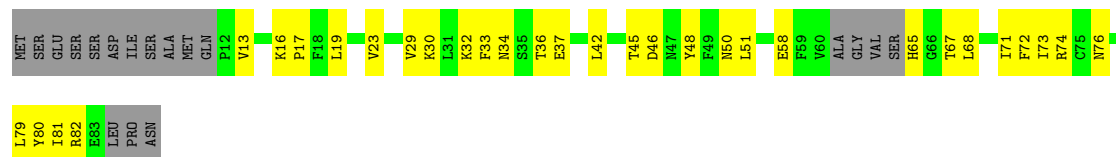
- Molecule 26: Small nuclear ribonucleoprotein G



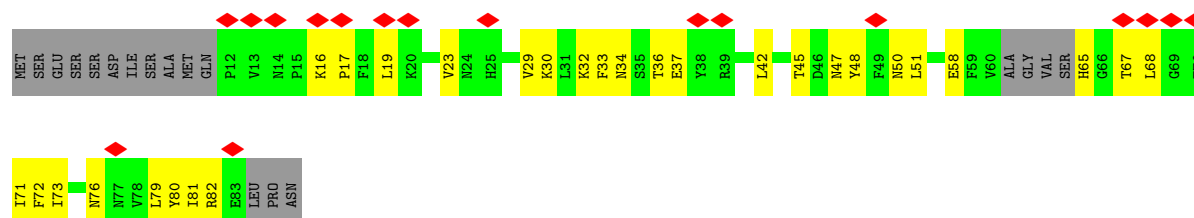
- Molecule 26: Small nuclear ribonucleoprotein G



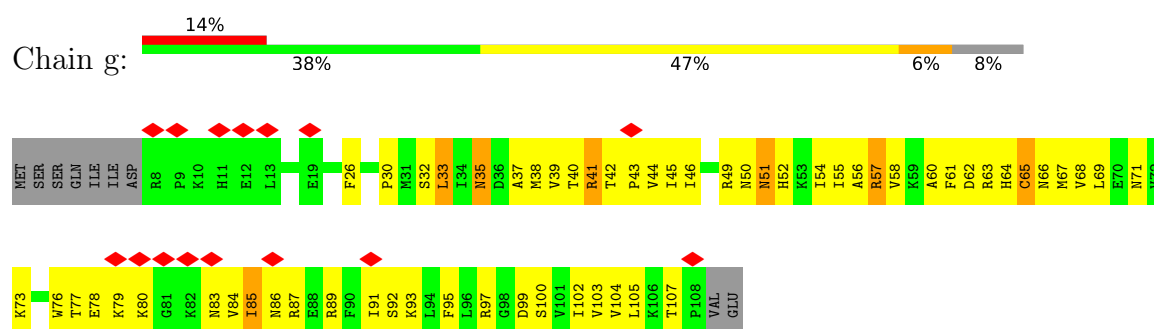
- Molecule 27: Small nuclear ribonucleoprotein F



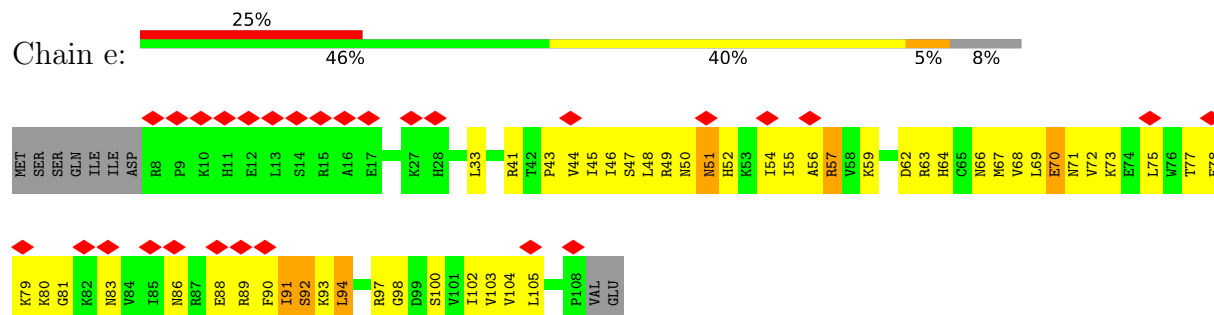
- Molecule 27: Small nuclear ribonucleoprotein F



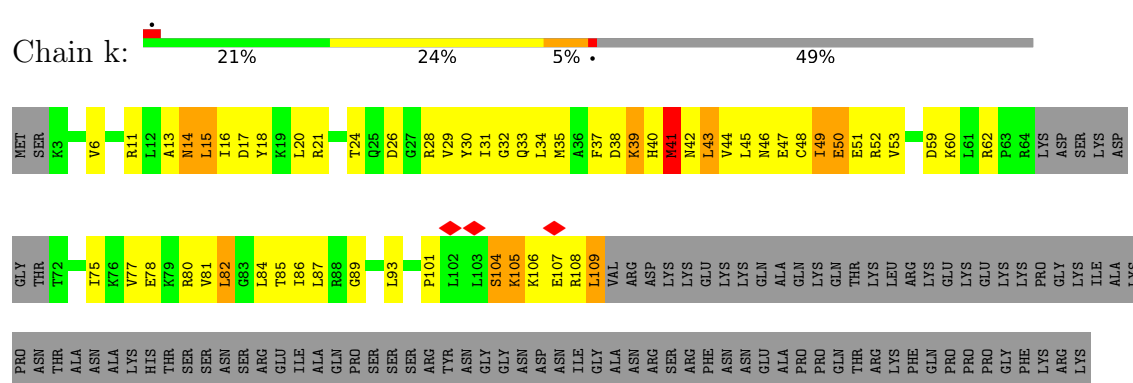
- Molecule 28: Small nuclear ribonucleoprotein Sm D2



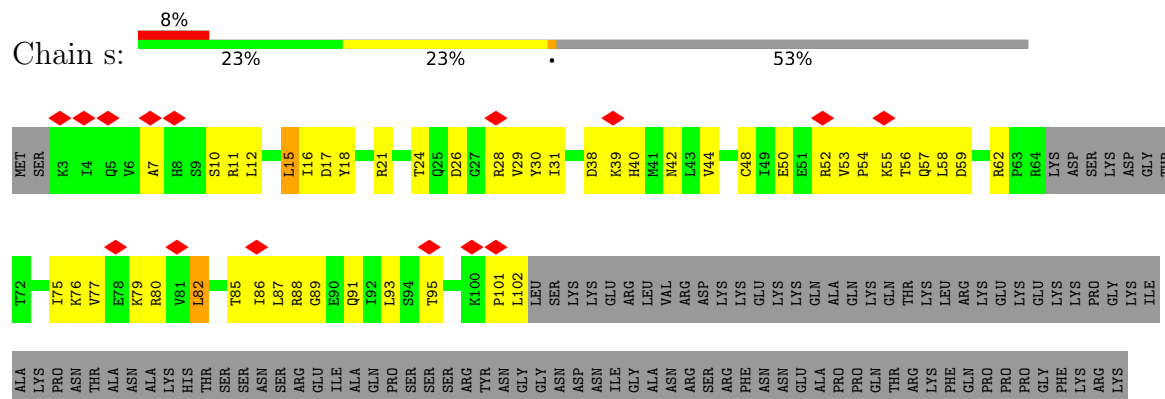
• Molecule 28: Small nuclear ribonucleoprotein Sm D2



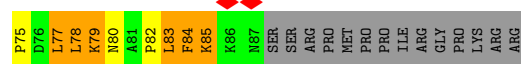
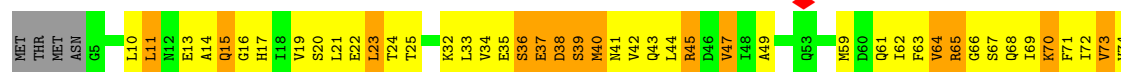
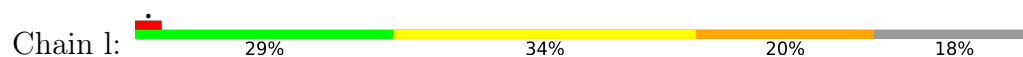
• Molecule 29: Small nuclear ribonucleoprotein-associated protein B



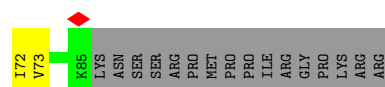
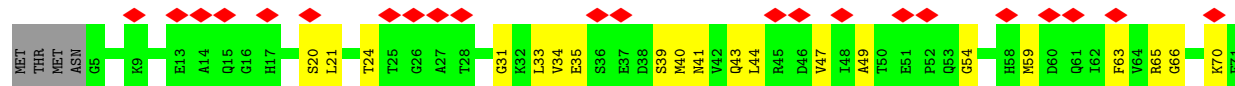
• Molecule 29: Small nuclear ribonucleoprotein-associated protein B



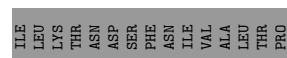
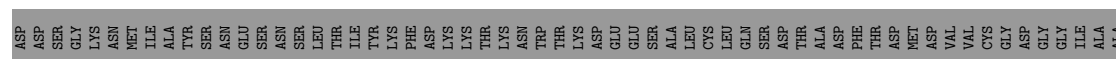
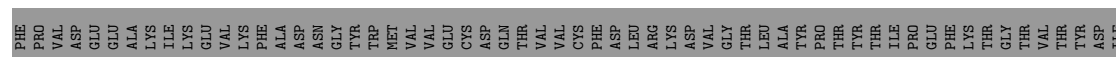
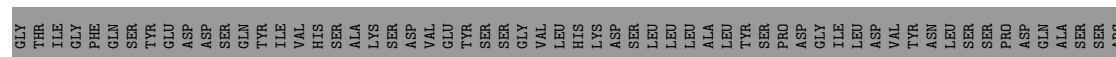
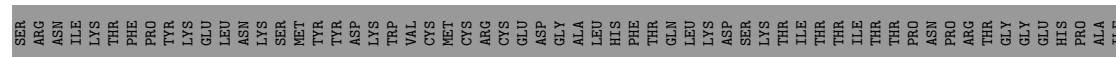
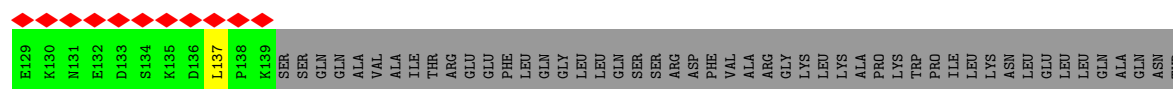
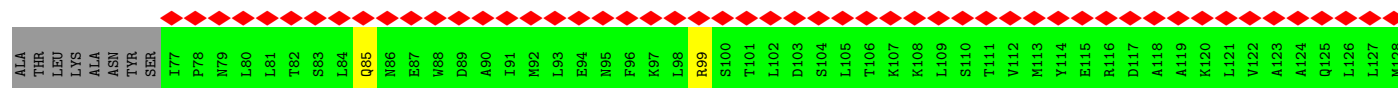
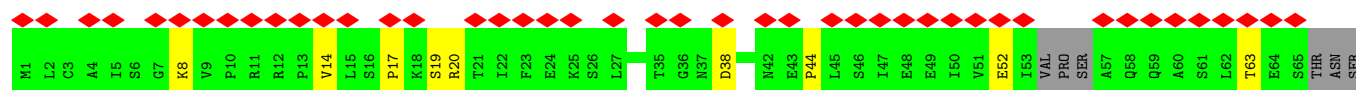
• Molecule 30: Small nuclear ribonucleoprotein Sm D3



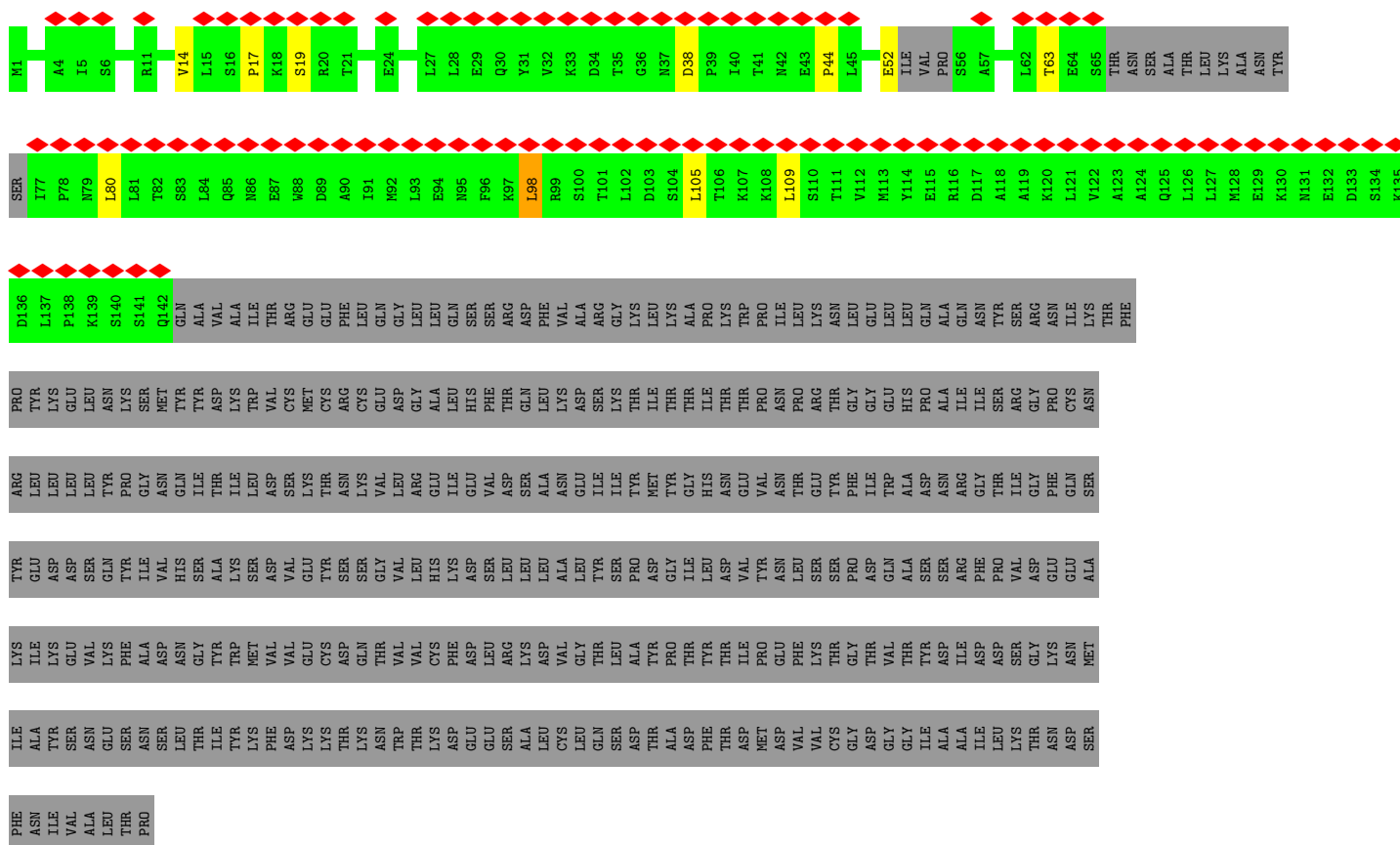
• Molecule 30: Small nuclear ribonucleoprotein Sm D3



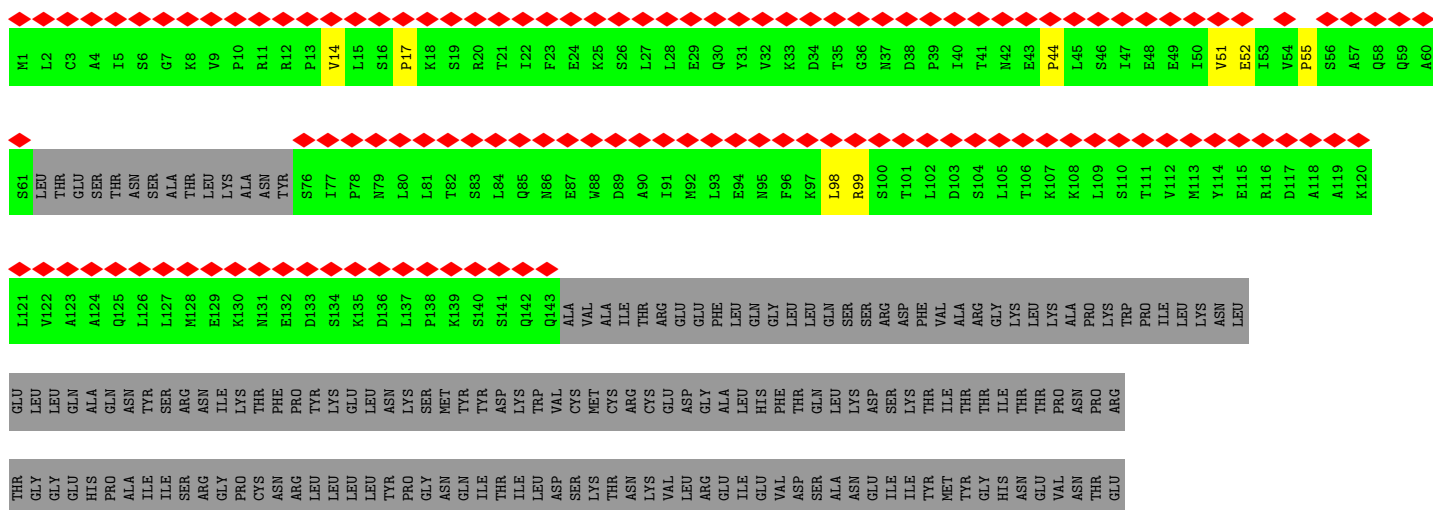
• Molecule 31: Pre-mRNA-processing factor 19

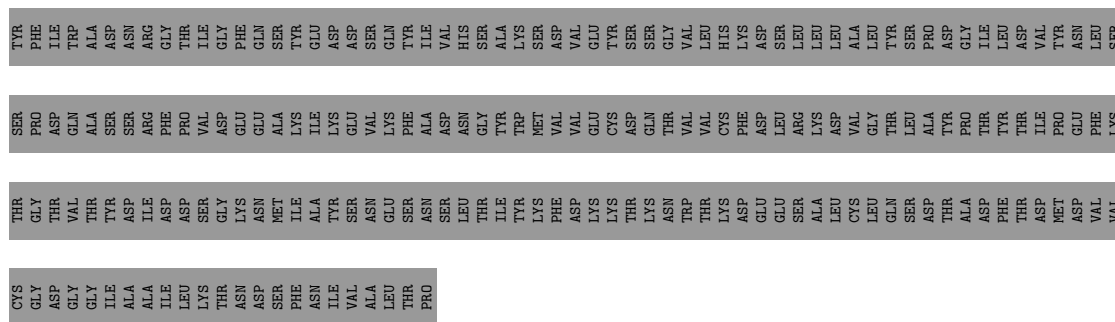


Chain p: 20% 23% 75%

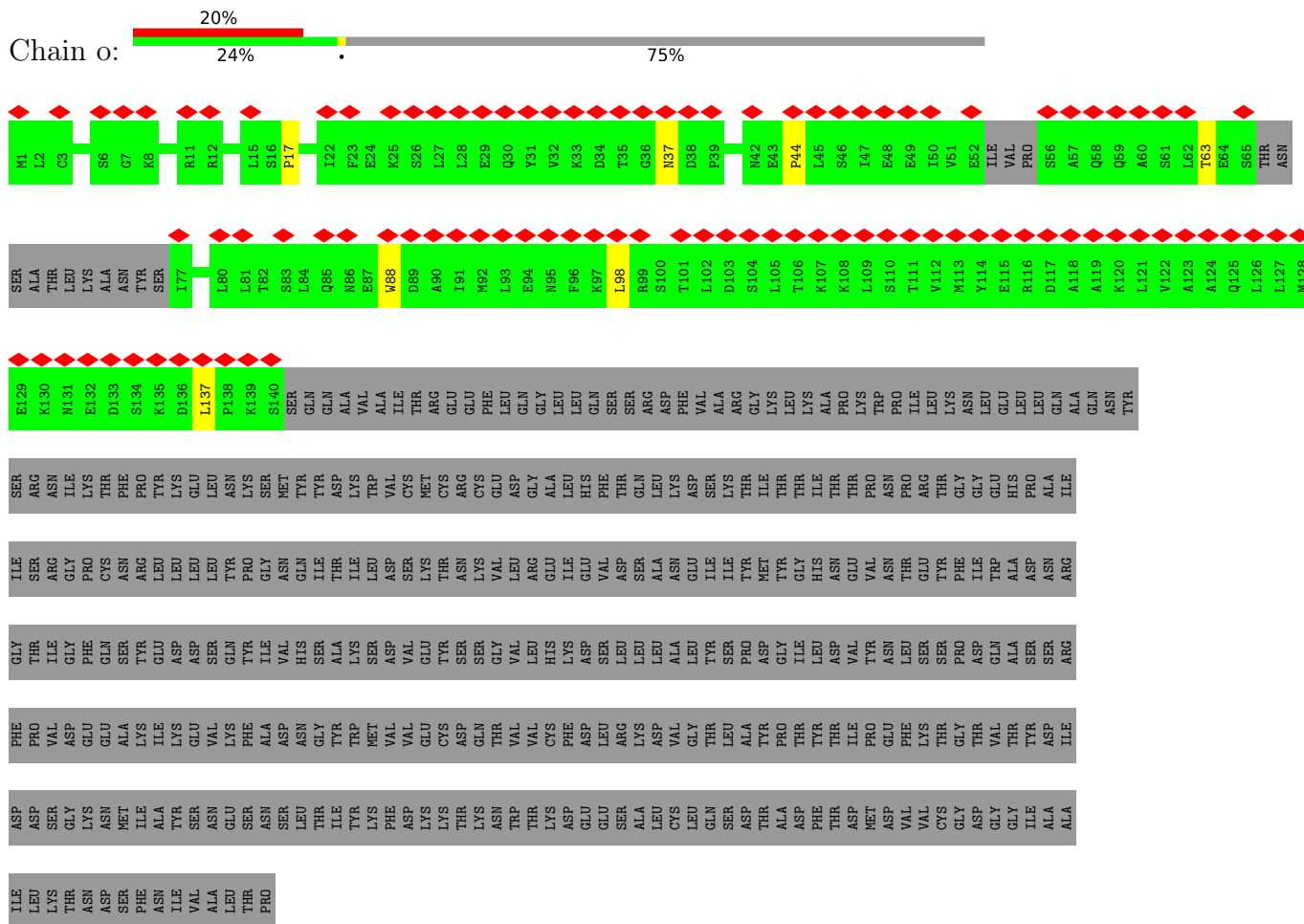


Chain q:

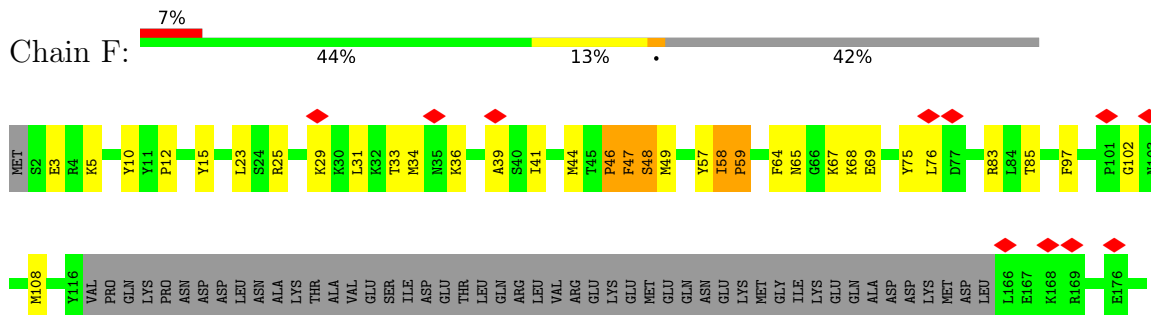


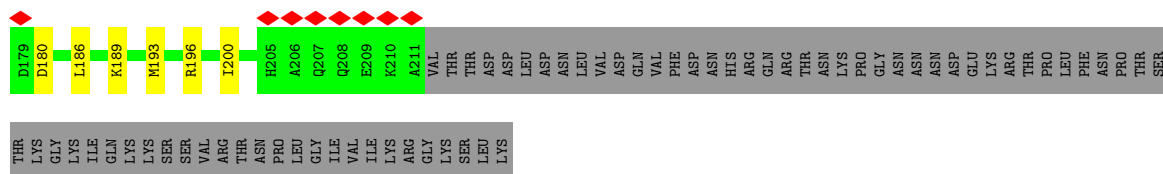


- Molecule 31: Pre-mRNA-processing factor 19



- Molecule 32: Splicing factor YJU2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	395458	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.3	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	0.114	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0116	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	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, MG, IHP, SEP, GTP

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	0.45	0/16198	0.58	2/21958 (0.0%)
2	C	0.43	0/7503	0.56	1/10159 (0.0%)
3	J	0.38	0/191	0.53	0/254
4	O	0.51	0/2872	0.63	0/3902
5	P	0.35	0/1629	0.50	0/2194
6	Q	0.42	0/2339	0.71	0/3154
7	R	0.45	0/2135	0.63	0/2871
8	S	0.42	0/581	0.59	0/776
9	T	0.38	0/1315	0.56	0/1759
10	Z	0.34	0/3712	0.54	0/5004
11	c	0.30	0/2996	0.50	0/4033
12	d	0.35	0/3931	0.61	2/5356 (0.0%)
13	I	0.34	0/826	0.53	0/1097
14	n	0.32	0/1894	0.57	0/2529
15	H	0.40	0/826	0.78	2/1108 (0.2%)
16	B	0.37	0/1347	0.54	0/2091
17	D	0.32	0/4239	0.46	1/6598 (0.0%)
18	E	0.45	1/2452 (0.0%)	0.52	1/3817 (0.0%)
19	L	0.36	0/4926	0.61	3/7641 (0.0%)
20	v	0.49	0/4662	0.76	4/6358 (0.1%)
21	a	0.63	0/415	1.14	0/577
22	b	1.07	0/839	1.44	8/1169 (0.7%)
23	t	0.29	0/924	0.54	0/1244
24	i	0.27	0/551	0.57	0/750
24	u	0.25	0/535	0.49	0/730
25	m	0.49	0/926	0.77	0/1257
25	z	0.32	0/833	0.62	0/1134
26	j	0.64	0/557	0.85	0/756
26	x	0.37	0/557	0.65	0/756
27	h	0.26	0/529	0.55	0/715
27	w	0.24	0/529	0.56	0/715
28	e	0.51	0/799	0.67	0/1078

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	g	0.56	0/799	0.78	0/1078
29	k	0.56	0/815	0.81	0/1092
29	s	0.44	0/755	0.73	0/1014
30	l	0.73	0/650	1.00	1/879 (0.1%)
30	y	0.31	0/625	0.58	0/847
31	o	0.23	0/835	0.56	2/1126 (0.2%)
31	p	0.18	0/848	0.44	0/1143
31	q	0.27	0/856	0.57	0/1155
31	r	0.30	0/828	0.57	0/1117
32	F	0.47	1/1333 (0.1%)	0.71	0/1775
All	All	0.42	2/82912 (0.0%)	0.62	27/114766 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	E	95	A	O3'-P	-11.49	1.44	1.61
32	F	41	ILE	C-N	11.27	1.49	1.33

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	b	43	MET	CA-C-N	8.56	128.69	119.28
22	b	43	MET	C-N-CA	8.56	128.69	119.28
22	b	4	THR	CA-C-N	7.90	127.46	118.85
22	b	4	THR	C-N-CA	7.90	127.46	118.85
20	v	681	SER	N-CA-C	-6.52	105.08	113.16
22	b	11	ALA	CA-C-N	6.50	127.97	119.84
22	b	11	ALA	C-N-CA	6.50	127.97	119.84
19	L	1092	A	C2'-C3'-O3'	-6.44	104.04	113.70
20	v	612	ILE	O-C-N	6.24	124.50	120.07
31	o	37	ASN	CA-C-N	6.00	129.94	121.61
31	o	37	ASN	C-N-CA	6.00	129.94	121.61
12	d	424	ARG	CA-C-N	5.97	128.55	120.38
12	d	424	ARG	C-N-CA	5.97	128.55	120.38
19	L	15	C	C4'-C3'-O3'	-5.68	104.48	113.00
1	A	1668	ILE	N-CA-C	-5.55	107.41	112.96
2	C	573	LYS	N-CA-CB	-5.52	107.88	114.17
19	L	6	U	C2'-C3'-O3'	-5.49	105.47	113.70
17	D	99	U	C4'-C3'-O3'	-5.44	104.83	113.00
15	H	34	ARG	CA-C-N	5.35	139.84	127.00
15	H	34	ARG	C-N-CA	5.35	139.84	127.00
22	b	81	LEU	CA-C-N	5.21	124.92	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	b	81	LEU	C-N-CA	5.21	124.92	119.92
18	E	60	G	C4'-C3'-O3'	-5.14	105.29	113.00
20	v	560	ALA	CA-C-N	5.05	130.49	122.61
20	v	560	ALA	C-N-CA	5.05	130.49	122.61
30	l	39	SER	N-CA-C	-5.03	105.92	111.71
1	A	1522	ASN	N-CA-C	5.01	116.43	110.97

There are no chirality outliers.

There are no planarity outliers.

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	15793	0	15768	396	0
2	C	7348	0	7520	109	0
3	J	190	0	186	5	0
4	O	2810	0	2804	70	0
5	P	1608	0	1631	34	0
6	Q	2301	0	2366	85	0
7	R	2089	0	2053	142	0
8	S	567	0	552	37	0
9	T	1291	0	1312	25	0
10	Z	3651	0	3707	93	0
11	c	2978	0	2459	56	0
12	d	3881	0	3041	142	0
13	I	822	0	845	23	0
14	n	1894	0	1406	23	0
15	H	810	0	799	48	0
16	B	1206	0	609	57	0
17	D	3795	0	1919	145	0
18	E	2192	0	1106	88	0
19	L	4425	0	2247	464	0
20	v	4625	0	3448	122	0
21	a	416	0	182	6	0
22	b	841	0	350	27	0
23	t	926	0	606	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	i	541	0	542	77	0
24	u	526	0	515	21	0
25	m	917	0	961	106	0
25	z	824	0	864	89	0
26	j	552	0	553	85	0
26	x	552	0	553	23	0
27	h	518	0	502	38	0
27	w	518	0	502	49	0
28	e	785	0	802	112	0
28	g	785	0	802	117	0
29	k	809	0	881	138	0
29	s	749	0	809	59	0
30	l	641	0	666	118	0
30	y	616	0	639	25	0
31	o	830	0	663	6	0
31	p	843	0	675	6	0
31	q	850	0	682	4	0
31	r	823	0	654	10	0
32	F	1316	0	1337	44	0
33	A	36	0	6	4	0
34	C	32	0	12	1	0
35	B	1	0	0	0	0
35	C	1	0	0	0	0
35	E	4	0	0	0	0
36	F	1	0	0	0	0
36	Q	2	0	0	0	0
36	R	1	0	0	0	0
36	T	3	0	0	0	0
All	All	80535	0	70536	2743	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 18.

All (2743) 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)
1:A:1992:TYR:CE1	1:A:2008:LEU:HD22	1.43	1.49
19:L:85:A:H2'	19:L:86:U:C5'	1.40	1.49
26:j:17:LEU:CD1	26:j:19:ILE:HD11	1.43	1.47
19:L:84:C:H2'	19:L:85:A:C8	1.50	1.46
29:k:31:ILE:CD1	29:k:49:ILE:HD11	1.45	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:g:35:ASN:HB2	28:g:61:PHE:CZ	1.52	1.43
28:e:56:ALA:HB2	28:e:72:VAL:CG2	1.48	1.41
19:L:46:C:H2'	19:L:47:U:C5	1.56	1.37
19:L:1137:U:H2'	19:L:1138:G:C1'	1.58	1.34
12:d:255:ALA:HB1	12:d:291:PHE:CE2	1.63	1.33
20:v:612:ILE:HG13	20:v:613:PRO:CD	1.60	1.28
7:R:151:LEU:HA	19:L:78:G:P	1.74	1.27
10:Z:181:LEU:CD1	10:Z:194:LEU:HD12	1.65	1.26
24:i:30:TRP:NE1	24:i:38:ARG:HD3	1.52	1.25
12:d:241:MET:HG2	12:d:279:LEU:CD1	1.66	1.24
29:k:31:ILE:HD11	29:k:49:ILE:CD1	1.68	1.23
25:m:84:TYR:CD2	29:k:6:VAL:HG11	1.73	1.23
29:k:48:CYS:SG	29:k:82:LEU:HD12	1.79	1.23
1:A:1232:SER:HB3	8:S:135:ARG:NH1	1.55	1.21
19:L:1154:U:O2'	19:L:1155:C:H5'	1.07	1.21
19:L:85:A:C2'	19:L:86:U:H5''	1.69	1.20
19:L:85:A:C2'	19:L:86:U:C5'	2.19	1.19
26:j:64:ARG:NH2	24:i:50:MET:HB3	1.56	1.19
28:e:56:ALA:CB	28:e:69:LEU:HD23	1.73	1.19
20:v:711:MET:HE1	20:v:748:PHE:CB	1.72	1.19
19:L:1154:U:O2'	19:L:1155:C:C5'	1.90	1.18
1:A:487:ASN:OD1	1:A:488:ARG:HD3	1.43	1.18
1:A:1992:TYR:HE1	1:A:2008:LEU:CD2	1.55	1.18
10:Z:181:LEU:HD12	10:Z:194:LEU:CD1	1.73	1.17
19:L:4:A:H1'	20:v:529:HIS:CD2	1.77	1.17
1:A:2024:MET:HE1	25:z:99:ASP:O	1.44	1.17
28:e:56:ALA:HB3	28:e:69:LEU:HD23	1.21	1.17
12:d:255:ALA:CB	12:d:291:PHE:CE2	2.27	1.17
1:A:1032:ILE:O	1:A:1035:LEU:HG	1.44	1.16
6:Q:300:ALA:HB2	7:R:154:ALA:HB1	1.17	1.16
10:Z:181:LEU:CD2	10:Z:186:LEU:HD22	1.76	1.15
25:m:19:LEU:HD22	25:m:91:THR:HG22	1.29	1.15
26:j:28:ILE:O	26:j:40:LEU:HB2	1.44	1.15
26:j:64:ARG:HH22	24:i:50:MET:HB3	1.10	1.14
29:k:49:ILE:HG22	29:k:81:VAL:HA	1.26	1.14
10:Z:181:LEU:HD11	10:Z:194:LEU:CB	1.77	1.14
19:L:74:C:O2'	19:L:75:A:H5'	1.46	1.14
31:r:99:ARG:HG2	31:o:98:LEU:HD11	1.18	1.13
1:A:1182:LEU:HD23	8:S:127:TRP:HZ2	1.11	1.13
26:j:57:LEU:HB3	24:i:91:THR:HG21	1.22	1.13
20:v:612:ILE:HG13	20:v:613:PRO:HD3	1.16	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:105:LYS:HA	29:k:108:ARG:HH21	1.07	1.12
6:Q:304:THR:CG2	7:R:153:PRO:HG2	1.80	1.12
15:H:26:TYR:O	15:H:27:LYS:HG2	1.49	1.12
26:j:17:LEU:HD12	26:j:19:ILE:HD11	1.24	1.11
19:L:113:U:O4	27:w:48:TYR:HA	1.46	1.11
19:L:1137:U:H2'	19:L:1138:G:H1'	1.26	1.11
7:R:155:GLN:HB3	19:L:78:G:H5''	1.31	1.11
19:L:85:A:H2'	19:L:86:U:H5''	1.25	1.11
1:A:1404:HIS:CD2	1:A:1437:ILE:HD13	1.86	1.11
25:m:17:ILE:HG23	25:m:92:ILE:CG2	1.79	1.10
29:k:86:ILE:HD11	30:l:11:LEU:HD12	1.33	1.10
28:e:56:ALA:HB2	28:e:72:VAL:HG23	1.17	1.10
29:k:31:ILE:CD1	29:k:49:ILE:CD1	2.27	1.10
30:l:21:LEU:HD23	30:l:72:ILE:HG12	1.32	1.09
10:Z:181:LEU:HD11	10:Z:194:LEU:CG	1.82	1.09
20:v:385:PHE:HA	20:v:388:LEU:HD12	1.20	1.09
29:s:54:PRO:HB2	29:s:57:GLN:HG2	1.31	1.09
24:i:30:TRP:CD1	24:i:38:ARG:HD3	1.86	1.09
12:d:271:ILE:HD13	12:d:281:LYS:HG3	1.12	1.09
1:A:2027:LEU:HD21	28:e:57:ARG:HH21	1.15	1.08
10:Z:181:LEU:HD11	10:Z:194:LEU:HB3	1.27	1.08
28:g:35:ASN:CB	28:g:61:PHE:CZ	2.37	1.08
29:k:49:ILE:CG2	29:k:81:VAL:HA	1.84	1.07
30:l:47:VAL:HG23	30:l:59:MET:HG3	1.31	1.07
17:D:128:A:H2'	17:D:129:G:H2'	1.08	1.07
25:m:84:TYR:CE2	29:k:6:VAL:HG11	1.89	1.07
20:v:711:MET:CE	20:v:748:PHE:CB	2.34	1.06
20:v:386:GLU:HA	20:v:389:ILE:HD12	1.38	1.06
19:L:1137:U:H2'	19:L:1138:G:O4'	1.55	1.06
26:j:17:LEU:HD13	26:j:19:ILE:HD11	1.32	1.06
6:Q:304:THR:HG22	7:R:153:PRO:HG2	1.09	1.05
10:Z:181:LEU:CD1	10:Z:194:LEU:HB3	1.86	1.05
25:m:17:ILE:HG23	25:m:92:ILE:HG22	1.36	1.05
6:Q:215:PRO:HB3	7:R:171:ASP:OD1	1.56	1.05
12:d:247:VAL:HG21	12:d:280:LEU:HD11	1.36	1.05
1:A:928:ARG:HH22	16:B:75:A:H5''	1.18	1.04
1:A:1384:PRO:HA	1:A:1431:HIS:HE1	1.21	1.04
17:D:175:G:O6	24:i:35:ILE:HD11	1.57	1.04
24:i:30:TRP:CD1	24:i:38:ARG:CD	2.40	1.04
19:L:84:C:C2'	19:L:85:A:C8	2.39	1.04
7:R:146:LEU:HD13	7:R:151:LEU:HD13	1.36	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1435:LYS:HG2	1:A:1436:LEU:H	1.23	1.03
29:k:105:LYS:HA	29:k:108:ARG:NH2	1.73	1.03
30:y:21:LEU:CD1	30:y:44:LEU:HD11	1.87	1.03
1:A:2030:PRO:HG3	28:e:73:LYS:HB2	1.38	1.03
29:k:31:ILE:CG1	29:k:49:ILE:CD1	2.36	1.03
26:j:27:GLY:HA3	26:j:40:LEU:HD12	1.36	1.03
6:Q:298:SER:HB3	19:L:75:A:N6	1.74	1.03
10:Z:181:LEU:HD21	10:Z:186:LEU:HD22	1.35	1.03
1:A:2024:MET:HA	28:e:71:ASN:HD21	1.23	1.02
25:m:17:ILE:CG2	25:m:92:ILE:CG2	2.36	1.02
1:A:930:ASN:HA	19:L:30:A:H5'	1.37	1.02
7:R:204:LEU:HD12	7:R:204:LEU:H	1.25	1.02
19:L:113:U:C5	27:w:48:TYR:CD1	2.46	1.02
28:g:40:THR:O	28:g:41:ARG:HG2	1.60	1.02
6:Q:304:THR:HG22	7:R:153:PRO:CG	1.90	1.02
26:j:17:LEU:CD1	26:j:19:ILE:CD1	2.37	1.02
28:g:35:ASN:HA	28:g:61:PHE:CE2	1.93	1.02
6:Q:248:CYS:SG	6:Q:316:LEU:HD12	2.00	1.01
6:Q:298:SER:HB3	19:L:75:A:H61	1.25	1.01
12:d:263:SER:HB3	12:d:287:PHE:CZ	1.93	1.01
32:F:47:PHE:HZ	32:F:97:PHE:CE1	1.78	1.01
5:P:34:ILE:HD13	12:d:155:LEU:CD1	1.91	1.01
7:R:51:PHE:CD2	7:R:80:MET:HG2	1.95	1.01
15:H:27:LYS:HD3	15:H:29:TYR:CE1	1.95	1.01
17:D:4:C:H2'	17:D:5:A:H8	1.25	1.01
16:B:0:G:H5'	16:B:1:G:H5''	1.42	1.01
1:A:928:ARG:NH2	16:B:75:A:H5''	1.75	1.00
17:D:128:A:C2'	17:D:129:G:H2'	1.91	1.00
19:L:85:A:H2'	19:L:86:U:H5'	1.03	1.00
20:v:541:SER:O	20:v:544:ILE:HG22	1.61	1.00
1:A:1229:GLU:OE2	8:S:128:ARG:HG2	1.62	1.00
19:L:1082:A:H2'	19:L:1083:A:H8	1.26	1.00
20:v:386:GLU:HA	20:v:389:ILE:CD1	1.92	1.00
12:d:267:TYR:CD2	12:d:284:LEU:HD23	1.97	0.99
29:k:48:CYS:SG	29:k:82:LEU:CD1	2.50	0.99
6:Q:303:GLY:HA3	6:Q:309:ASN:OD1	1.62	0.99
24:u:35:ILE:CD1	27:w:79:LEU:CD1	2.40	0.99
1:A:1232:SER:HB3	8:S:135:ARG:HH11	1.18	0.99
1:A:1384:PRO:HA	1:A:1431:HIS:CE1	1.98	0.99
1:A:1435:LYS:HB2	1:A:1437:ILE:CD1	1.91	0.99
10:Z:181:LEU:HD22	10:Z:191:ARG:HG2	1.39	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:241:MET:HG2	12:d:279:LEU:HD13	1.42	0.98
12:d:255:ALA:HB1	12:d:291:PHE:CD2	1.99	0.98
19:L:3:G:O2'	19:L:4:A:N7	1.96	0.98
7:R:151:LEU:CA	19:L:78:G:P	2.52	0.98
1:A:1870:VAL:HG22	19:L:47:U:OP1	1.62	0.98
19:L:46:C:H2'	19:L:47:U:C6	1.98	0.98
19:L:1137:U:O2'	19:L:1138:G:H4'	1.63	0.98
22:b:50:LEU:C	22:b:55:HIS:CB	2.36	0.97
1:A:1035:LEU:HD11	1:A:1038:ILE:HD13	1.46	0.97
12:d:271:ILE:CD1	12:d:281:LYS:HG3	1.93	0.97
24:i:28:THR:HG22	24:i:40:LYS:HD2	1.45	0.97
28:e:56:ALA:HB2	28:e:72:VAL:HG21	1.47	0.97
5:P:34:ILE:HD13	12:d:155:LEU:HD13	1.43	0.97
6:Q:300:ALA:HB2	7:R:154:ALA:CB	1.95	0.97
19:L:46:C:H2'	19:L:47:U:H5	1.28	0.97
25:m:96:ILE:HD11	28:g:89:ARG:HH22	1.29	0.97
22:b:110:ARG:HA	22:b:134:VAL:CB	1.95	0.97
29:s:59:ASP:HA	29:s:62:ARG:HH21	1.31	0.96
1:A:2027:LEU:HD21	28:e:57:ARG:NH2	1.80	0.96
7:R:155:GLN:HG2	19:L:78:G:OP2	1.65	0.96
29:k:49:ILE:HG22	29:k:81:VAL:CA	1.94	0.96
19:L:1082:A:H2'	19:L:1083:A:C8	2.00	0.96
11:c:189:ARG:CZ	12:d:38:LEU:HD13	1.95	0.96
1:A:1992:TYR:HH	1:A:2005:PHE:HD1	1.12	0.96
18:E:55:G:O2'	18:E:56:A:H5'	1.64	0.96
12:d:267:TYR:O	12:d:271:ILE:HG22	1.64	0.96
12:d:241:MET:CG	12:d:279:LEU:CD1	2.44	0.95
22:b:110:ARG:CA	22:b:134:VAL:CB	2.44	0.95
1:A:1182:LEU:HD23	8:S:127:TRP:CZ2	2.01	0.95
29:k:31:ILE:HG13	29:k:49:ILE:CD1	1.94	0.95
18:E:100:U:H5'	18:E:100:U:H6	1.30	0.95
19:L:50:U:H2'	19:L:51:C:C2	2.01	0.95
19:L:1085:G:C2	19:L:1086:U:C5	2.54	0.95
28:e:56:ALA:CB	28:e:72:VAL:CG2	2.42	0.95
30:l:14:ALA:O	30:l:17:HIS:HB2	1.67	0.95
28:e:56:ALA:CB	28:e:72:VAL:HG23	1.96	0.95
7:R:155:GLN:HB3	19:L:78:G:C5'	1.96	0.95
18:E:99:A:H2'	18:E:100:U:H5''	1.49	0.94
4:O:327:CYS:SG	4:O:328:THR:N	2.28	0.94
7:R:40:GLY:HA2	15:H:26:TYR:OH	1.64	0.94
19:L:28:U:O2'	19:L:29:C:H5'	1.66	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:121:C:H1'	28:e:49:ARG:HG2	1.48	0.94
19:L:84:C:H2'	19:L:85:A:H8	1.29	0.93
25:m:47:LEU:HD11	25:m:61:ALA:CB	1.98	0.93
12:d:241:MET:HG2	12:d:279:LEU:HD11	1.51	0.93
24:u:35:ILE:HD13	27:w:79:LEU:CD1	1.98	0.93
10:Z:181:LEU:CD2	10:Z:191:ARG:HG2	1.98	0.93
28:g:50:ASN:HD22	28:g:52:HIS:HE1	0.99	0.92
1:A:1869:ASN:HA	19:L:47:U:H5'	1.52	0.92
31:r:99:ARG:HG2	31:o:98:LEU:CD1	1.98	0.92
10:Z:449:PHE:HB3	10:Z:477:MET:CE	2.00	0.92
6:Q:248:CYS:SG	6:Q:316:LEU:CD1	2.58	0.92
29:k:13:ALA:HB2	29:k:37:PHE:HZ	1.31	0.92
29:s:48:CYS:SG	29:s:82:LEU:O	2.27	0.92
28:g:35:ASN:HB2	28:g:61:PHE:HZ	1.25	0.92
19:L:151:A:H61	19:L:1086:U:H3	1.11	0.92
29:k:44:VAL:HG22	29:k:86:ILE:HG22	1.52	0.92
28:g:50:ASN:HD22	28:g:52:HIS:CE1	1.87	0.91
16:B:1:G:OP1	16:B:1:G:N2	2.02	0.91
25:m:47:LEU:HD11	25:m:61:ALA:HB1	1.53	0.91
30:l:59:MET:SD	30:l:62:ILE:HD12	2.09	0.91
28:g:40:THR:C	28:g:41:ARG:HG2	1.94	0.91
29:k:35:MET:HB3	30:l:84:PHE:HE2	1.34	0.91
29:k:31:ILE:HG13	29:k:49:ILE:HD12	1.51	0.91
1:A:1182:LEU:CD2	8:S:127:TRP:HZ2	1.83	0.91
10:Z:181:LEU:CD1	10:Z:194:LEU:CD1	2.38	0.91
27:w:32:LYS:HG3	27:w:33:PHE:CD1	2.06	0.91
16:B:71:C:O2'	16:B:72:A:H5''	1.71	0.91
1:A:581:LEU:HG	7:R:33:TRP:CE3	2.05	0.90
17:D:168:U:H2'	24:i:49:PHE:CD1	2.06	0.90
17:D:173:U:H1'	28:g:99:ASP:HB3	1.48	0.90
30:y:21:LEU:HD11	30:y:44:LEU:HD11	1.51	0.90
19:L:113:U:C4	27:w:48:TYR:HA	2.05	0.90
10:Z:450:PRO:O	10:Z:451:LEU:HB2	1.69	0.90
12:d:255:ALA:CB	12:d:291:PHE:HE2	1.81	0.90
26:j:17:LEU:HD13	26:j:19:ILE:CD1	2.01	0.90
29:k:86:ILE:HD11	30:l:11:LEU:CD1	2.02	0.90
16:B:72:A:H2'	16:B:73:A:O4'	1.71	0.90
6:Q:207:LEU:HD23	6:Q:290:ILE:HG22	1.51	0.90
1:A:928:ARG:HD3	19:L:32:G:C2	2.07	0.90
7:R:145:ALA:HB1	7:R:204:LEU:CD1	2.02	0.90
19:L:84:C:H2'	19:L:85:A:N7	1.86	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:g:76:TRP:CZ2	28:g:87:ARG:HD3	2.07	0.89
5:P:34:ILE:CD1	12:d:155:LEU:HD13	2.03	0.89
1:A:1435:LYS:HB2	1:A:1437:ILE:HD11	1.54	0.89
19:L:117:U:O2	25:z:35:GLN:HB3	1.71	0.89
20:v:385:PHE:CA	20:v:388:LEU:HD12	2.03	0.89
30:l:21:LEU:CD2	30:l:72:ILE:HG12	2.02	0.89
1:A:1960:GLU:C	1:A:1961:LEU:HD12	1.97	0.89
1:A:930:ASN:HA	19:L:30:A:C5'	2.03	0.89
1:A:1992:TYR:CE1	1:A:2008:LEU:CD2	2.40	0.89
19:L:118:U:H3	28:e:66:ASN:HD22	1.17	0.89
29:k:40:HIS:O	29:k:41:MET:HB2	1.70	0.89
10:Z:181:LEU:CD1	10:Z:194:LEU:CG	2.51	0.89
1:A:1843:LEU:HD23	1:A:1849:LYS:HZ3	1.38	0.88
1:A:1182:LEU:CD2	8:S:127:TRP:CZ2	2.56	0.88
6:Q:207:LEU:CD2	6:Q:290:ILE:HG22	2.03	0.88
25:z:47:LEU:HD21	25:z:61:ALA:CB	2.02	0.88
30:l:17:HIS:CG	30:l:75:PRO:HG2	2.07	0.88
19:L:152:C:H42	19:L:1085:G:H1	1.20	0.88
15:H:26:TYR:CZ	15:H:28:ASP:OD1	2.26	0.88
30:l:65:ARG:HH11	30:l:65:ARG:HG3	1.36	0.88
19:L:67:A:O2'	19:L:68:U:H5'	1.74	0.88
10:Z:449:PHE:HB3	10:Z:477:MET:HE3	1.53	0.88
28:g:76:TRP:CH2	28:g:87:ARG:HD3	2.09	0.88
30:l:75:PRO:HB2	30:l:78:LEU:HD13	1.56	0.88
12:d:289:LYS:HE2	20:v:643:HIS:HE1	1.36	0.88
30:y:33:LEU:HA	30:y:44:LEU:HD23	1.54	0.88
1:A:1228:TRP:CZ2	8:S:135:ARG:NH2	2.41	0.87
24:u:35:ILE:HD11	27:w:79:LEU:CD1	2.03	0.87
26:j:27:GLY:CA	26:j:40:LEU:HD12	2.05	0.87
26:j:61:THR:HG22	24:i:91:THR:HG23	1.55	0.87
17:D:17:C:H4'	17:D:18:A:OP2	1.75	0.87
1:A:743:LYS:HE3	1:A:749:ARG:NH1	1.89	0.87
19:L:85:A:O2'	19:L:86:U:H5''	1.72	0.87
19:L:151:A:N6	19:L:1086:U:H3	1.72	0.87
19:L:1130:U:H2'	19:L:1131:U:O4'	1.73	0.87
11:c:237:ILE:HD11	12:d:114:CYS:SG	2.14	0.87
28:g:50:ASN:HB3	28:g:52:HIS:ND1	1.90	0.87
16:B:2:U:O2'	16:B:3:A:OP2	1.93	0.87
28:g:45:ILE:HD12	28:g:55:ILE:HG12	1.57	0.87
19:L:85:A:C2'	19:L:86:U:H5'	1.97	0.87
30:l:82:PRO:O	30:l:85:LYS:HD2	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:386:GLU:CA	20:v:389:ILE:HD12	2.04	0.86
18:E:64:U:O2'	18:E:65:U:OP1	1.93	0.86
2:C:681:CYS:SG	2:C:714:PRO:HG3	2.15	0.86
19:L:1146:G:H2'	19:L:1147:A:C8	2.11	0.86
19:L:1154:U:HO2'	19:L:1155:C:H5'	1.37	0.86
11:c:200:ILE:HG21	12:d:45:GLU:HG3	1.58	0.86
19:L:66:A:H2'	19:L:67:A:H8	1.41	0.86
6:Q:300:ALA:CB	7:R:154:ALA:HB1	2.04	0.86
15:H:88:GLU:HG2	15:H:92:TRP:HZ3	1.41	0.86
29:k:29:VAL:O	29:k:50:GLU:HA	1.76	0.86
10:Z:450:PRO:O	10:Z:451:LEU:CD2	2.25	0.85
14:n:51:PHE:HE1	14:n:55:GLU:HG3	1.39	0.85
7:R:209:ASP:OD1	19:L:79:A:H5''	1.77	0.85
25:m:52:LEU:HD21	28:g:79:LYS:C	2.00	0.85
10:Z:181:LEU:HD11	10:Z:194:LEU:HG	1.58	0.85
30:y:21:LEU:HD12	30:y:44:LEU:HD11	1.56	0.85
19:L:1154:U:H2'	19:L:1155:C:C6	2.11	0.85
1:A:1235:PRO:HD3	8:S:133:PHE:CZ	2.11	0.85
12:d:229:VAL:HG12	12:d:274:TRP:CZ2	2.12	0.85
28:g:50:ASN:ND2	28:g:52:HIS:HE1	1.75	0.85
17:D:4:C:H2'	17:D:5:A:C8	2.12	0.84
30:l:49:ALA:HB2	30:l:59:MET:HE3	1.59	0.84
1:A:143:ILE:HD12	1:A:143:ILE:O	1.77	0.84
1:A:1843:LEU:HD23	1:A:1849:LYS:NZ	1.91	0.84
19:L:1137:U:C2'	19:L:1138:G:H1'	2.05	0.84
1:A:1870:VAL:CG2	19:L:47:U:OP1	2.24	0.84
7:R:155:GLN:CB	19:L:78:G:H5''	2.06	0.84
19:L:1:A:H1'	19:L:2:C:C5	2.12	0.84
1:A:184:GLU:OE1	1:A:187:LYS:HD2	1.78	0.84
1:A:1663:PHE:HZ	1:A:1902:GLN:HE21	1.23	0.84
7:R:151:LEU:HD23	19:L:78:G:C5'	2.07	0.84
10:Z:181:LEU:HD23	10:Z:186:LEU:HD22	1.58	0.84
1:A:1032:ILE:O	1:A:1035:LEU:CG	2.25	0.84
25:m:39:ILE:HD11	25:m:84:TYR:CE1	2.13	0.84
28:g:43:PRO:O	28:g:107:THR:CB	2.26	0.84
16:B:0:G:C5'	16:B:1:G:H5''	2.07	0.83
12:d:289:LYS:HG3	20:v:609:GLU:HG2	1.58	0.83
20:v:385:PHE:HA	20:v:388:LEU:CD1	2.05	0.83
29:s:54:PRO:CB	29:s:57:GLN:HG2	2.08	0.83
1:A:205:THR:OG1	1:A:495:ARG:HD2	1.79	0.83
22:b:14:TYR:O	29:s:102:LEU:CD1	2.26	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:35:MET:HB3	30:l:84:PHE:CE2	2.13	0.83
18:E:59:A:H2'	18:E:60:G:O4'	1.79	0.83
18:E:102:U:H2'	18:E:103:A:N9	1.94	0.83
12:d:255:ALA:CB	12:d:291:PHE:CD2	2.60	0.83
1:A:2027:LEU:CD2	28:e:57:ARG:NH2	2.42	0.82
11:c:181:ARG:NH2	11:c:185:LEU:HD11	1.94	0.82
19:L:68:U:O2'	19:L:69:G:H5'	1.78	0.82
2:C:684:GLU:HB3	2:C:712:ALA:O	1.79	0.82
12:d:247:VAL:HG21	12:d:280:LEU:CD1	2.07	0.82
1:A:1663:PHE:CZ	1:A:1902:GLN:HG3	2.13	0.82
12:d:284:LEU:O	12:d:284:LEU:HD22	1.79	0.82
19:L:82:C:O2'	19:L:83:U:H5'	1.79	0.82
24:i:30:TRP:NE1	24:i:38:ARG:CD	2.39	0.82
15:H:26:TYR:O	15:H:27:LYS:CG	2.25	0.82
17:D:129:G:O4'	17:D:130:A:H3'	1.79	0.82
1:A:1035:LEU:O	1:A:1035:LEU:HD12	1.79	0.82
26:x:19:ILE:O	26:x:23:ARG:HB2	1.78	0.82
18:E:55:G:C2'	18:E:56:A:H5'	2.10	0.82
25:m:52:LEU:HD21	28:g:80:LYS:N	1.94	0.82
30:l:47:VAL:HG23	30:l:59:MET:CG	2.10	0.82
19:L:15:C:H1'	19:L:16:U:C5	2.14	0.81
19:L:69:G:O2'	19:L:70:A:H5'	1.79	0.81
19:L:73:U:O2'	19:L:74:C:H5'	1.80	0.81
5:P:148:HIS:HB2	12:d:131:ARG:HG3	1.60	0.81
7:R:51:PHE:HD2	7:R:80:MET:HG2	1.44	0.81
26:j:6:GLU:HG2	30:l:37:GLU:OE2	1.80	0.81
26:j:64:ARG:HG3	24:i:50:MET:SD	2.20	0.81
29:k:42:ASN:HB3	29:k:89:GLY:H	1.45	0.81
29:k:49:ILE:CG2	29:k:81:VAL:CA	2.57	0.81
1:A:2030:PRO:HG3	28:e:73:LYS:CB	2.10	0.81
19:L:4:A:C1'	20:v:529:HIS:CD2	2.63	0.81
24:u:35:ILE:CD1	27:w:79:LEU:HD12	2.09	0.81
18:E:102:U:O3'	18:E:103:A:O4'	1.98	0.81
18:E:102:U:H3'	18:E:103:A:C8	2.16	0.81
30:l:15:GLN:C	30:l:15:GLN:HE21	1.89	0.81
25:m:3:LEU:CD2	28:g:95:PHE:HE1	1.94	0.81
19:L:46:C:C2'	19:L:47:U:C5	2.53	0.81
29:k:13:ALA:HA	29:k:37:PHE:CE2	2.16	0.81
29:k:42:ASN:HB3	29:k:89:GLY:N	1.95	0.81
19:L:1085:G:N2	19:L:1086:U:C4	2.49	0.81
20:v:612:ILE:CG1	20:v:613:PRO:HD3	2.07	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:84:LEU:HD23	30:l:75:PRO:O	1.81	0.81
25:z:47:LEU:HD21	25:z:61:ALA:HB3	1.62	0.81
25:m:4:VAL:HG22	25:m:36:MET:HE2	1.63	0.81
26:j:27:GLY:HA3	26:j:40:LEU:CD1	2.09	0.81
1:A:607:THR:CG2	16:B:2:U:H5'	2.10	0.80
19:L:1085:G:C2	19:L:1086:U:C4	2.68	0.80
25:m:96:ILE:CD1	28:g:89:ARG:HH22	1.92	0.80
28:g:35:ASN:HB2	28:g:61:PHE:CE2	2.15	0.80
1:A:2024:MET:HA	28:e:71:ASN:ND2	1.95	0.80
2:C:681:CYS:SG	2:C:714:PRO:CD	2.69	0.80
19:L:79:A:O2'	19:L:80:G:H5'	1.81	0.80
1:A:1035:LEU:HD11	1:A:1038:ILE:CD1	2.11	0.80
1:A:1964:PRO:O	1:A:1965:PHE:HB2	1.81	0.80
19:L:1137:U:C2'	19:L:1138:G:C4'	2.60	0.80
32:F:47:PHE:CZ	32:F:97:PHE:CE1	2.67	0.80
12:d:263:SER:HB3	12:d:287:PHE:HZ	1.42	0.80
30:l:17:HIS:ND1	30:l:75:PRO:HG2	1.96	0.80
26:j:17:LEU:HD12	26:j:19:ILE:CD1	2.07	0.80
12:d:267:TYR:HE2	12:d:287:PHE:HB3	1.47	0.80
20:v:662:CYS:SG	20:v:665:ILE:HD11	2.22	0.79
29:k:86:ILE:CD1	30:l:11:LEU:HD12	2.11	0.79
29:k:105:LYS:CA	29:k:108:ARG:HH21	1.91	0.79
7:R:41:PHE:CZ	7:R:43:GLY:CA	2.66	0.79
11:c:181:ARG:CZ	12:d:49:ARG:NH1	2.45	0.79
25:z:72:GLN:HE22	25:z:79:ILE:HD11	1.46	0.79
7:R:155:GLN:CG	19:L:78:G:H5'	2.13	0.79
18:E:84:C:O2'	18:E:85:C:OP1	1.99	0.79
1:A:1404:HIS:CG	1:A:1437:ILE:CD1	2.65	0.79
27:h:71:ILE:HG23	28:g:103:VAL:HG23	1.64	0.79
6:Q:206:PHE:HD2	6:Q:291:ILE:CD1	1.96	0.79
7:R:155:GLN:HG2	19:L:78:G:H5'	1.65	0.79
4:O:373:LEU:HD12	4:O:373:LEU:O	1.83	0.79
7:R:152:LYS:HB3	7:R:153:PRO:HD2	1.65	0.79
28:g:35:ASN:O	28:g:39:VAL:HG23	1.83	0.79
11:c:189:ARG:NH2	12:d:38:LEU:HD13	1.95	0.79
19:L:16:U:H5'	19:L:18:U:C5	2.18	0.79
19:L:1085:G:N2	19:L:1086:U:C5	2.51	0.79
19:L:1137:U:C2'	19:L:1138:G:C1'	2.53	0.79
25:m:72:GLN:HE22	25:m:79:ILE:HD11	1.47	0.79
15:H:26:TYR:CE1	15:H:28:ASP:OD1	2.36	0.79
6:Q:214:ILE:HD11	6:Q:283:ILE:HG12	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:167:A:H2'	27:h:48:TYR:CE2	2.18	0.79
19:L:66:A:O2'	19:L:67:A:H5'	1.83	0.79
19:L:51:C:H2'	19:L:52:A:O4'	1.84	0.79
17:D:3:G:O2'	17:D:4:C:H5'	1.83	0.78
18:E:100:U:H6	18:E:100:U:C5'	1.94	0.78
22:b:14:TYR:O	29:s:102:LEU:HD12	1.84	0.78
14:n:51:PHE:CE1	14:n:55:GLU:CG	2.67	0.78
25:m:17:ILE:CG2	25:m:92:ILE:HG22	2.07	0.78
1:A:1434:GLU:N	1:A:1434:GLU:OE2	2.16	0.78
12:d:330:ILE:HA	12:d:334:PHE:HB2	1.64	0.78
1:A:1232:SER:CB	8:S:135:ARG:NH1	2.44	0.78
30:l:11:LEU:HD11	30:l:72:ILE:CD1	2.13	0.78
24:i:40:LYS:HG3	24:i:60:ILE:CD1	2.13	0.78
7:R:145:ALA:HB1	7:R:204:LEU:HD12	1.64	0.78
19:L:81:G:O2'	19:L:82:C:H5'	1.84	0.78
19:L:113:U:C5	27:w:48:TYR:CE1	2.71	0.78
19:L:1136:U:O3'	19:L:1137:U:H4'	1.82	0.78
19:L:113:U:O4	27:w:48:TYR:CA	2.31	0.78
30:y:21:LEU:CD2	30:y:72:ILE:HG12	2.14	0.78
19:L:66:A:H2'	19:L:67:A:C8	2.19	0.78
25:m:19:LEU:HD22	25:m:91:THR:CG2	2.10	0.78
30:l:21:LEU:HD23	30:l:72:ILE:CG1	2.13	0.78
1:A:928:ARG:NH2	16:B:75:A:C5'	2.47	0.78
29:s:59:ASP:HA	29:s:62:ARG:NH2	1.99	0.78
7:R:159:ARG:HG3	7:R:159:ARG:HH11	1.46	0.77
19:L:72:C:O2'	19:L:73:U:H5'	1.84	0.77
28:e:56:ALA:HB1	28:e:69:LEU:HD23	1.65	0.77
30:y:21:LEU:HD12	30:y:44:LEU:CD1	2.12	0.77
19:L:1137:U:H2'	19:L:1138:G:C4'	2.13	0.77
28:e:68:VAL:C	28:e:69:LEU:HD12	2.09	0.77
29:k:13:ALA:CB	29:k:37:PHE:HZ	1.97	0.77
12:d:267:TYR:CE2	12:d:287:PHE:HB3	2.20	0.77
18:E:58:C:H2'	18:E:59:A:H5'	1.65	0.77
18:E:67:C:H6	18:E:67:C:H5''	1.49	0.77
25:m:93:ARG:HH11	25:m:93:ARG:HG3	1.50	0.77
2:C:685:SER:HB3	2:C:852:THR:HG22	1.65	0.77
25:m:39:ILE:HD11	25:m:84:TYR:HE1	1.49	0.77
19:L:1101:C:H5'	19:L:1102:C:OP2	1.84	0.77
29:k:35:MET:CB	30:l:84:PHE:HE2	1.97	0.77
1:A:1964:PRO:HG3	1:A:2016:LYS:NZ	2.00	0.77
28:e:59:LYS:CG	28:e:70:GLU:HG2	2.13	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:i:32:PHE:HD1	24:i:86:ASN:O	1.68	0.77
1:A:1229:GLU:OE2	8:S:128:ARG:CG	2.33	0.76
29:s:57:GLN:HB3	29:s:75:ILE:HG23	1.67	0.76
1:A:1435:LYS:HG2	1:A:1436:LEU:N	2.00	0.76
12:d:329:LEU:HD23	20:v:642:GLU:HG3	1.67	0.76
19:L:70:A:O2'	19:L:71:C:H5'	1.85	0.76
29:s:54:PRO:HB2	29:s:57:GLN:CG	2.15	0.76
30:l:33:LEU:HD21	30:l:35:GLU:O	1.85	0.76
19:L:1137:U:C2'	19:L:1138:G:H4'	2.15	0.76
19:L:1:A:P	19:L:1:A:H2'	2.25	0.76
19:L:125:C:H5''	28:e:80:LYS:HA	1.67	0.76
1:A:1404:HIS:CG	1:A:1437:ILE:HD13	2.20	0.76
19:L:80:G:O2'	19:L:81:G:H5'	1.85	0.76
20:v:612:ILE:HG13	20:v:613:PRO:HD2	1.67	0.76
20:v:617:PRO:O	20:v:618:GLU:HB2	1.84	0.76
1:A:607:THR:HG23	16:B:2:U:H5'	1.68	0.76
20:v:612:ILE:CG1	20:v:613:PRO:CD	2.55	0.76
25:m:86:ASN:HD21	29:k:41:MET:CE	1.99	0.76
30:y:35:GLU:HB2	30:y:43:GLN:HG2	1.68	0.76
24:u:35:ILE:HD13	27:w:79:LEU:HD12	1.64	0.75
26:j:61:THR:CG2	24:i:91:THR:HG23	2.16	0.75
1:A:581:LEU:HG	7:R:33:TRP:CZ3	2.22	0.75
4:O:348:GLU:C	4:O:349:LYS:HG2	2.10	0.75
24:i:30:TRP:CG	24:i:38:ARG:NE	2.54	0.75
1:A:1122:ASP:OD1	1:A:1163:ARG:HD3	1.87	0.75
12:d:255:ALA:HB3	12:d:291:PHE:HE2	1.51	0.75
19:L:1114:G:H2'	19:L:1115:G:O4'	1.87	0.75
17:D:4:C:O2'	17:D:5:A:H5'	1.86	0.75
19:L:74:C:H2'	19:L:75:A:H8	1.51	0.75
6:Q:215:PRO:CB	7:R:171:ASP:OD1	2.33	0.75
30:l:17:HIS:ND1	30:l:75:PRO:CG	2.50	0.75
1:A:2011:LEU:HG	1:A:2040:TRP:CH2	2.20	0.75
7:R:41:PHE:H	15:H:26:TYR:HE1	1.34	0.75
1:A:1435:LYS:HB2	1:A:1437:ILE:HD12	1.68	0.75
7:R:145:ALA:O	7:R:205:LEU:HD21	1.87	0.75
24:u:35:ILE:HD13	27:w:79:LEU:HD11	1.67	0.75
25:m:41:THR:O	25:m:83:GLN:HG2	1.86	0.75
18:E:100:U:H5'	18:E:100:U:C6	2.20	0.74
30:y:31:GLY:HA3	30:y:47:VAL:HG12	1.68	0.74
7:R:206:LEU:N	7:R:206:LEU:HD23	2.02	0.74
26:j:14:LYS:HG2	26:j:74:LEU:HD11	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:13:ALA:HB2	29:k:37:PHE:CZ	2.21	0.74
29:k:49:ILE:HD12	29:k:49:ILE:H	1.52	0.74
7:R:155:GLN:CB	19:L:78:G:C5'	2.63	0.74
12:d:267:TYR:CD2	12:d:284:LEU:CD2	2.69	0.74
1:A:1964:PRO:CG	1:A:2016:LYS:NZ	2.50	0.74
7:R:51:PHE:HD2	7:R:80:MET:CG	1.99	0.74
7:R:145:ALA:CB	7:R:204:LEU:CD1	2.66	0.74
12:d:267:TYR:HE2	12:d:287:PHE:CD2	2.05	0.74
29:k:15:LEU:HB2	29:k:18:TYR:CD2	2.22	0.74
7:R:159:ARG:HG3	7:R:159:ARG:NH1	2.00	0.74
17:D:130:A:H4'	17:D:131:A:O5'	1.86	0.74
29:s:28:ARG:HD3	29:s:52:ARG:HE	1.51	0.74
27:w:32:LYS:HG3	27:w:33:PHE:HD1	1.53	0.74
25:z:23:THR:HG22	25:z:47:LEU:HD11	1.68	0.74
19:L:67:A:H2'	19:L:68:U:H6	1.50	0.74
30:l:24:THR:HA	30:l:70:LYS:NZ	2.03	0.74
17:D:167:A:H2'	27:h:48:TYR:HE2	1.51	0.74
26:j:29:LEU:HD23	26:j:29:LEU:C	2.13	0.74
26:j:57:LEU:HB3	24:i:91:THR:CG2	2.11	0.74
1:A:1235:PRO:HD3	8:S:133:PHE:CE1	2.23	0.74
1:A:2084:LEU:HD12	1:A:2085:GLY:H	1.53	0.74
2:C:681:CYS:SG	2:C:714:PRO:HD3	2.28	0.73
7:R:145:ALA:CB	7:R:204:LEU:HD11	2.18	0.73
14:n:51:PHE:CE1	14:n:55:GLU:HG2	2.23	0.73
19:L:117:U:C2	25:z:35:GLN:HB3	2.22	0.73
19:L:1085:G:N3	19:L:1086:U:C5	2.55	0.73
28:e:59:LYS:HG2	28:e:70:GLU:CG	2.18	0.73
2:C:406:VAL:CG1	2:C:427:LEU:HD23	2.18	0.73
17:D:123:U:C2'	17:D:124:C:H5'	2.17	0.73
19:L:1137:U:C2'	19:L:1138:G:O4'	2.35	0.73
7:R:44:ASN:O	7:R:45:THR:HB	1.88	0.73
10:Z:181:LEU:HD12	10:Z:194:LEU:HD12	0.82	0.73
19:L:1129:U:H2'	19:L:1130:U:H5'	1.71	0.73
26:j:23:ARG:H	26:j:23:ARG:HD3	1.52	0.73
29:s:52:ARG:O	29:s:77:VAL:HG13	1.87	0.73
7:R:41:PHE:CE1	7:R:43:GLY:N	2.56	0.73
19:L:1105:C:H1'	19:L:1106:G:C1'	2.19	0.73
25:z:45:LEU:HD11	25:z:65:LEU:HD13	1.68	0.73
19:L:4:A:H1'	20:v:529:HIS:NE2	2.03	0.73
28:g:78:GLU:HG2	28:g:85:ILE:CG2	2.19	0.73
6:Q:295:SER:CB	19:L:73:U:OP1	2.37	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:450:PRO:O	10:Z:451:LEU:CB	2.37	0.73
1:A:1960:GLU:O	1:A:1961:LEU:HD12	1.88	0.73
28:e:56:ALA:HB2	28:e:72:VAL:CB	2.17	0.73
1:A:2027:LEU:CD2	28:e:57:ARG:HH21	1.96	0.73
15:H:27:LYS:HD3	15:H:29:TYR:CZ	2.23	0.73
17:D:100:A:H3'	17:D:101:C:H5''	1.71	0.73
30:l:24:THR:HA	30:l:70:LYS:HZ2	1.54	0.73
25:z:47:LEU:HD21	25:z:61:ALA:HB1	1.70	0.73
1:A:1663:PHE:CZ	1:A:1902:GLN:CG	2.72	0.73
1:A:1842:GLU:O	1:A:1843:LEU:HG	1.89	0.73
17:D:173:U:C2	28:g:97:ARG:CZ	2.72	0.73
25:m:82:LEU:HD11	25:m:85:ILE:HB	1.70	0.72
25:m:45:LEU:HD11	25:m:65:LEU:HD13	1.69	0.72
26:j:18:ASN:C	26:j:19:ILE:HD13	2.14	0.72
29:k:109:LEU:C	29:k:109:LEU:HD12	2.15	0.72
28:e:59:LYS:HG2	28:e:70:GLU:HG2	1.69	0.72
7:R:151:LEU:HD23	19:L:78:G:H4'	1.72	0.72
16:B:9:A:H1'	16:B:10:A:OP1	1.88	0.72
19:L:15:C:O2'	19:L:16:U:H5''	1.88	0.72
1:A:1889:LEU:HD11	1:A:1991:ILE:HG23	1.71	0.72
29:k:15:LEU:C	29:k:15:LEU:HD12	2.14	0.72
16:B:69:A:N3	16:B:71:C:N4	2.37	0.72
5:P:34:ILE:HD13	12:d:155:LEU:HD12	1.70	0.72
1:A:1964:PRO:HG3	1:A:2016:LYS:HZ3	1.55	0.72
14:n:51:PHE:CE1	14:n:55:GLU:HG3	2.24	0.72
7:R:155:GLN:HG3	19:L:78:G:H8	1.55	0.72
12:d:263:SER:CB	12:d:287:PHE:CZ	2.71	0.72
27:w:34:ASN:HB3	27:w:36:THR:HG23	1.72	0.72
7:R:41:PHE:CD1	7:R:42:ALA:N	2.57	0.72
7:R:155:GLN:HG3	19:L:78:G:C8	2.24	0.72
19:L:71:C:H2'	19:L:72:C:H6	1.55	0.72
28:g:50:ASN:HB3	28:g:52:HIS:HD1	1.53	0.72
1:A:1843:LEU:HA	1:A:1849:LYS:HZ3	1.54	0.72
10:Z:181:LEU:HD21	10:Z:186:LEU:CD2	2.16	0.72
29:k:109:LEU:HD12	29:k:109:LEU:O	1.90	0.72
24:i:30:TRP:CD2	24:i:38:ARG:NE	2.58	0.72
1:A:1430:THR:O	1:A:1431:HIS:HB2	1.87	0.71
20:v:608:TYR:O	20:v:612:ILE:HG23	1.90	0.71
27:h:34:ASN:HB3	27:h:36:THR:HG23	1.72	0.71
2:C:681:CYS:O	2:C:682:SER:OG	2.06	0.71
11:c:189:ARG:CZ	12:d:38:LEU:CD1	2.69	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:267:TYR:OH	12:d:287:PHE:HB2	1.90	0.71
17:D:55:U:H1'	17:D:60:U:O4	1.90	0.71
19:L:73:U:H2'	19:L:74:C:H6	1.55	0.71
28:e:48:LEU:HD22	28:e:52:HIS:NE2	2.05	0.71
1:A:495:ARG:NH1	1:A:495:ARG:HB2	2.06	0.71
2:C:681:CYS:SG	2:C:714:PRO:CG	2.77	0.71
25:m:19:LEU:CD2	25:m:91:THR:HG22	2.16	0.71
30:l:70:LYS:HZ2	30:l:70:LYS:HB2	1.55	0.71
27:w:32:LYS:HG3	27:w:33:PHE:CE1	2.25	0.71
12:d:267:TYR:CE2	12:d:287:PHE:CD2	2.79	0.71
19:L:28:U:C2'	19:L:29:C:H5'	2.20	0.71
20:v:388:LEU:HA	20:v:391:LEU:HD12	1.72	0.71
24:u:35:ILE:CD1	27:w:79:LEU:HD11	2.20	0.71
28:g:33:LEU:C	28:g:33:LEU:HD12	2.15	0.71
28:g:50:ASN:CB	28:g:52:HIS:CE1	2.73	0.71
19:L:1:A:H1'	19:L:2:C:N4	2.05	0.71
24:i:30:TRP:CD2	24:i:38:ARG:CZ	2.73	0.71
2:C:728:LEU:HD12	2:C:755:TYR:OH	1.91	0.71
25:m:47:LEU:HD11	25:m:61:ALA:HB3	1.73	0.71
10:Z:446:ASP:HA	10:Z:449:PHE:O	1.91	0.71
15:H:29:TYR:OH	15:H:46:GLU:HG2	1.90	0.71
20:v:365:ASP:HA	20:v:399:VAL:HG22	1.72	0.71
30:y:21:LEU:HD23	30:y:72:ILE:HG12	1.73	0.71
5:P:143:VAL:HG11	12:d:124:ARG:HG3	1.73	0.71
6:Q:295:SER:HB3	19:L:73:U:OP1	1.91	0.71
27:h:68:LEU:HD23	27:h:71:ILE:HD11	1.73	0.71
30:l:65:ARG:HG3	30:l:65:ARG:NH1	1.99	0.71
12:d:70:ARG:NH1	18:E:88:U:H1'	2.06	0.70
19:L:16:U:H5'	19:L:18:U:C6	2.26	0.70
19:L:46:C:O2'	19:L:47:U:P	2.49	0.70
19:L:117:U:C5	25:z:88:ARG:NH1	2.59	0.70
25:m:3:LEU:HG	28:g:95:PHE:HE1	1.55	0.70
25:m:84:TYR:CD2	29:k:6:VAL:CG1	2.64	0.70
6:Q:102:GLU:OE2	12:d:82:ARG:NH2	2.24	0.70
7:R:38:SER:O	7:R:39:GLN:O	2.09	0.70
15:H:27:LYS:CD	15:H:29:TYR:CZ	2.75	0.70
18:E:56:A:O2'	18:E:57:U:H5'	1.91	0.70
19:L:72:C:H2'	19:L:73:U:H6	1.56	0.70
24:i:40:LYS:HG3	24:i:60:ILE:HD11	1.74	0.70
19:L:78:G:O2'	19:L:79:A:H5'	1.92	0.70
29:k:52:ARG:NH2	29:k:78:GLU:OE2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1430:THR:HG22	1:A:1431:HIS:N	2.07	0.70
20:v:385:PHE:O	20:v:389:ILE:HD12	1.92	0.70
1:A:1961:LEU:HD23	1:A:2084:LEU:HB2	1.73	0.70
1:A:1963:LEU:HD12	1:A:1963:LEU:N	2.07	0.70
7:R:10:LYS:NZ	7:R:10:LYS:HB3	2.05	0.70
12:d:147:ASN:ND2	13:l:160:LEU:HD21	2.06	0.70
16:B:63:U:H3	19:L:41:C:H42	1.39	0.70
17:D:128:A:H1'	17:D:129:G:C4	2.27	0.70
18:E:67:C:H5''	18:E:67:C:C6	2.25	0.70
19:L:83:U:H2'	19:L:84:C:H6	1.55	0.70
1:A:1992:TYR:CZ	1:A:2008:LEU:HD22	2.21	0.70
1:A:2084:LEU:CD1	1:A:2085:GLY:H	2.05	0.70
7:R:204:LEU:HD12	7:R:204:LEU:N	2.03	0.70
15:H:18:GLN:OE1	32:F:23:LEU:CD2	2.40	0.70
29:k:40:HIS:O	29:k:41:MET:CB	2.40	0.70
30:l:11:LEU:HD11	30:l:72:ILE:HD12	1.73	0.70
1:A:2033:THR:HG22	28:e:43:PRO:HG3	1.72	0.70
26:x:14:LYS:HG2	26:x:74:LEU:HD11	1.74	0.70
31:r:99:ARG:CG	31:o:98:LEU:HD11	2.12	0.70
14:n:305:GLY:O	14:n:306:SER:C	2.34	0.70
19:L:40:U:O2'	19:L:41:C:OP1	2.08	0.70
28:g:105:LEU:C	28:g:105:LEU:HD12	2.16	0.70
29:k:31:ILE:HD11	29:k:49:ILE:HD11	0.73	0.70
20:v:388:LEU:HB3	20:v:392:TYR:OH	1.92	0.69
20:v:797:TYR:C	20:v:799:ASP:H	1.99	0.69
19:L:1146:G:H3'	19:L:1147:A:H5''	1.75	0.69
22:b:54:THR:HA	22:b:77:HIS:CB	2.22	0.69
7:R:10:LYS:HB3	7:R:10:LYS:HZ2	1.57	0.69
19:L:2:C:C6	19:L:3:G:N1	2.61	0.69
19:L:106:A:O2'	19:L:107:U:O5'	2.09	0.69
25:z:39:ILE:HD11	25:z:84:TYR:HE1	1.56	0.69
3:J:24:LEU:H	10:Z:310:HIS:HD2	1.40	0.69
25:m:20:LYS:HG2	25:m:91:THR:O	1.92	0.69
27:w:68:LEU:HD23	27:w:71:ILE:HD11	1.73	0.69
1:A:2084:LEU:CG	1:A:2085:GLY:H	2.05	0.69
6:Q:298:SER:CB	19:L:75:A:N6	2.53	0.69
18:E:65:U:H5''	18:E:66:C:OP2	1.91	0.69
19:L:50:U:OP1	19:L:50:U:H4'	1.93	0.69
19:L:54:U:H2'	19:L:55:G:C8	2.26	0.69
1:A:1228:TRP:CE2	8:S:135:ARG:NH2	2.59	0.69
12:d:267:TYR:HE2	12:d:287:PHE:CB	2.06	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:71:C:O2'	19:L:72:C:H5'	1.92	0.69
1:A:1080:ASP:O	11:c:82:ASN:ND2	2.26	0.69
4:O:111:ILE:HG22	12:d:194:MET:O	1.92	0.69
14:n:51:PHE:HE1	14:n:55:GLU:CG	2.02	0.69
17:D:128:A:H3'	17:D:128:A:N3	2.08	0.69
18:E:68:C:H4'	18:E:68:C:OP1	1.92	0.69
19:L:46:C:C2'	19:L:47:U:C6	2.76	0.69
19:L:53:G:H3'	19:L:53:G:N3	2.08	0.69
22:b:14:TYR:C	29:s:102:LEU:HD12	2.17	0.69
25:m:3:LEU:CG	28:g:95:PHE:HE1	2.06	0.69
28:e:59:LYS:HD3	28:e:70:GLU:OE1	1.93	0.69
4:O:229:THR:HG21	4:O:271:GLN:HA	1.75	0.69
18:E:13:A:H4'	18:E:14:C:OP1	1.93	0.69
18:E:84:C:H3'	18:E:85:C:H5''	1.73	0.69
20:v:396:LEU:HD23	20:v:396:LEU:C	2.18	0.69
1:A:1962:ARG:C	1:A:1963:LEU:HD12	2.18	0.69
10:Z:450:PRO:O	10:Z:451:LEU:HD23	1.93	0.69
28:g:35:ASN:CA	28:g:61:PHE:CE2	2.72	0.69
29:k:82:LEU:HD13	29:k:85:THR:HG21	1.75	0.69
12:d:289:LYS:HE2	20:v:643:HIS:CE1	2.25	0.68
30:l:82:PRO:O	30:l:85:LYS:CD	2.41	0.68
24:i:29:ILE:HG22	24:i:90:ILE:HA	1.76	0.68
24:i:30:TRP:CD1	24:i:38:ARG:CG	2.76	0.68
12:d:284:LEU:HD13	12:d:284:LEU:C	2.18	0.68
19:L:1118:U:H2'	19:L:1119:C:C6	2.28	0.68
20:v:530:ARG:CA	20:v:530:ARG:HH11	2.06	0.68
29:k:49:ILE:HG23	29:k:81:VAL:HA	1.75	0.68
29:s:50:GLU:OE2	29:s:80:ARG:NE	2.23	0.68
4:O:330:ASP:OD2	4:O:332:ARG:NE	2.26	0.68
10:Z:449:PHE:CD2	10:Z:465:PHE:HE2	2.10	0.68
17:D:174:G:H3'	28:g:49:ARG:HH12	1.58	0.68
19:L:105:A:N6	19:L:106:A:C6	2.61	0.68
24:i:54:ILE:HG13	24:i:57:ALA:HB2	1.73	0.68
1:A:581:LEU:HG	7:R:33:TRP:HE3	1.58	0.68
1:A:1841:ALA:C	1:A:1842:GLU:HG2	2.17	0.68
19:L:84:C:C2'	19:L:85:A:H8	1.91	0.68
19:L:105:A:H2'	19:L:106:A:H5'	1.76	0.68
28:e:89:ARG:NH2	28:e:91:ILE:HD11	2.07	0.68
2:C:251:GLN:HE21	2:C:255:GLN:HE21	1.40	0.68
1:A:2040:TRP:HE3	1:A:2041:PRO:HD3	1.57	0.68
17:D:176:A:H1'	27:h:33:PHE:HE1	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1:A:H1'	19:L:2:C:H41	1.58	0.68
19:L:42:U:H2'	19:L:43:G:H8	1.59	0.68
26:j:20:ASN:HD22	26:j:21:GLY:N	1.90	0.68
30:y:20:SER:HB2	30:y:73:VAL:HB	1.75	0.68
25:m:103:LEU:HD13	28:g:93:LYS:HD3	1.76	0.68
26:j:28:ILE:O	26:j:40:LEU:CB	2.33	0.68
25:m:88:ARG:HH11	25:m:90:ASN:ND2	1.92	0.68
1:A:743:LYS:HE3	1:A:749:ARG:HH11	1.58	0.68
19:L:1093:C:H6	19:L:1093:C:C5'	2.07	0.68
26:j:23:ARG:HD3	26:j:23:ARG:N	2.08	0.68
28:g:33:LEU:HD12	28:g:33:LEU:O	1.94	0.68
7:R:145:ALA:HB1	7:R:204:LEU:HD11	1.74	0.68
10:Z:445:LEU:H	10:Z:445:LEU:HD12	1.59	0.68
13:I:209:ARG:HD3	19:L:15:C:N4	2.08	0.68
28:g:50:ASN:ND2	28:g:52:HIS:CE1	2.54	0.68
1:A:1404:HIS:CD2	1:A:1437:ILE:CD1	2.72	0.67
6:Q:295:SER:HB2	19:L:73:U:P	2.33	0.67
9:T:150:CYS:SG	9:T:151:ARG:N	2.67	0.67
17:D:129:G:C4'	17:D:130:A:H3'	2.24	0.67
19:L:1117:G:O2'	19:L:1118:U:H5'	1.94	0.67
28:e:49:ARG:NH2	27:w:76:ASN:OD1	2.27	0.67
28:e:93:LYS:HB3	25:z:97:LEU:HD11	1.76	0.67
2:C:286:LEU:HD21	10:Z:182:GLN:O	1.94	0.67
6:Q:189:LYS:NZ	19:L:72:C:P	2.67	0.67
7:R:208:SER:O	19:L:79:A:H4'	1.93	0.67
29:s:28:ARG:HG2	29:s:52:ARG:HG2	1.75	0.67
12:d:229:VAL:HG12	12:d:274:TRP:HZ2	1.60	0.67
19:L:1125:U:H2'	19:L:1126:G:C8	2.30	0.67
24:u:29:ILE:HG22	24:u:90:ILE:HA	1.75	0.67
25:m:86:ASN:HD21	29:k:41:MET:HE1	1.59	0.67
26:j:57:LEU:CB	24:i:91:THR:HG21	2.14	0.67
8:S:134:GLY:C	8:S:135:ARG:HG2	2.20	0.67
26:j:27:GLY:CA	26:j:40:LEU:CD1	2.69	0.67
28:e:56:ALA:HB3	28:e:69:LEU:CD2	2.14	0.67
30:l:70:LYS:NZ	30:l:70:LYS:HB2	2.07	0.67
1:A:1093:LYS:NZ	19:L:27:A:OP1	2.26	0.67
7:R:152:LYS:HB3	7:R:153:PRO:CD	2.23	0.67
1:A:972:MET:HE1	16:B:74:A:N1	2.09	0.67
19:L:114:U:O4'	26:x:64:ARG:NH1	2.26	0.67
19:L:1119:C:O5'	19:L:1119:C:H6	1.78	0.67
29:k:50:GLU:HG3	29:k:50:GLU:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:52:ARG:HG2	29:k:52:ARG:HH11	1.60	0.67
1:A:745:THR:HG21	4:O:203:ASP:HB2	1.75	0.67
12:d:267:TYR:CG	12:d:284:LEU:HD23	2.29	0.67
19:L:5:A:H2'	19:L:5:A:N3	2.09	0.67
29:k:15:LEU:HB2	29:k:18:TYR:CE2	2.29	0.67
30:l:20:SER:OG	30:l:73:VAL:CG2	2.43	0.67
4:O:197:LEU:HB3	4:O:209:TRP:HB2	1.76	0.67
19:L:1168:U:O5'	19:L:1168:U:H6	1.78	0.67
25:m:43:VAL:HG21	25:m:85:ILE:CG2	2.25	0.67
7:R:207:PRO:C	7:R:209:ASP:H	2.03	0.67
19:L:54:U:H2'	19:L:55:G:H8	1.60	0.67
19:L:70:A:H61	19:L:82:C:H42	1.42	0.67
19:L:117:U:C5	25:z:88:ARG:CZ	2.78	0.67
19:L:125:C:OP1	25:z:55:LEU:HD11	1.94	0.67
1:A:1035:LEU:CD1	1:A:1038:ILE:HG12	2.25	0.67
2:C:316:THR:N	34:C:1500:GTP:O6	2.28	0.67
11:c:187:LYS:HE3	15:H:66:TYR:HE2	1.59	0.67
20:v:395:TYR:O	20:v:398:ASP:HB3	1.95	0.67
25:m:103:LEU:CD1	28:g:93:LYS:HD3	2.25	0.67
30:l:47:VAL:CG2	30:l:59:MET:HG3	2.19	0.67
19:L:82:C:H2'	19:L:83:U:H6	1.60	0.66
19:L:1146:G:H2'	19:L:1147:A:N9	2.10	0.66
25:m:21:ASN:HD21	29:k:93:LEU:HD11	1.60	0.66
6:Q:248:CYS:SG	6:Q:316:LEU:HD11	2.34	0.66
12:d:241:MET:CG	12:d:279:LEU:HD11	2.17	0.66
15:H:28:ASP:O	15:H:29:TYR:HB2	1.93	0.66
28:e:78:GLU:CG	25:z:52:LEU:HD22	2.24	0.66
24:i:40:LYS:CG	24:i:60:ILE:CD1	2.73	0.66
2:C:728:LEU:CD1	2:C:755:TYR:OH	2.43	0.66
17:D:17:C:O5'	17:D:17:C:H6	1.77	0.66
25:m:17:ILE:CG2	25:m:92:ILE:HG23	2.26	0.66
29:s:82:LEU:HD13	29:s:85:THR:HG21	1.75	0.66
25:z:45:LEU:HD11	25:z:65:LEU:CD1	2.26	0.66
7:R:159:ARG:NH1	7:R:204:LEU:O	2.29	0.66
16:B:0:G:H22	17:D:96:U:H3	1.43	0.66
17:D:168:U:C6	24:i:49:PHE:CE1	2.83	0.66
19:L:114:U:H1'	26:x:66:ASN:HB2	1.76	0.66
1:A:1435:LYS:CG	1:A:1436:LEU:H	2.03	0.66
2:C:684:GLU:O	2:C:685:SER:HB2	1.94	0.66
19:L:51:C:O2'	19:L:52:A:OP1	2.11	0.66
19:L:110:A:N6	25:z:34:PRO:HB2	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:125:C:H4'	28:e:81:GLY:N	2.09	0.66
19:L:1105:C:H1'	19:L:1106:G:H1'	1.78	0.66
20:v:711:MET:HE1	20:v:748:PHE:CA	2.26	0.66
30:l:21:LEU:HD22	30:l:69:ILE:HD13	1.77	0.66
1:A:1430:THR:HG22	1:A:1431:HIS:H	1.61	0.66
19:L:1093:C:H6	19:L:1093:C:O5'	1.78	0.66
22:b:32:ARG:HA	22:b:60:THR:O	1.96	0.66
23:t:111:VAL:O	23:t:114:LEU:N	2.29	0.66
29:s:44:VAL:HG22	29:s:86:ILE:HG22	1.77	0.66
20:v:746:ILE:CB	20:v:771:LEU:CB	2.73	0.66
30:l:43:GLN:C	30:l:44:LEU:HD23	2.20	0.66
1:A:1964:PRO:CG	1:A:2016:LYS:HZ3	2.09	0.66
19:L:1:A:H1'	19:L:2:C:C4	2.30	0.66
19:L:125:C:OP1	25:z:55:LEU:CD1	2.42	0.66
28:g:40:THR:C	28:g:41:ARG:CG	2.69	0.66
28:e:56:ALA:CB	28:e:72:VAL:HB	2.25	0.66
1:A:1965:PHE:CE1	1:A:2012:LEU:HD13	2.31	0.66
17:D:96:U:O2'	17:D:97:U:H5'	1.95	0.66
19:L:38:U:O2'	19:L:39:A:H5'	1.95	0.66
19:L:74:C:H2'	19:L:75:A:C8	2.31	0.66
19:L:1129:U:H2'	19:L:1130:U:C5'	2.26	0.66
25:m:3:LEU:HG	28:g:95:PHE:CE1	2.31	0.66
1:A:996:ASP:OD2	1:A:1511:ARG:NH2	2.29	0.65
7:R:28:LEU:HD21	15:H:16:GLN:HB3	1.79	0.65
10:Z:454:ASP:HB2	10:Z:457:HIS:ND1	2.10	0.65
29:s:93:LEU:HD11	25:z:21:ASN:HD21	1.60	0.65
7:R:152:LYS:HB2	7:R:155:GLN:OE1	1.96	0.65
18:E:99:A:C2'	18:E:100:U:H5''	2.25	0.65
25:m:88:ARG:HH11	25:m:90:ASN:HD22	1.42	0.65
29:k:86:ILE:CG2	30:l:10:LEU:HD23	2.26	0.65
7:R:145:ALA:HB2	7:R:221:LEU:HB3	1.78	0.65
12:d:267:TYR:CE2	12:d:287:PHE:CB	2.79	0.65
18:E:58:C:C2'	18:E:59:A:H5'	2.27	0.65
19:L:121:C:H1'	28:e:49:ARG:CG	2.24	0.65
25:m:43:VAL:HG21	25:m:85:ILE:HG21	1.78	0.65
28:e:89:ARG:CZ	28:e:91:ILE:HD11	2.26	0.65
24:i:58:VAL:HG12	24:i:76:PRO:HA	1.79	0.65
1:A:1229:GLU:CD	8:S:128:ARG:HG2	2.21	0.65
1:A:1859:ARG:NH2	1:A:1876:ASN:O	2.29	0.65
17:D:27:G:H4'	17:D:28:G:OP1	1.95	0.65
19:L:1150:U:OP1	29:s:55:LYS:HG3	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:g:38:MET:HA	28:g:58:VAL:O	1.96	0.65
29:k:48:CYS:HG	29:k:82:LEU:HD12	1.60	0.65
7:R:152:LYS:CD	7:R:153:PRO:HD2	2.26	0.65
11:c:187:LYS:HZ1	15:H:62:SER:C	2.04	0.65
1:A:1965:PHE:HE1	1:A:2012:LEU:HD13	1.61	0.65
7:R:151:LEU:HD23	19:L:78:G:C4'	2.27	0.65
9:T:98:THR:HG22	18:E:25:C:O2	1.97	0.65
19:L:81:G:H2'	19:L:82:C:H6	1.61	0.65
1:A:2040:TRP:HE3	1:A:2041:PRO:CD	2.10	0.65
19:L:1137:U:C4	21:a:67:LYS:O	2.50	0.65
28:g:50:ASN:HB3	28:g:52:HIS:CE1	2.32	0.65
25:z:51:ARG:O	25:z:54:LYS:N	2.29	0.65
17:D:176:A:N3	27:h:33:PHE:HD1	1.94	0.65
27:h:71:ILE:HG23	28:g:103:VAL:CG2	2.25	0.65
26:j:63:ILE:HG13	24:i:89:LEU:CD2	2.26	0.65
26:j:64:ARG:HH22	24:i:50:MET:CB	2.00	0.65
1:A:607:THR:OG1	16:B:2:U:H3'	1.97	0.65
1:A:1385:PRO:HD3	1:A:1431:HIS:ND1	2.11	0.65
17:D:10:U:O5'	17:D:10:U:H6	1.80	0.65
17:D:26:A:H5''	17:D:131:A:C8	2.32	0.65
19:L:69:G:H1	19:L:83:U:H3	1.43	0.65
28:e:48:LEU:HD22	28:e:52:HIS:CE1	2.33	0.65
24:i:30:TRP:CE2	24:i:38:ARG:CZ	2.80	0.65
1:A:1807:LYS:O	1:A:1946:VAL:HG11	1.95	0.64
10:Z:181:LEU:CD1	10:Z:194:LEU:CB	2.55	0.64
19:L:121:C:C1'	28:e:49:ARG:HG2	2.24	0.64
22:b:110:ARG:CB	22:b:134:VAL:CB	2.74	0.64
25:m:3:LEU:CD2	28:g:95:PHE:CE1	2.79	0.64
29:k:30:TYR:CD1	29:k:50:GLU:HB3	2.32	0.64
28:e:93:LYS:HB3	25:z:97:LEU:CD1	2.27	0.64
29:s:88:ARG:NH1	30:y:40:MET:SD	2.70	0.64
30:y:34:VAL:HG12	30:y:35:GLU:HG2	1.77	0.64
1:A:1073:ILE:HG13	1:A:1074:VAL:HG23	1.79	0.64
10:Z:454:ASP:CB	10:Z:457:HIS:ND1	2.60	0.64
16:B:9:A:H1'	16:B:10:A:P	2.37	0.64
19:L:68:U:H2'	19:L:69:G:H8	1.60	0.64
19:L:114:U:O2	26:x:64:ARG:HG2	1.98	0.64
17:D:16:U:OP2	17:D:17:C:N4	2.30	0.64
17:D:136:G:O2'	17:D:137:U:O4'	2.16	0.64
27:w:32:LYS:CG	27:w:33:PHE:CE1	2.80	0.64
7:R:209:ASP:OD1	19:L:79:A:C5'	2.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:270:ALA:CB	12:d:280:LEU:HD21	2.27	0.64
25:m:45:LEU:CD1	25:m:65:LEU:HD13	2.27	0.64
26:j:11:MET:O	26:j:12:ASP:HB2	1.97	0.64
24:i:32:PHE:CD1	24:i:86:ASN:O	2.50	0.64
12:d:147:ASN:HD22	13:l:160:LEU:HD21	1.62	0.64
12:d:284:LEU:HD13	12:d:285:LEU:N	2.12	0.64
19:L:67:A:C2'	19:L:68:U:H5'	2.27	0.64
25:z:45:LEU:CD1	25:z:65:LEU:HD13	2.27	0.64
1:A:1286:TRP:NE1	1:A:1348:GLU:OE2	2.30	0.64
18:E:101:U:C6	18:E:101:U:H5''	2.32	0.64
25:m:15:VAL:HG23	25:m:96:ILE:O	1.96	0.64
25:m:45:LEU:HD11	25:m:65:LEU:CD1	2.27	0.64
29:k:60:LYS:HD2	29:k:75:ILE:HD13	1.78	0.64
29:k:84:LEU:HG	30:l:74:VAL:HG23	1.80	0.64
19:L:1086:U:O5'	19:L:1086:U:H6	1.81	0.64
22:b:110:ARG:N	22:b:134:VAL:CB	2.60	0.64
32:F:47:PHE:CZ	32:F:97:PHE:CZ	2.86	0.64
9:T:123:ARG:NH2	18:E:26:A:O2'	2.31	0.64
28:e:93:LYS:HD2	25:z:97:LEU:CD1	2.27	0.64
2:C:187:ARG:NH1	2:C:653:ASP:OD2	2.31	0.63
2:C:422:LYS:O	2:C:426:GLN:HG3	1.98	0.63
26:j:69:ILE:HA	30:l:68:GLN:HG3	1.80	0.63
6:Q:300:ALA:CB	7:R:154:ALA:CB	2.70	0.63
17:D:3:G:C2'	17:D:4:C:H5'	2.27	0.63
25:m:67:LEU:HB3	29:k:29:VAL:HG21	1.80	0.63
11:c:252:GLY:CA	12:d:38:LEU:O	2.46	0.63
18:E:102:U:H2'	18:E:103:A:C1'	2.29	0.63
19:L:73:U:H2'	19:L:74:C:C6	2.34	0.63
29:k:28:ARG:HG2	29:k:52:ARG:HG2	1.81	0.63
1:A:143:ILE:HD12	1:A:143:ILE:C	2.24	0.63
6:Q:206:PHE:HD2	6:Q:291:ILE:HD11	1.63	0.63
17:D:9:U:H3	17:D:156:G:H1	1.46	0.63
26:j:63:ILE:HG13	24:i:89:LEU:HD23	1.79	0.63
11:c:41:GLN:HB3	11:c:151:MET:HE2	1.80	0.63
11:c:187:LYS:HE3	15:H:66:TYR:CE2	2.33	0.63
17:D:22:G:H1	17:D:149:U:H3	1.47	0.63
17:D:167:A:H3'	27:h:48:TYR:OH	1.98	0.63
19:L:72:C:H2'	19:L:73:U:C6	2.34	0.63
19:L:141:A:C2	19:L:1168:U:O2	2.51	0.63
2:C:187:ARG:NH2	2:C:654:CYS:SG	2.72	0.63
7:R:151:LEU:C	19:L:78:G:P	2.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:83:GLN:NE2	25:m:84:TYR:HB2	2.13	0.63
7:R:149:LYS:HB2	7:R:151:LEU:HD11	1.79	0.63
12:d:270:ALA:HB3	12:d:280:LEU:HD21	1.80	0.63
19:L:67:A:H2'	19:L:68:U:C6	2.31	0.63
25:m:89:GLY:O	25:m:92:ILE:HG13	1.99	0.63
29:k:11:ARG:O	29:k:14:ASN:N	2.31	0.63
30:l:17:HIS:O	30:l:19:VAL:HG13	1.98	0.63
17:D:131:A:H5''	17:D:132:A:N7	2.14	0.63
25:m:17:ILE:HG23	25:m:92:ILE:HG21	1.76	0.63
29:s:29:VAL:HG21	25:z:67:LEU:HB3	1.79	0.63
24:i:30:TRP:CD1	24:i:38:ARG:NE	2.66	0.63
4:O:280:GLN:NE2	5:P:66:CYS:SG	2.71	0.62
11:c:233:GLU:OE2	12:d:116:ASN:N	2.23	0.62
1:A:1934:ILE:HG12	1:A:1957:ARG:HB2	1.80	0.62
2:C:90:LEU:HD23	4:O:211:LEU:HD22	1.81	0.62
6:Q:13:CYS:HB2	6:Q:16:CYS:SG	2.39	0.62
10:Z:449:PHE:CD2	10:Z:465:PHE:CE2	2.86	0.62
17:D:174:G:C3'	28:g:49:ARG:HH12	2.12	0.62
19:L:46:C:O2'	19:L:47:U:OP1	2.17	0.62
29:k:13:ALA:HA	29:k:37:PHE:HE2	1.64	0.62
26:x:27:GLY:HA3	26:x:40:LEU:HD13	1.80	0.62
24:u:58:VAL:HG12	24:u:76:PRO:HA	1.79	0.62
10:Z:403:LYS:HG2	10:Z:445:LEU:HB3	1.80	0.62
19:L:1:A:H5'	19:L:1:A:N3	2.14	0.62
19:L:50:U:H2'	19:L:51:C:O2	2.00	0.62
26:j:63:ILE:HG21	26:j:68:ILE:HD11	1.80	0.62
29:k:105:LYS:HA	29:k:108:ARG:CZ	2.30	0.62
19:L:1090:A:O2'	19:L:1091:G:H5'	2.00	0.62
29:s:54:PRO:HG2	29:s:76:LYS:O	1.98	0.62
1:A:487:ASN:CG	1:A:488:ARG:HD3	2.22	0.62
1:A:1710:GLU:HG2	1:A:1728:ILE:HG12	1.81	0.62
7:R:40:GLY:CA	15:H:26:TYR:OH	2.43	0.62
25:m:86:ASN:ND2	29:k:41:MET:HE1	2.15	0.62
25:m:93:ARG:HG3	25:m:93:ARG:NH1	2.14	0.62
28:g:76:TRP:CZ2	28:g:87:ARG:CD	2.79	0.62
30:l:77:LEU:HD23	30:l:77:LEU:H	1.64	0.62
1:A:488:ARG:NH2	1:A:488:ARG:HG3	2.14	0.62
1:A:495:ARG:HH11	1:A:495:ARG:CG	2.12	0.62
19:L:71:C:H2'	19:L:72:C:C6	2.33	0.62
1:A:1296:ARG:NH1	10:Z:430:GLU:OE2	2.33	0.62
7:R:207:PRO:HD2	7:R:208:SER:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:v:612:ILE:N	20:v:613:PRO:HD2	2.15	0.62
26:j:64:ARG:NH2	24:i:50:MET:CB	2.47	0.62
17:D:55:U:O5'	17:D:55:U:H6	1.83	0.62
17:D:123:U:O2'	17:D:124:C:H5'	2.00	0.62
19:L:16:U:O2'	19:L:17:U:OP1	2.17	0.62
19:L:40:U:H1'	19:L:41:C:OP2	2.00	0.62
26:j:19:ILE:CG2	24:i:88:THR:HG23	2.29	0.62
28:g:38:MET:SD	28:g:60:ALA:HA	2.38	0.62
29:s:42:ASN:HB3	29:s:89:GLY:H	1.65	0.62
1:A:495:ARG:HH11	1:A:495:ARG:HG3	1.65	0.62
1:A:676:GLN:HG2	1:A:714:PHE:HB2	1.81	0.62
19:L:1154:U:H2'	19:L:1155:C:H6	1.63	0.62
20:v:385:PHE:O	20:v:388:LEU:HB2	2.00	0.62
6:Q:189:LYS:HZ2	19:L:72:C:P	2.22	0.61
9:T:98:THR:HG22	18:E:25:C:H1'	1.82	0.61
10:Z:101:MET:O	10:Z:105:GLN:NE2	2.33	0.61
11:c:252:GLY:HA2	12:d:38:LEU:O	2.00	0.61
20:v:322:CYS:O	20:v:326:LEU:N	2.28	0.61
20:v:580:LEU:HB3	20:v:582:LEU:HD23	1.82	0.61
28:g:78:GLU:CD	28:g:85:ILE:HG23	2.25	0.61
1:A:1228:TRP:CH2	8:S:135:ARG:NH2	2.68	0.61
2:C:498:THR:HG22	2:C:538:GLU:HG2	1.81	0.61
1:A:749:ARG:HH21	1:A:749:ARG:CG	2.13	0.61
1:A:1663:PHE:HZ	1:A:1902:GLN:NE2	1.97	0.61
2:C:684:GLU:CB	2:C:712:ALA:O	2.47	0.61
4:O:343:THR:HB	5:P:47:ARG:HB2	1.82	0.61
17:D:173:U:O2	28:g:97:ARG:NE	2.32	0.61
19:L:31:A:O2'	19:L:32:G:H5'	2.01	0.61
19:L:115:U:C2	30:y:39:SER:OG	2.53	0.61
28:e:56:ALA:CB	28:e:72:VAL:CB	2.77	0.61
24:i:30:TRP:HA	24:i:38:ARG:HG3	1.82	0.61
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.33	0.61
22:b:65:ILE:HA	22:b:85:ASN:O	2.01	0.61
30:l:41:ASN:HB3	30:l:66:GLY:H	1.65	0.61
4:O:111:ILE:HG21	12:d:197:PRO:HD3	1.82	0.61
19:L:1083:A:H2'	19:L:1084:A:H8	1.65	0.61
20:v:582:LEU:HD12	20:v:582:LEU:O	2.00	0.61
32:F:58:ILE:HG22	32:F:58:ILE:O	2.01	0.61
2:C:133:ILE:HG22	2:C:209:MET:HB3	1.80	0.61
2:C:681:CYS:SG	2:C:682:SER:N	2.74	0.61
17:D:43:G:H2'	17:D:45:A:OP1	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:173:U:C2	28:g:97:ARG:NH1	2.68	0.61
29:k:13:ALA:CA	29:k:37:PHE:CZ	2.83	0.61
30:l:13:GLU:OE1	30:l:13:GLU:HA	2.01	0.61
1:A:1896:THR:HA	1:A:1899:TRP:HD1	1.66	0.61
4:O:371:GLY:HA3	4:O:400:ARG:HG2	1.83	0.61
7:R:234:ALA:HA	7:R:237:ARG:HE	1.65	0.61
17:D:79:C:H5''	17:D:80:G:H2'	1.82	0.61
19:L:3:G:H5''	19:L:3:G:C8	2.35	0.61
19:L:54:U:OP2	19:L:55:G:OP2	2.17	0.61
19:L:1095:U:H2'	19:L:1096:C:C6	2.35	0.61
19:L:1137:U:C5	21:a:67:LYS:O	2.54	0.61
20:v:396:LEU:HD23	20:v:396:LEU:O	1.99	0.61
30:l:39:SER:O	30:l:40:MET:HB3	2.01	0.61
32:F:75:TYR:OH	32:F:102:GLY:HA3	2.00	0.61
1:A:1992:TYR:OH	1:A:2005:PHE:HD1	1.82	0.61
11:c:248:VAL:HG11	12:d:43:LEU:HD22	1.83	0.61
18:E:101:U:H3'	18:E:102:U:C6	2.36	0.61
28:g:62:ASP:OD1	28:g:63:ARG:N	2.26	0.61
29:k:13:ALA:HA	29:k:37:PHE:CZ	2.34	0.61
12:d:267:TYR:HE2	12:d:287:PHE:CG	2.18	0.61
16:B:62:A:H61	19:L:42:U:H3	1.48	0.61
19:L:4:A:O5'	19:L:4:A:H8	1.83	0.61
32:F:46:PRO:C	32:F:47:PHE:HD1	2.08	0.61
1:A:488:ARG:HH21	1:A:488:ARG:CG	2.14	0.61
7:R:146:LEU:HD13	7:R:151:LEU:CD1	2.22	0.61
18:E:102:U:C3'	18:E:103:A:C8	2.84	0.61
19:L:70:A:H2'	19:L:71:C:H6	1.65	0.61
19:L:126:A:P	28:e:80:LYS:CB	2.89	0.61
1:A:1154:LYS:HA	1:A:1159:ARG:HH12	1.64	0.60
19:L:117:U:C6	25:z:88:ARG:NH1	2.69	0.60
19:L:1085:G:N3	19:L:1085:G:H2'	2.16	0.60
19:L:1125:U:H2'	19:L:1126:G:H8	1.64	0.60
29:k:43:LEU:CD1	29:k:87:LEU:HD22	2.31	0.60
29:k:105:LYS:O	29:k:108:ARG:HG2	2.01	0.60
28:e:62:ASP:OD1	28:e:63:ARG:N	2.33	0.60
1:A:1993:ASP:CG	1:A:2039:LEU:H	2.08	0.60
19:L:119:G:H2'	19:L:120:G:H5'	1.82	0.60
20:v:387:SER:O	20:v:391:LEU:HG	2.01	0.60
30:l:42:VAL:HG22	30:l:64:VAL:HG22	1.83	0.60
11:c:189:ARG:NH2	12:d:38:LEU:CD1	2.64	0.60
17:D:28:G:C2	17:D:29:G:C4	2.89	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:4:A:C1'	20:v:529:HIS:CG	2.84	0.60
19:L:4:A:H8	19:L:4:A:P	2.24	0.60
19:L:83:U:H2'	19:L:84:C:C6	2.34	0.60
1:A:2013:ARG:NH1	1:A:2082:ILE:O	2.34	0.60
19:L:50:U:O3'	19:L:51:C:O4'	2.19	0.60
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.83	0.60
1:A:2024:MET:CE	25:z:99:ASP:O	2.35	0.60
2:C:183:GLN:HE22	2:C:654:CYS:HA	1.65	0.60
2:C:780:PRO:HA	2:C:783:ILE:HB	1.84	0.60
11:c:214:ASN:HD21	12:d:44:ARG:HG3	1.66	0.60
25:m:67:LEU:HD11	29:k:53:VAL:HG23	1.82	0.60
17:D:27:G:C4'	17:D:28:G:OP1	2.50	0.60
10:Z:450:PRO:O	10:Z:451:LEU:HD22	1.99	0.60
11:c:109:GLU:HB3	32:F:196:ARG:HG2	1.82	0.60
19:L:54:U:OP2	19:L:54:U:H3'	2.01	0.60
25:m:52:LEU:O	25:m:52:LEU:HD12	2.01	0.60
1:A:162:LEU:HD22	7:R:33:TRP:CH2	2.36	0.60
19:L:1107:C:H2'	19:L:1108:A:OP2	2.01	0.60
25:m:41:THR:O	25:m:83:GLN:HA	2.02	0.60
1:A:928:ARG:HD3	19:L:32:G:N3	2.17	0.60
7:R:204:LEU:C	7:R:205:LEU:HD22	2.26	0.60
19:L:1117:G:C2'	19:L:1118:U:H5'	2.31	0.60
20:v:680:ILE:O	20:v:680:ILE:HG22	2.00	0.60
26:j:20:ASN:OD1	24:i:32:PHE:CE2	2.55	0.60
6:Q:213:SER:O	6:Q:214:ILE:HG22	2.02	0.60
16:B:3:A:H5''	16:B:4:U:C5	2.37	0.60
16:B:52:U:H2'	16:B:53:U:O4'	2.01	0.60
1:A:2033:THR:HG22	28:e:43:PRO:CG	2.32	0.59
1:A:2084:LEU:HD12	1:A:2085:GLY:N	2.17	0.59
7:R:152:LYS:HD2	7:R:153:PRO:HD2	1.82	0.59
7:R:207:PRO:O	7:R:209:ASP:N	2.35	0.59
12:d:342:PHE:O	12:d:346:ILE:N	2.31	0.59
20:v:530:ARG:NH1	20:v:530:ARG:HB2	2.17	0.59
20:v:797:TYR:O	20:v:799:ASP:N	2.34	0.59
30:l:20:SER:OG	30:l:73:VAL:HG23	2.01	0.59
19:L:1:A:C1'	19:L:2:C:C5	2.85	0.59
19:L:1106:G:H4'	19:L:1107:C:OP1	2.00	0.59
28:e:46:ILE:HD12	28:e:54:ILE:HD11	1.84	0.59
1:A:1921:VAL:O	1:A:1929:GLN:NE2	2.35	0.59
1:A:1965:PHE:O	1:A:1966:SER:HB3	2.01	0.59
7:R:41:PHE:CZ	7:R:43:GLY:HA2	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:56:G:H1	19:L:47:U:H3	1.49	0.59
17:D:2:A:C2	17:D:3:G:C5	2.90	0.59
19:L:85:A:C3'	19:L:86:U:C5'	2.80	0.59
1:A:743:LYS:HB3	1:A:749:ARG:NH1	2.17	0.59
1:A:2080:LYS:C	1:A:2084:LEU:CD2	2.75	0.59
4:O:97:PHE:HB3	12:d:231:ASN:OD1	2.02	0.59
18:E:55:G:HO2'	18:E:56:A:H5'	1.66	0.59
19:L:4:A:N3	19:L:5:A:C8	2.71	0.59
19:L:74:C:O2'	19:L:75:A:C5'	2.38	0.59
25:m:39:ILE:CD1	25:m:84:TYR:CE1	2.85	0.59
29:s:12:LEU:HD12	29:s:15:LEU:HD11	1.84	0.59
1:A:1433:ASP:OD1	1:A:1433:ASP:N	2.35	0.59
1:A:1642:LYS:HE2	1:A:1646:ILE:HD11	1.82	0.59
6:Q:251:LEU:HG	6:Q:251:LEU:O	2.02	0.59
12:d:57:TYR:CE2	18:E:86:G:C2	2.91	0.59
14:n:375:LYS:O	14:n:376:ILE:HB	2.03	0.59
19:L:4:A:H2'	19:L:5:A:H8	1.67	0.59
19:L:1142:G:C2'	19:L:1143:C:H5'	2.32	0.59
24:u:35:ILE:HD11	27:w:79:LEU:HD13	1.82	0.59
1:A:255:ILE:HG23	1:A:640:ARG:HG2	1.85	0.59
2:C:866:ILE:HB	2:C:902:VAL:HB	1.84	0.59
15:H:26:TYR:O	15:H:27:LYS:CB	2.50	0.59
19:L:6:U:OP1	19:L:6:U:H6	1.86	0.59
27:h:33:PHE:CZ	28:g:49:ARG:CD	2.86	0.59
28:g:46:ILE:HD12	28:g:54:ILE:HD11	1.84	0.59
28:e:78:GLU:HG2	25:z:52:LEU:HD22	1.85	0.59
24:i:40:LYS:CD	24:i:60:ILE:HD13	2.32	0.59
5:P:110:HIS:CE1	6:Q:20:GLU:O	2.56	0.59
7:R:159:ARG:HH11	7:R:159:ARG:CG	2.14	0.59
9:T:98:THR:CG2	18:E:25:C:H1'	2.33	0.59
15:H:18:GLN:OE1	32:F:23:LEU:HD21	2.02	0.59
15:H:53:GLN:HA	15:H:56:LYS:HE2	1.83	0.59
17:D:167:A:O4'	28:g:64:HIS:NE2	2.25	0.59
18:E:101:U:C6	18:E:101:U:C5'	2.86	0.59
19:L:1:A:H2'	19:L:1:A:OP2	2.03	0.59
25:m:16:THR:OG1	25:m:96:ILE:HB	2.03	0.59
29:k:43:LEU:HD11	29:k:87:LEU:HD22	1.85	0.59
30:l:17:HIS:HE1	30:l:77:LEU:HD11	1.66	0.59
32:F:69:GLU:OE1	32:F:83:ARG:NH2	2.35	0.59
6:Q:296:GLY:N	19:L:74:C:OP2	2.35	0.59
15:H:27:LYS:HD2	15:H:29:TYR:CZ	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:3:G:O5'	17:D:3:G:H8	1.86	0.59
26:j:6:GLU:OE2	30:l:35:GLU:HB3	2.03	0.59
28:e:91:ILE:HD13	25:z:96:ILE:HD11	1.84	0.59
1:A:416:GLU:HG2	1:A:418:ASP:H	1.68	0.59
1:A:2027:LEU:O	28:e:71:ASN:HB3	2.03	0.59
6:Q:213:SER:C	6:Q:214:ILE:HG22	2.28	0.59
12:d:284:LEU:HD22	12:d:284:LEU:C	2.28	0.59
14:n:376:ILE:O	14:n:393:GLY:HA2	2.02	0.59
15:H:27:LYS:C	15:H:28:ASP:CG	2.69	0.59
17:D:6:G:H4'	29:k:11:ARG:NH2	2.17	0.59
17:D:167:A:C5	27:h:48:TYR:CE1	2.91	0.59
19:L:40:U:HO2'	19:L:41:C:P	2.26	0.59
19:L:80:G:H2'	19:L:81:G:H8	1.68	0.59
28:e:93:LYS:HZ2	25:z:103:LEU:CD1	2.15	0.59
7:R:51:PHE:CD2	7:R:80:MET:CG	2.74	0.58
19:L:1093:C:C5'	19:L:1093:C:C6	2.85	0.58
25:m:18:GLU:OE1	25:m:94:GLN:OE1	2.20	0.58
28:g:50:ASN:O	28:g:51:ASN:HB3	2.03	0.58
32:F:49:MET:HB2	32:F:58:ILE:HB	1.85	0.58
11:c:163:GLN:HB3	11:c:167:ALA:HB3	1.85	0.58
19:L:1146:G:C2'	19:L:1147:A:C8	2.85	0.58
28:g:37:ALA:HB1	28:g:44:VAL:HG11	1.83	0.58
28:g:105:LEU:HD12	28:g:105:LEU:O	2.04	0.58
29:k:52:ARG:HH11	29:k:52:ARG:CG	2.15	0.58
19:L:113:U:O4	27:w:47:ASN:O	2.21	0.58
19:L:1107:C:C2'	19:L:1108:A:OP2	2.51	0.58
19:L:1142:G:H2'	19:L:1143:C:H5'	1.84	0.58
26:j:61:THR:HG22	24:i:91:THR:CG2	2.31	0.58
1:A:162:LEU:HD22	7:R:33:TRP:CZ3	2.38	0.58
1:A:1035:LEU:HD13	1:A:1038:ILE:HG23	1.84	0.58
5:P:34:ILE:HG21	12:d:155:LEU:HD12	1.85	0.58
1:A:864:GLN:HE22	1:A:1101:TYR:H	1.52	0.58
4:O:259:VAL:HG11	5:P:74:ILE:HG23	1.85	0.58
16:B:9:A:C1'	16:B:10:A:P	2.91	0.58
26:j:23:ARG:HH21	26:j:23:ARG:HB2	1.68	0.58
30:l:11:LEU:CD1	30:l:72:ILE:HD12	2.33	0.58
25:z:16:THR:OG1	25:z:96:ILE:HB	2.03	0.58
1:A:2080:LYS:O	1:A:2084:LEU:HD23	2.03	0.58
10:Z:181:LEU:HD13	10:Z:194:LEU:HB3	1.80	0.58
28:e:73:LYS:NZ	28:e:75:LEU:HD21	2.17	0.58
2:C:141:PRO:O	2:C:146:LYS:NZ	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:n:312:SER:OG	14:n:314:ASP:OD1	2.22	0.58
19:L:15:C:H1'	19:L:16:U:C6	2.38	0.58
19:L:79:A:H2'	19:L:80:G:H8	1.68	0.58
15:H:18:GLN:OE1	32:F:23:LEU:HD23	2.03	0.58
18:E:14:C:H4'	18:E:15:C:OP2	2.02	0.58
19:L:69:G:H2'	19:L:70:A:H8	1.68	0.58
19:L:1137:U:O2'	19:L:1138:G:C4'	2.43	0.58
1:A:988:GLU:OE1	1:A:1085:LYS:NZ	2.37	0.58
2:C:138:VAL:HG21	2:C:150:MET:HE3	1.86	0.58
19:L:4:A:P	19:L:4:A:C8	2.97	0.58
20:v:323:GLY:O	20:v:327:LYS:N	2.29	0.58
25:m:17:ILE:HG21	25:m:92:ILE:CG2	2.33	0.58
18:E:11:U:O4	18:E:15:C:N4	2.37	0.58
19:L:110:A:H62	25:z:34:PRO:HB2	1.69	0.58
19:L:1118:U:O2'	19:L:1119:C:H5'	2.04	0.58
28:g:40:THR:O	28:g:40:THR:HG22	2.04	0.58
28:e:56:ALA:CA	28:e:72:VAL:HG23	2.33	0.58
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.32	0.57
2:C:708:ILE:HD13	2:C:841:LEU:HD12	1.85	0.57
7:R:149:LYS:HB2	7:R:151:LEU:CD1	2.33	0.57
25:m:52:LEU:HD12	25:m:52:LEU:C	2.28	0.57
25:m:82:LEU:C	25:m:82:LEU:HD12	2.29	0.57
1:A:2043:PHE:HE2	1:A:2047:GLN:H	1.50	0.57
2:C:685:SER:O	2:C:852:THR:HB	2.04	0.57
12:d:330:ILE:CG2	12:d:339:MET:HA	2.34	0.57
29:k:15:LEU:HD12	29:k:15:LEU:O	2.03	0.57
28:e:56:ALA:HB1	28:e:69:LEU:HB3	1.86	0.57
1:A:2081:ASP:HA	1:A:2084:LEU:HG	1.86	0.57
7:R:41:PHE:CZ	7:R:43:GLY:HA3	2.38	0.57
25:m:84:TYR:HD2	29:k:6:VAL:HG21	1.68	0.57
24:i:30:TRP:CE3	24:i:38:ARG:NH2	2.72	0.57
4:O:145:VAL:HG22	4:O:157:THR:HG22	1.86	0.57
17:D:173:U:O2'	27:h:74:ARG:NH2	2.37	0.57
19:L:71:C:C2	19:L:72:C:C5	2.93	0.57
19:L:82:C:H2'	19:L:83:U:C6	2.38	0.57
20:v:690:GLY:HA3	20:v:710:ARG:HE	1.68	0.57
25:m:52:LEU:HD21	28:g:79:LYS:CA	2.34	0.57
29:s:29:VAL:O	29:s:50:GLU:HA	2.05	0.57
29:s:91:GLN:HG3	30:y:70:LYS:HG3	1.87	0.57
32:F:58:ILE:O	32:F:59:PRO:C	2.47	0.57
1:A:1602:PRO:HA	19:L:35:U:OP1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2011:LEU:CG	1:A:2040:TRP:CH2	2.87	0.57
7:R:50:PRO:HB2	7:R:51:PHE:CE1	2.40	0.57
19:L:72:C:C2	19:L:73:U:C5	2.93	0.57
19:L:78:G:H2'	19:L:79:A:H8	1.70	0.57
28:g:46:ILE:HG12	28:g:104:VAL:HG22	1.87	0.57
26:x:47:ASN:OD1	26:x:48:GLY:N	2.31	0.57
32:F:57:TYR:O	32:F:59:PRO:HD3	2.05	0.57
6:Q:51:ARG:NH2	18:E:29:U:OP2	2.37	0.57
8:S:10:GLU:O	18:E:64:U:H5''	2.04	0.57
10:Z:413:CYS:SG	10:Z:414:PRO:HD2	2.45	0.57
10:Z:449:PHE:CD1	10:Z:449:PHE:N	2.73	0.57
17:D:10:U:H2'	17:D:11:A:C8	2.40	0.57
19:L:2:C:C6	19:L:3:G:C2	2.92	0.57
19:L:2:C:H6	19:L:2:C:H3'	1.69	0.57
19:L:32:G:O5'	19:L:32:G:H8	1.87	0.57
25:m:90:ASN:OD1	25:m:91:THR:N	2.38	0.57
30:l:44:LEU:HD12	30:l:47:VAL:CG1	2.35	0.57
6:Q:295:SER:HB2	19:L:73:U:OP1	2.02	0.57
11:c:74:LEU:HD13	32:F:200:ILE:HG21	1.85	0.57
17:D:3:G:C6	17:D:4:C:N4	2.73	0.57
19:L:109:C:P	25:z:8:LYS:HZ2	2.27	0.57
2:C:97:ARG:NH1	17:D:43:G:OP1	2.38	0.57
2:C:728:LEU:HD11	2:C:755:TYR:CZ	2.40	0.57
7:R:152:LYS:CB	7:R:155:GLN:OE1	2.53	0.57
15:H:38:VAL:HG21	15:H:91:ARG:HG3	1.86	0.57
19:L:83:U:C2	19:L:84:C:C5	2.93	0.57
22:b:14:TYR:C	29:s:102:LEU:CD1	2.76	0.57
26:j:16:LEU:HD22	26:j:72:GLU:OE2	2.05	0.57
29:k:30:TYR:HD1	29:k:50:GLU:HB3	1.69	0.57
29:k:49:ILE:CG2	29:k:81:VAL:CB	2.83	0.57
28:e:46:ILE:HG12	28:e:104:VAL:HG22	1.87	0.57
12:d:289:LYS:CG	20:v:609:GLU:HG2	2.32	0.56
19:L:12:U:C2	19:L:13:G:C8	2.93	0.56
27:h:58:GLU:O	27:h:65:HIS:N	2.38	0.56
1:A:495:ARG:NH1	1:A:498:ASP:OD2	2.38	0.56
11:c:513:ILE:O	11:c:517:VAL:N	2.38	0.56
20:v:530:ARG:HB2	20:v:530:ARG:CZ	2.34	0.56
20:v:610:LYS:O	20:v:613:PRO:HG2	2.05	0.56
1:A:1521:ARG:NH1	16:B:74:A:O2'	2.38	0.56
4:O:391:GLU:OE2	4:O:400:ARG:NH1	2.38	0.56
6:Q:299:ALA:O	6:Q:300:ALA:HB3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:445:LEU:HD13	10:Z:445:LEU:O	2.04	0.56
13:I:209:ARG:HD3	19:L:15:C:C4	2.41	0.56
15:H:88:GLU:HG2	15:H:92:TRP:CZ3	2.32	0.56
16:B:69:A:O2'	16:B:70:A:C5	2.58	0.56
17:D:99:U:H5''	17:D:99:U:H6	1.69	0.56
19:L:125:C:H5''	28:e:80:LYS:CA	2.34	0.56
19:L:1106:G:H5'	19:L:1107:C:OP1	2.05	0.56
29:k:11:ARG:H	29:k:14:ASN:HB2	1.69	0.56
28:e:68:VAL:O	28:e:69:LEU:HD12	2.06	0.56
32:F:58:ILE:O	32:F:59:PRO:O	2.22	0.56
1:A:749:ARG:NH2	1:A:749:ARG:HG2	2.20	0.56
1:A:966:PRO:HB3	1:A:1089:VAL:HB	1.87	0.56
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.87	0.56
2:C:804:LYS:HD3	2:C:805:GLU:HG3	1.86	0.56
16:B:52:U:C4	16:B:53:U:C2	2.94	0.56
18:E:101:U:H3'	18:E:102:U:H6	1.70	0.56
19:L:81:G:C4	19:L:82:C:C5	2.93	0.56
20:v:349:PHE:O	20:v:353:CYS:N	2.37	0.56
29:s:53:VAL:HG23	25:z:67:LEU:HD11	1.86	0.56
30:l:17:HIS:HB3	30:l:75:PRO:CG	2.35	0.56
1:A:488:ARG:HG3	1:A:488:ARG:HH21	1.69	0.56
10:Z:319:ASN:HA	10:Z:322:LYS:HD3	1.87	0.56
19:L:1:A:OP1	19:L:1:A:H3'	2.05	0.56
22:b:14:TYR:O	29:s:102:LEU:HD13	2.03	0.56
7:R:41:PHE:CE1	7:R:43:GLY:CA	2.89	0.56
19:L:50:U:H2'	19:L:51:C:N1	2.21	0.56
19:L:73:U:C2	19:L:74:C:C5	2.93	0.56
28:g:38:MET:HB2	28:g:58:VAL:HG12	1.88	0.56
29:k:35:MET:HE2	29:k:46:ASN:HB2	1.87	0.56
29:k:86:ILE:CD1	30:l:11:LEU:CD1	2.78	0.56
26:x:7:LEU:HD23	26:x:29:LEU:HD11	1.87	0.56
1:A:769:MET:HE2	4:O:352:ILE:HD12	1.87	0.56
1:A:903:LEU:HD11	1:A:948:HIS:HE1	1.70	0.56
1:A:1035:LEU:HD12	1:A:1038:ILE:HG12	1.87	0.56
2:C:788:LEU:HD11	2:C:823:ILE:HG21	1.85	0.56
12:d:267:TYR:CE2	12:d:287:PHE:CG	2.94	0.56
19:L:1:A:P	19:L:1:A:C2'	2.94	0.56
20:v:392:TYR:HA	20:v:395:TYR:HD2	1.70	0.56
26:j:19:ILE:HD12	26:j:68:ILE:HD13	1.87	0.56
24:i:40:LYS:CG	24:i:60:ILE:HD13	2.36	0.56
1:A:1906:SER:OG	16:B:61:U:OP1	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:63:PHE:O	10:Z:69:ASN:ND2	2.34	0.56
17:D:128:A:C8	17:D:129:G:N2	2.73	0.56
19:L:81:G:H2'	19:L:82:C:C6	2.41	0.56
19:L:82:C:C2	19:L:83:U:C5	2.92	0.56
1:A:1403:SER:OG	1:A:1429:MET:SD	2.60	0.56
2:C:231:ALA:O	2:C:487:ARG:NH1	2.39	0.56
4:O:105:GLU:HG2	4:O:106:VAL:HG23	1.88	0.56
10:Z:10:ASP:OD2	10:Z:244:LYS:NZ	2.39	0.56
11:c:181:ARG:HH21	11:c:185:LEU:HD11	1.71	0.56
18:E:51:A:N7	32:F:65:ASN:ND2	2.51	0.56
28:e:54:ILE:HD13	28:e:72:VAL:HG21	1.88	0.56
30:l:10:LEU:HD12	30:l:10:LEU:O	2.04	0.56
24:i:30:TRP:CG	24:i:38:ARG:HE	2.24	0.56
27:w:58:GLU:O	27:w:65:HIS:N	2.38	0.56
1:A:749:ARG:HD2	1:A:753:TYR:CE2	2.39	0.56
6:Q:270:LEU:HD12	6:Q:289:PHE:HE1	1.71	0.56
7:R:152:LYS:HD3	7:R:153:PRO:HD3	1.87	0.56
11:c:181:ARG:CZ	11:c:181:ARG:HB3	2.35	0.56
17:D:28:G:O2'	17:D:29:G:OP1	2.23	0.56
19:L:6:U:H6	19:L:6:U:P	2.29	0.56
20:v:530:ARG:HH11	20:v:530:ARG:HA	1.70	0.56
26:j:14:LYS:CG	26:j:74:LEU:HD11	2.34	0.56
28:g:78:GLU:HG2	28:g:85:ILE:HG22	1.88	0.56
28:g:102:ILE:HG13	28:g:103:VAL:H	1.70	0.56
1:A:1964:PRO:CG	1:A:2016:LYS:HZ1	2.18	0.55
4:O:329:ASP:O	4:O:347:SER:OG	2.24	0.55
17:D:28:G:N2	17:D:29:G:C4	2.74	0.55
30:l:21:LEU:CD2	30:l:69:ILE:HD13	2.36	0.55
25:z:23:THR:HG22	25:z:47:LEU:CD1	2.34	0.55
19:L:1:A:H1'	19:L:2:C:H5	1.70	0.55
20:v:542:LEU:HD23	20:v:582:LEU:HD12	1.88	0.55
4:O:414:LEU:HB3	4:O:426:TRP:HB2	1.87	0.55
10:Z:448:MET:HB3	10:Z:449:PHE:CD1	2.41	0.55
19:L:116:U:N3	29:s:40:HIS:CD2	2.74	0.55
26:j:19:ILE:HG21	24:i:88:THR:HG23	1.88	0.55
29:k:49:ILE:HD12	29:k:49:ILE:N	2.16	0.55
28:e:73:LYS:HG3	28:e:90:PHE:CD2	2.41	0.55
25:z:39:ILE:HD11	25:z:84:TYR:CE1	2.40	0.55
1:A:1232:SER:CB	8:S:135:ARG:HH11	2.05	0.55
1:A:1294:LYS:O	10:Z:429:ASN:ND2	2.38	0.55
1:A:1663:PHE:CE1	1:A:1902:GLN:HG3	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:194:GLU:O	6:Q:291:ILE:HG21	2.05	0.55
13:I:102:LYS:NZ	13:I:106:GLU:OE2	2.39	0.55
17:D:99:U:H5''	17:D:99:U:C6	2.41	0.55
19:L:70:A:C4	19:L:71:C:C5	2.94	0.55
20:v:385:PHE:N	20:v:385:PHE:CD1	2.73	0.55
28:e:93:LYS:NZ	25:z:103:LEU:HD13	2.21	0.55
6:Q:215:PRO:HG2	6:Q:218:LYS:HB2	1.89	0.55
7:R:19:PRO:O	9:T:40:LYS:NZ	2.26	0.55
19:L:120:G:H4'	19:L:121:C:O5'	2.06	0.55
20:v:386:GLU:HA	20:v:389:ILE:HD13	1.84	0.55
28:g:35:ASN:CB	28:g:61:PHE:CE2	2.81	0.55
1:A:1430:THR:CG2	1:A:1431:HIS:H	2.20	0.55
1:A:2080:LYS:O	1:A:2084:LEU:HG	2.06	0.55
2:C:466:GLY:O	2:C:581:LYS:NZ	2.40	0.55
14:n:57:LYS:NZ	18:E:1:G:OP2	2.39	0.55
19:L:67:A:C4	19:L:68:U:C5	2.95	0.55
19:L:152:C:N4	19:L:1085:G:H1	1.97	0.55
19:L:1129:U:C2'	19:L:1130:U:C5'	2.85	0.55
28:g:37:ALA:CB	28:g:44:VAL:HG11	2.37	0.55
24:i:30:TRP:O	24:i:88:THR:HB	2.07	0.55
1:A:2011:LEU:HD11	1:A:2040:TRP:HH2	1.72	0.55
2:C:500:ARG:NH1	2:C:536:SER:OG	2.39	0.55
9:T:3:ARG:NH2	9:T:85:LYS:O	2.40	0.55
17:D:50:G:H1	17:D:65:U:H3	1.53	0.55
28:e:102:ILE:HG13	28:e:103:VAL:H	1.70	0.55
1:A:2080:LYS:HG3	1:A:2084:LEU:HD21	1.89	0.55
2:C:684:GLU:OE1	2:C:713:GLU:HG3	2.07	0.55
2:C:947:LYS:NZ	2:C:984:ASN:O	2.40	0.55
10:Z:445:LEU:HD12	10:Z:445:LEU:N	2.21	0.55
17:D:9:U:O2	17:D:9:U:H2'	2.07	0.55
29:k:49:ILE:HG23	29:k:81:VAL:HG23	1.88	0.55
28:e:97:ARG:NH2	25:z:36:MET:SD	2.79	0.55
26:x:74:LEU:O	26:x:74:LEU:HD12	2.07	0.55
1:A:1182:LEU:HD21	8:S:127:TRP:CZ2	2.41	0.55
6:Q:212:ALA:O	7:R:237:ARG:NH1	2.39	0.55
20:v:325:LEU:O	20:v:329:SER:N	2.38	0.55
7:R:229:ASP:O	7:R:235:GLN:NE2	2.39	0.55
17:D:26:A:O4'	17:D:131:A:OP1	2.25	0.55
29:k:44:VAL:HG13	29:k:85:THR:O	2.06	0.55
24:i:30:TRP:CE2	24:i:38:ARG:NE	2.75	0.55
1:A:143:ILE:HD11	1:A:573:ARG:CZ	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1964:PRO:HG2	1:A:2016:LYS:NZ	2.22	0.54
4:O:271:GLN:HG2	4:O:314:THR:H	1.71	0.54
19:L:113:U:C6	27:w:48:TYR:CE1	2.96	0.54
4:O:126:HIS:HB2	4:O:384:TYR:CE2	2.42	0.54
4:O:285:SER:OG	4:O:287:ASP:OD1	2.23	0.54
7:R:41:PHE:CD1	7:R:41:PHE:C	2.85	0.54
7:R:55:PRO:HB3	7:R:93:ILE:HD11	1.88	0.54
17:D:9:U:O4	17:D:156:G:O6	2.26	0.54
19:L:105:A:H2'	19:L:106:A:C5'	2.37	0.54
24:u:44:VAL:HB	24:u:53:VAL:HG23	1.89	0.54
29:k:49:ILE:HG22	29:k:80:ARG:C	2.32	0.54
29:s:53:VAL:HG23	25:z:67:LEU:CD1	2.37	0.54
1:A:1163:ARG:HG2	1:A:1163:ARG:HH11	1.72	0.54
2:C:675:THR:HG22	2:C:909:ILE:HD13	1.89	0.54
4:O:259:VAL:HG12	4:O:260:ILE:HG13	1.88	0.54
7:R:41:PHE:CD1	7:R:43:GLY:N	2.74	0.54
20:v:255:GLU:O	20:v:259:LYS:N	2.40	0.54
26:j:35:PHE:HB2	26:j:37:ASN:ND2	2.23	0.54
26:j:47:ASN:OD1	26:j:48:GLY:N	2.31	0.54
1:A:2080:LYS:O	1:A:2084:LEU:CD2	2.56	0.54
11:c:233:GLU:OE2	12:d:115:ILE:N	2.41	0.54
15:H:47:ALA:HA	15:H:50:TRP:HD1	1.72	0.54
17:D:172:U:N3	25:m:37:ASN:OD1	2.41	0.54
19:L:12:U:C4	19:L:13:G:N7	2.76	0.54
19:L:109:C:O2'	19:L:110:A:OP2	2.23	0.54
29:k:39:LYS:HG3	29:k:40:HIS:N	2.23	0.54
1:A:1035:LEU:HD11	1:A:1038:ILE:CG1	2.37	0.54
1:A:1286:TRP:HB2	1:A:1300:ALA:HB3	1.90	0.54
1:A:1800:ASN:OD1	1:A:1803:ARG:NH2	2.39	0.54
7:R:151:LEU:HD23	19:L:78:G:H5''	1.88	0.54
10:Z:440:LEU:HD13	10:Z:449:PHE:CZ	2.43	0.54
12:d:211:ARG:HG2	20:v:520:ILE:CG1	2.38	0.54
15:H:27:LYS:O	15:H:28:ASP:OD2	2.25	0.54
19:L:1:A:H2'	19:L:1:A:OP1	2.07	0.54
26:j:63:ILE:CG1	24:i:89:LEU:CD2	2.86	0.54
24:i:44:VAL:HB	24:i:53:VAL:HG23	1.89	0.54
7:R:150:HIS:C	7:R:150:HIS:CD2	2.86	0.54
18:E:64:U:O2'	18:E:65:U:P	2.65	0.54
20:v:711:MET:HE2	20:v:748:PHE:CB	2.33	0.54
30:l:21:LEU:HD12	30:l:44:LEU:HD11	1.90	0.54
1:A:674:MET:HE1	1:A:1621:VAL:HG21	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:230:PRO:HD2	16:B:14:U:H2'	1.88	0.54
12:d:141:ILE:HG23	13:I:105:TYR:CE1	2.42	0.54
19:L:2:C:C6	19:L:2:C:H3'	2.43	0.54
28:e:56:ALA:HB1	28:e:72:VAL:HB	1.89	0.54
32:F:46:PRO:C	32:F:47:PHE:CD1	2.85	0.54
1:A:1056:GLU:HB2	1:A:1059:GLU:HB3	1.89	0.54
2:C:352:VAL:O	2:C:372:THR:OG1	2.23	0.54
7:R:162:PHE:CE1	19:L:75:A:O2'	2.60	0.54
10:Z:450:PRO:HD2	10:Z:477:MET:HE2	1.89	0.54
11:c:226:GLY:HA3	12:d:120:ASN:CG	2.32	0.54
12:d:319:ASP:OD1	12:d:319:ASP:N	2.40	0.54
25:m:86:ASN:ND2	29:k:41:MET:CE	2.70	0.54
1:A:1435:LYS:CB	1:A:1437:ILE:HD11	2.31	0.54
1:A:1647:GLN:O	1:A:1650:ARG:NH1	2.38	0.54
11:c:35:LYS:HE2	18:E:54:U:O2'	2.08	0.54
12:d:298:GLU:HA	12:d:301:ILE:HG22	1.88	0.54
17:D:3:G:C6	17:D:4:C:C4	2.95	0.54
19:L:4:A:C2	19:L:5:A:C5	2.96	0.54
19:L:38:U:C2'	19:L:39:A:H5'	2.37	0.54
19:L:107:U:O5'	19:L:107:U:H6	1.91	0.54
1:A:1855:THR:HG22	1:A:1937:ARG:HH21	1.73	0.54
2:C:286:LEU:CD2	10:Z:182:GLN:O	2.55	0.54
2:C:681:CYS:SG	2:C:714:PRO:N	2.81	0.54
10:Z:402:LEU:HD12	10:Z:405:ILE:HD13	1.89	0.54
27:h:71:ILE:CG2	28:g:103:VAL:HG23	2.37	0.54
29:k:51:GLU:OE1	29:k:77:VAL:HG11	2.07	0.54
32:F:25:ARG:HH12	32:F:29:LYS:HE2	1.73	0.54
1:A:139:LEU:O	1:A:143:ILE:HG22	2.08	0.53
1:A:1435:LYS:O	1:A:1436:LEU:HB2	2.07	0.53
1:A:2084:LEU:HG	1:A:2085:GLY:H	1.71	0.53
7:R:207:PRO:C	7:R:209:ASP:N	2.66	0.53
12:d:267:TYR:HD2	12:d:284:LEU:HD23	1.70	0.53
20:v:686:ILE:HG12	20:v:713:ILE:HG21	1.89	0.53
22:b:125:LYS:O	22:b:152:GLU:CB	2.55	0.53
28:g:79:LYS:HA	28:g:83:ASN:O	2.08	0.53
29:k:52:ARG:HB3	29:k:52:ARG:NH1	2.23	0.53
29:s:16:ILE:O	29:s:17:ASP:HB2	2.08	0.53
25:z:27:GLY:HA3	25:z:43:VAL:HG12	1.90	0.53
32:F:47:PHE:CZ	32:F:49:MET:HE1	2.43	0.53
1:A:591:LEU:HD11	1:A:613:SER:HB2	1.91	0.53
1:A:1993:ASP:HB3	1:A:2038:HIS:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:n:274:HIS:HB2	14:n:287:GLN:HB2	1.89	0.53
17:D:130:A:H1'	17:D:131:A:OP2	2.08	0.53
19:L:52:A:H2'	19:L:52:A:N3	2.23	0.53
19:L:1155:C:H6	19:L:1155:C:O5'	1.90	0.53
26:j:71:LEU:HB3	30:l:63:PHE:HB3	1.90	0.53
30:l:63:PHE:CD1	30:l:63:PHE:C	2.85	0.53
1:A:2080:LYS:C	1:A:2084:LEU:HD23	2.33	0.53
1:A:2081:ASP:OD1	1:A:2085:GLY:HA2	2.07	0.53
4:O:373:LEU:HD11	4:O:387:LEU:HB2	1.89	0.53
17:D:123:U:H2'	17:D:124:C:H5'	1.90	0.53
17:D:147:C:H2'	17:D:148:G:H8	1.72	0.53
19:L:49:U:O2	19:L:49:U:H2'	2.07	0.53
29:k:31:ILE:CG1	29:k:49:ILE:HD13	2.37	0.53
29:k:31:ILE:O	29:k:48:CYS:HA	2.09	0.53
30:l:11:LEU:HD23	30:l:36:SER:HB3	1.90	0.53
1:A:1850:LEU:HD13	1:A:1930:PRO:HG3	1.90	0.53
6:Q:39:LEU:HD23	6:Q:63:ARG:HH12	1.74	0.53
19:L:1129:U:C2'	19:L:1130:U:H5'	2.38	0.53
22:b:160:THR:O	22:b:163:GLU:N	2.42	0.53
26:j:23:ARG:HH21	26:j:23:ARG:CG	2.22	0.53
28:e:50:ASN:O	28:e:51:ASN:CB	2.57	0.53
30:l:71:PHE:C	30:l:71:PHE:CD1	2.85	0.53
26:x:35:PHE:HB2	26:x:37:ASN:ND2	2.23	0.53
1:A:1711:VAL:HA	1:A:1791:PHE:HA	1.91	0.53
1:A:2011:LEU:HD11	1:A:2040:TRP:CH2	2.43	0.53
6:Q:304:THR:HG23	7:R:154:ALA:HB2	1.89	0.53
17:D:43:G:C2'	17:D:45:A:OP1	2.56	0.53
28:e:54:ILE:HB	28:e:72:VAL:CG2	2.38	0.53
24:i:30:TRP:HE1	24:i:38:ARG:HD3	1.62	0.53
1:A:2011:LEU:CD1	1:A:2040:TRP:CH2	2.92	0.53
11:c:252:GLY:HA3	12:d:38:LEU:O	2.09	0.53
19:L:109:C:H3'	19:L:109:C:H6	1.73	0.53
19:L:1137:U:H5'	21:a:66:LYS:O	2.09	0.53
1:A:1159:ARG:HE	1:A:1173:HIS:HB3	1.73	0.53
4:O:384:TYR:CD1	4:O:384:TYR:C	2.85	0.53
6:Q:303:GLY:CA	6:Q:309:ASN:OD1	2.48	0.53
7:R:28:LEU:HB3	7:R:39:GLN:HB2	1.91	0.53
15:H:27:LYS:O	15:H:28:ASP:CG	2.52	0.53
17:D:3:G:H2'	17:D:4:C:C6	2.43	0.53
20:v:391:LEU:HB3	20:v:395:TYR:CE2	2.43	0.53
25:m:27:GLY:HA3	25:m:43:VAL:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:x:63:ILE:HG21	26:x:68:ILE:HD11	1.90	0.53
6:Q:252:ARG:HG3	6:Q:297:PHE:CE1	2.43	0.53
7:R:151:LEU:O	19:L:78:G:P	2.67	0.53
7:R:152:LYS:CB	7:R:153:PRO:CD	2.83	0.53
17:D:161:U:O2'	17:D:162:G:H5'	2.08	0.53
17:D:166:U:H3'	17:D:166:U:H6	1.74	0.53
19:L:6:U:O2	19:L:6:U:H2'	2.09	0.53
19:L:1107:C:H6	19:L:1107:C:H5'	1.74	0.53
20:v:357:ILE:O	20:v:361:LEU:N	2.35	0.53
26:j:10:TYR:HB3	26:j:15:ILE:HD11	1.90	0.53
29:s:58:LEU:HD11	25:z:62:MET:HE3	1.91	0.53
26:x:71:LEU:N	30:y:63:PHE:O	2.28	0.53
1:A:1430:THR:CG2	1:A:1431:HIS:N	2.72	0.53
1:A:1808:ALA:HB1	1:A:1947:HIS:NE2	2.23	0.53
13:I:197:ASN:OD1	13:I:200:ASN:ND2	2.42	0.53
17:D:165:A:H4'	17:D:166:U:OP1	2.08	0.53
18:E:79:A:OP1	18:E:81:G:O2'	2.27	0.53
20:v:489:LEU:HD22	20:v:547:LYS:HD3	1.89	0.53
28:e:45:ILE:HB	28:e:105:LEU:HG	1.90	0.53
26:x:14:LYS:CG	26:x:74:LEU:HD11	2.39	0.53
12:d:211:ARG:HG2	20:v:520:ILE:HG13	1.91	0.53
16:B:55:U:H2'	16:B:56:G:C8	2.43	0.53
19:L:4:A:C2	19:L:5:A:C8	2.97	0.53
26:j:27:GLY:C	26:j:40:LEU:HD12	2.34	0.53
26:j:29:LEU:HD23	26:j:29:LEU:O	2.09	0.53
1:A:1235:PRO:HD3	8:S:133:PHE:HZ	1.71	0.52
1:A:1405:ILE:HD13	10:Z:303:LEU:HB2	1.90	0.52
1:A:1660:SER:OG	1:A:1809:ASN:OD1	2.24	0.52
7:R:40:GLY:CA	15:H:26:TYR:CZ	2.93	0.52
12:d:342:PHE:O	12:d:345:ALA:N	2.42	0.52
16:B:69:A:H2'	16:B:71:C:H41	1.73	0.52
17:D:2:A:N1	17:D:3:G:C6	2.77	0.52
28:g:35:ASN:HA	28:g:61:PHE:CD2	2.40	0.52
1:A:746:THR:OG1	1:A:749:ARG:NH2	2.41	0.52
1:A:1773:VAL:HA	1:A:1788:GLY:HA3	1.91	0.52
4:O:385:GLN:NE2	4:O:387:LEU:HD21	2.24	0.52
10:Z:105:GLN:OE1	10:Z:108:ARG:NH2	2.43	0.52
11:c:509:LEU:O	11:c:513:ILE:N	2.39	0.52
17:D:167:A:C6	27:h:48:TYR:CD1	2.98	0.52
18:E:13:A:HO2'	18:E:14:C:H5	1.57	0.52
18:E:100:U:O2'	18:E:101:U:OP1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:84:TYR:CD2	29:k:6:VAL:HG21	2.44	0.52
29:k:18:TYR:CE1	29:k:101:PRO:HD3	2.44	0.52
30:l:10:LEU:O	30:l:13:GLU:HB2	2.09	0.52
32:F:47:PHE:HZ	32:F:97:PHE:CZ	2.21	0.52
1:A:743:LYS:CE	1:A:749:ARG:HH11	2.21	0.52
19:L:74:C:C2'	19:L:75:A:H5'	2.38	0.52
19:L:114:U:O2	26:x:64:ARG:CG	2.57	0.52
25:z:52:LEU:HD23	25:z:55:LEU:HD22	1.92	0.52
1:A:860:GLU:OE2	1:A:863:ARG:NH2	2.36	0.52
1:A:1012:TRP:HB2	1:A:1162:THR:HA	1.91	0.52
1:A:1382:ARG:NH2	1:A:1635:HIS:O	2.42	0.52
6:Q:189:LYS:NZ	19:L:72:C:OP1	2.42	0.52
12:d:330:ILE:HG22	12:d:339:MET:HA	1.90	0.52
16:B:1:G:H21	16:B:1:G:P	2.27	0.52
19:L:1125:U:H6	19:L:1125:U:H5''	1.74	0.52
28:e:93:LYS:NZ	25:z:103:LEU:CD1	2.73	0.52
1:A:1380:PRO:O	1:A:1431:HIS:NE2	2.41	0.52
5:P:171:ASN:OD1	5:P:185:ARG:O	2.27	0.52
7:R:152:LYS:HD3	7:R:153:PRO:CD	2.39	0.52
7:R:205:LEU:CD2	7:R:205:LEU:N	2.73	0.52
17:D:147:C:H2'	17:D:148:G:C8	2.45	0.52
19:L:2:C:C6	19:L:2:C:C3'	2.93	0.52
19:L:1101:C:H2'	19:L:1101:C:O2	2.09	0.52
20:v:683:SER:O	20:v:687:LEU:N	2.40	0.52
26:j:19:ILE:HG21	24:i:88:THR:CG2	2.40	0.52
28:g:68:VAL:C	28:g:69:LEU:HD12	2.35	0.52
29:s:42:ASN:HB3	29:s:89:GLY:N	2.23	0.52
30:l:79:LYS:HG3	30:l:80:ASN:N	2.25	0.52
1:A:743:LYS:HB3	1:A:749:ARG:HH11	1.75	0.52
1:A:1521:ARG:HD3	16:B:74:A:H1'	1.91	0.52
4:O:134:VAL:HG22	4:O:424:LYS:HG2	1.92	0.52
7:R:38:SER:C	7:R:39:GLN:O	2.50	0.52
7:R:41:PHE:CG	7:R:42:ALA:N	2.77	0.52
19:L:2:C:H3'	19:L:2:C:OP2	2.10	0.52
19:L:4:A:O4'	20:v:529:HIS:CG	2.63	0.52
19:L:113:U:C6	27:w:48:TYR:CD1	2.96	0.52
20:v:467:ARG:HA	20:v:470:TRP:HD1	1.75	0.52
20:v:612:ILE:HD13	20:v:624:TRP:CZ2	2.44	0.52
26:j:64:ARG:HH21	24:i:50:MET:HB3	1.64	0.52
27:w:29:VAL:HG12	27:w:81:ILE:HG12	1.91	0.52
1:A:1404:HIS:CG	1:A:1437:ILE:HD12	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2011:LEU:HG	1:A:2040:TRP:CZ2	2.44	0.52
19:L:67:A:HO2'	19:L:68:U:H5'	1.75	0.52
28:g:50:ASN:O	28:g:51:ASN:CB	2.57	0.52
28:e:44:VAL:HG22	28:e:56:ALA:O	2.10	0.52
28:e:93:LYS:CB	25:z:97:LEU:CD1	2.87	0.52
30:l:17:HIS:CG	30:l:75:PRO:CG	2.88	0.52
27:w:32:LYS:HA	27:w:79:LEU:HD12	1.92	0.52
18:E:100:U:C5'	18:E:100:U:C6	2.85	0.52
18:E:102:U:C2'	18:E:103:A:C1'	2.88	0.52
19:L:70:A:H2'	19:L:71:C:C6	2.45	0.52
20:v:530:ARG:NH1	20:v:530:ARG:CB	2.73	0.52
25:m:99:ASP:OD1	28:g:92:SER:HB3	2.09	0.52
27:h:13:VAL:HG12	24:i:44:VAL:HG11	1.92	0.52
27:h:29:VAL:HG12	27:h:81:ILE:HG12	1.91	0.52
28:g:32:SER:O	28:g:35:ASN:ND2	2.37	0.52
28:g:41:ARG:HG3	28:g:41:ARG:NH2	2.25	0.52
30:l:44:LEU:HD12	30:l:47:VAL:HG11	1.91	0.52
32:F:46:PRO:O	32:F:47:PHE:HB3	2.08	0.52
5:P:76:ARG:HE	6:Q:5:ILE:HD12	1.74	0.52
7:R:158:SER:OG	19:L:75:A:H2	1.92	0.52
11:c:189:ARG:NH2	12:d:42:GLU:OE2	2.40	0.52
19:L:1:A:C1'	19:L:2:C:N4	2.73	0.52
25:m:17:ILE:HD12	25:m:40:LEU:HD11	1.92	0.52
28:g:37:ALA:HB1	28:g:44:VAL:CG1	2.39	0.52
28:e:93:LYS:HZ3	25:z:103:LEU:HD13	1.74	0.52
30:l:22:GLU:HB3	30:l:71:PHE:CE1	2.44	0.52
1:A:1616:ARG:NH2	1:A:1744:ASP:OD1	2.42	0.52
1:A:1865:THR:HB	1:A:1869:ASN:H	1.75	0.52
2:C:205:SER:O	30:l:83:LEU:HD23	2.10	0.52
2:C:360:ARG:HH11	2:C:362:LYS:HE3	1.74	0.52
6:Q:213:SER:O	6:Q:214:ILE:CG2	2.58	0.52
17:D:129:G:H4'	17:D:130:A:OP1	2.10	0.52
30:l:21:LEU:HD22	30:l:42:VAL:HG21	1.92	0.52
27:w:23:VAL:HA	27:w:42:LEU:HD22	1.92	0.52
27:w:32:LYS:CG	27:w:33:PHE:CD1	2.88	0.52
2:C:905:GLN:OE1	2:C:938:ARG:NH2	2.40	0.51
9:T:82:ILE:HG21	9:T:89:LYS:HD3	1.91	0.51
16:B:69:A:O2'	16:B:70:A:C8	2.64	0.51
17:D:128:A:H1'	17:D:129:G:N3	2.25	0.51
27:h:32:LYS:HA	27:h:79:LEU:HD12	1.92	0.51
1:A:1432:GLU:HG3	1:A:1433:ASP:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:851:LEU:HB2	2:C:989:LEU:HD13	1.92	0.51
7:R:151:LEU:HD23	19:L:78:G:O5'	2.10	0.51
7:R:152:LYS:CB	7:R:153:PRO:HD2	2.38	0.51
32:F:12:PRO:HG2	32:F:15:TYR:HB2	1.93	0.51
1:A:495:ARG:NH1	1:A:495:ARG:CG	2.73	0.51
6:Q:306:THR:HG23	6:Q:307:ALA:N	2.26	0.51
13:I:117:GLN:HB3	13:I:121:LYS:NZ	2.26	0.51
16:B:52:U:H3'	16:B:52:U:H6	1.75	0.51
17:D:128:A:N3	17:D:128:A:C3'	2.74	0.51
19:L:53:G:N3	19:L:53:G:C2'	2.73	0.51
19:L:53:G:N3	19:L:53:G:C3'	2.73	0.51
19:L:68:U:H2'	19:L:69:G:C8	2.44	0.51
19:L:1127:A:C2'	19:L:1128:C:O5'	2.58	0.51
28:g:76:TRP:CH2	28:g:87:ARG:CD	2.86	0.51
28:e:59:LYS:HG3	28:e:70:GLU:HG2	1.90	0.51
1:A:1035:LEU:CD1	1:A:1038:ILE:CG1	2.88	0.51
1:A:1324:GLY:HA3	16:B:72:A:H4'	1.93	0.51
2:C:406:VAL:HG13	2:C:427:LEU:HG	1.92	0.51
12:d:141:ILE:CG2	13:I:105:TYR:CD1	2.94	0.51
17:D:128:A:H1'	17:D:129:G:C2	2.45	0.51
19:L:78:G:C2'	19:L:79:A:H5'	2.40	0.51
27:h:23:VAL:HA	27:h:42:LEU:HD22	1.92	0.51
28:e:70:GLU:OE2	28:e:71:ASN:OD1	2.28	0.51
1:A:273:ASP:HA	1:A:310:ASN:HD21	1.75	0.51
1:A:1011:ASN:HB2	1:A:1144:PHE:HA	1.91	0.51
5:P:170:SER:OG	5:P:173:LYS:O	2.29	0.51
11:c:35:LYS:HD3	18:E:55:G:N7	2.25	0.51
17:D:179:U:OP1	28:g:79:LYS:O	2.27	0.51
18:E:102:U:H2'	18:E:103:A:C8	2.43	0.51
19:L:2:C:C5	19:L:3:G:N1	2.76	0.51
19:L:46:C:HO2'	19:L:47:U:H6	1.58	0.51
19:L:119:G:N7	28:e:49:ARG:HD2	2.24	0.51
29:s:18:TYR:CE1	29:s:101:PRO:HD3	2.44	0.51
6:Q:70:ILE:HD13	6:Q:84:ILE:HD11	1.91	0.51
7:R:19:PRO:HG3	7:R:51:PHE:HZ	1.76	0.51
9:T:98:THR:O	18:E:1:G:N2	2.41	0.51
16:B:69:A:C2	16:B:71:C:N4	2.79	0.51
17:D:131:A:H5''	17:D:132:A:C8	2.46	0.51
26:j:19:ILE:HD13	26:j:19:ILE:N	2.23	0.51
27:h:74:ARG:HE	27:h:76:ASN:ND2	2.08	0.51
28:g:78:GLU:CG	28:g:85:ILE:CG2	2.88	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:s:24:THR:OG1	29:s:26:ASP:OD1	2.25	0.51
31:r:8:LYS:CG	31:o:88:TRP:HH2	2.24	0.51
4:O:206:VAL:HB	4:O:220:TYR:HB2	1.93	0.51
7:R:152:LYS:CD	7:R:153:PRO:CD	2.88	0.51
12:d:269:ILE:O	12:d:273:LYS:HB2	2.11	0.51
15:H:27:LYS:CD	15:H:29:TYR:CE1	2.81	0.51
28:g:76:TRP:CZ2	28:g:87:ARG:NE	2.79	0.51
24:i:28:THR:CG2	24:i:40:LYS:HD2	2.31	0.51
24:i:30:TRP:CE2	24:i:38:ARG:HD3	2.38	0.51
2:C:233:ASP:OD1	2:C:487:ARG:NH2	2.43	0.51
2:C:626:SER:HB2	2:C:634:ILE:HD12	1.93	0.51
2:C:869:HIS:HA	2:C:899:LEU:HA	1.93	0.51
7:R:40:GLY:HA2	15:H:26:TYR:CZ	2.44	0.51
10:Z:473:LEU:CD1	10:Z:473:LEU:N	2.73	0.51
12:d:301:ILE:HD11	20:v:646:PHE:CG	2.46	0.51
18:E:102:U:O5'	18:E:103:A:OP2	2.28	0.51
19:L:33:U:H2'	19:L:34:G:O4'	2.11	0.51
19:L:46:C:O2'	19:L:47:U:O5'	2.29	0.51
20:v:365:ASP:CA	20:v:399:VAL:HG22	2.39	0.51
20:v:729:TYR:CE1	20:v:749:SER:CB	2.94	0.51
25:m:4:VAL:HG11	25:m:34:PRO:O	2.11	0.51
25:m:47:LEU:HD23	25:m:48:PRO:HD2	1.92	0.51
1:A:144:ASN:HB3	9:T:36:ASP:HB2	1.91	0.51
1:A:488:ARG:NH2	1:A:488:ARG:CG	2.73	0.51
4:O:373:LEU:HD12	4:O:373:LEU:C	2.36	0.51
29:k:13:ALA:CB	29:k:37:PHE:CZ	2.85	0.51
29:k:24:THR:OG1	29:k:26:ASP:OD1	2.25	0.51
1:A:1035:LEU:HD12	1:A:1035:LEU:C	2.35	0.51
7:R:41:PHE:N	15:H:26:TYR:HE1	2.06	0.51
7:R:150:HIS:O	7:R:152:LYS:N	2.44	0.50
19:L:1090:A:C2'	19:L:1091:G:H5'	2.41	0.50
19:L:1146:G:C6	19:L:1147:A:C6	3.00	0.50
19:L:1154:U:C2'	19:L:1155:C:O5'	2.58	0.50
30:y:21:LEU:CD1	30:y:44:LEU:CD1	2.71	0.50
1:A:1361:VAL:HG21	1:A:1407:ILE:HD11	1.93	0.50
6:Q:67:GLN:NE2	6:Q:116:LYS:O	2.44	0.50
8:S:8:GLN:HB3	18:E:63:G:O2'	2.12	0.50
10:Z:443:SER:O	10:Z:444:LYS:C	2.54	0.50
11:c:152:LEU:HD21	11:c:156:ARG:HH21	1.75	0.50
11:c:187:LYS:NZ	15:H:62:SER:O	2.30	0.50
26:j:71:LEU:HD23	26:j:71:LEU:C	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:e:89:ARG:NH2	28:e:91:ILE:CD1	2.72	0.50
25:z:30:GLN:HB2	25:z:39:ILE:HG23	1.92	0.50
11:c:14:THR:HG23	11:c:17:GLU:H	1.77	0.50
11:c:189:ARG:HH21	12:d:42:GLU:CD	2.19	0.50
14:n:305:GLY:O	14:n:307:LYS:N	2.44	0.50
17:D:127:U:H6	17:D:127:U:OP2	1.94	0.50
19:L:1:A:P	19:L:1:A:C3'	3.00	0.50
29:k:38:ASP:OD1	29:k:39:LYS:N	2.41	0.50
30:l:41:ASN:HB3	30:l:66:GLY:N	2.26	0.50
1:A:1435:LYS:HD3	1:A:1435:LYS:H	1.77	0.50
1:A:1853:ASP:HB3	1:A:1880:PHE:HB3	1.92	0.50
4:O:159:SER:OG	4:O:160:ASN:N	2.44	0.50
12:d:175:PHE:HA	12:d:178:ARG:NH2	2.27	0.50
19:L:117:U:H5'	25:z:90:ASN:HB3	1.93	0.50
20:v:530:ARG:CA	20:v:530:ARG:NH1	2.73	0.50
26:j:62:VAL:CG1	24:i:90:ILE:HB	2.41	0.50
29:s:85:THR:HG22	30:y:73:VAL:HG22	1.93	0.50
1:A:1163:ARG:HG2	1:A:1163:ARG:NH1	2.27	0.50
1:A:1404:HIS:NE2	1:A:1437:ILE:HD13	2.22	0.50
2:C:682:SER:O	2:C:683:ASN:ND2	2.45	0.50
6:Q:214:ILE:HG23	6:Q:214:ILE:O	2.12	0.50
25:z:17:ILE:HD12	25:z:40:LEU:HD11	1.92	0.50
1:A:1182:LEU:HD21	8:S:127:TRP:CH2	2.46	0.50
1:A:1810:PRO:HB3	1:A:1911:TRP:NE1	2.26	0.50
1:A:1991:ILE:O	1:A:2040:TRP:CD1	2.65	0.50
16:B:60:U:H3	19:L:43:G:H1	1.58	0.50
26:x:10:TYR:HB3	26:x:15:ILE:HD11	1.94	0.50
25:z:16:THR:HA	25:z:25:VAL:O	2.11	0.50
6:Q:207:LEU:HD22	6:Q:290:ILE:HG22	1.93	0.50
12:d:141:ILE:HG23	13:I:105:TYR:CD1	2.47	0.50
19:L:109:C:OP1	25:z:8:LYS:NZ	2.45	0.50
19:L:1106:G:C4'	19:L:1107:C:OP1	2.60	0.50
28:g:41:ARG:HG3	28:g:41:ARG:HH21	1.75	0.50
30:l:61:GLN:HG3	30:l:62:ILE:N	2.25	0.50
25:z:19:LEU:HD22	25:z:91:THR:HG22	1.93	0.50
1:A:495:ARG:NH1	1:A:495:ARG:CB	2.73	0.50
1:A:854:ARG:HH21	19:L:25:A:H5''	1.77	0.50
1:A:1852:VAL:HB	1:A:1935:VAL:HG22	1.94	0.50
6:Q:207:LEU:CD2	6:Q:290:ILE:CG2	2.83	0.50
13:I:117:GLN:HB3	13:I:121:LYS:HZ1	1.76	0.50
17:D:10:U:H2'	17:D:11:A:N7	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:175:G:O5'	28:g:49:ARG:NH1	2.45	0.50
19:L:1105:C:H1'	19:L:1106:G:O4'	2.12	0.50
24:u:35:ILE:HG23	24:u:37:ILE:H	1.77	0.50
1:A:1201:TYR:OH	1:A:1248:VAL:O	2.30	0.50
1:A:1965:PHE:O	1:A:1966:SER:CB	2.60	0.50
4:O:121:GLN:NE2	5:P:49:SER:O	2.39	0.50
11:c:145:GLU:HB3	11:c:149:LYS:HE3	1.93	0.50
19:L:4:A:C2	19:L:5:A:N7	2.80	0.50
19:L:105:A:C2'	19:L:106:A:H5'	2.40	0.50
19:L:1154:U:C2'	19:L:1155:C:C5'	2.87	0.50
20:v:530:ARG:NH1	20:v:530:ARG:N	2.60	0.50
28:g:71:ASN:N	28:g:92:SER:O	2.41	0.50
29:k:52:ARG:CG	29:k:52:ARG:NH1	2.74	0.50
30:l:21:LEU:CD1	30:l:44:LEU:HD11	2.42	0.50
24:i:46:PHE:HB3	24:i:52:VAL:HG12	1.94	0.50
1:A:495:ARG:CB	1:A:495:ARG:CZ	2.90	0.49
4:O:385:GLN:HE21	4:O:387:LEU:HD21	1.76	0.49
6:Q:250:GLY:C	6:Q:297:PHE:CZ	2.90	0.49
19:L:1127:A:H8	19:L:1127:A:O5'	1.95	0.49
22:b:67:ILE:CB	22:b:89:VAL:CB	2.90	0.49
25:m:16:THR:HA	25:m:25:VAL:O	2.11	0.49
32:F:186:LEU:HD23	32:F:189:LYS:HD2	1.92	0.49
1:A:140:ARG:O	1:A:143:ILE:HG23	2.12	0.49
5:P:105:LEU:HD13	5:P:112:ILE:HD12	1.94	0.49
17:D:128:A:C2'	17:D:128:A:N3	2.74	0.49
20:v:396:LEU:C	20:v:396:LEU:CD2	2.86	0.49
28:e:73:LYS:HE3	28:e:90:PHE:HE2	1.78	0.49
24:i:54:ILE:CG1	24:i:57:ALA:HB2	2.41	0.49
30:y:24:THR:HA	30:y:70:LYS:HE3	1.93	0.49
6:Q:71:CYS:SG	6:Q:74:CYS:N	2.84	0.49
7:R:158:SER:OG	19:L:75:A:C2	2.65	0.49
19:L:68:U:HO2'	19:L:69:G:H5'	1.75	0.49
20:v:667:ILE:HA	20:v:670:SER:HB3	1.94	0.49
28:e:63:ARG:HH11	28:e:64:HIS:HE1	1.59	0.49
30:y:33:LEU:HA	30:y:44:LEU:CD2	2.35	0.49
1:A:1304:VAL:H	1:A:1353:THR:HG21	1.78	0.49
6:Q:206:PHE:CD2	6:Q:291:ILE:CD1	2.87	0.49
10:Z:32:LEU:HD23	10:Z:76:LEU:HD23	1.94	0.49
19:L:51:C:C4	19:L:52:A:N7	2.81	0.49
19:L:1084:A:O3'	19:L:1085:G:H8	1.95	0.49
29:k:49:ILE:HG22	29:k:81:VAL:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:84:LEU:O	30:l:74:VAL:HG22	2.12	0.49
1:A:1035:LEU:CD1	1:A:1038:ILE:CG2	2.90	0.49
6:Q:283:ILE:HD12	6:Q:283:ILE:N	2.26	0.49
8:S:132:ALA:O	8:S:133:PHE:HB3	2.12	0.49
19:L:1168:U:H2'	19:L:1169:C:C6	2.46	0.49
1:A:173:LEU:HD12	1:A:715:LEU:HB3	1.94	0.49
1:A:1716:LEU:HD23	1:A:1718:HIS:H	1.77	0.49
2:C:880:MET:HE3	2:C:886:SER:HB3	1.93	0.49
4:O:275:THR:OG1	4:O:279:PRO:O	2.30	0.49
12:d:60:ARG:NH1	18:E:84:C:H4'	2.27	0.49
16:B:57:C:N4	19:L:46:C:H42	2.10	0.49
18:E:102:U:H3'	18:E:103:A:H8	1.75	0.49
19:L:1095:U:H3'	19:L:1096:C:C6	2.48	0.49
28:e:59:LYS:HG3	25:z:103:LEU:HD22	1.94	0.49
30:l:44:LEU:HB2	30:l:47:VAL:CG1	2.43	0.49
4:O:345:PHE:HE2	4:O:364:LEU:HD13	1.77	0.49
10:Z:445:LEU:C	10:Z:445:LEU:CD1	2.86	0.49
10:Z:449:PHE:CB	10:Z:477:MET:CE	2.85	0.49
17:D:176:A:H1'	27:h:33:PHE:CE1	2.43	0.49
19:L:2:C:N1	19:L:3:G:N2	2.60	0.49
19:L:5:A:N3	19:L:5:A:C2'	2.76	0.49
20:v:365:ASP:CB	20:v:399:VAL:HG22	2.42	0.49
22:b:49:HIS:O	22:b:50:LEU:CB	2.61	0.49
26:j:19:ILE:HG22	24:i:88:THR:HG23	1.94	0.49
1:A:749:ARG:HH21	1:A:749:ARG:HG2	1.76	0.49
1:A:1163:ARG:HG3	1:A:1168:ILE:HG22	1.93	0.49
2:C:406:VAL:HG13	2:C:427:LEU:CD2	2.43	0.49
2:C:778:THR:HG23	2:C:781:ASP:H	1.77	0.49
11:c:166:LYS:HD3	18:E:52:G:H4'	1.94	0.49
18:E:77:G:H5''	18:E:77:G:H8	1.78	0.49
24:u:35:ILE:HD11	27:w:79:LEU:HD12	1.86	0.49
25:m:14:GLN:HB3	25:m:26:TRP:CH2	2.48	0.49
26:j:63:ILE:CG1	24:i:89:LEU:HD23	2.43	0.49
27:h:72:PHE:O	28:g:103:VAL:HA	2.13	0.49
28:g:77:THR:HB	28:g:86:ASN:HD22	1.78	0.49
28:e:93:LYS:CD	25:z:97:LEU:HD11	2.43	0.49
29:s:93:LEU:HD11	25:z:21:ASN:ND2	2.28	0.49
1:A:372:ARG:HB3	2:C:973:ARG:HH11	1.78	0.49
1:A:1446:THR:OG1	1:A:1449:ASN:ND2	2.46	0.49
4:O:392:MET:HG2	8:S:158:ASN:HB2	1.93	0.49
5:P:134:VAL:HG22	6:Q:111:ARG:HD3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:18:GLN:CD	32:F:23:LEU:HD21	2.38	0.49
18:E:55:G:H2'	18:E:56:A:C8	2.48	0.49
19:L:1107:C:H3'	19:L:1107:C:OP2	2.12	0.49
28:e:91:ILE:HG21	25:z:96:ILE:HG12	1.95	0.49
1:A:607:THR:OG1	16:B:2:U:H5'	2.13	0.49
2:C:107:THR:HG23	2:C:549:TYR:HB3	1.94	0.49
7:R:149:LYS:CB	7:R:151:LEU:CD1	2.91	0.49
9:T:102:LYS:O	9:T:153:CYS:HB3	2.13	0.49
13:I:186:ALA:O	13:I:201:LYS:NZ	2.44	0.49
19:L:2:C:C2	19:L:3:G:N2	2.81	0.49
19:L:1106:G:N2	21:a:69:ARG:O	2.46	0.49
19:L:1150:U:OP1	29:s:55:LYS:CG	2.61	0.49
29:k:35:MET:CB	30:l:84:PHE:CE2	2.85	0.49
30:l:65:ARG:HD3	30:l:67:SER:HB3	1.94	0.49
1:A:607:THR:HG21	16:B:2:U:H4'	1.93	0.48
1:A:782:ILE:HD13	5:P:165:ILE:HD13	1.94	0.48
1:A:1967:ALA:O	1:A:1971:ILE:N	2.38	0.48
2:C:348:LEU:HD12	2:C:372:THR:HG22	1.95	0.48
6:Q:194:GLU:O	6:Q:291:ILE:CG2	2.61	0.48
6:Q:254:GLN:O	6:Q:255:SER:CB	2.61	0.48
6:Q:280:VAL:HG23	6:Q:280:VAL:O	2.13	0.48
9:T:151:ARG:HD3	14:n:71:SER:HA	1.95	0.48
10:Z:73:ILE:HG22	10:Z:123:ILE:HD12	1.94	0.48
15:H:44:ILE:HG13	15:H:96:ILE:HG12	1.95	0.48
17:D:10:U:O2	17:D:156:G:N1	2.45	0.48
17:D:80:G:OP1	17:D:114:G:O2'	2.30	0.48
19:L:51:C:H6	19:L:51:C:O5'	1.96	0.48
24:u:35:ILE:HD12	27:w:32:LYS:O	2.12	0.48
25:m:46:THR:HB	25:m:79:ILE:HA	1.95	0.48
30:l:15:GLN:HE21	30:l:16:GLY:N	2.11	0.48
30:l:21:LEU:CD2	30:l:72:ILE:CG1	2.81	0.48
30:l:39:SER:O	30:l:40:MET:CB	2.60	0.48
24:i:40:LYS:O	24:i:57:ALA:HA	2.13	0.48
27:w:32:LYS:HD2	27:w:33:PHE:HE1	1.77	0.48
1:A:1602:PRO:CA	19:L:35:U:OP1	2.61	0.48
10:Z:443:SER:HB3	10:Z:445:LEU:HG	1.95	0.48
15:H:18:GLN:CD	32:F:23:LEU:CD2	2.86	0.48
19:L:1114:G:H2'	19:L:1115:G:C1'	2.42	0.48
20:v:617:PRO:O	20:v:618:GLU:CB	2.60	0.48
28:g:64:HIS:O	28:g:65:CYS:CB	2.61	0.48
30:l:44:LEU:CB	30:l:47:VAL:HG13	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:z:14:GLN:HB3	25:z:26:TRP:CH2	2.48	0.48
2:C:606:VAL:HG22	2:C:643:VAL:HG22	1.94	0.48
4:O:102:PHE:HZ	12:d:202:TRP:HH2	1.60	0.48
7:R:69:GLN:HG3	7:R:71:PHE:H	1.76	0.48
10:Z:322:LYS:HE3	10:Z:357:TRP:CE2	2.48	0.48
31:r:8:LYS:CG	31:o:88:TRP:CH2	2.96	0.48
2:C:189:LEU:HD21	2:C:650:LEU:HD21	1.95	0.48
15:H:18:GLN:NE2	32:F:23:LEU:HG	2.28	0.48
24:u:46:PHE:HB3	24:u:52:VAL:HG12	1.94	0.48
25:m:19:LEU:HD23	25:m:92:ILE:HA	1.94	0.48
28:g:41:ARG:HB2	28:g:57:ARG:HD3	1.95	0.48
31:r:137:LEU:HD23	31:o:137:LEU:HD23	1.95	0.48
1:A:376:ARG:HG3	2:C:909:ILE:HG13	1.96	0.48
1:A:1125:LEU:O	1:A:1233:ARG:NH1	2.44	0.48
2:C:507:SER:HB2	2:C:591:PHE:HB3	1.95	0.48
15:H:56:LYS:HD2	16:B:8:U:O2'	2.13	0.48
26:j:64:ARG:HD2	24:i:87:ILE:HB	1.95	0.48
28:g:38:MET:HG3	28:g:58:VAL:O	2.13	0.48
28:e:59:LYS:HG2	28:e:70:GLU:HG3	1.96	0.48
31:r:14:VAL:HG12	31:r:52:GLU:HA	1.95	0.48
1:A:487:ASN:OD1	1:A:488:ARG:CD	2.37	0.48
1:A:1327:THR:HA	1:A:1603:ASN:HD21	1.79	0.48
1:A:1801:SER:O	1:A:1804:THR:OG1	2.31	0.48
2:C:468:LEU:HD21	2:C:493:LEU:HD12	1.96	0.48
5:P:92:ARG:NH1	17:D:110:U:OP1	2.45	0.48
7:R:40:GLY:HA3	15:H:26:TYR:CE1	2.48	0.48
11:c:181:ARG:NE	12:d:49:ARG:NH1	2.62	0.48
2:C:84:GLN:HE21	2:C:88:THR:HG21	1.78	0.48
2:C:139:ILE:HD12	2:C:252:LEU:HD22	1.96	0.48
4:O:231:SER:HG	4:O:274:CYS:HG	1.54	0.48
9:T:154:ALA:HB3	9:T:157:ASP:OD1	2.14	0.48
17:D:168:U:C4	24:i:49:PHE:CZ	3.02	0.48
20:v:652:LEU:HD11	20:v:666:PHE:CZ	2.49	0.48
30:l:17:HIS:CB	30:l:75:PRO:HG2	2.44	0.48
1:A:742:VAL:HB	4:O:224:LEU:HD23	1.95	0.48
1:A:2047:GLN:O	1:A:2051:ILE:N	2.36	0.48
6:Q:252:ARG:HH12	19:L:75:A:H3'	1.79	0.48
7:R:54:GLN:H	7:R:58:HIS:HD2	1.62	0.48
7:R:155:GLN:CB	19:L:78:G:H5'	2.35	0.48
7:R:204:LEU:C	7:R:205:LEU:CD2	2.86	0.48
19:L:25:A:H2'	19:L:27:A:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:1085:G:P	19:L:1085:G:C8	3.06	0.48
20:v:608:TYR:CD2	20:v:627:TYR:HD1	2.32	0.48
26:j:11:MET:HA	26:j:29:LEU:HD22	1.96	0.48
29:s:28:ARG:CG	29:s:52:ARG:HG2	2.42	0.48
29:s:53:VAL:CG2	25:z:67:LEU:CD1	2.91	0.48
31:r:20:ARG:CB	31:q:51:VAL:HG13	2.44	0.48
1:A:1229:GLU:CD	8:S:128:ARG:CG	2.83	0.48
1:A:1602:PRO:HD2	1:A:1605:ARG:HH11	1.78	0.48
28:e:45:ILE:HD12	28:e:55:ILE:HG12	1.96	0.48
26:x:35:PHE:O	26:x:36:LEU:HB3	2.14	0.48
1:A:709:ARG:NH2	17:D:82:A:O3'	2.46	0.48
1:A:1111:SER:HB2	1:A:1510:ILE:HG13	1.95	0.48
1:A:1183:THR:HB	1:A:1222:LEU:HD23	1.96	0.48
1:A:1440:ILE:HA	1:A:1443:TYR:HD2	1.78	0.48
1:A:1794:LEU:O	1:A:1798:ILE:N	2.36	0.48
1:A:1960:GLU:C	1:A:1961:LEU:CD1	2.78	0.48
1:A:2084:LEU:CG	1:A:2085:GLY:N	2.74	0.48
5:P:30:LEU:O	5:P:30:LEU:HD12	2.14	0.48
6:Q:304:THR:CG2	7:R:153:PRO:CG	2.68	0.48
19:L:4:A:OP1	20:v:530:ARG:NH2	2.46	0.48
19:L:105:A:C6	19:L:106:A:C6	3.02	0.48
19:L:1107:C:HO2'	19:L:1108:A:P	2.37	0.48
27:h:29:VAL:O	27:h:37:GLU:HA	2.14	0.48
25:z:82:LEU:HD11	25:z:85:ILE:HB	1.96	0.48
1:A:2011:LEU:CD1	1:A:2040:TRP:HH2	2.27	0.47
6:Q:56:ILE:HG12	7:R:105:ARG:HH12	1.79	0.47
10:Z:443:SER:CB	10:Z:445:LEU:HG	2.44	0.47
11:c:237:ILE:CD1	12:d:85:ARG:HH22	2.27	0.47
19:L:105:A:H62	19:L:106:A:N6	2.11	0.47
12:d:241:MET:CG	12:d:279:LEU:HD12	2.41	0.47
28:g:67:MET:HG3	28:g:69:LEU:CD1	2.44	0.47
29:k:33:GLN:O	29:k:45:LEU:HA	2.14	0.47
29:k:49:ILE:CG2	29:k:81:VAL:HB	2.43	0.47
29:s:48:CYS:SG	29:s:82:LEU:HD12	2.54	0.47
32:F:31:LEU:HB2	32:F:34:MET:HG3	1.96	0.47
1:A:697:LYS:HB3	33:A:3000:IHP:O46	2.14	0.47
4:O:135:ILE:HB	4:O:423:ILE:HB	1.97	0.47
17:D:10:U:H1'	17:D:156:G:N2	2.28	0.47
20:v:403:GLN:HG2	20:v:439:LYS:HB2	1.95	0.47
25:m:21:ASN:ND2	29:k:93:LEU:HD11	2.28	0.47
25:m:25:VAL:HG22	25:m:45:LEU:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:F:39:ALA:O	32:F:68:LYS:N	2.40	0.47
1:A:244:ASP:HB2	1:A:594:ASP:HB3	1.95	0.47
19:L:108:A:O3'	25:z:8:LYS:NZ	2.47	0.47
20:v:365:ASP:O	20:v:399:VAL:HG13	2.14	0.47
20:v:385:PHE:HA	20:v:388:LEU:HB2	1.95	0.47
22:b:65:ILE:O	22:b:86:ILE:HA	2.14	0.47
26:j:23:ARG:HH21	26:j:23:ARG:CB	2.27	0.47
30:l:77:LEU:O	30:l:79:LYS:N	2.47	0.47
27:w:29:VAL:O	27:w:37:GLU:HA	2.14	0.47
1:A:1361:VAL:HG22	1:A:1403:SER:HB2	1.96	0.47
1:A:1841:ALA:O	1:A:1842:GLU:HG2	2.15	0.47
10:Z:454:ASP:HB3	10:Z:457:HIS:ND1	2.29	0.47
19:L:120:G:H4'	19:L:121:C:C5'	2.45	0.47
27:h:19:LEU:HD11	24:i:81:LEU:HD22	1.96	0.47
28:e:102:ILE:HG13	28:e:103:VAL:N	2.30	0.47
1:A:1964:PRO:HG3	1:A:2016:LYS:HZ1	1.77	0.47
1:A:2011:LEU:CG	1:A:2040:TRP:HH2	2.26	0.47
2:C:825:VAL:HG13	2:C:826:PRO:HD2	1.95	0.47
6:Q:208:TYR:HB2	6:Q:316:LEU:HD13	1.95	0.47
9:T:13:PRO:HG2	9:T:77:LEU:HA	1.96	0.47
22:b:60:THR:HA	22:b:82:GLY:O	2.15	0.47
25:m:92:ILE:HG13	25:m:92:ILE:H	1.45	0.47
28:g:89:ARG:NH2	28:g:91:ILE:HD11	2.29	0.47
30:l:11:LEU:HD23	30:l:36:SER:CB	2.45	0.47
1:A:495:ARG:HB2	1:A:495:ARG:CZ	2.44	0.47
2:C:468:LEU:HB3	2:C:579:SER:HB3	1.96	0.47
4:O:193:ARG:HH22	4:O:237:ASP:H	1.62	0.47
5:P:193:GLU:OE1	5:P:195:ASN:N	2.43	0.47
16:B:75:A:H2'	16:B:76:U:C6	2.50	0.47
17:D:148:G:H2'	17:D:149:U:C6	2.49	0.47
19:L:50:U:H2'	19:L:51:C:C1'	2.44	0.47
25:m:86:ASN:ND2	25:m:86:ASN:C	2.73	0.47
26:j:63:ILE:CG2	26:j:68:ILE:HD11	2.45	0.47
29:s:7:ALA:HB3	29:s:10:SER:HB2	1.96	0.47
25:z:25:VAL:HG22	25:z:45:LEU:HB2	1.97	0.47
1:A:427:SER:HA	10:Z:202:GLN:HB3	1.96	0.47
5:P:129:LYS:NZ	8:S:23:THR:O	2.47	0.47
10:Z:421:LYS:HG3	10:Z:468:ILE:HG23	1.97	0.47
20:v:577:VAL:HG12	20:v:583:ILE:HB	1.97	0.47
26:j:37:ASN:OD1	26:j:64:ARG:HA	2.14	0.47
29:k:45:LEU:O	29:k:84:LEU:HA	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2080:LYS:O	1:A:2084:LEU:CG	2.63	0.47
2:C:863:GLU:OE2	2:C:934:HIS:ND1	2.47	0.47
19:L:2:C:H2'	19:L:3:G:C2	2.50	0.47
19:L:5:A:C8	19:L:5:A:O5'	2.68	0.47
19:L:1083:A:H2'	19:L:1084:A:C8	2.47	0.47
19:L:1127:A:H2'	19:L:1128:C:O5'	2.14	0.47
28:e:93:LYS:CB	25:z:97:LEU:HD12	2.45	0.47
30:l:42:VAL:HG22	30:l:64:VAL:CG2	2.44	0.47
2:C:406:VAL:CG1	2:C:427:LEU:CD2	2.93	0.47
6:Q:214:ILE:HD12	6:Q:283:ILE:HG21	1.96	0.47
14:n:386:GLY:O	14:n:387:ILE:CB	2.63	0.47
19:L:52:A:O2'	19:L:53:G:OP1	2.30	0.47
19:L:108:A:C6	19:L:109:C:N4	2.83	0.47
20:v:389:ILE:HA	20:v:392:TYR:CD2	2.50	0.47
28:e:49:ARG:NH2	27:w:76:ASN:CG	2.73	0.47
29:s:54:PRO:HG2	29:s:57:GLN:HG3	1.96	0.47
29:s:95:THR:OG1	25:z:86:ASN:HB3	2.15	0.47
1:A:1032:ILE:O	1:A:1035:LEU:CD1	2.63	0.46
1:A:1204:ARG:HH21	1:A:1260:PHE:HA	1.80	0.46
2:C:117:ARG:NH1	2:C:156:ASP:O	2.47	0.46
6:Q:254:GLN:O	6:Q:255:SER:OG	2.33	0.46
10:Z:77:SER:HA	10:Z:80:ILE:HD12	1.97	0.46
17:D:28:G:N1	17:D:29:G:C5	2.83	0.46
18:E:77:G:H5''	18:E:77:G:C8	2.49	0.46
20:v:397:ASN:HB3	20:v:411:TRP:HD1	1.79	0.46
22:b:137:LEU:O	22:b:140:TYR:CB	2.63	0.46
28:g:54:ILE:HA	28:g:73:LYS:O	2.14	0.46
30:l:63:PHE:C	30:l:63:PHE:HD1	2.24	0.46
25:z:33:SER:HB2	25:z:37:ASN:HB2	1.97	0.46
1:A:372:ARG:HD2	2:C:973:ARG:HD2	1.97	0.46
1:A:688:TYR:CE2	33:A:3000:IHP:O21	2.69	0.46
1:A:1964:PRO:HG2	1:A:2016:LYS:HZ1	1.80	0.46
2:C:406:VAL:HG13	2:C:427:LEU:HD23	1.97	0.46
2:C:501:ILE:HD13	2:C:567:ILE:HG23	1.97	0.46
4:O:200:VAL:HG13	4:O:230:VAL:HG22	1.97	0.46
5:P:110:HIS:HE1	6:Q:20:GLU:O	1.95	0.46
9:T:1:MET:N	9:T:84:GLU:OE2	2.48	0.46
12:d:219:ARG:HA	12:d:222:TYR:HB2	1.98	0.46
12:d:269:ILE:HA	12:d:272:GLU:HG2	1.96	0.46
17:D:159:C:O2'	17:D:161:U:OP2	2.26	0.46
18:E:47:A:OP1	32:F:36:LYS:NZ	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:L:113:U:O4	27:w:47:ASN:C	2.58	0.46
19:L:118:U:N3	28:e:66:ASN:ND2	2.58	0.46
19:L:1146:G:H5'	19:L:1147:A:OP2	2.15	0.46
24:u:81:LEU:HD22	27:w:19:LEU:HD11	1.98	0.46
26:j:30:ARG:HE	26:j:30:ARG:HB2	1.60	0.46
28:g:102:ILE:HG13	28:g:103:VAL:N	2.30	0.46
29:k:30:TYR:CE1	29:k:50:GLU:HB3	2.50	0.46
29:s:38:ASP:OD1	29:s:39:LYS:N	2.39	0.46
30:y:44:LEU:CB	30:y:47:VAL:HG11	2.45	0.46
1:A:291:LYS:HE3	1:A:292:LYS:HE2	1.98	0.46
4:O:321:PHE:HB2	5:P:57:LEU:HD23	1.95	0.46
12:d:141:ILE:CG2	13:I:105:TYR:CE1	2.97	0.46
18:E:101:U:O2	18:E:101:U:H2'	2.13	0.46
19:L:110:A:H62	25:z:34:PRO:CB	2.28	0.46
20:v:442:THR:HG1	20:v:445:SER:HG	1.57	0.46
20:v:479:PRO:HB3	20:v:530:ARG:HD3	1.97	0.46
20:v:505:PHE:O	20:v:509:GLU:N	2.46	0.46
20:v:797:TYR:C	20:v:799:ASP:N	2.66	0.46
23:t:111:VAL:O	23:t:112:SER:C	2.58	0.46
28:g:78:GLU:HG2	28:g:85:ILE:HG23	1.94	0.46
29:k:11:ARG:H	29:k:14:ASN:CB	2.27	0.46
1:A:1639:PRO:HG3	32:F:5:LYS:HD3	1.98	0.46
2:C:246:THR:OG1	2:C:247:PHE:N	2.48	0.46
11:c:106:LEU:O	32:F:196:ARG:HD3	2.15	0.46
11:c:160:LEU:HD23	13:I:196:ILE:HG12	1.98	0.46
12:d:281:LYS:O	12:d:284:LEU:HB3	2.15	0.46
20:v:385:PHE:O	20:v:389:ILE:CD1	2.63	0.46
20:v:729:TYR:HE1	20:v:749:SER:CB	2.28	0.46
25:m:53:ASN:O	25:m:54:LYS:HB3	2.15	0.46
26:j:74:LEU:O	26:j:75:ASP:CB	2.64	0.46
28:g:26:PHE:HE1	28:g:63:ARG:HA	1.80	0.46
31:p:19:SER:OG	31:p:38:ASP:OD2	2.26	0.46
1:A:1406:LEU:N	10:Z:307:GLU:OE2	2.46	0.46
4:O:348:GLU:O	4:O:349:LYS:HG2	2.15	0.46
5:P:112:ILE:HD11	6:Q:17:LEU:HD21	1.97	0.46
6:Q:295:SER:CB	19:L:73:U:P	3.03	0.46
10:Z:454:ASP:O	10:Z:457:HIS:N	2.34	0.46
19:L:7:C:O2'	19:L:8:U:H5'	2.16	0.46
19:L:1095:U:C3'	19:L:1096:C:C6	2.99	0.46
30:l:21:LEU:HD21	30:l:72:ILE:CD1	2.45	0.46
10:Z:454:ASP:N	10:Z:454:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:c:30:THR:O	11:c:33:TRP:NE1	2.48	0.46
19:L:1107:C:O2'	19:L:1108:A:P	2.74	0.46
19:L:1137:U:O4	21:a:67:LYS:O	2.33	0.46
28:g:67:MET:HG3	28:g:69:LEU:HD11	1.97	0.46
1:A:1643:ILE:HD12	19:L:37:G:OP2	2.15	0.46
1:A:1771:THR:HA	1:A:1789:ASN:HD21	1.80	0.46
5:P:34:ILE:CD1	12:d:155:LEU:CD1	2.71	0.46
6:Q:79:ARG:HG2	6:Q:80:TRP:CD1	2.51	0.46
7:R:19:PRO:HG3	7:R:51:PHE:CZ	2.51	0.46
9:T:94:LYS:HB2	9:T:103:LEU:HD23	1.97	0.46
10:Z:305:GLY:HA3	10:Z:345:ILE:HG23	1.98	0.46
11:c:35:LYS:HE2	18:E:54:U:HO2'	1.80	0.46
19:L:66:A:C2	19:L:67:A:C5	3.04	0.46
19:L:1105:C:O3'	19:L:1106:G:O4'	2.34	0.46
19:L:1117:G:H2'	19:L:1118:U:H5'	1.98	0.46
28:g:41:ARG:CB	28:g:57:ARG:HD3	2.45	0.46
28:e:93:LYS:CD	25:z:97:LEU:CD1	2.94	0.46
29:s:53:VAL:CG2	25:z:67:LEU:HD11	2.45	0.46
30:l:77:LEU:C	30:l:79:LYS:H	2.24	0.46
24:i:51:ASN:HB3	24:i:84:GLY:H	1.81	0.46
1:A:209:ILE:HG22	1:A:211:PRO:HD2	1.97	0.46
1:A:460:PRO:HG2	2:C:375:GLU:HG2	1.98	0.46
1:A:1017:ASP:OD1	1:A:1508:HIS:ND1	2.49	0.46
1:A:2035:LYS:HB2	1:A:2038:HIS:HB2	1.97	0.46
2:C:993:ILE:HG12	2:C:997:LEU:HD22	1.97	0.46
19:L:11:U:O2'	19:L:12:U:O5'	2.34	0.46
19:L:121:C:N4	27:w:33:PHE:CG	2.84	0.46
24:u:51:ASN:HB3	24:u:84:GLY:H	1.81	0.46
2:C:608:GLN:HE21	2:C:669:LYS:HD2	1.80	0.46
4:O:102:PHE:CZ	12:d:224:LEU:HD21	2.50	0.46
4:O:244:ARG:HH12	8:S:8:GLN:NE2	2.14	0.46
12:d:320:TYR:CD1	12:d:356:LYS:HA	2.50	0.46
19:L:35:U:H2'	19:L:36:A:C8	2.50	0.46
21:a:67:LYS:O	21:a:68:GLN:CB	2.64	0.46
29:k:16:ILE:O	29:k:17:ASP:HB2	2.16	0.46
28:e:33:LEU:HD23	27:w:72:PHE:HB2	1.98	0.46
30:l:11:LEU:HD11	30:l:72:ILE:HD13	1.94	0.46
1:A:1522:ASN:OD1	1:A:1522:ASN:N	2.49	0.46
1:A:1716:LEU:O	1:A:1795:LYS:NZ	2.49	0.46
4:O:220:TYR:HE1	4:O:256:ARG:HG2	1.81	0.46
7:R:170:ILE:HD13	7:R:173:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:205:LEU:O	7:R:206:LEU:HG	2.16	0.46
10:Z:450:PRO:CD	10:Z:477:MET:HE2	2.46	0.46
12:d:306:LYS:NZ	12:d:326:TYR:OH	2.40	0.46
17:D:161:U:C2'	17:D:162:G:H5'	2.46	0.46
26:j:23:ARG:CG	26:j:23:ARG:NH2	2.79	0.46
29:k:84:LEU:HD21	30:l:78:LEU:HB2	1.98	0.46
31:p:105:LEU:O	31:p:109:LEU:N	2.47	0.46
1:A:1035:LEU:HD13	1:A:1038:ILE:CG2	2.45	0.45
1:A:1145:MET:HE3	1:A:1145:MET:HB2	1.76	0.45
2:C:129:ILE:HG12	30:l:16:GLY:O	2.16	0.45
4:O:373:LEU:CD1	4:O:387:LEU:HB2	2.46	0.45
10:Z:317:ILE:HD13	10:Z:325:VAL:HG21	1.97	0.45
17:D:168:U:C6	24:i:49:PHE:HE1	2.33	0.45
17:D:173:U:C5	28:g:64:HIS:CE1	3.04	0.45
25:m:82:LEU:HD12	25:m:83:GLN:N	2.31	0.45
1:A:1262:MET:HG3	1:A:1263:CYS:H	1.81	0.45
2:C:780:PRO:O	2:C:784:SER:N	2.43	0.45
9:T:95:TRP:HE1	9:T:103:LEU:HB3	1.81	0.45
10:Z:181:LEU:CD1	10:Z:194:LEU:HG	2.32	0.45
11:c:181:ARG:HB3	11:c:181:ARG:NH1	2.32	0.45
15:H:28:ASP:O	15:H:29:TYR:CB	2.63	0.45
18:E:48:C:H2'	18:E:49:A:H8	1.81	0.45
26:x:37:ASN:OD1	26:x:64:ARG:HA	2.16	0.45
32:F:47:PHE:O	32:F:48:SER:C	2.58	0.45
1:A:674:MET:HE1	1:A:1621:VAL:CG2	2.46	0.45
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.51	0.45
1:A:1286:TRP:CD1	1:A:1448:GLU:HB2	2.52	0.45
1:A:1936:THR:OG1	1:A:1937:ARG:N	2.49	0.45
2:C:200:CYS:HB2	2:C:210:ILE:HD12	1.98	0.45
9:T:95:TRP:NE1	9:T:103:LEU:HB3	2.31	0.45
11:c:181:ARG:CZ	12:d:49:ARG:HH12	2.26	0.45
17:D:17:C:C4'	17:D:18:A:OP2	2.56	0.45
17:D:167:A:C1'	28:g:64:HIS:HE2	2.27	0.45
25:m:18:GLU:HG3	25:m:24:THR:HG22	1.98	0.45
26:j:18:ASN:ND2	26:j:18:ASN:N	2.60	0.45
28:e:91:ILE:HG21	25:z:96:ILE:HD13	1.97	0.45
29:s:50:GLU:O	29:s:79:LYS:HA	2.17	0.45
30:l:44:LEU:HB2	30:l:47:VAL:HG13	1.98	0.45
1:A:905:TYR:OH	1:A:1002:GLU:OE2	2.33	0.45
1:A:1384:PRO:CA	1:A:1431:HIS:HE1	2.10	0.45
12:d:263:SER:CB	12:d:287:PHE:HZ	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:n:253:VAL:HG21	14:n:298:ALA:HA	1.97	0.45
17:D:168:U:C4	24:i:49:PHE:HZ	2.35	0.45
19:L:46:C:C2'	19:L:47:U:H5	2.12	0.45
19:L:117:U:C5	25:z:88:ARG:NH2	2.84	0.45
20:v:509:GLU:OE2	20:v:548:TYR:OH	2.23	0.45
26:j:20:ASN:OD1	24:i:32:PHE:CD2	2.70	0.45
27:h:46:ASP:N	28:g:30:PRO:HG2	2.31	0.45
30:l:23:LEU:HB3	30:l:25:THR:HG22	1.98	0.45
26:x:15:ILE:HG23	26:x:72:GLU:O	2.16	0.45
4:O:307:HIS:ND1	4:O:327:CYS:HB3	2.30	0.45
4:O:329:ASP:OD1	4:O:347:SER:O	2.35	0.45
11:c:106:LEU:HD13	32:F:193:MET:O	2.16	0.45
12:d:267:TYR:OH	12:d:287:PHE:CB	2.61	0.45
19:L:51:C:C2	19:L:52:A:C8	3.05	0.45
19:L:1129:U:H2'	19:L:1130:U:O5'	2.16	0.45
28:g:62:ASP:HB3	28:g:66:ASN:OD1	2.17	0.45
30:l:65:ARG:HH11	30:l:65:ARG:CG	2.14	0.45
31:p:14:VAL:HG12	31:p:52:GLU:HA	1.97	0.45
1:A:177:GLU:HA	1:A:712:LEU:HD21	1.99	0.45
1:A:928:ARG:HD3	19:L:32:G:N2	2.30	0.45
1:A:1411:ASP:H	3:J:6:ILE:HG22	1.82	0.45
1:A:1670:ASP:HA	1:A:1673:LEU:HB3	1.98	0.45
4:O:210:ASP:O	4:O:214:ASN:N	2.48	0.45
12:d:272:GLU:HG3	12:d:273:LYS:N	2.30	0.45
13:I:157:ASP:OD1	13:I:157:ASP:N	2.48	0.45
24:u:91:THR:HG21	26:x:57:LEU:HB3	1.99	0.45
28:g:78:GLU:CG	28:g:85:ILE:HG23	2.47	0.45
28:e:62:ASP:HB3	28:e:66:ASN:OD1	2.17	0.45
28:e:91:ILE:HG21	25:z:96:ILE:CG1	2.47	0.45
27:w:33:PHE:CD1	27:w:33:PHE:N	2.84	0.45
32:F:44:MET:O	32:F:46:PRO:HD3	2.17	0.45
1:A:194:HIS:CD2	5:P:122:LEU:HD22	2.52	0.45
2:C:248:VAL:HA	2:C:933:TRP:HH2	1.80	0.45
17:D:3:G:C5	17:D:4:C:C4	3.05	0.45
17:D:173:U:C2	28:g:97:ARG:NE	2.84	0.45
18:E:102:U:H2'	18:E:103:A:C4	2.49	0.45
19:L:1146:G:H3'	19:L:1147:A:C5'	2.44	0.45
22:b:148:VAL:O	22:b:149:PRO:CB	2.64	0.45
25:m:17:ILE:CG2	25:m:92:ILE:HG21	2.38	0.45
26:j:19:ILE:HG22	26:j:67:SER:HB2	1.98	0.45
29:k:45:LEU:HD12	29:k:87:LEU:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:s:54:PRO:CG	29:s:76:LYS:O	2.65	0.45
7:R:152:LYS:O	7:R:156:ILE:HD12	2.17	0.45
7:R:207:PRO:CD	7:R:208:SER:H	2.30	0.45
14:n:221:PHE:HB3	14:n:233:TRP:HB2	1.98	0.45
18:E:100:U:C6	18:E:100:U:C4'	2.99	0.45
19:L:4:A:N9	20:v:529:HIS:CE1	2.84	0.45
19:L:68:U:C2'	19:L:69:G:H5'	2.47	0.45
19:L:116:U:C2	29:s:40:HIS:CD2	3.04	0.45
20:v:570:THR:HG21	20:v:594:PHE:CZ	2.51	0.45
20:v:645:ARG:NH2	20:v:673:GLU:OE2	2.43	0.45
22:b:54:THR:CA	22:b:77:HIS:CB	2.94	0.45
22:b:97:ASN:O	22:b:98:VAL:CB	2.64	0.45
30:l:14:ALA:HB1	30:l:19:VAL:HG11	1.98	0.45
1:A:903:LEU:HG	32:F:180:ASP:OD1	2.17	0.45
2:C:234:LEU:HD21	2:C:439:ILE:HG23	1.99	0.45
4:O:343:THR:HA	5:P:45:PRO:HB3	1.99	0.45
6:Q:283:ILE:N	6:Q:283:ILE:CD1	2.79	0.45
14:n:51:PHE:CZ	14:n:59:ARG:HD2	2.52	0.45
16:B:69:A:O2'	16:B:70:A:N7	2.49	0.45
20:v:324:ASP:O	20:v:328:LYS:N	2.47	0.45
26:j:35:PHE:O	26:j:36:LEU:CB	2.64	0.45
29:k:45:LEU:HD12	29:k:87:LEU:HD13	1.98	0.45
29:k:86:ILE:HG22	30:l:10:LEU:HD23	1.99	0.45
28:e:48:LEU:HD22	28:e:52:HIS:HE2	1.77	0.45
29:s:54:PRO:CG	29:s:57:GLN:CG	2.94	0.45
30:l:33:LEU:CD2	30:l:35:GLU:O	2.63	0.45
25:z:18:GLU:HG3	25:z:24:THR:HG22	1.98	0.45
1:A:1329:THR:HG21	1:A:1601:ILE:H	1.82	0.45
1:A:1549:ALA:HA	10:Z:297:LEU:HD21	1.98	0.45
10:Z:299:LEU:HD21	10:Z:343:TYR:HE1	1.82	0.45
12:d:47:GLN:NE2	12:d:78:GLN:OE1	2.39	0.45
18:E:102:U:H6	18:E:102:U:OP2	1.99	0.45
19:L:1095:U:H2'	19:L:1096:C:N1	2.32	0.45
20:v:412:MET:HE2	20:v:428:TYR:HA	1.99	0.45
20:v:415:VAL:HG21	20:v:427:VAL:HG21	1.98	0.45
30:l:21:LEU:CD2	30:l:42:VAL:HG21	2.46	0.45
1:A:2018:ASN:HD22	1:A:2021:SER:HB2	1.81	0.44
7:R:83:LEU:HB2	7:R:87:CYS:HB2	1.99	0.44
11:c:189:ARG:NE	12:d:38:LEU:HD13	2.29	0.44
17:D:19:A:N6	17:D:151:A:N1	2.54	0.44
19:L:78:G:H2'	19:L:79:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:m:14:GLN:NE2	25:m:28:THR:OG1	2.50	0.44
29:k:15:LEU:HD13	29:k:18:TYR:HB2	1.99	0.44
25:z:14:GLN:NE2	25:z:28:THR:OG1	2.50	0.44
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.99	0.44
1:A:854:ARG:NH2	19:L:25:A:H5''	2.32	0.44
1:A:1373:LEU:HD11	17:D:95:C:H5''	1.99	0.44
4:O:200:VAL:HG12	4:O:206:VAL:HG22	1.99	0.44
6:Q:302:PHE:O	6:Q:312:LEU:HD13	2.18	0.44
7:R:10:LYS:NZ	7:R:10:LYS:CB	2.73	0.44
7:R:143:ASP:OD1	7:R:143:ASP:N	2.50	0.44
7:R:155:GLN:H	7:R:155:GLN:CD	2.25	0.44
12:d:267:TYR:CB	12:d:284:LEU:HD23	2.47	0.44
16:B:56:G:H8	16:B:56:G:O5'	1.99	0.44
17:D:28:G:C2	17:D:29:G:C5	3.05	0.44
17:D:163:C:O2'	17:D:165:A:OP1	2.27	0.44
19:L:114:U:C2	26:x:64:ARG:HG3	2.52	0.44
25:m:39:ILE:CD1	25:m:84:TYR:HE1	2.22	0.44
28:e:52:HIS:CD2	28:e:52:HIS:O	2.71	0.44
30:l:34:VAL:HG12	30:l:35:GLU:HG2	1.98	0.44
30:l:38:ASP:OD1	30:l:38:ASP:N	2.43	0.44
25:z:8:LYS:HE2	25:z:8:LYS:HB3	1.59	0.44
1:A:946:ASN:HB3	1:A:949:ASP:HB2	2.00	0.44
1:A:1270:LEU:HD13	1:A:1275:MET:HG2	1.99	0.44
4:O:365:PHE:CE1	4:O:373:LEU:HB2	2.53	0.44
6:Q:190:LEU:HD11	6:Q:312:LEU:HD11	1.99	0.44
10:Z:474:THR:OG1	10:Z:478:ARG:NH1	2.50	0.44
11:c:233:GLU:CD	12:d:116:ASN:H	2.19	0.44
12:d:293:ASP:OD1	12:d:293:ASP:N	2.46	0.44
17:D:54:C:C2'	17:D:55:U:H5'	2.47	0.44
19:L:3:G:C5	19:L:3:G:OP2	2.70	0.44
19:L:4:A:C4	19:L:5:A:C8	3.06	0.44
19:L:117:U:H5'	25:z:90:ASN:CB	2.48	0.44
25:m:72:GLN:NE2	25:m:75:ALA:HB2	2.33	0.44
27:h:33:PHE:CZ	28:g:49:ARG:NE	2.85	0.44
27:h:80:TYR:HE1	27:h:82:ARG:HD2	1.82	0.44
28:g:63:ARG:HE	28:g:63:ARG:HB3	1.60	0.44
28:e:49:ARG:N	28:e:100:SER:O	2.49	0.44
28:e:66:ASN:HB3	28:e:98:GLY:H	1.81	0.44
28:e:73:LYS:HG3	28:e:90:PHE:HD2	1.83	0.44
30:l:70:LYS:NZ	30:l:70:LYS:CB	2.79	0.44
6:Q:204:SER:OG	6:Q:252:ARG:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S:133:PHE:CD1	8:S:133:PHE:O	2.70	0.44
16:B:10:A:C8	16:B:10:A:OP2	2.71	0.44
19:L:6:U:O5'	19:L:6:U:C6	2.70	0.44
19:L:7:C:OP2	19:L:7:C:C6	2.70	0.44
19:L:51:C:O5'	19:L:51:C:C6	2.71	0.44
19:L:1093:C:C5	19:L:1093:C:OP2	2.70	0.44
26:j:5:PRO:HA	30:l:37:GLU:OE1	2.17	0.44
27:h:16:LYS:HB3	27:h:17:PRO:HD3	2.00	0.44
29:k:30:TYR:CD1	29:k:50:GLU:CB	2.98	0.44
27:w:16:LYS:HB3	27:w:17:PRO:HD3	1.99	0.44
25:z:72:GLN:NE2	25:z:75:ALA:HB2	2.33	0.44
1:A:1262:MET:O	1:A:1264:GLY:N	2.51	0.44
1:A:1637:LYS:NZ	32:F:3:GLU:OE1	2.43	0.44
1:A:1663:PHE:CZ	1:A:1902:GLN:NE2	2.79	0.44
2:C:683:ASN:HB3	2:C:684:GLU:H	1.59	0.44
4:O:392:MET:HE2	8:S:156:TYR:HD2	1.82	0.44
12:d:271:ILE:HD13	12:d:281:LYS:CG	2.08	0.44
19:L:53:G:N3	19:L:53:G:H2'	2.33	0.44
20:v:479:PRO:HB3	20:v:530:ARG:CD	2.47	0.44
28:g:56:ALA:HB3	28:g:69:LEU:HD23	2.00	0.44
1:A:1406:LEU:HB3	1:A:1425:PHE:HB3	1.99	0.44
7:R:196:LYS:NZ	18:E:38:U:O2	2.45	0.44
12:d:298:GLU:O	12:d:301:ILE:HG22	2.17	0.44
14:n:60:ARG:HH22	18:E:1:G:H8	1.65	0.44
17:D:28:G:HO2'	17:D:29:G:P	2.40	0.44
17:D:128:A:O2'	17:D:129:G:O5'	2.36	0.44
18:E:71:G:H21	18:E:75:A:H62	1.64	0.44
19:L:1:A:C1'	19:L:2:C:C4	3.01	0.44
19:L:1107:C:OP2	19:L:1107:C:C6	2.70	0.44
19:L:1129:U:O2'	19:L:1130:U:C5'	2.65	0.44
20:v:549:ILE:HD12	20:v:587:MET:HE3	1.99	0.44
25:m:36:MET:HE3	25:m:36:MET:HB2	1.90	0.44
29:k:49:ILE:HG22	29:k:80:ARG:O	2.17	0.44
29:k:105:LYS:HA	29:k:108:ARG:NE	2.32	0.44
29:s:54:PRO:HG2	29:s:57:GLN:CG	2.48	0.44
26:x:33:ASP:OD1	26:x:37:ASN:N	2.51	0.44
31:q:14:VAL:HG12	31:q:52:GLU:HA	2.00	0.44
1:A:481:HIS:NE2	2:C:275:LEU:O	2.50	0.44
1:A:609:GLU:OE2	18:E:43:C:O2'	2.34	0.44
1:A:1486:ARG:HH22	10:Z:337:SER:HB2	1.82	0.44
1:A:1914:ALA:HA	1:A:1944:LEU:HD23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:308:LYS:HA	5:P:148:HIS:CE1	2.52	0.44
7:R:34:TYR:O	7:R:36:LYS:N	2.50	0.44
7:R:232:PRO:HA	7:R:235:GLN:HB2	1.98	0.44
10:Z:450:PRO:HB2	10:Z:451:LEU:H	1.65	0.44
17:D:101:C:O2'	17:D:102:C:H5'	2.17	0.44
19:L:4:A:H2'	19:L:5:A:C8	2.50	0.44
19:L:6:U:H6	19:L:6:U:O5'	2.00	0.44
19:L:16:U:H2'	19:L:18:U:O4	2.17	0.44
19:L:1085:G:C8	19:L:1085:G:OP2	2.70	0.44
19:L:1093:C:OP2	19:L:1093:C:H5	2.01	0.44
19:L:1154:U:H2'	19:L:1155:C:C5	2.49	0.44
20:v:391:LEU:O	20:v:395:TYR:CD2	2.70	0.44
25:m:43:VAL:HG21	25:m:85:ILE:HG22	1.96	0.44
27:h:13:VAL:O	24:i:53:VAL:HG21	2.17	0.44
29:k:15:LEU:C	29:k:15:LEU:CD1	2.86	0.44
28:e:93:LYS:NZ	25:z:101:LEU:O	2.51	0.44
30:y:44:LEU:HB3	30:y:47:VAL:HG11	2.00	0.44
11:c:181:ARG:NH2	12:d:49:ARG:HH12	2.16	0.44
14:n:51:PHE:CD1	14:n:55:GLU:HG2	2.53	0.44
14:n:208:PRO:C	14:n:225:SER:HG	2.26	0.44
15:H:26:TYR:CG	15:H:27:LYS:N	2.86	0.44
17:D:176:A:N3	27:h:33:PHE:CD1	2.81	0.44
19:L:116:U:C4	29:s:40:HIS:NE2	2.86	0.44
19:L:1136:U:OP1	19:L:1136:U:C6	2.70	0.44
20:v:549:ILE:HD12	20:v:587:MET:CE	2.48	0.44
26:j:33:ASP:OD1	26:j:37:ASN:N	2.51	0.44
2:C:649:GLU:OE2	2:C:913:GLY:N	2.38	0.44
12:d:320:TYR:CE1	12:d:356:LYS:HA	2.53	0.44
15:H:11:VAL:HG22	15:H:14:ARG:HH21	1.83	0.44
17:D:2:A:N1	17:D:3:G:O6	2.51	0.44
17:D:169:U:O2	26:j:66:ASN:N	2.51	0.44
18:E:8:A:H2'	18:E:9:A:C8	2.53	0.44
19:L:5:A:C2	19:L:6:U:C5	3.05	0.44
19:L:1093:C:C6	19:L:1093:C:H5''	2.52	0.44
24:u:31:LEU:HD21	24:u:82:LEU:HD21	2.00	0.44
24:i:31:LEU:HD21	24:i:82:LEU:HD21	2.00	0.44
1:A:1840:TYR:O	1:A:1840:TYR:CG	2.70	0.43
1:A:1961:LEU:CD1	1:A:1961:LEU:N	2.81	0.43
4:O:385:GLN:HE22	4:O:387:LEU:HD11	1.83	0.43
7:R:149:LYS:CB	7:R:151:LEU:HD12	2.48	0.43
17:D:149:U:H2'	17:D:150:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:E:102:U:C6	18:E:102:U:OP2	2.70	0.43
20:v:385:PHE:C	20:v:389:ILE:HD12	2.43	0.43
24:i:30:TRP:CE2	24:i:38:ARG:CD	2.99	0.43
32:F:58:ILE:HD12	32:F:64:PHE:HZ	1.83	0.43
2:C:802:ALA:HB2	2:C:843:LYS:HA	2.00	0.43
4:O:317:HIS:HD2	4:O:318:PRO:HD2	1.83	0.43
19:L:113:U:H5	27:w:48:TYR:CE1	2.30	0.43
20:v:612:ILE:N	20:v:613:PRO:CD	2.81	0.43
25:m:26:TRP:O	25:m:43:VAL:HA	2.17	0.43
25:m:103:LEU:HD23	25:m:107:LEU:HD11	2.01	0.43
29:k:32:GLY:HA3	29:k:47:GLU:O	2.18	0.43
28:e:91:ILE:HG21	25:z:96:ILE:CD1	2.48	0.43
1:A:1993:ASP:OD2	1:A:2039:LEU:N	2.37	0.43
2:C:794:GLN:HA	2:C:797:GLN:HB3	1.99	0.43
10:Z:446:ASP:OD1	10:Z:446:ASP:N	2.45	0.43
14:n:316:THR:HA	14:n:332:SER:HA	2.00	0.43
17:D:167:A:C8	27:h:48:TYR:CZ	3.06	0.43
19:L:3:G:O2'	19:L:4:A:OP1	2.36	0.43
19:L:1146:G:H2'	19:L:1147:A:C1'	2.48	0.43
22:b:77:HIS:HA	22:b:98:VAL:HA	1.99	0.43
25:m:47:LEU:CD1	25:m:61:ALA:HB1	2.38	0.43
26:j:62:VAL:HG12	24:i:90:ILE:HB	2.00	0.43
29:k:28:ARG:CD	29:k:52:ARG:HG2	2.48	0.43
29:k:52:ARG:HB3	29:k:52:ARG:CZ	2.48	0.43
30:l:33:LEU:HD23	30:l:33:LEU:C	2.43	0.43
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.83	0.43
2:C:940:VAL:HA	2:C:941:PRO:HD3	1.92	0.43
7:R:51:PHE:HE2	7:R:80:MET:HE3	1.83	0.43
9:T:151:ARG:NH2	14:n:71:SER:HB3	2.33	0.43
11:c:170:LYS:HD2	11:c:170:LYS:HA	1.62	0.43
12:d:139:TYR:CG	12:d:155:LEU:HD21	2.53	0.43
19:L:1097:G:C2	19:L:1146:G:C4	3.07	0.43
28:g:105:LEU:C	28:g:105:LEU:CD1	2.88	0.43
29:k:35:MET:CE	29:k:46:ASN:HB2	2.49	0.43
29:s:54:PRO:CG	29:s:57:GLN:HG2	2.47	0.43
1:A:305:LEU:HD12	1:A:472:ASN:HB3	2.00	0.43
1:A:674:MET:CE	1:A:1621:VAL:HG21	2.49	0.43
1:A:1331:VAL:HG12	1:A:1367:ILE:HG23	1.99	0.43
2:C:398:ASN:OD1	2:C:401:ARG:NH2	2.52	0.43
2:C:968:MET:HE1	2:C:986:GLY:HA2	2.00	0.43
4:O:224:LEU:HD13	8:S:12:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:84:ASN:HD22	10:Z:129:VAL:HG13	1.83	0.43
18:E:53:A:H5'	18:E:54:U:OP2	2.18	0.43
19:L:7:C:H2'	19:L:8:U:C6	2.54	0.43
19:L:1086:U:OP2	19:L:1086:U:C6	2.70	0.43
29:k:104:SER:O	29:k:107:GLU:HB3	2.17	0.43
1:A:607:THR:OG1	16:B:2:U:C3'	2.65	0.43
1:A:1040:ASP:O	1:A:1045:GLN:NE2	2.52	0.43
1:A:1478:GLU:HA	1:A:1481:GLU:HB2	2.01	0.43
1:A:1570:TRP:HA	1:A:1573:LEU:HD12	1.99	0.43
1:A:1808:ALA:O	1:A:1911:TRP:CE3	2.71	0.43
10:Z:16:GLU:HA	10:Z:19:GLU:HB3	2.00	0.43
12:d:364:ILE:O	12:d:368:MET:N	2.48	0.43
17:D:6:G:H4'	29:k:11:ARG:HH22	1.81	0.43
19:L:1107:C:O2'	19:L:1108:A:O5'	2.37	0.43
19:L:1126:G:H8	19:L:1126:G:O5'	2.01	0.43
26:j:15:ILE:HG12	26:j:73:ALA:HA	2.00	0.43
30:l:36:SER:C	30:l:37:GLU:HG2	2.44	0.43
27:w:32:LYS:CG	27:w:33:PHE:HE1	2.30	0.43
25:z:26:TRP:O	25:z:43:VAL:HA	2.17	0.43
25:z:31:SER:O	25:z:39:ILE:HG22	2.18	0.43
1:A:190:LYS:HD3	1:A:559:GLN:HE21	1.83	0.43
1:A:205:THR:HG1	1:A:495:ARG:HD2	1.80	0.43
1:A:749:ARG:CG	1:A:749:ARG:NH2	2.73	0.43
1:A:1216:ILE:HG13	1:A:1254:ASN:HB3	1.99	0.43
2:C:135:ASN:O	2:C:233:ASP:N	2.45	0.43
7:R:87:CYS:HB3	7:R:91:HIS:HE1	1.84	0.43
8:S:3:THR:OG1	8:S:4:SER:N	2.51	0.43
13:I:121:LYS:HZ3	20:v:529:HIS:HB3	1.82	0.43
16:B:53:U:H6	16:B:53:U:H5''	1.83	0.43
17:D:128:A:H2'	17:D:128:A:N3	2.34	0.43
19:L:109:C:C3'	19:L:109:C:C6	3.01	0.43
20:v:728:LEU:O	20:v:732:CYS:N	2.48	0.43
24:i:32:PHE:HB3	24:i:34:GLN:OE1	2.18	0.43
25:z:15:VAL:HG11	25:z:29:LEU:HD12	2.00	0.43
1:A:2011:LEU:CD1	1:A:2040:TRP:CZ2	3.01	0.43
1:A:2040:TRP:CE3	1:A:2041:PRO:CD	2.98	0.43
8:S:12:ARG:NH2	18:E:66:C:OP2	2.44	0.43
17:D:128:A:C8	17:D:128:A:OP2	2.70	0.43
19:L:1:A:P	19:L:1:A:H3'	2.58	0.43
20:v:454:GLY:O	20:v:458:TRP:N	2.52	0.43
25:m:84:TYR:CG	25:m:84:TYR:O	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:86:ILE:HG21	30:l:10:LEU:HD23	1.99	0.43
29:k:105:LYS:O	29:k:108:ARG:NE	2.52	0.43
28:e:77:THR:HB	28:e:86:ASN:HD22	1.84	0.43
28:e:79:LYS:HA	28:e:83:ASN:O	2.19	0.43
27:w:80:TYR:HE1	27:w:82:ARG:HD2	1.83	0.43
30:y:49:ALA:HB2	30:y:59:MET:HE3	2.01	0.43
1:A:244:ASP:N	1:A:244:ASP:OD1	2.51	0.43
7:R:102:LEU:O	7:R:106:THR:OG1	2.32	0.43
11:c:57:ASN:HB3	11:c:60:LEU:HG	2.01	0.43
12:d:203:LEU:HA	12:d:206:VAL:HG22	2.01	0.43
25:m:17:ILE:HG21	25:m:92:ILE:HG23	1.98	0.43
27:h:67:THR:C	27:h:68:LEU:HD12	2.44	0.43
29:s:21:ARG:HD3	25:z:67:LEU:O	2.19	0.43
27:w:67:THR:C	27:w:68:LEU:HD12	2.44	0.43
1:A:139:LEU:HD13	1:A:193:TYR:CG	2.54	0.43
1:A:404:ASN:ND2	2:C:927:MET:SD	2.92	0.43
1:A:903:LEU:HD11	1:A:948:HIS:CE1	2.52	0.43
4:O:292:LEU:HD12	4:O:302:LYS:HB3	2.00	0.43
19:L:47:U:H6	19:L:47:U:O5'	2.02	0.43
19:L:106:A:O2'	19:L:107:U:O4'	2.37	0.43
19:L:120:G:H4'	19:L:121:C:H5'	2.01	0.43
19:L:1147:A:O2'	19:L:1148:U:H5'	2.19	0.43
25:m:33:SER:HB2	25:m:37:ASN:HB2	2.01	0.43
25:m:96:ILE:CD1	28:g:89:ARG:NH2	2.73	0.43
1:A:199:ILE:HD13	1:A:578:MET:HE1	2.01	0.42
2:C:218:HIS:CD2	2:C:650:LEU:HD23	2.54	0.42
6:Q:206:PHE:HB3	6:Q:291:ILE:HD12	2.00	0.42
6:Q:208:TYR:HB2	6:Q:316:LEU:CD1	2.48	0.42
12:d:289:LYS:HD3	12:d:289:LYS:HA	1.90	0.42
12:d:298:GLU:HA	12:d:301:ILE:CG2	2.49	0.42
17:D:2:A:C2	17:D:3:G:C6	3.07	0.42
17:D:100:A:H3'	17:D:101:C:C5'	2.46	0.42
19:L:40:U:H1'	19:L:41:C:P	2.58	0.42
19:L:45:U:O2'	19:L:46:C:H5'	2.19	0.42
19:L:125:C:H4'	28:e:81:GLY:H	1.83	0.42
20:v:593:LEU:HD22	20:v:593:LEU:HA	1.84	0.42
25:m:15:VAL:HG22	25:m:16:THR:N	2.33	0.42
25:m:67:LEU:O	29:k:21:ARG:HD3	2.19	0.42
28:e:91:ILE:HD12	28:e:94:LEU:CD1	2.48	0.42
30:l:21:LEU:HD13	30:l:42:VAL:HG21	2.00	0.42
1:A:743:LYS:HE3	1:A:749:ARG:HH12	1.74	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:834:ILE:HG12	1:A:840:VAL:HG11	2.01	0.42
2:C:683:ASN:O	2:C:684:GLU:HB3	2.19	0.42
5:P:36:LYS:O	5:P:39:LYS:NZ	2.46	0.42
7:R:231:ASP:N	7:R:231:ASP:OD1	2.52	0.42
8:S:6:ARG:NH2	18:E:85:C:OP1	2.52	0.42
17:D:74:U:O2'	17:D:77:A:N3	2.42	0.42
17:D:128:A:OP2	17:D:128:A:C4	2.71	0.42
17:D:175:G:P	28:g:49:ARG:HH12	2.42	0.42
18:E:99:A:H2'	18:E:100:U:C5'	2.33	0.42
19:L:12:U:O2'	19:L:13:G:H5'	2.19	0.42
20:v:385:PHE:CD1	20:v:388:LEU:HD12	2.54	0.42
25:z:45:LEU:HG	25:z:45:LEU:O	2.20	0.42
12:d:137:TYR:CD1	13:I:105:TYR:CG	3.08	0.42
17:D:129:G:H4'	17:D:130:A:H3'	1.97	0.42
17:D:173:U:C1'	28:g:99:ASP:HB3	2.34	0.42
19:L:1:A:H5'	19:L:1:A:C4	2.54	0.42
19:L:104:C:O2'	19:L:105:A:H5'	2.19	0.42
20:v:397:ASN:HD22	20:v:397:ASN:HA	1.66	0.42
20:v:529:HIS:CG	20:v:529:HIS:O	2.71	0.42
26:j:23:ARG:NH2	26:j:23:ARG:HG2	2.34	0.42
29:k:51:GLU:HB3	29:k:77:VAL:HG11	2.02	0.42
30:l:77:LEU:C	30:l:79:LYS:N	2.76	0.42
1:A:535:HIS:HE2	17:D:105:A:P	2.42	0.42
1:A:748:GLN:HE22	18:E:77:G:P	2.43	0.42
1:A:2061:THR:O	1:A:2065:ARG:N	2.42	0.42
2:C:132:ARG:NH2	30:l:13:GLU:O	2.40	0.42
2:C:234:LEU:HD23	2:C:443:TYR:HB2	2.01	0.42
2:C:660:ARG:NH2	2:C:670:ILE:HD12	2.33	0.42
6:Q:306:THR:CG2	6:Q:307:ALA:N	2.82	0.42
10:Z:84:ASN:ND2	10:Z:220:TYR:OH	2.52	0.42
10:Z:454:ASP:O	10:Z:456:GLU:N	2.53	0.42
16:B:9:A:OP2	16:B:10:A:C2	2.72	0.42
17:D:128:A:C8	17:D:129:G:C2	3.07	0.42
19:L:10:U:O2'	19:L:11:U:H5'	2.19	0.42
19:L:105:A:N6	19:L:106:A:N6	2.68	0.42
28:e:54:ILE:HB	28:e:72:VAL:HG22	2.01	0.42
30:y:41:ASN:HB3	30:y:66:GLY:H	1.83	0.42
4:O:433:THR:OG1	4:O:435:GLU:O	2.31	0.42
5:P:30:LEU:HD21	12:d:151:ILE:HG12	2.00	0.42
7:R:155:GLN:CD	7:R:155:GLN:N	2.78	0.42
9:T:150:CYS:SG	9:T:152:GLY:N	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:B:9:A:C4'	16:B:10:A:OP2	2.67	0.42
16:B:69:A:C2'	16:B:70:A:OP2	2.67	0.42
17:D:169:U:H1'	26:j:66:ASN:HB2	2.01	0.42
19:L:1082:A:C2	19:L:1083:A:C5	3.07	0.42
20:v:342:ILE:O	20:v:346:TYR:N	2.45	0.42
25:m:84:TYR:CG	29:k:6:VAL:HG11	2.41	0.42
26:j:74:LEU:H	26:j:74:LEU:HG	1.65	0.42
29:k:35:MET:HE2	29:k:46:ASN:CA	2.50	0.42
28:e:78:GLU:HG3	25:z:52:LEU:HD22	2.00	0.42
29:s:31:ILE:O	29:s:48:CYS:HA	2.19	0.42
3:J:12:LYS:NZ	17:D:92:U:O2	2.48	0.42
7:R:176:VAL:HG12	7:R:179:LYS:H	1.85	0.42
8:S:7:PRO:HD2	19:L:20:G:N3	2.34	0.42
10:Z:449:PHE:HB3	10:Z:477:MET:HE2	1.95	0.42
28:g:50:ASN:CB	28:g:52:HIS:ND1	2.69	0.42
29:k:35:MET:SD	30:l:84:PHE:CE2	3.13	0.42
32:F:108:MET:HE3	32:F:108:MET:HB2	1.87	0.42
1:A:1938:LYS:HA	1:A:1941:LEU:HG	2.01	0.42
2:C:274:ILE:HG21	2:C:385:PHE:CD2	2.54	0.42
2:C:827:SER:O	2:C:828:ASP:CB	2.67	0.42
10:Z:445:LEU:C	10:Z:447:GLY:N	2.76	0.42
12:d:241:MET:HG3	12:d:279:LEU:CD1	2.45	0.42
19:L:1084:A:H2'	19:L:1084:A:N3	2.34	0.42
19:L:1146:G:C4	19:L:1147:A:C5	3.07	0.42
23:t:105:PRO:O	23:t:109:SER:OG	2.37	0.42
26:j:74:LEU:O	26:j:74:LEU:HD12	2.20	0.42
1:A:139:LEU:HD21	1:A:570:GLN:OE1	2.20	0.42
1:A:148:ASP:OD1	1:A:148:ASP:N	2.53	0.42
1:A:205:THR:OG1	1:A:495:ARG:CD	2.58	0.42
1:A:535:HIS:NE2	17:D:105:A:OP1	2.46	0.42
1:A:1848:ILE:HB	1:A:1930:PRO:HA	1.99	0.42
2:C:685:SER:HB3	2:C:852:THR:CG2	2.44	0.42
7:R:145:ALA:HB3	7:R:204:LEU:CD1	2.48	0.42
10:Z:181:LEU:CD2	10:Z:186:LEU:CD2	2.70	0.42
12:d:334:PHE:O	12:d:335:PRO:C	2.62	0.42
19:L:1097:G:H21	19:L:1146:G:H1'	1.84	0.42
28:e:91:ILE:CG2	25:z:96:ILE:CG2	2.98	0.42
2:C:425:LEU:O	2:C:428:ILE:O	2.38	0.42
2:C:428:ILE:O	2:C:429:PHE:HB2	2.19	0.42
6:Q:252:ARG:HG3	6:Q:297:PHE:CZ	2.55	0.42
10:Z:39:GLU:OE2	10:Z:42:ARG:NH1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:70:ARG:HD3	18:E:89:U:OP1	2.20	0.42
12:d:270:ALA:HB1	12:d:280:LEU:HD11	2.02	0.42
12:d:271:ILE:O	12:d:274:TRP:C	2.63	0.42
30:l:41:ASN:ND2	30:l:63:PHE:CZ	2.88	0.42
1:A:659:HIS:HE1	33:A:3000:IHP:O42	2.03	0.42
1:A:1292:ARG:HD3	1:A:1293:THR:HG23	2.01	0.42
1:A:1963:LEU:N	1:A:1963:LEU:CD1	2.77	0.42
12:d:269:ILE:O	12:d:273:LYS:CB	2.68	0.42
16:B:2:U:HO2'	16:B:3:A:P	2.41	0.42
17:D:166:U:C3'	17:D:166:U:C6	3.03	0.42
17:D:168:U:H2'	24:i:49:PHE:CE1	2.53	0.42
29:s:54:PRO:CB	29:s:57:GLN:CG	2.88	0.42
25:z:103:LEU:HD23	25:z:107:LEU:HD11	2.01	0.42
1:A:854:ARG:HH21	19:L:25:A:C5'	2.33	0.41
2:C:220:ASN:HB3	2:C:651:TYR:HB2	2.01	0.41
4:O:147:ILE:HD12	4:O:155:PHE:HB3	2.01	0.41
10:Z:454:ASP:C	10:Z:456:GLU:N	2.78	0.41
17:D:130:A:N7	17:D:147:C:H4'	2.35	0.41
19:L:1095:U:C2'	19:L:1096:C:C6	3.03	0.41
24:u:28:THR:N	24:u:91:THR:O	2.49	0.41
25:m:104:ASP:OD1	25:m:105:SER:N	2.53	0.41
29:k:44:VAL:CG2	29:k:86:ILE:HG22	2.36	0.41
30:l:44:LEU:HD23	30:l:44:LEU:N	2.32	0.41
24:i:28:THR:N	24:i:91:THR:O	2.49	0.41
27:w:45:THR:HA	27:w:50:ASN:O	2.20	0.41
1:A:162:LEU:HG	1:A:730:ILE:HD12	2.01	0.41
1:A:774:ILE:HG23	1:A:778:LYS:HB2	2.01	0.41
1:A:1365:THR:HG21	3:J:15:SER:HB3	2.02	0.41
9:T:94:LYS:CB	9:T:103:LEU:HD23	2.50	0.41
10:Z:44:LEU:HD21	10:Z:56:ILE:HD11	2.02	0.41
11:c:158:ARG:HG3	18:E:55:G:H5'	2.02	0.41
16:B:52:U:C3'	16:B:52:U:C6	3.02	0.41
17:D:174:G:H2'	28:g:49:ARG:NH1	2.35	0.41
19:L:119:G:OP2	27:w:76:ASN:ND2	2.39	0.41
19:L:1093:C:O2'	30:y:54:GLY:HA3	2.20	0.41
25:m:52:LEU:CD2	28:g:79:LYS:CA	2.98	0.41
26:j:14:LYS:CD	26:j:74:LEU:HD11	2.49	0.41
26:j:15:ILE:O	26:j:26:ALA:HA	2.19	0.41
1:A:607:THR:HG21	16:B:2:U:OP1	2.20	0.41
1:A:1283:GLU:OE2	10:Z:341:LYS:N	2.52	0.41
2:C:644:ILE:HG22	2:C:652:MET:HE1	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:106:VAL:HG11	4:O:109:GLU:HG2	2.01	0.41
4:O:420:ASP:OD1	4:O:422:SER:OG	2.36	0.41
12:d:125:ALA:HB1	12:d:135:LEU:HD22	2.02	0.41
18:E:102:U:C2'	18:E:103:A:C8	3.03	0.41
19:L:4:A:C1'	20:v:529:HIS:NE2	2.79	0.41
19:L:1137:U:H3'	19:L:1137:U:H6	1.85	0.41
25:m:45:LEU:HG	25:m:45:LEU:O	2.20	0.41
27:h:45:THR:HA	27:h:50:ASN:O	2.20	0.41
27:h:74:ARG:NE	28:g:99:ASP:HA	2.35	0.41
31:p:98:LEU:HG	31:q:99:ARG:HE	1.84	0.41
1:A:1941:LEU:HD23	1:A:1941:LEU:HA	1.86	0.41
2:C:476:VAL:HG12	2:C:478:TYR:HB2	2.02	0.41
4:O:119:LEU:O	4:O:122:ARG:NH1	2.39	0.41
4:O:329:ASP:O	4:O:347:SER:CB	2.69	0.41
7:R:69:GLN:HG2	7:R:89:TYR:HA	2.03	0.41
10:Z:105:GLN:HA	10:Z:108:ARG:HB2	2.01	0.41
10:Z:449:PHE:CE2	10:Z:465:PHE:CE2	3.08	0.41
11:c:107:GLU:HG2	32:F:196:ARG:NH1	2.35	0.41
15:H:26:TYR:CE2	15:H:28:ASP:OD1	2.71	0.41
16:B:57:C:H42	19:L:46:C:H42	1.67	0.41
17:D:3:G:H2'	17:D:4:C:H5'	2.01	0.41
18:E:8:A:H2'	18:E:9:A:H8	1.85	0.41
18:E:88:U:O2'	19:L:17:U:OP2	2.28	0.41
19:L:2:C:H3'	19:L:2:C:P	2.61	0.41
20:v:442:THR:HA	20:v:443:PRO:HD3	1.91	0.41
20:v:552:LEU:HD13	20:v:570:THR:HA	2.02	0.41
20:v:686:ILE:HG21	20:v:713:ILE:HG21	2.03	0.41
22:b:84:ASN:O	22:b:106:ASN:HA	2.21	0.41
28:e:89:ARG:NH1	28:e:91:ILE:HD11	2.35	0.41
30:l:44:LEU:HB2	30:l:62:ILE:HG22	2.02	0.41
30:l:44:LEU:CB	30:l:47:VAL:CG1	2.97	0.41
24:i:35:ILE:HG22	24:i:37:ILE:HG12	2.02	0.41
1:A:165:LEU:HD13	1:A:578:MET:HB3	2.03	0.41
1:A:347:PRO:HG3	3:J:2:SER:HB3	2.01	0.41
1:A:856:TRP:CD1	8:S:174:VAL:HG21	2.55	0.41
6:Q:316:LEU:O	6:Q:319:LEU:N	2.53	0.41
9:T:95:TRP:CD1	9:T:103:LEU:HB3	2.56	0.41
9:T:100:TYR:CE1	18:E:26:A:H4'	2.55	0.41
11:c:544:LEU:HA	11:c:547:HIS:HB2	2.02	0.41
15:H:34:ARG:HH22	15:H:36:ARG:HH11	1.67	0.41
19:L:1082:A:O2'	19:L:1083:A:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:k:86:ILE:CG1	30:l:72:ILE:HB	2.51	0.41
30:l:34:VAL:CG2	30:l:45:ARG:HB2	2.51	0.41
30:l:83:LEU:HD12	30:l:84:PHE:N	2.35	0.41
6:Q:67:GLN:NE2	6:Q:114:SER:O	2.54	0.41
6:Q:207:LEU:O	6:Q:249:GLY:N	2.50	0.41
13:I:184:GLN:HA	13:I:187:LYS:HZ3	1.86	0.41
19:L:1143:C:HO2'	19:L:1145:U:P	2.44	0.41
26:j:72:GLU:O	26:j:72:GLU:HG3	2.19	0.41
29:k:28:ARG:HD2	29:k:50:GLU:OE1	2.21	0.41
28:e:57:ARG:HD2	28:e:70:GLU:CD	2.46	0.41
1:A:554:THR:HG21	5:P:121:PRO:HD3	2.02	0.41
1:A:1207:TRP:O	1:A:1212:ARG:NH2	2.54	0.41
1:A:1430:THR:O	1:A:1431:HIS:CB	2.64	0.41
1:A:2040:TRP:CE3	1:A:2041:PRO:HD2	2.56	0.41
10:Z:37:LEU:HD23	10:Z:214:ILE:HG13	2.02	0.41
13:I:196:ILE:HB	13:I:200:ASN:ND2	2.36	0.41
13:I:206:LYS:HD2	19:L:18:U:H1'	2.03	0.41
17:D:28:G:H2'	17:D:29:G:O5'	2.21	0.41
29:k:59:ASP:HA	29:k:62:ARG:HH21	1.86	0.41
29:s:15:LEU:O	29:s:16:ILE:HD13	2.20	0.41
29:s:48:CYS:SG	29:s:85:THR:HG23	2.60	0.41
26:x:35:PHE:O	26:x:36:LEU:CB	2.68	0.41
1:A:600:LYS:HB2	32:F:10:TYR:HB2	2.03	0.41
1:A:748:GLN:OE1	18:E:76:A:H5''	2.21	0.41
1:A:1126:LEU:HD11	1:A:1161:TYR:CG	2.55	0.41
2:C:485:LEU:HD12	2:C:485:LEU:HA	1.91	0.41
5:P:197:ILE:HG23	11:c:90:MET:HE2	2.02	0.41
15:H:52:ARG:O	15:H:56:LYS:HG3	2.21	0.41
17:D:60:U:C6	17:D:61:U:C6	3.09	0.41
19:L:2:C:H6	19:L:2:C:C3'	2.33	0.41
19:L:109:C:H3'	19:L:109:C:C6	2.55	0.41
19:L:1085:G:N2	19:L:1086:U:C6	2.87	0.41
19:L:1097:G:N2	19:L:1146:G:H1'	2.36	0.41
25:m:3:LEU:HD21	28:g:95:PHE:HE1	1.83	0.41
27:h:33:PHE:HZ	28:g:49:ARG:NE	2.19	0.41
25:z:104:ASP:OD1	25:z:105:SER:N	2.53	0.41
1:A:1408:PRO:HB3	1:A:1422:ILE:HG23	2.03	0.41
1:A:1847:ASP:OD1	1:A:1847:ASP:N	2.53	0.41
1:A:1992:TYR:OH	1:A:2005:PHE:CD1	2.61	0.41
2:C:406:VAL:HG13	2:C:427:LEU:CG	2.51	0.41
2:C:514:GLN:NE2	2:C:587:LYS:O	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:34:ILE:HD13	12:d:155:LEU:HA	2.02	0.41
6:Q:269:THR:HG22	6:Q:279:GLY:HA2	2.02	0.41
7:R:63:ARG:HD3	9:T:143:HIS:CD2	2.56	0.41
8:S:6:ARG:HH22	18:E:85:C:P	2.44	0.41
10:Z:148:LEU:HA	10:Z:151:VAL:HG12	2.02	0.41
10:Z:394:TYR:OH	10:Z:430:GLU:OE1	2.30	0.41
11:c:249:ASN:ND2	12:d:40:LEU:HD13	2.36	0.41
13:I:199:LYS:NZ	19:L:17:U:O3'	2.54	0.41
15:H:27:LYS:HG3	15:H:28:ASP:N	2.36	0.41
17:D:168:U:C5	24:i:49:PHE:CE1	3.08	0.41
19:L:5:A:C2'	19:L:6:U:OP1	2.69	0.41
20:v:687:LEU:HD22	20:v:688:ARG:HH21	1.85	0.41
22:b:68:PRO:O	22:b:69:ASP:CB	2.69	0.41
25:m:3:LEU:HD23	28:g:95:PHE:CE1	2.53	0.41
29:k:18:TYR:HE1	29:k:101:PRO:HD3	1.84	0.41
29:k:84:LEU:O	30:l:74:VAL:CG2	2.68	0.41
28:e:67:MET:HG3	28:e:69:LEU:CD1	2.50	0.41
29:s:30:TYR:HD2	29:s:87:LEU:HD21	1.86	0.41
30:l:71:PHE:C	30:l:71:PHE:HD1	2.27	0.41
27:w:30:LYS:HD2	27:w:80:TYR:CE2	2.55	0.41
27:w:79:LEU:HD22	27:w:80:TYR:HD2	1.86	0.41
31:p:98:LEU:HD12	31:q:98:LEU:HG	2.03	0.41
2:C:683:ASN:O	2:C:684:GLU:CB	2.69	0.41
7:R:41:PHE:C	7:R:41:PHE:HD1	2.26	0.41
8:S:7:PRO:CD	19:L:20:G:H1'	2.51	0.41
12:d:270:ALA:HB1	12:d:280:LEU:HD21	2.01	0.41
12:d:391:LEU:O	12:d:395:ILE:N	2.53	0.41
16:B:2:U:O2'	16:B:3:A:P	2.79	0.41
17:D:124:C:O2'	17:D:125:C:H5'	2.20	0.41
19:L:114:U:O2'	30:y:65:ARG:NH2	2.53	0.41
20:v:711:MET:HE1	20:v:748:PHE:HA	1.99	0.41
25:m:33:SER:HB2	25:m:37:ASN:CB	2.50	0.41
25:m:67:LEU:HB3	29:k:29:VAL:CG2	2.49	0.41
28:g:26:PHE:CE1	28:g:63:ARG:HA	2.56	0.41
28:g:49:ARG:N	28:g:100:SER:O	2.49	0.41
29:k:20:LEU:HD12	29:k:34:LEU:HB2	2.03	0.41
30:l:17:HIS:CE1	30:l:77:LEU:HD11	2.52	0.41
30:l:21:LEU:CD2	30:l:72:ILE:CD1	2.99	0.41
32:F:47:PHE:O	32:F:47:PHE:CG	2.73	0.41
1:A:167:TYR:HB3	1:A:201:PHE:HZ	1.86	0.40
4:O:328:THR:O	4:O:329:ASP:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:d:255:ALA:HB2	12:d:291:PHE:CD2	2.48	0.40
13:I:142:LYS:HB3	13:I:144:GLN:HE22	1.86	0.40
13:I:209:ARG:CD	19:L:15:C:C4	3.04	0.40
14:n:51:PHE:CZ	14:n:59:ARG:CD	3.04	0.40
16:B:55:U:H6	16:B:55:U:H5''	1.85	0.40
18:E:7:G:H2'	18:E:8:A:C8	2.56	0.40
19:L:1:A:H4'	19:L:2:C:O5'	2.20	0.40
26:j:29:LEU:C	26:j:29:LEU:CD2	2.86	0.40
29:k:29:VAL:O	29:k:50:GLU:CA	2.58	0.40
29:k:85:THR:HG22	30:l:73:VAL:HG13	2.03	0.40
28:e:50:ASN:O	28:e:51:ASN:HB3	2.21	0.40
28:e:57:ARG:HD3	28:e:70:GLU:OE1	2.20	0.40
1:A:1040:ASP:OD2	1:A:1045:GLN:NE2	2.54	0.40
4:O:358:ILE:HG12	4:O:364:LEU:HD12	2.03	0.40
9:T:73:ILE:HB	9:T:77:LEU:HD23	2.03	0.40
12:d:240:ASP:CG	12:d:277:ASN:HB3	2.46	0.40
19:L:1129:U:C2'	19:L:1130:U:O5'	2.69	0.40
27:h:51:LEU:HB2	27:h:73:ILE:HB	2.04	0.40
29:k:28:ARG:CG	29:k:52:ARG:HG2	2.48	0.40
29:k:30:TYR:HH	30:l:71:PHE:HD2	1.69	0.40
28:e:69:LEU:HD12	28:e:69:LEU:N	2.36	0.40
25:z:93:ARG:HG2	25:z:94:GLN:HG3	2.03	0.40
1:A:607:THR:OG1	16:B:2:U:C5'	2.69	0.40
7:R:205:LEU:C	7:R:206:LEU:HG	2.46	0.40
12:d:51:ARG:NE	12:d:75:GLU:OE2	2.51	0.40
12:d:189:TYR:HA	12:d:192:TYR:HB3	2.03	0.40
17:D:169:U:C6	26:j:35:PHE:CD1	3.10	0.40
19:L:117:U:O2	25:z:35:GLN:O	2.39	0.40
19:L:1085:G:N3	19:L:1086:U:H5	2.11	0.40
28:g:77:THR:CB	28:g:86:ASN:HD22	2.34	0.40
29:k:30:TYR:CE1	29:k:50:GLU:CB	3.04	0.40
29:k:105:LYS:HA	29:k:108:ARG:HE	1.86	0.40
24:i:31:LEU:HD12	24:i:37:ILE:HG13	2.04	0.40
24:i:54:ILE:CD1	24:i:57:ALA:CB	3.00	0.40
1:A:1025:VAL:HG22	1:A:1262:MET:HB3	2.03	0.40
1:A:1035:LEU:CD1	1:A:1038:ILE:CD1	2.94	0.40
1:A:1287:ASP:HB3	1:A:1296:ARG:HG2	2.04	0.40
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	2.04	0.40
1:A:1971:ILE:HG22	1:A:1974:LEU:H	1.86	0.40
2:C:124:LEU:HD13	2:C:124:LEU:HA	1.87	0.40
4:O:224:LEU:N	4:O:245:ASP:OD2	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:251:LEU:HD11	6:Q:253:PHE:CZ	2.56	0.40
12:d:288:GLU:HB3	12:d:297:ILE:HG13	2.03	0.40
12:d:330:ILE:HG21	12:d:339:MET:HA	2.02	0.40
24:u:90:ILE:HB	26:x:62:VAL:CG1	2.52	0.40
25:m:83:GLN:HE22	25:m:84:TYR:HB2	1.82	0.40
27:h:30:LYS:HD2	27:h:80:TYR:CE2	2.56	0.40
28:e:47:SER:HB2	28:e:103:VAL:HG12	2.04	0.40
28:e:89:ARG:HH22	28:e:91:ILE:CD1	2.33	0.40
28:e:92:SER:CB	25:z:99:ASP:OD1	2.69	0.40
31:r:19:SER:OG	31:r:38:ASP:OD2	2.34	0.40
31:r:85:GLN:HG2	31:p:80:LEU:HD21	2.03	0.40
1:A:748:GLN:NE2	18:E:77:G:OP1	2.54	0.40
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.57	0.40
1:A:1752:VAL:HG12	1:A:1787:TYR:HB3	2.03	0.40
33:A:3000:IHP:P3	33:A:3000:IHP:O14	2.79	0.40
6:Q:4:GLU:HG2	6:Q:5:ILE:HG23	2.04	0.40
15:H:9:ASN:HD21	32:F:33:THR:HG21	1.85	0.40
17:D:67:U:H2'	17:D:68:A:C8	2.57	0.40
18:E:55:G:H2'	18:E:56:A:H8	1.87	0.40
19:L:53:G:O4'	19:L:53:G:P	2.79	0.40
19:L:121:C:N4	27:w:33:PHE:CD1	2.90	0.40
20:v:385:PHE:HD1	20:v:388:LEU:HD12	1.85	0.40
22:b:104:SER:HA	22:b:130:ILE:O	2.21	0.40
25:m:4:VAL:CG2	25:m:36:MET:HE2	2.45	0.40
26:j:15:ILE:HG12	26:j:73:ALA:CB	2.51	0.40
27:h:79:LEU:HD22	27:h:80:TYR:HD2	1.86	0.40
28:g:50:ASN:HB2	28:g:52:HIS:CE1	2.55	0.40
28:e:73:LYS:HE3	28:e:90:PHE:CE2	2.56	0.40
27:w:51:LEU:HB2	27:w:73:ILE:HB	2.04	0.40
25:z:46:THR:OG1	25:z:78:ASN:O	2.29	0.40
25:z:47:LEU:CD2	25:z:61:ALA:HB3	2.43	0.40
32:F:67:LYS:HB2	32:F:85:THR:HG1	1.86	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	1905/2413 (79%)	1801 (94%)	91 (5%)	13 (1%)	18	50
2	C	914/1008 (91%)	871 (95%)	39 (4%)	4 (0%)	30	60
3	J	25/135 (18%)	21 (84%)	4 (16%)	0	100	100
4	O	355/451 (79%)	321 (90%)	30 (8%)	4 (1%)	11	42
5	P	197/379 (52%)	190 (96%)	7 (4%)	0	100	100
6	Q	288/364 (79%)	266 (92%)	19 (7%)	3 (1%)	12	43
7	R	259/339 (76%)	238 (92%)	13 (5%)	8 (3%)	3	26
8	S	64/175 (37%)	61 (95%)	3 (5%)	0	100	100
9	T	155/157 (99%)	145 (94%)	9 (6%)	1 (1%)	21	52
10	Z	443/577 (77%)	417 (94%)	19 (4%)	7 (2%)	7	35
11	c	418/590 (71%)	397 (95%)	20 (5%)	1 (0%)	43	72
12	d	534/687 (78%)	513 (96%)	16 (3%)	5 (1%)	14	45
13	I	98/215 (46%)	95 (97%)	3 (3%)	0	100	100
14	n	279/455 (61%)	253 (91%)	20 (7%)	6 (2%)	5	31
15	H	93/235 (40%)	86 (92%)	4 (4%)	3 (3%)	3	25
20	v	666/859 (78%)	642 (96%)	22 (3%)	2 (0%)	36	65
21	a	82/111 (74%)	78 (95%)	3 (4%)	1 (1%)	10	40
22	b	165/238 (69%)	138 (84%)	20 (12%)	7 (4%)	2	20
23	t	150/175 (86%)	145 (97%)	4 (3%)	1 (1%)	18	50
24	i	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
24	u	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
25	m	117/146 (80%)	111 (95%)	6 (5%)	0	100	100
25	z	106/146 (73%)	100 (94%)	6 (6%)	0	100	100
26	j	73/77 (95%)	67 (92%)	5 (7%)	1 (1%)	9	37
26	x	73/77 (95%)	65 (89%)	7 (10%)	1 (1%)	9	37
27	h	64/86 (74%)	60 (94%)	4 (6%)	0	100	100
27	w	64/86 (74%)	61 (95%)	3 (5%)	0	100	100
28	e	99/110 (90%)	95 (96%)	3 (3%)	1 (1%)	12	43
28	g	99/110 (90%)	93 (94%)	4 (4%)	2 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	k	96/196 (49%)	90 (94%)	5 (5%)	1 (1%)	12	43
29	s	89/196 (45%)	83 (93%)	6 (7%)	0	100	100
30	l	81/101 (80%)	79 (98%)	0	2 (2%)	4	29
30	y	79/101 (78%)	75 (95%)	4 (5%)	0	100	100
31	o	120/503 (24%)	115 (96%)	5 (4%)	0	100	100
31	p	122/503 (24%)	118 (97%)	4 (3%)	0	100	100
31	q	125/503 (25%)	116 (93%)	9 (7%)	0	100	100
31	r	119/503 (24%)	112 (94%)	7 (6%)	0	100	100
32	F	157/278 (56%)	147 (94%)	4 (2%)	6 (4%)	2	22
All	All	8913/13473 (66%)	8399 (94%)	434 (5%)	80 (1%)	16	45

All (80) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1431	HIS
1	A	1435	LYS
1	A	1966	SER
2	C	682	SER
2	C	828	ASP
4	O	329	ASP
7	R	39	GLN
7	R	41	PHE
7	R	45	THR
7	R	152	LYS
7	R	208	SER
9	T	104	CYS
10	Z	448	MET
10	Z	450	PRO
10	Z	451	LEU
12	d	181	ASN
12	d	353	GLU
14	n	306	SER
21	a	68	GLN
22	b	68	PRO
22	b	95	PRO
22	b	125	LYS
22	b	149	PRO
26	j	75	ASP
32	F	47	PHE

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Mol	Chain	Res	Type
32	F	58	ILE
32	F	59	PRO
1	A	260	PRO
1	A	1263	CYS
1	A	1432	GLU
2	C	683	ASN
2	C	684	GLU
4	O	351	GLY
7	R	151	LEU
10	Z	452	GLU
10	Z	455	ALA
14	n	291	HIS
14	n	304	ASP
14	n	387	ILE
15	H	27	LYS
20	v	798	LYS
22	b	98	VAL
23	t	112	SER
28	g	51	ASN
28	g	65	CYS
29	k	41	MET
28	e	51	ASN
30	l	78	LEU
1	A	510	PRO
1	A	1965	PHE
4	O	327	CYS
4	O	352	ILE
6	Q	255	SER
10	Z	182	GLN
12	d	63	LEU
12	d	336	LYS
20	v	515	PRO
22	b	67	ILE
22	b	94	LEU
32	F	48	SER
1	A	1164	TYR
1	A	1843	LEU
1	A	1964	PRO
7	R	43	GLY
14	n	305	GLY
30	l	40	MET
26	x	75	ASP

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Mol	Chain	Res	Type
32	F	76	LEU
15	H	26	TYR
15	H	28	ASP
6	Q	215	PRO
10	Z	446	ASP
14	n	427	LYS
1	A	1157	PRO
1	A	1156	HIS
6	Q	191	PRO
7	R	153	PRO
11	c	418	PRO
12	d	334	PHE
32	F	46	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1737/2182 (80%)	1714 (99%)	23 (1%)	61	71
2	C	830/910 (91%)	822 (99%)	8 (1%)	68	74
3	J	21/121 (17%)	21 (100%)	0	100	100
4	O	312/397 (79%)	306 (98%)	6 (2%)	50	65
5	P	175/328 (53%)	174 (99%)	1 (1%)	78	79
6	Q	265/332 (80%)	262 (99%)	3 (1%)	65	73
7	R	224/296 (76%)	211 (94%)	13 (6%)	18	45
8	S	57/151 (38%)	52 (91%)	5 (9%)	9	33
9	T	141/141 (100%)	140 (99%)	1 (1%)	76	77
10	Z	417/538 (78%)	405 (97%)	12 (3%)	37	57
11	c	214/525 (41%)	205 (96%)	9 (4%)	26	51
12	d	274/633 (43%)	267 (97%)	7 (3%)	40	60
13	I	92/193 (48%)	91 (99%)	1 (1%)	65	73
14	n	122/412 (30%)	109 (89%)	13 (11%)	6	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	H	88/216 (41%)	86 (98%)	2 (2%)	44	62
20	v	294/786 (37%)	278 (95%)	16 (5%)	20	46
23	t	39/165 (24%)	26 (67%)	13 (33%)	0	1
24	i	55/83 (66%)	52 (94%)	3 (6%)	19	46
24	u	52/83 (63%)	51 (98%)	1 (2%)	50	65
25	m	106/129 (82%)	93 (88%)	13 (12%)	4	22
25	z	95/129 (74%)	92 (97%)	3 (3%)	34	56
26	j	56/66 (85%)	47 (84%)	9 (16%)	2	14
26	x	56/66 (85%)	55 (98%)	1 (2%)	51	67
27	h	51/77 (66%)	51 (100%)	0	100	100
27	w	51/77 (66%)	51 (100%)	0	100	100
28	e	82/103 (80%)	75 (92%)	7 (8%)	10	35
28	g	82/103 (80%)	75 (92%)	7 (8%)	10	35
29	k	92/176 (52%)	80 (87%)	12 (13%)	4	20
29	s	85/176 (48%)	81 (95%)	4 (5%)	23	48
30	l	72/89 (81%)	54 (75%)	18 (25%)	0	4
30	y	68/89 (76%)	68 (100%)	0	100	100
31	o	60/451 (13%)	57 (95%)	3 (5%)	22	48
31	p	62/451 (14%)	58 (94%)	4 (6%)	15	43
31	q	62/451 (14%)	59 (95%)	3 (5%)	23	48
31	r	60/451 (13%)	57 (95%)	3 (5%)	22	48
32	F	145/256 (57%)	145 (100%)	0	100	100
All	All	6694/11832 (57%)	6470 (97%)	224 (3%)	34	55

All (224) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	ILE
1	A	249	LEU
1	A	261	LEU
1	A	305	LEU
1	A	488	ARG
1	A	495	ARG
1	A	570	GLN

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Mol	Chain	Res	Type
1	A	621	LEU
1	A	674	MET
1	A	742	VAL
1	A	749	ARG
1	A	903	LEU
1	A	1182	LEU
1	A	1222	LEU
1	A	1433	ASP
1	A	1434	GLU
1	A	1435	LYS
1	A	1437	ILE
1	A	1661	ILE
1	A	1842	GLU
1	A	1963	LEU
1	A	1991	ILE
1	A	2084	LEU
2	C	107	THR
2	C	148	SER
2	C	267	ILE
2	C	545	LEU
2	C	683	ASN
2	C	684	GLU
2	C	697	ARG
2	C	841	LEU
4	O	230	VAL
4	O	236	LEU
4	O	327	CYS
4	O	330	ASP
4	O	349	LYS
4	O	350	THR
5	P	30	LEU
6	Q	251	LEU
6	Q	282	LEU
6	Q	291	ILE
7	R	10	LYS
7	R	28	LEU
7	R	39	GLN
7	R	41	PHE
7	R	44	ASN
7	R	54	GLN
7	R	150	HIS
7	R	152	LYS

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Mol	Chain	Res	Type
7	R	159	ARG
7	R	204	LEU
7	R	205	LEU
7	R	206	LEU
7	R	208	SER
8	S	12	ARG
8	S	35	THR
8	S	36	THR
8	S	128	ARG
8	S	135	ARG
9	T	153	CYS
10	Z	194	LEU
10	Z	444	LYS
10	Z	445	LEU
10	Z	446	ASP
10	Z	448	MET
10	Z	449	PHE
10	Z	451	LEU
10	Z	452	GLU
10	Z	454	ASP
10	Z	463	ASN
10	Z	470	LEU
10	Z	473	LEU
11	c	20	ILE
11	c	170	LYS
11	c	181	ARG
11	c	504	PRO
11	c	505	PRO
11	c	506	THR
11	c	517	VAL
11	c	532	PRO
11	c	550	PRO
12	d	62	ARG
12	d	155	LEU
12	d	263	SER
12	d	271	ILE
12	d	284	LEU
12	d	285	LEU
12	d	334	PHE
13	I	121	LYS
14	n	51	PHE
14	n	159	PRO

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Mol	Chain	Res	Type
14	n	162	PRO
14	n	208	PRO
14	n	257	PRO
14	n	258	THR
14	n	260	PRO
14	n	327	PRO
14	n	340	PRO
14	n	373	PRO
14	n	424	PRO
14	n	428	PRO
14	n	436	PRO
15	H	28	ASP
15	H	38	VAL
20	v	385	PHE
20	v	386	GLU
20	v	397	ASN
20	v	398	ASP
20	v	438	ARG
20	v	529	HIS
20	v	530	ARG
20	v	538	LEU
20	v	544	ILE
20	v	576	THR
20	v	582	LEU
20	v	593	LEU
20	v	612	ILE
20	v	652	LEU
20	v	665	ILE
20	v	719	THR
23	t	13	PRO
23	t	76	THR
23	t	77	PRO
23	t	85	THR
23	t	96	PRO
23	t	100	THR
23	t	105	PRO
23	t	108	SER
23	t	109	SER
23	t	111	VAL
23	t	133	PRO
23	t	136	VAL
23	t	150	THR

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Mol	Chain	Res	Type
24	u	35	ILE
25	m	33	SER
25	m	35	GLN
25	m	37	ASN
25	m	39	ILE
25	m	45	LEU
25	m	46	THR
25	m	47	LEU
25	m	52	LEU
25	m	60	ILE
25	m	85	ILE
25	m	86	ASN
25	m	92	ILE
25	m	93	ARG
26	j	18	ASN
26	j	19	ILE
26	j	20	ASN
26	j	22	SER
26	j	23	ARG
26	j	29	LEU
26	j	39	VAL
26	j	64	ARG
26	j	74	LEU
28	g	33	LEU
28	g	35	ASN
28	g	41	ARG
28	g	42	THR
28	g	57	ARG
28	g	84	VAL
28	g	85	ILE
29	k	14	ASN
29	k	15	LEU
29	k	39	LYS
29	k	41	MET
29	k	43	LEU
29	k	49	ILE
29	k	50	GLU
29	k	82	LEU
29	k	104	SER
29	k	105	LYS
29	k	106	LYS
29	k	109	LEU

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Mol	Chain	Res	Type
28	e	41	ARG
28	e	57	ARG
28	e	70	GLU
28	e	88	GLU
28	e	91	ILE
28	e	92	SER
28	e	94	LEU
29	s	11	ARG
29	s	15	LEU
29	s	56	THR
29	s	82	LEU
30	l	11	LEU
30	l	15	GLN
30	l	23	LEU
30	l	32	LYS
30	l	36	SER
30	l	37	GLU
30	l	38	ASP
30	l	45	ARG
30	l	47	VAL
30	l	64	VAL
30	l	65	ARG
30	l	70	LYS
30	l	73	VAL
30	l	77	LEU
30	l	79	LYS
30	l	83	LEU
30	l	84	PHE
30	l	85	LYS
24	i	18	PHE
24	i	22	GLN
24	i	40	LYS
26	x	74	LEU
25	z	45	LEU
25	z	54	LYS
25	z	55	LEU
31	r	17	PRO
31	r	44	PRO
31	r	63	THR
31	p	17	PRO
31	p	44	PRO
31	p	63	THR

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Mol	Chain	Res	Type
31	p	98	LEU
31	q	17	PRO
31	q	44	PRO
31	q	55	PRO
31	o	17	PRO
31	o	44	PRO
31	o	63	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (132) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	265	ASN
1	A	310	ASN
1	A	429	ASN
1	A	509	HIS
1	A	532	ASN
1	A	541	ASN
1	A	580	ASN
1	A	658	ASN
1	A	659	HIS
1	A	675	HIS
1	A	685	HIS
1	A	830	ASN
1	A	848	ASN
1	A	864	GLN
1	A	948	HIS
1	A	952	ASN
1	A	1034	ASN
1	A	1067	ASN
1	A	1077	ASN
1	A	1087	ASN
1	A	1128	GLN
1	A	1368	GLN
1	A	1449	ASN
1	A	1466	GLN
1	A	1500	HIS
1	A	1529	ASN
1	A	1540	ASN
1	A	1618	ASN
1	A	1677	GLN
1	A	1687	HIS
1	A	1737	GLN

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Mol	Chain	Res	Type
1	A	2018	ASN
1	A	2068	ASN
2	C	84	GLN
2	C	108	GLN
2	C	183	GLN
2	C	251	GLN
2	C	289	ASN
2	C	294	ASN
2	C	355	HIS
2	C	410	GLN
2	C	423	HIS
2	C	444	GLN
2	C	511	GLN
2	C	560	GLN
2	C	608	GLN
2	C	647	ASN
2	C	764	ASN
2	C	797	GLN
2	C	869	HIS
2	C	929	GLN
2	C	1004	ASN
3	J	19	HIS
4	O	99	ASN
4	O	271	GLN
5	P	87	ASN
5	P	110	HIS
6	Q	85	GLN
6	Q	106	ASN
6	Q	141	ASN
7	R	39	GLN
7	R	58	HIS
7	R	91	HIS
7	R	150	HIS
7	R	201	ASN
7	R	257	ASN
8	S	27	HIS
8	S	34	HIS
8	S	173	HIS
9	T	56	HIS
9	T	57	HIS
9	T	143	HIS
10	Z	84	ASN

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Mol	Chain	Res	Type
10	Z	116	ASN
10	Z	310	HIS
10	Z	354	HIS
10	Z	441	ASN
10	Z	463	ASN
11	c	32	GLN
11	c	214	ASN
12	d	79	HIS
12	d	123	ASN
12	d	147	ASN
12	d	248	ASN
12	d	315	ASN
12	d	316	ASN
13	I	184	GLN
15	H	9	ASN
15	H	74	GLN
20	v	397	ASN
20	v	529	HIS
20	v	596	GLN
20	v	643	HIS
23	t	143	ASN
24	u	24	GLN
24	u	86	ASN
25	m	5	ASN
25	m	12	ASN
25	m	14	GLN
25	m	21	ASN
25	m	30	GLN
25	m	83	GLN
25	m	86	ASN
25	m	94	GLN
26	j	20	ASN
26	j	54	ASN
27	h	50	ASN
28	g	50	ASN
28	g	52	HIS
28	g	86	ASN
29	k	14	ASN
28	e	50	ASN
28	e	64	HIS
28	e	66	ASN
28	e	71	ASN

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Mol	Chain	Res	Type
28	e	86	ASN
30	l	15	GLN
30	l	41	ASN
30	l	43	GLN
30	l	68	GLN
24	i	22	GLN
24	i	24	GLN
26	x	20	ASN
30	y	53	GLN
25	z	5	ASN
25	z	12	ASN
25	z	14	GLN
25	z	21	ASN
25	z	30	GLN
31	r	85	GLN
31	q	85	GLN
32	F	115	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	B	55/246 (22%)	29 (52%)	3 (5%)
17	D	177/214 (82%)	55 (31%)	8 (4%)
18	E	102/112 (91%)	45 (44%)	3 (2%)
19	L	201/1175 (17%)	86 (42%)	15 (7%)
All	All	535/1747 (30%)	215 (40%)	29 (5%)

All (215) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	B	-11	U
16	B	-10	G
16	B	-8	U
16	B	-6	U
16	B	-1	A
16	B	0	G
16	B	2	U
16	B	3	A
16	B	4	U
16	B	9	A
16	B	10	A

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Mol	Chain	Res	Type
16	B	11	A
16	B	12	G
16	B	13	U
16	B	52	U
16	B	55	U
16	B	58	U
16	B	59	C
16	B	62	A
16	B	63	U
16	B	64	U
16	B	67	C
16	B	68	U
16	B	70	A
16	B	71	C
16	B	72	A
16	B	73	A
16	B	74	A
16	B	75	A
17	D	2	A
17	D	4	C
17	D	9	U
17	D	12	C
17	D	13	A
17	D	18	A
17	D	20	U
17	D	27	G
17	D	28	G
17	D	29	G
17	D	31	G
17	D	33	U
17	D	38	A
17	D	41	A
17	D	42	A
17	D	43	G
17	D	44	A
17	D	45	A
17	D	75	A
17	D	77	A
17	D	79	C
17	D	80	G
17	D	81	A
17	D	84	A

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Mol	Chain	Res	Type
17	D	92	U
17	D	96	U
17	D	100	A
17	D	101	C
17	D	103	A
17	D	104	G
17	D	109	A
17	D	113	G
17	D	124	C
17	D	127	U
17	D	128	A
17	D	130	A
17	D	131	A
17	D	132	A
17	D	139	A
17	D	141	G
17	D	142	C
17	D	151	A
17	D	160	U
17	D	161	U
17	D	162	G
17	D	163	C
17	D	164	C
17	D	165	A
17	D	166	U
17	D	168	U
17	D	170	U
17	D	171	U
17	D	174	G
17	D	175	G
17	D	178	C
18	E	5	G
18	E	12	A
18	E	13	A
18	E	14	C
18	E	15	C
18	E	16	C
18	E	23	G
18	E	31	G
18	E	33	C
18	E	36	U
18	E	39	G

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Mol	Chain	Res	Type
18	E	40	A
18	E	42	A
18	E	51	A
18	E	52	G
18	E	54	U
18	E	56	A
18	E	59	A
18	E	60	G
18	E	62	A
18	E	63	G
18	E	64	U
18	E	65	U
18	E	66	C
18	E	67	C
18	E	68	C
18	E	73	A
18	E	74	U
18	E	77	G
18	E	80	U
18	E	81	G
18	E	84	C
18	E	85	C
18	E	86	G
18	E	87	U
18	E	88	U
18	E	90	U
18	E	91	A
18	E	92	C
18	E	98	G
18	E	99	A
18	E	100	U
18	E	101	U
18	E	102	U
18	E	103	A
19	L	2	C
19	L	4	A
19	L	5	A
19	L	6	U
19	L	7	C
19	L	9	C
19	L	12	U
19	L	16	U

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Mol	Chain	Res	Type
19	L	17	U
19	L	18	U
19	L	19	U
19	L	21	G
19	L	23	U
19	L	25	A
19	L	26	G
19	L	29	C
19	L	30	A
19	L	31	A
19	L	32	G
19	L	33	U
19	L	36	A
19	L	39	A
19	L	41	C
19	L	44	U
19	L	47	U
19	L	50	U
19	L	51	C
19	L	52	A
19	L	53	G
19	L	54	U
19	L	68	U
19	L	84	C
19	L	85	A
19	L	86	U
19	L	106	A
19	L	107	U
19	L	109	C
19	L	110	A
19	L	111	C
19	L	115	U
19	L	119	G
19	L	120	G
19	L	121	C
19	L	124	C
19	L	129	A
19	L	141	A
19	L	153	U
19	L	1084	A
19	L	1085	G
19	L	1086	U

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Mol	Chain	Res	Type
19	L	1091	G
19	L	1092	A
19	L	1093	C
19	L	1094	G
19	L	1096	C
19	L	1098	C
19	L	1099	G
19	L	1100	A
19	L	1101	C
19	L	1102	C
19	L	1103	C
19	L	1104	U
19	L	1105	C
19	L	1106	G
19	L	1107	C
19	L	1108	A
19	L	1115	G
19	L	1120	G
19	L	1122	U
19	L	1123	C
19	L	1124	U
19	L	1125	U
19	L	1126	G
19	L	1128	C
19	L	1130	U
19	L	1137	U
19	L	1138	G
19	L	1139	G
19	L	1140	U
19	L	1144	U
19	L	1145	U
19	L	1146	G
19	L	1147	A
19	L	1149	G
19	L	1152	U
19	L	1166	G

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	B	2	U
16	B	3	A

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Mol	Chain	Res	Type
16	B	9	A
17	D	17	C
17	D	27	G
17	D	28	G
17	D	83	C
17	D	99	U
17	D	130	A
17	D	150	U
17	D	163	C
18	E	14	C
18	E	64	U
18	E	101	U
19	L	1	A
19	L	3	G
19	L	5	A
19	L	40	U
19	L	46	C
19	L	51	C
19	L	53	G
19	L	109	C
19	L	120	G
19	L	1085	G
19	L	1092	A
19	L	1093	C
19	L	1106	G
19	L	1107	C
19	L	1146	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
14	SEP	n	73	14	8,9,10	0.67	0	7,12,14	0.61	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	SEP	n	73	14	-	5/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	n	73	SEP	C-CA-CB-OG
14	n	73	SEP	CB-OG-P-O1P
14	n	73	SEP	CB-OG-P-O2P
14	n	73	SEP	CB-OG-P-O3P
14	n	73	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 13 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	$\# Z > 2$
33	IHP	A	3000	-	36,36,36	0.78	0	60,60,60	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	GTP	C	1500	35	33,34,34	0.50	0	50,54,54	0.49	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	IHP	A	3000	-	-	9/30/54/54	0/1/1/1
34	GTP	C	1500	35	-	2/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
33	A	3000	IHP	C3-C2-O12-P2
33	A	3000	IHP	C2-C3-O13-P3
33	A	3000	IHP	C4-C3-O13-P3
33	A	3000	IHP	C1-C2-O12-P2
34	C	1500	GTP	PA-O3A-PB-O2B
34	C	1500	GTP	PA-O3A-PB-O1B
33	A	3000	IHP	C1-O11-P1-O21
33	A	3000	IHP	C3-O13-P3-O23
33	A	3000	IHP	C4-O14-P4-O24
33	A	3000	IHP	C3-O13-P3-O33
33	A	3000	IHP	C3-O13-P3-O43

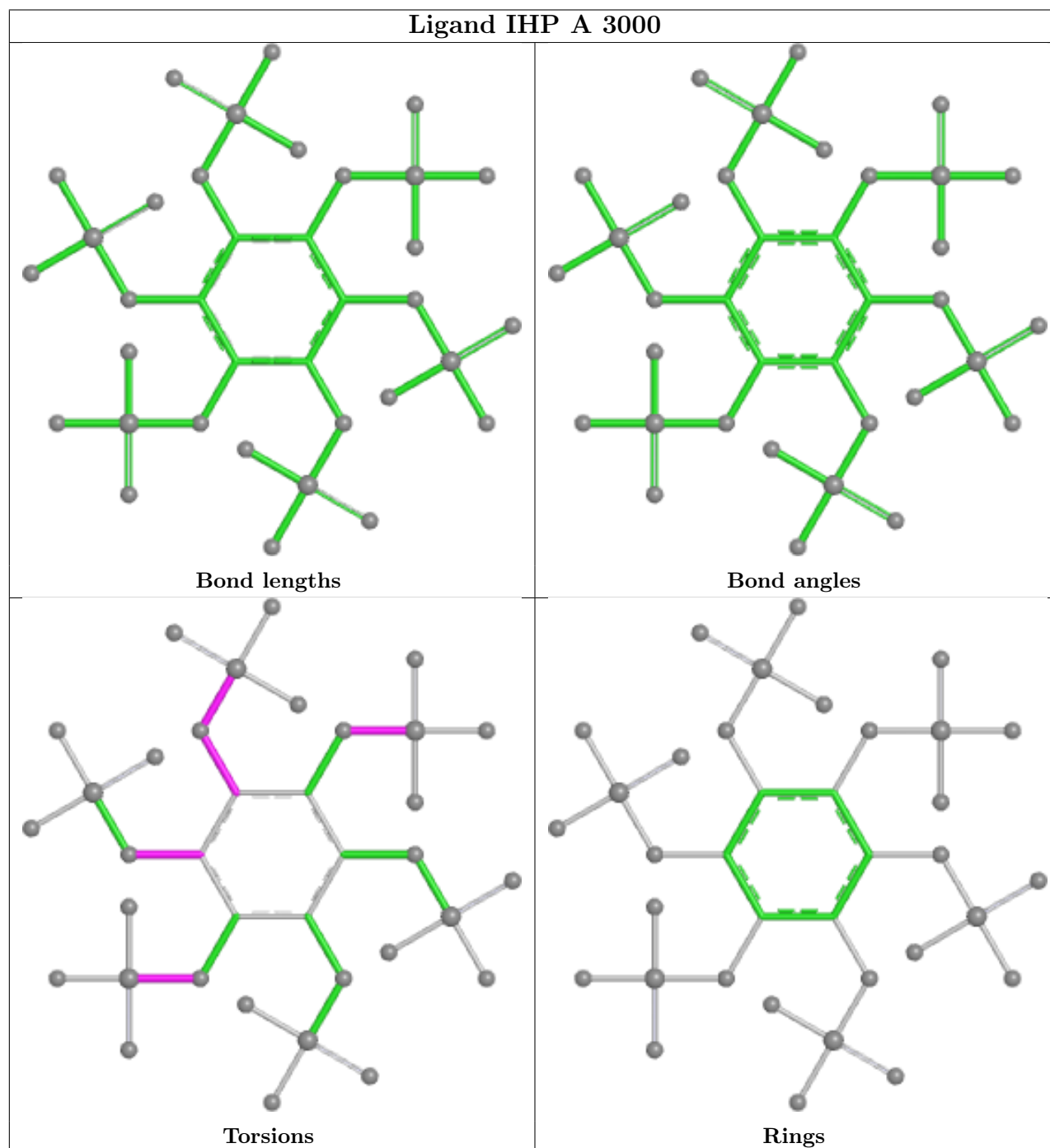
There are no ring outliers.

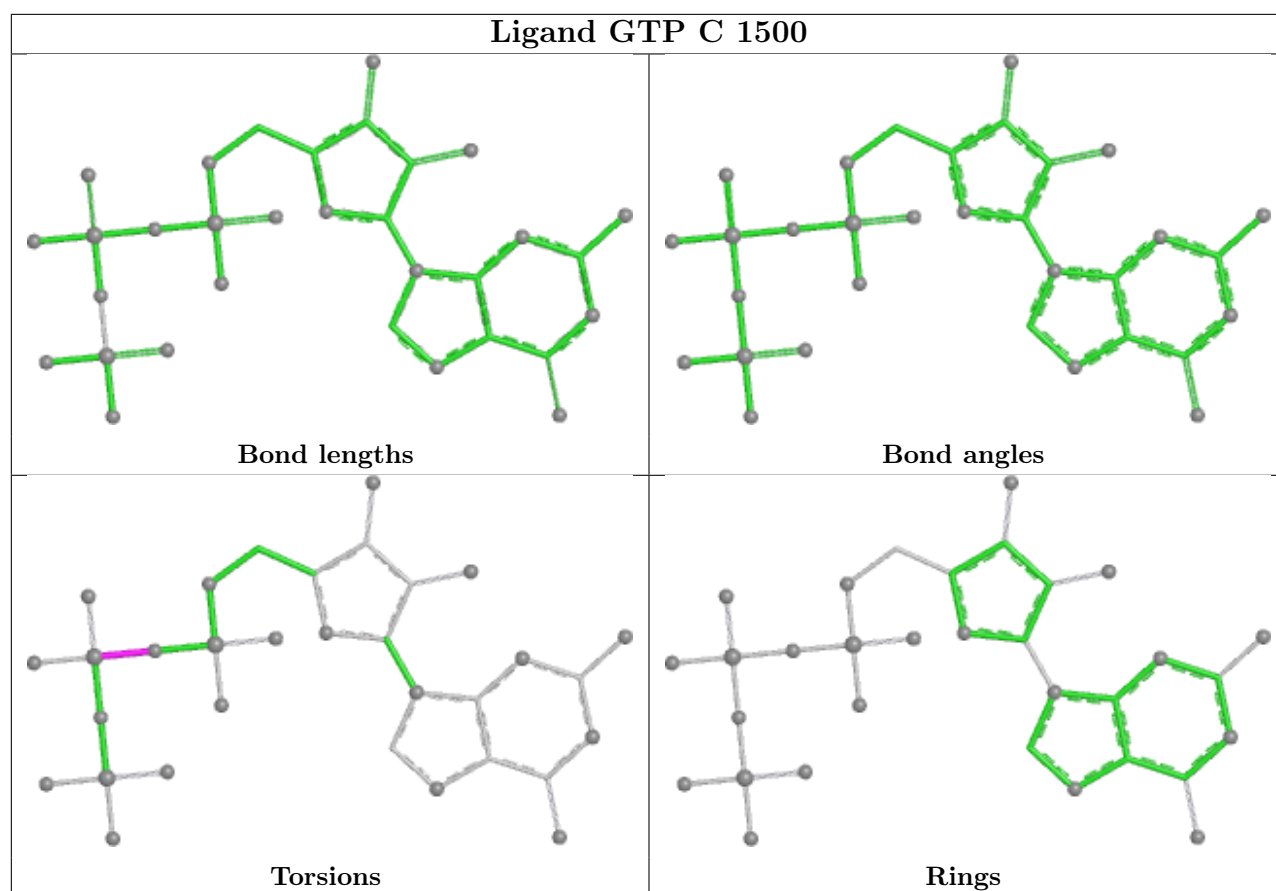
2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	A	3000	IHP	4	0
34	C	1500	GTP	1	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.

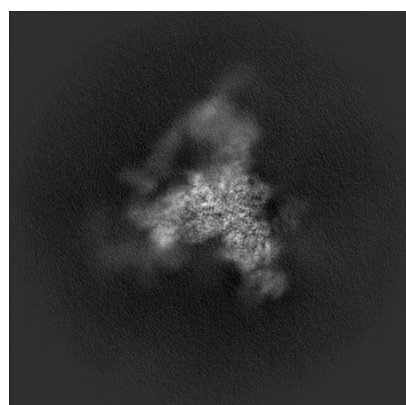
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0692. These allow visual inspection of the internal detail of the map and identification of artifacts.

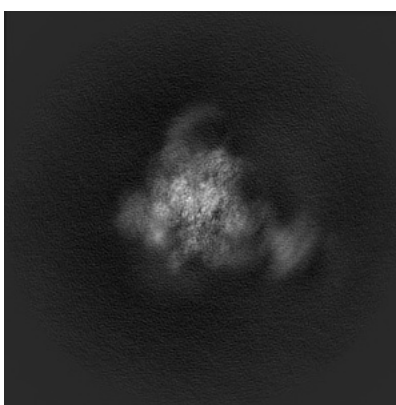
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

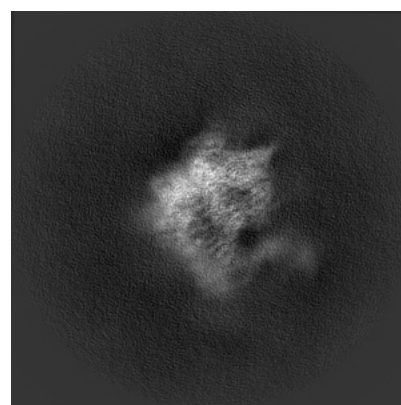
6.1.1 Primary map



X



Y

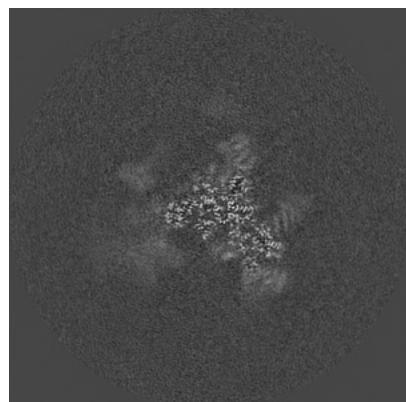


Z

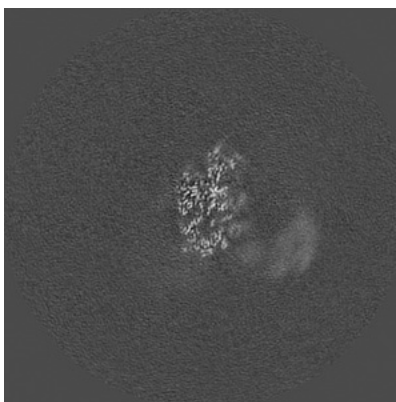
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

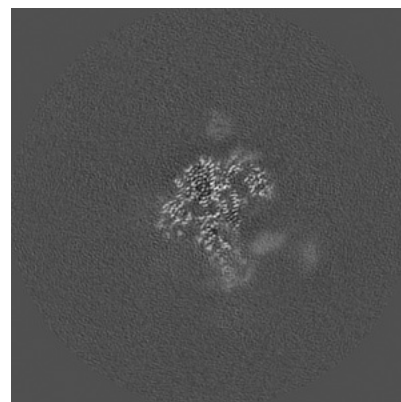
6.2.1 Primary map



X Index: 200



Y Index: 200

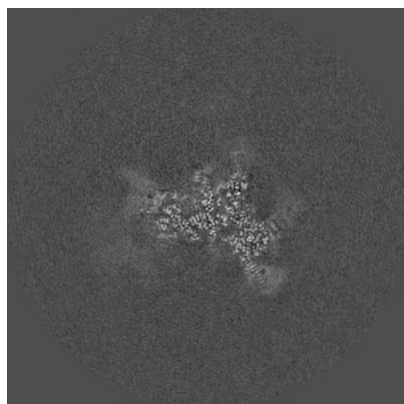


Z Index: 200

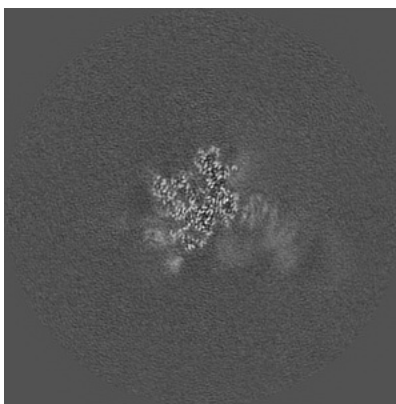
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

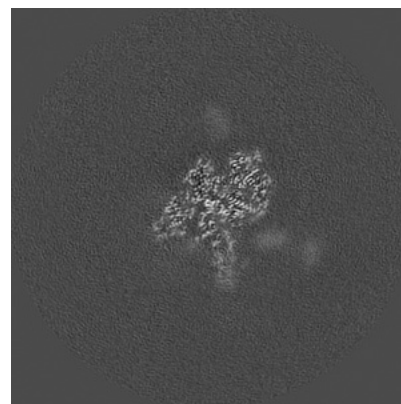
6.3.1 Primary map



X Index: 210



Y Index: 228

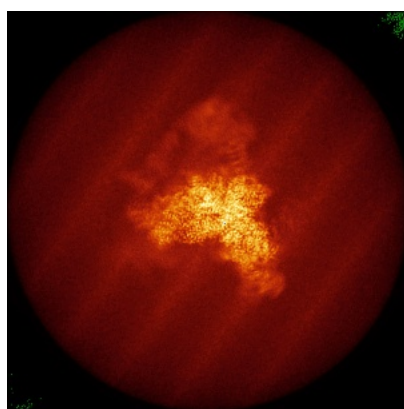


Z Index: 206

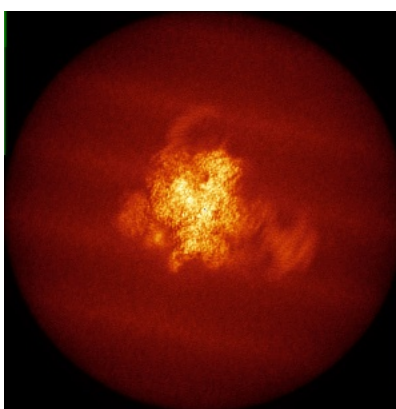
The images above show the largest variance slices of the map in three orthogonal directions.

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

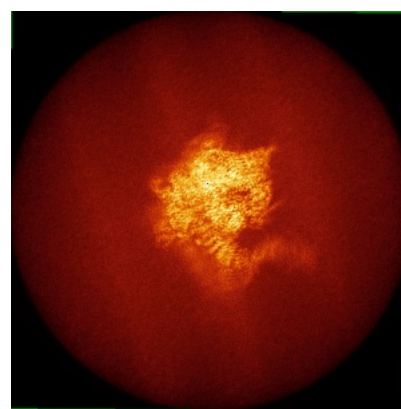
6.4.1 Primary map



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

This section was not generated.

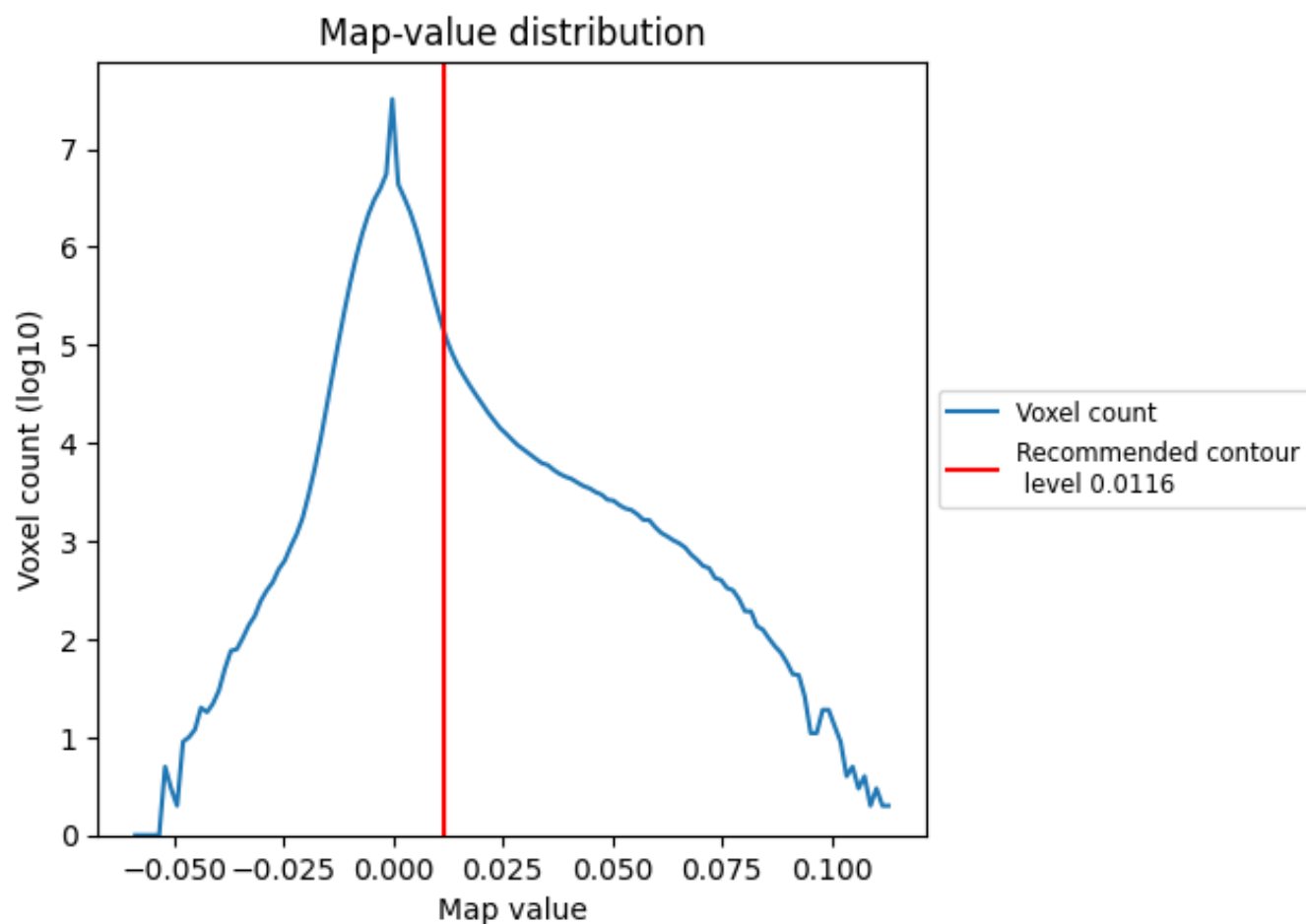
6.6 Mask visualisation

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

7 Map analysis [i](#)

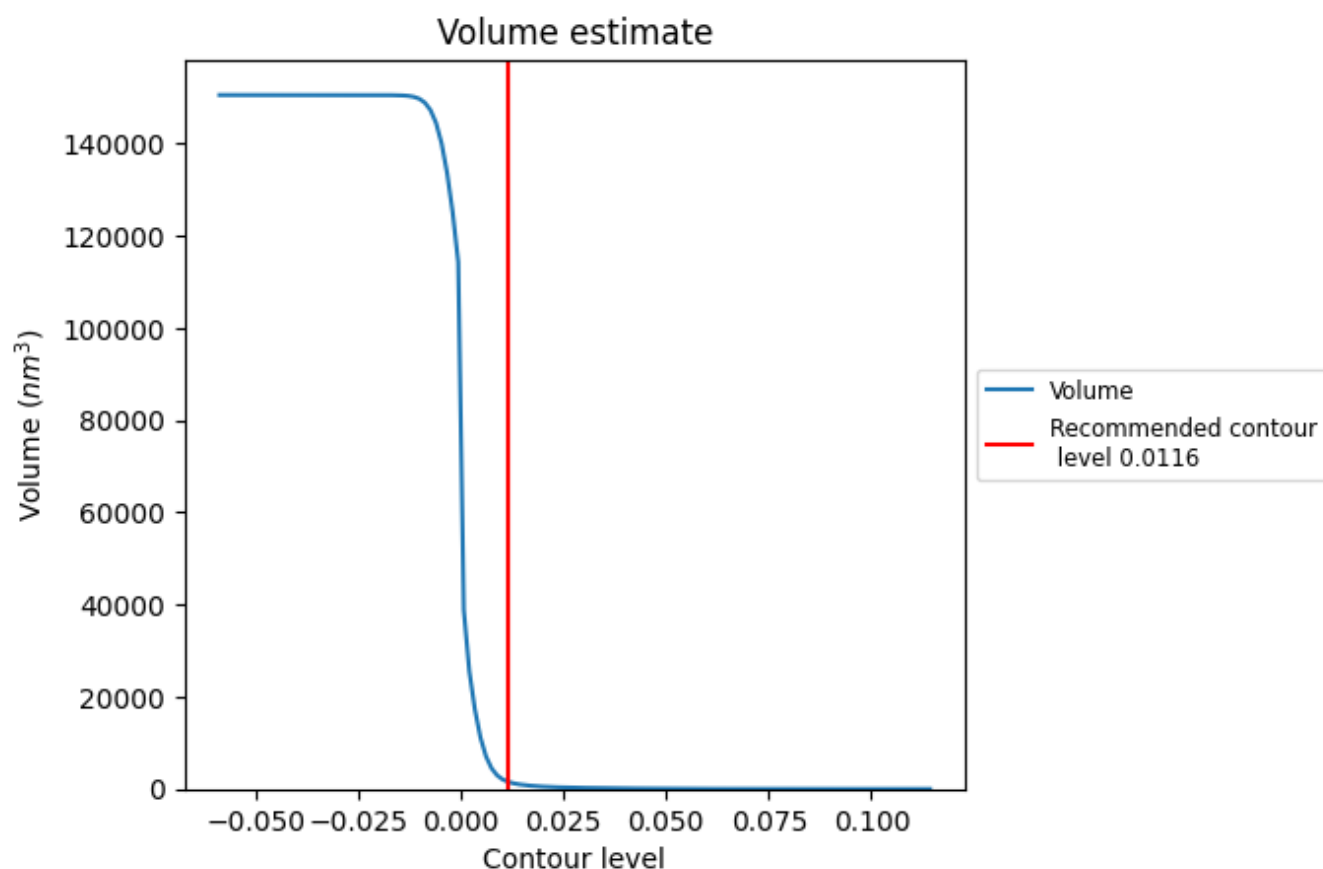
This section contains the results of statistical analysis of the map.

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.

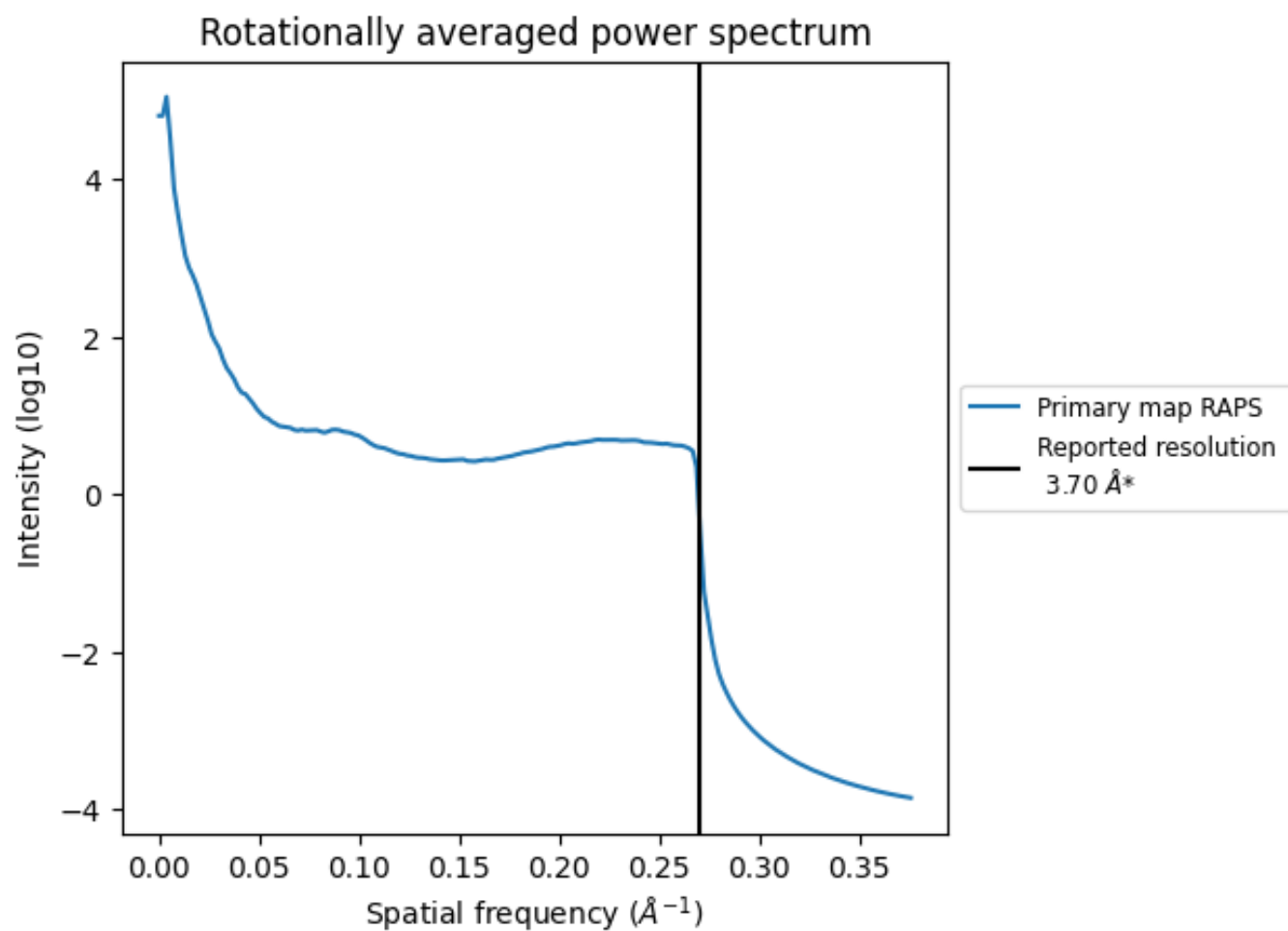
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1527 nm³; this corresponds to an approximate mass of 1379 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 0.270 Å⁻¹

8 Fourier-Shell correlation

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

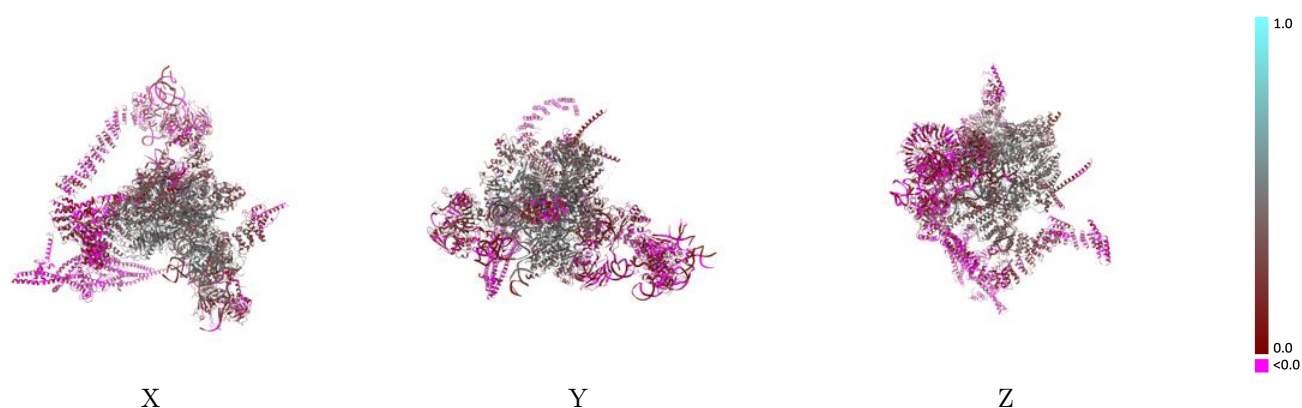
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0692 and PDB model 6J6Q. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

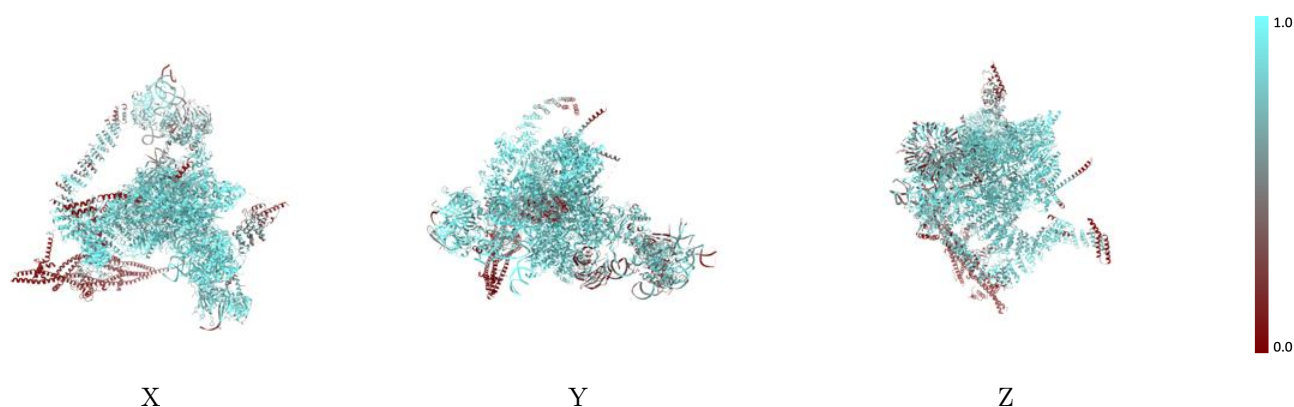
This section was not generated.

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



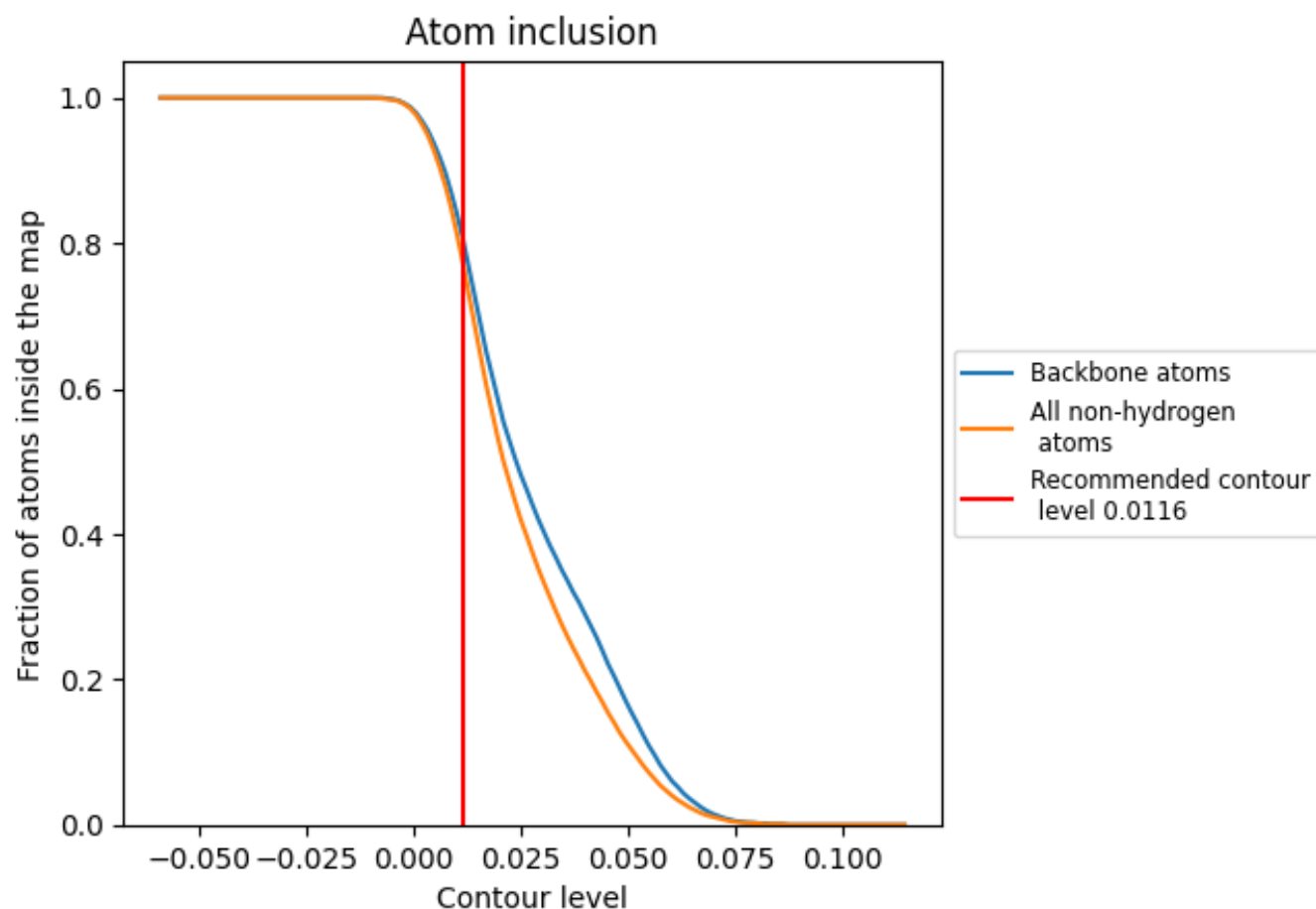
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0116).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 77% 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 (0.0116) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7720	 0.2610
A	 0.8990	 0.3880
B	 0.8990	 0.2650
C	 0.9180	 0.4100
D	 0.9370	 0.2600
E	 0.9840	 0.3810
F	 0.7000	 0.2500
H	 0.7630	 0.2450
I	 0.8080	 0.3130
J	 0.9570	 0.4300
L	 0.7160	 0.0950
O	 0.9270	 0.4520
P	 0.7950	 0.3440
Q	 0.8850	 0.3490
R	 0.9160	 0.4110
S	 0.8250	 0.4020
T	 0.9240	 0.4170
Z	 0.6350	 0.2470
a	 0.8000	 0.0310
b	 0.7430	 0.0480
c	 0.5280	 0.2150
d	 0.8100	 0.2390
e	 0.5770	 0.0670
g	 0.7400	 0.0900
h	 0.8970	 0.1570
i	 0.8310	 0.1170
j	 0.8030	 0.1820
k	 0.8210	 0.2480
l	 0.8660	 0.3040
m	 0.7080	 0.1410
n	 0.4090	 0.0650
o	 0.1910	 -0.0040
p	 0.1690	 -0.0030
q	 0.0380	 -0.0430
r	 0.1390	 -0.0080



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Chain	Atom inclusion	Q-score
s	 0.6960	 0.0420
t	 0.0920	 -0.0130
u	 0.5750	 0.0410
v	 0.7560	 0.1080
w	 0.6430	 0.0560
x	 0.5220	 0.0500
y	 0.5830	 0.0270
z	 0.6320	 0.0620