



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 11:38 AM UTC

PDB ID : 7W5A / pdb_00007w5a
EMDB ID : EMD-32319
Title : The cryo-EM structure of human pre-C*-II complex
Authors : Zhan, X.; Lu, Y.; Shi, Y.
Deposited on : 2021-11-29
Resolution : 3.60 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

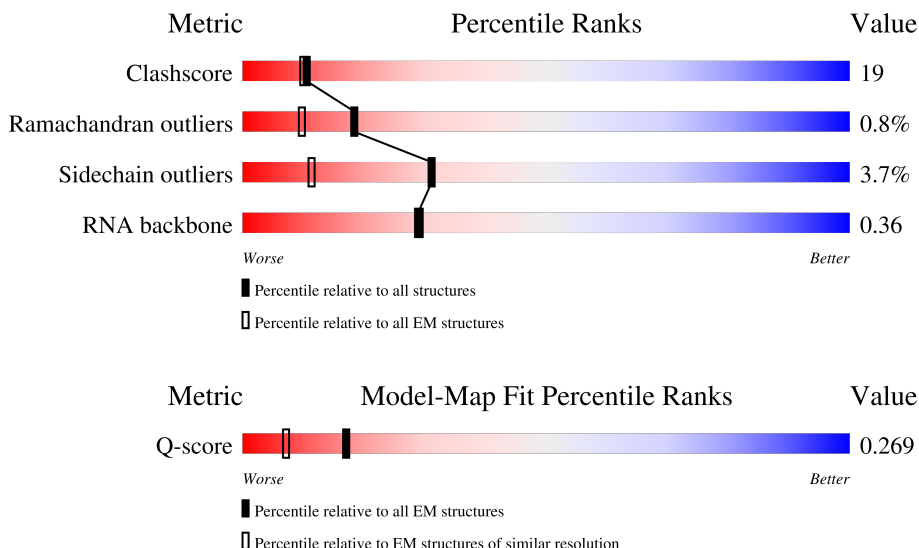
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	A	2335	
2	B	117	
3	C	972	

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Mol	Chain	Length	Quality of chain
4	E	357	
5	F	107	
6	4	46	
7	G	174	
8	H	188	
9	I	855	
10	J	848	
11	K	225	
12	L	802	
13	M	243	
14	N	144	
15	O	420	
16	P	229	
17	Q	1485	
18	R	536	
19	S	166	
20	T	514	
21	U	2752	
22	V	908	
23	W	579	
24	X	254	
25	Y	1220	
26	Z	758	
27	2	184	
28	z	112	

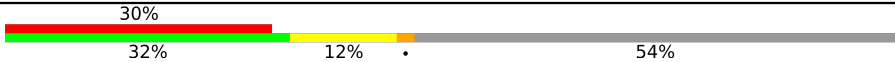
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Mol	Chain	Length	Quality of chain
29	b	240	
29	i	240	
30	y	301	
31	a	126	
31	h	126	
32	c	119	
32	j	119	
33	d	118	
33	k	118	
34	f	86	
34	m	86	
35	e	92	
35	l	92	
36	g	76	
36	n	76	
37	v	146	
38	w	174	
39	u	411	
40	x	703	
41	q	504	
41	r	504	
41	s	504	
41	t	504	
42	o	255	
43	p	225	

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Mol	Chain	Length	Quality of chain
44	1	586	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
45	IHP	A	3000	-	-	X	-

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 96822 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1984	Total	C	N	O	S	0	0
			16449	10601	2879	2899	70		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	P	0	0
			1768	792	295	597	84		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	862	Total	C	N	O	S	0	0
			6791	4341	1138	1280	32		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	299	Total	C	N	O	S	0	0
			2338	1470	410	445	13		

- Molecule 5 is a RNA chain called U6 snRNA.

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

- Molecule 6 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	13	Total	C	N	O	P	0	0
			276	123	50	90	13		

- Molecule 7 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	82	Total	C	N	O	P	0	0
			1510	666	210	552	82		

- Molecule 8 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	140	Total	C	N	O	P	0	0
			2966	1326	510	990	140		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	618	Total	C	N	O	S	0	0
			3857	2389	722	735	11		

- Molecule 10 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	567	Total	C	N	O	S	0	0
			3809	2373	716	714	6		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	155	Total	C	N	O	0	0
			772	462	155	155		

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	437	Total	C	N	O	S	0	0
			3015	1859	584	565	7		

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

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

- Molecule 14 is a protein called Protein BUD31 homolog.

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

- Molecule 15 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	285	Total	C	N	O	S	0	0
			2296	1442	408	426	20		

- Molecule 16 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	113	Total	C	N	O	S	0	0
			953	583	189	179	2		

- Molecule 17 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	1322	Total	C	N	O	S	4	0
			6562	3918	1322	1322			

- Molecule 18 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	261	Total	C	N	O	P S	0	0
			2073	1300	373	386	2 12		

- Molecule 19 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

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

- Molecule 20 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	312	Total	C	N	O	S	0	0
			2454	1550	446	450	8		

- Molecule 21 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	72	Total	C	N	O	S	0	0
			422	257	82	82	1		

- Molecule 22 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	452	Total	C	N	O	S	0	0
			2632	1639	492	495	6		

- Molecule 23 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	509	Total	C	N	O	S	0	0
			4129	2628	715	762	24		

- Molecule 24 is a protein called PSME3-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	87	Total	C	N	O	S	0	0
			702	431	128	142	1		

- Molecule 25 is a protein called ATP-dependent RNA helicase DHX8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	667	Total	C	N	O	S	4	0
			3431	2057	680	693	1		

- Molecule 26 is a protein called Cactin.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	101	Total	C	N	O	S	0	0
			902	592	167	141	2		

- Molecule 27 is a protein called PRKR-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	123	Total	C	N	O	S	0	0
			1013	635	193	180	5		

- Molecule 28 is a protein called Protein FAM32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	z	60	Total	C	N	O	S	0	0
			504	314	96	92	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	102	Total	C	N	O	S	0	0
			786	492	148	139	7		
29	i	86	Total	C	N	O	S	0	0
			690	434	126	123	7		

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

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

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	77	Total	C	N	O	S	0	0
			609	381	108	115	5		
31	h	81	Total	C	N	O	S	0	0
			633	397	112	118	6		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	82	Total	C	N	O	S	0	0
			649	413	113	119	4		
32	j	82	Total	C	N	O	S	0	0
			649	413	113	119	4		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	97	Total	C	N	O	S	0	0
			776	488	143	140	5		
33	k	85	Total	C	N	O	S	0	0
			688	432	125	126	5		

- Molecule 34 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		
34	m	74	Total	C	N	O	S	0	0
			572	370	94	103	5		

- Molecule 35 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	79	Total	C	N	O	S	0	0
			652	412	116	119	5		
35	l	79	Total	C	N	O	S	0	0
			652	412	116	119	5		

- Molecule 36 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		
36	n	69	Total	C	N	O	S	0	0
			542	345	97	94	6		

- Molecule 37 is a protein called Protein mago nashi homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	v	144	Total	C	N	O	0	0
			711	423	144	144		

- Molecule 38 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	w	91	Total	C	N	O	0	0
			445	263	91	91		

- Molecule 39 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	u	386	Total	C	N	O	0	0
			1907	1135	386	386		

- Molecule 40 is a protein called Protein CASC3.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	x	25	Total	C	N	O	0	0
			124	74	25	25		

- Molecule 41 is a protein called Pre-mRNA-processing factor 19.

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

- Molecule 42 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	162	Total	C	N	O	S	0	0
			1282	820	219	240	3		

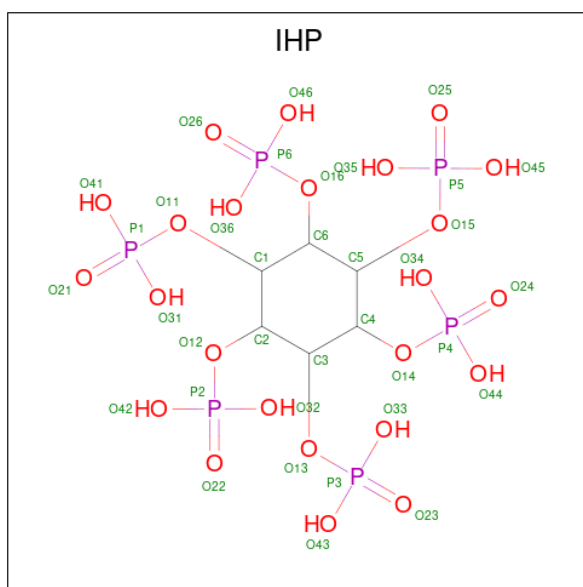
- Molecule 43 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	94	Total	C	N	O	S	0	0
			760	488	135	132	5		

- Molecule 44 is a protein called Pre-mRNA-splicing factor SLU7.

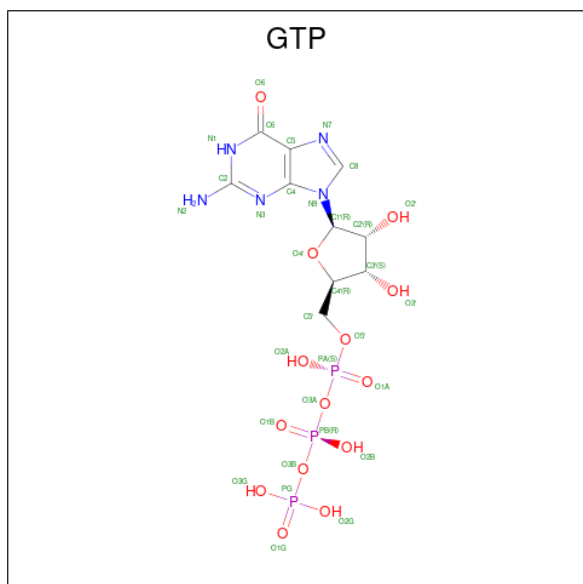
Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	267	Total	C	N	O	S	0	0
			2194	1378	392	416	8		

- Molecule 45 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 46 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



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

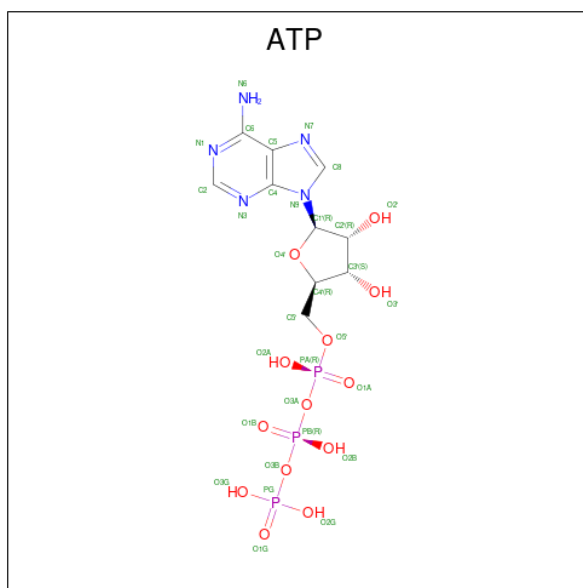
- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
47	C	1	Total	Mg	0
			1	1	
47	F	6	Total	Mg	0
			6	6	
47	Q	2	Total	Mg	0
			2	2	

- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
48	N	3	Total	Zn	0
			3	3	
48	O	3	Total	Zn	0
			3	3	
48	1	1	Total	Zn	0
			1	1	

- Molecule 49 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

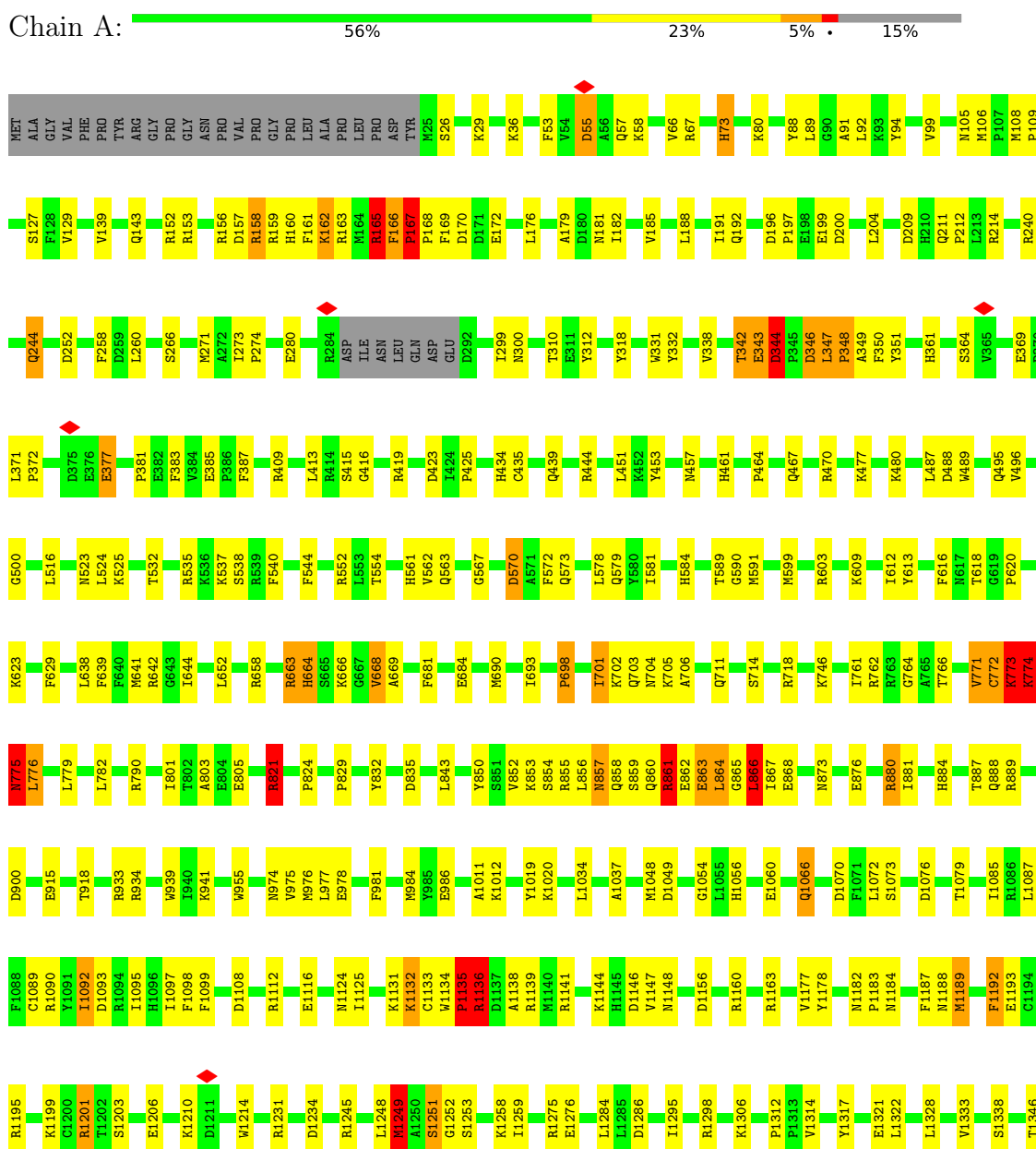


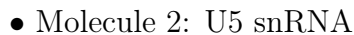
Mol	Chain	Residues	Atoms					AltConf
49	Q	1	Total	C	N	O	P	0
			31	10	5	13	3	

3 Residue-property plots

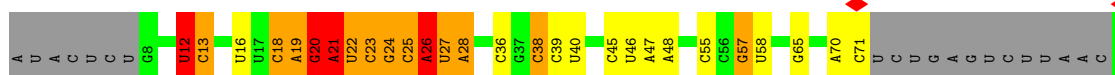
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

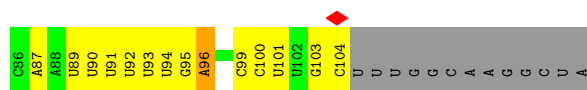
- Molecule 1: Pre-mRNA-processing-splicing factor 8





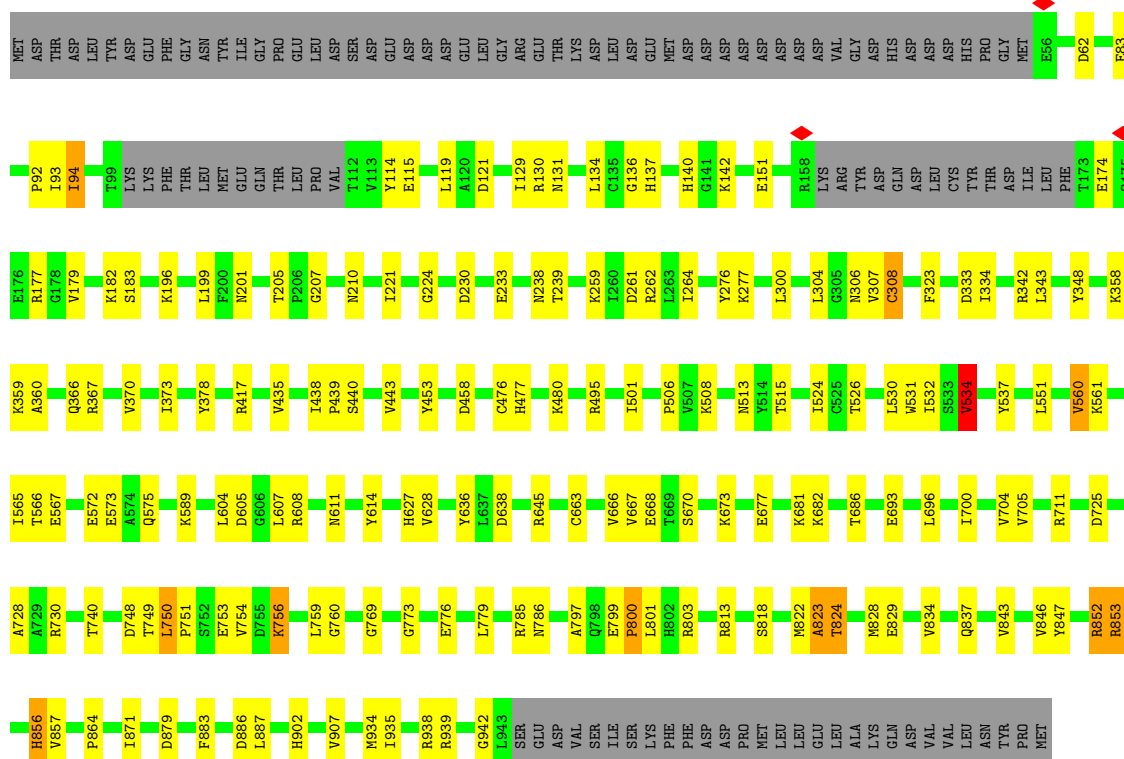
Frequency	Percentage
Daily	36%
Often	22%
Sometimes	10%
Rarely	2%
Never	28%





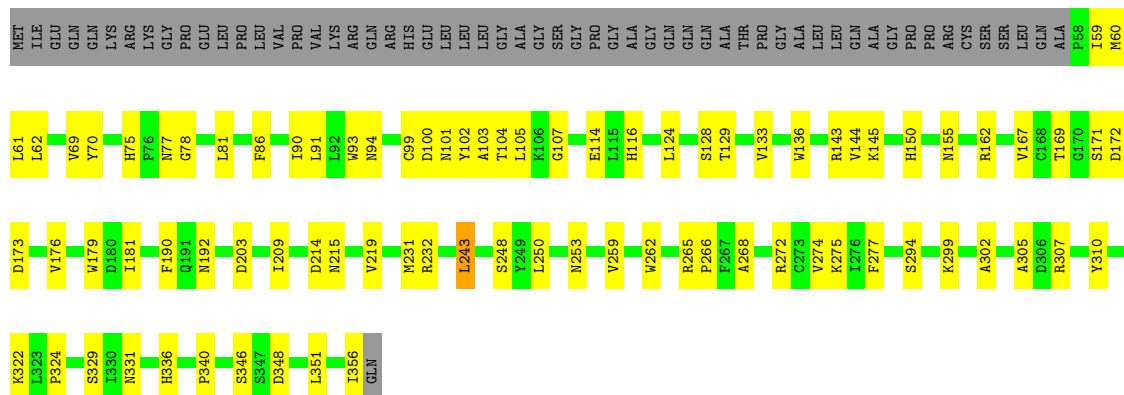
- Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

Chain C: 71% 17% 11%



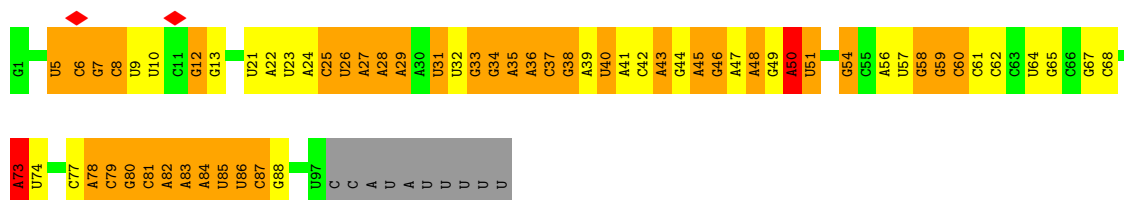
- Molecule 4: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain E: 61% 23% 16%



- Molecule 5: U6 snRNA

Chain F: 31% 23% 35% 9%



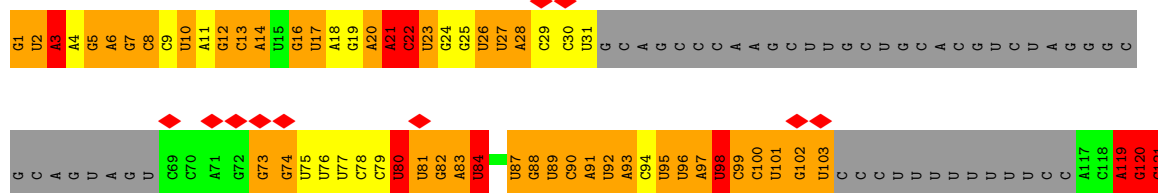
• Molecule 6: Pre-mRNA

Chain 4: 7% 13% . 72%



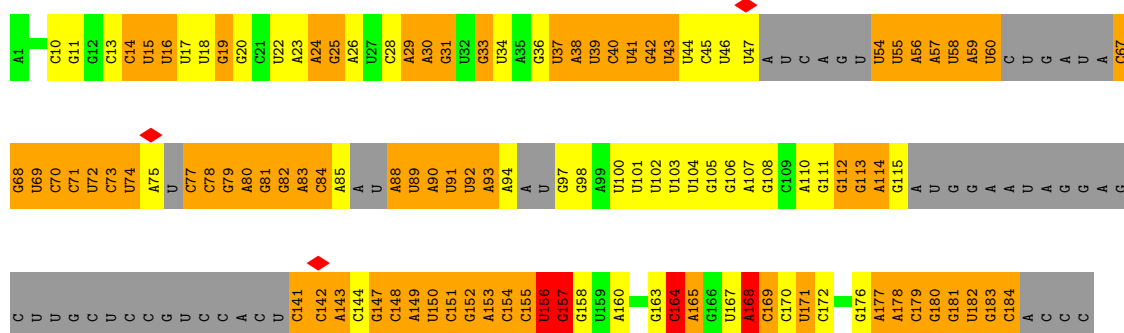
• Molecule 7: Pre-mRNA

Chain G: 7% 6% 10% 24% 7% 53%



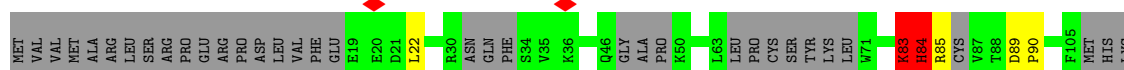
• Molecule 8: U2 snRNA

Chain H: 12% 22% 38% . 26%

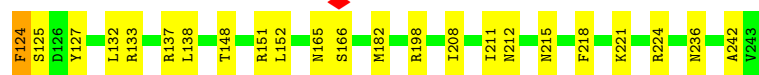


• Molecule 9: Pre-mRNA-splicing factor SYF1

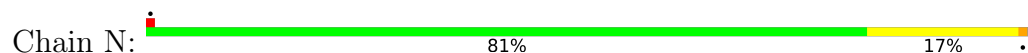
Chain I: 59% 11% . 28%



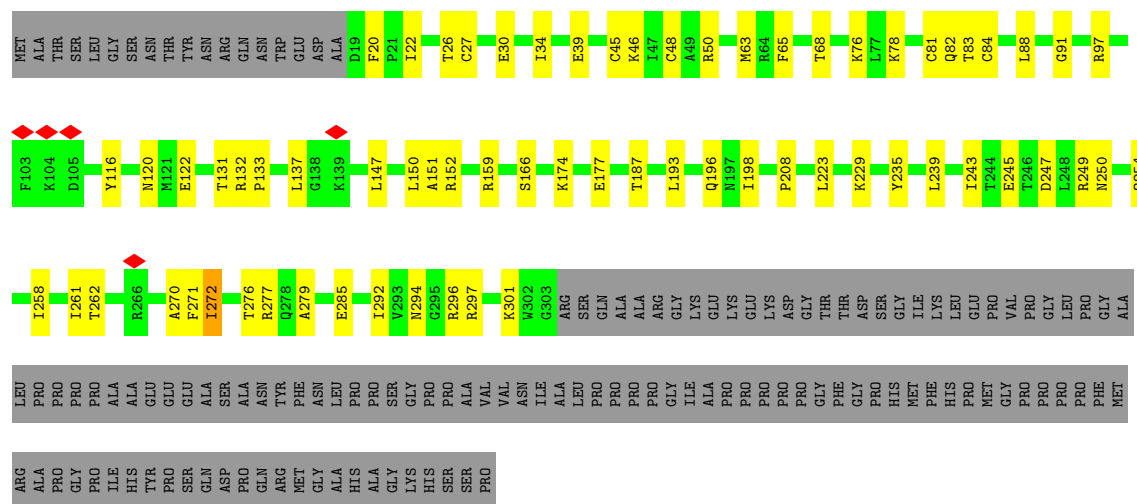
MET	ALA	ALA	ALA	ILE	ALA	ALA	SER	GLU	VAL	LEU	VAL	ASP	SER	ALA	GLU	GLU	SER	GLY	LEU	ALA	ALA	ALA	ALA	GLU	LYS	ARG	GLU	GLN	ARG	LEU	LYS	PHE	ARG	GLU	LEU	HIS	LEU	MET	ASN	ASN	GLN	GLU	VAL	VAL	GLU	ASP	LYS
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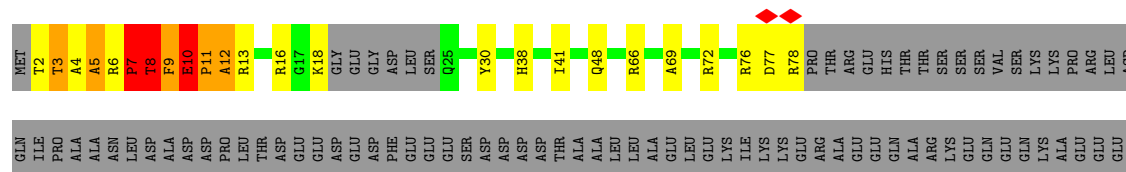
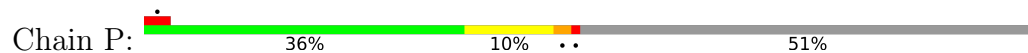
- Molecule 14: Protein BUD31 homolog



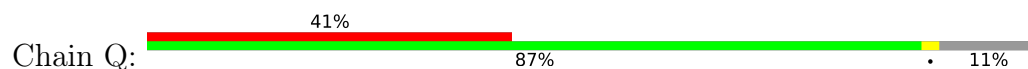
- Molecule 15: Pre-mRNA-splicing factor RBM22



- Molecule 16: Spliceosome-associated protein CWC15 homolog



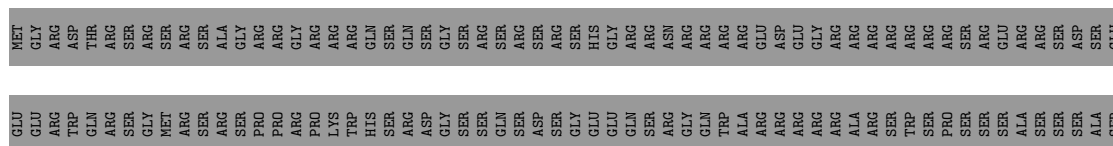
- Molecule 17: RNA helicase aquarius

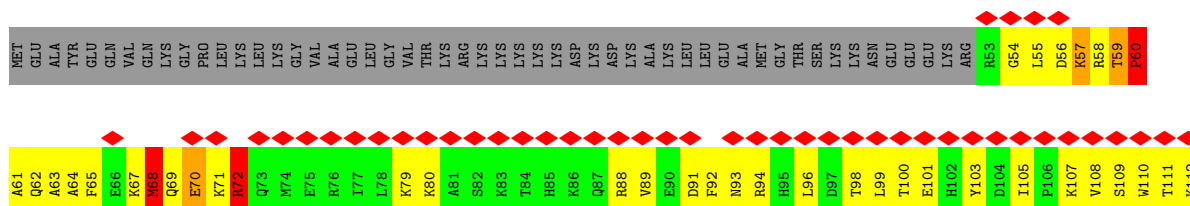
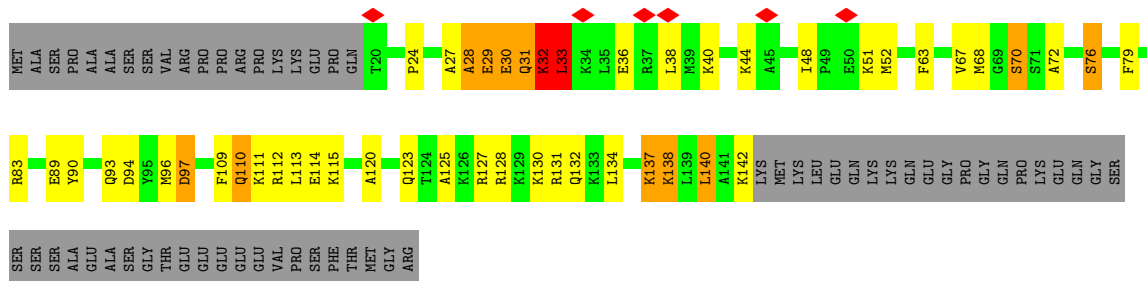
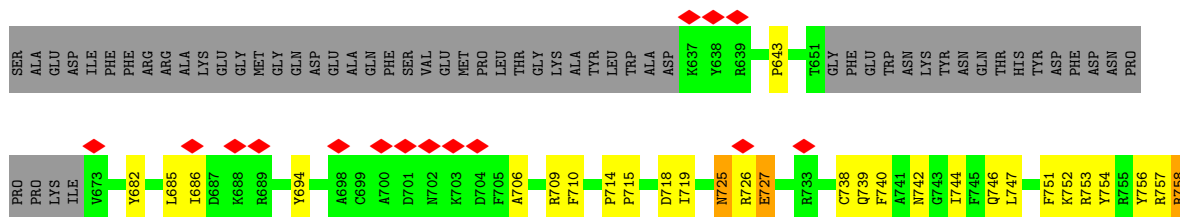


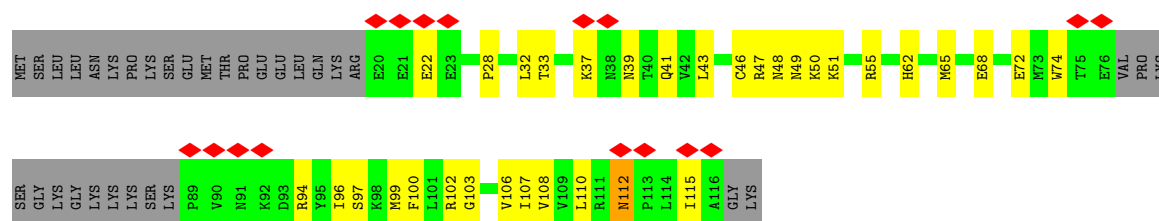
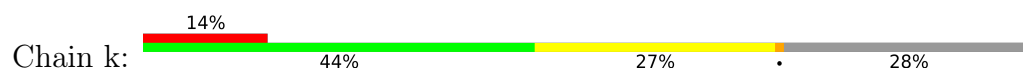




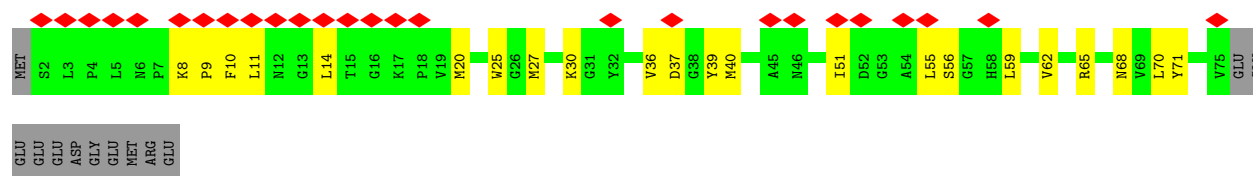
- Molecule 26: Cactin



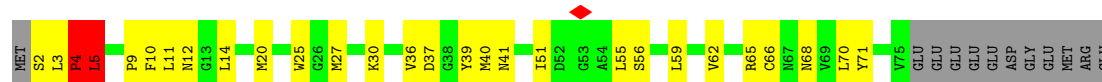




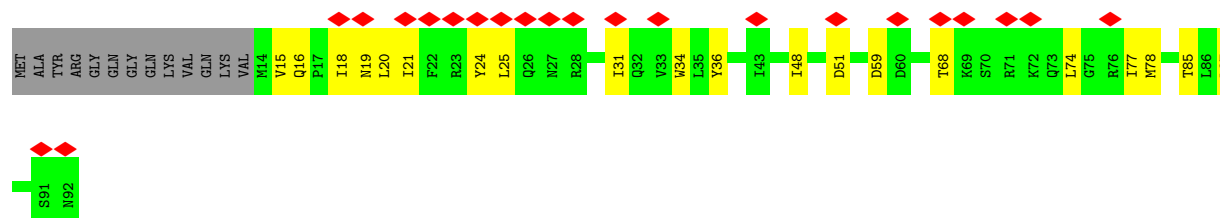
• Molecule 34: Small nuclear ribonucleoprotein F



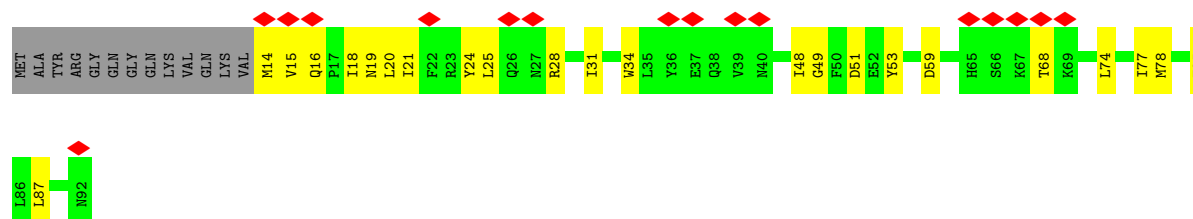
• Molecule 34: Small nuclear ribonucleoprotein F



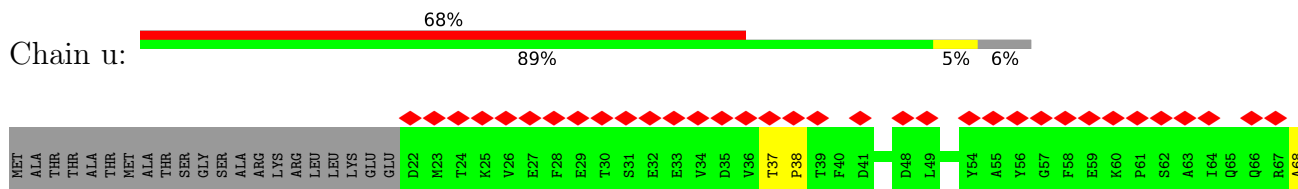
• Molecule 35: Small nuclear ribonucleoprotein E



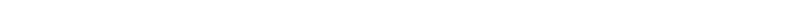
• Molecule 35: Small nuclear ribonucleoprotein E

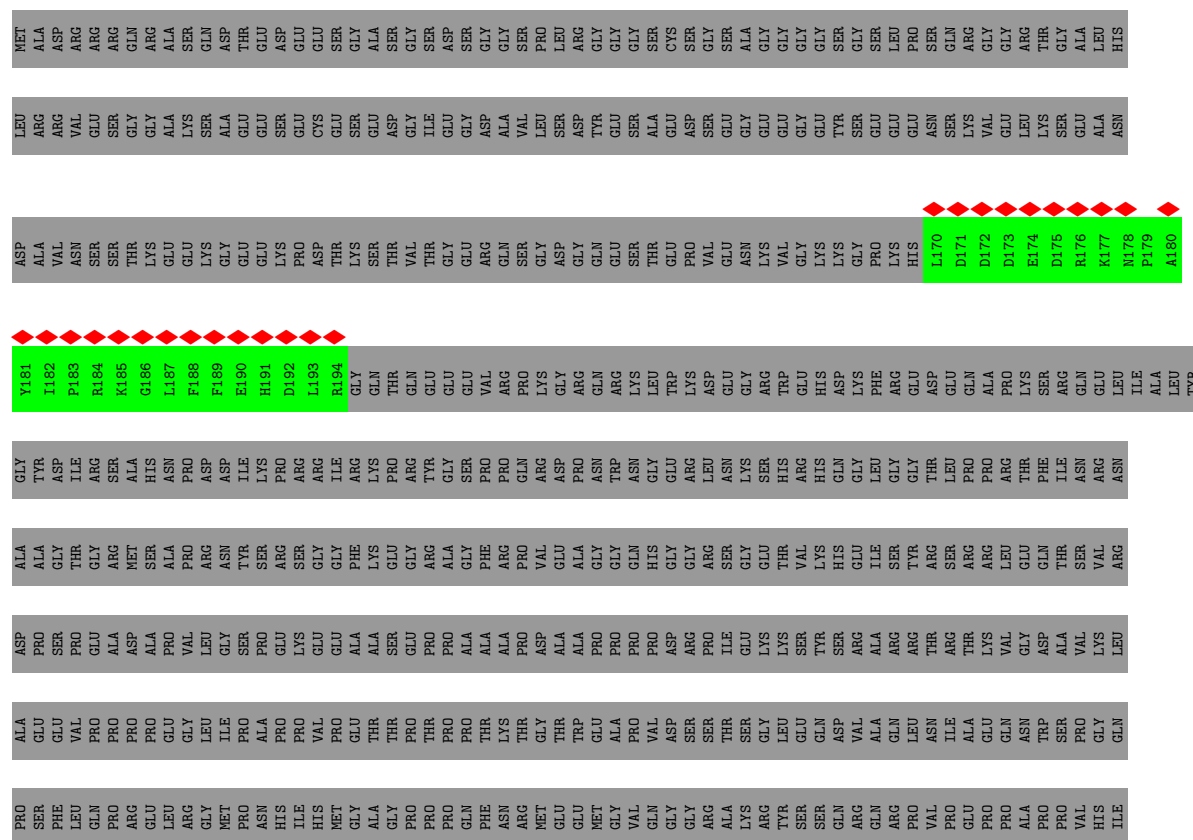


• Molecule 36: Small nuclear ribonucleoprotein G

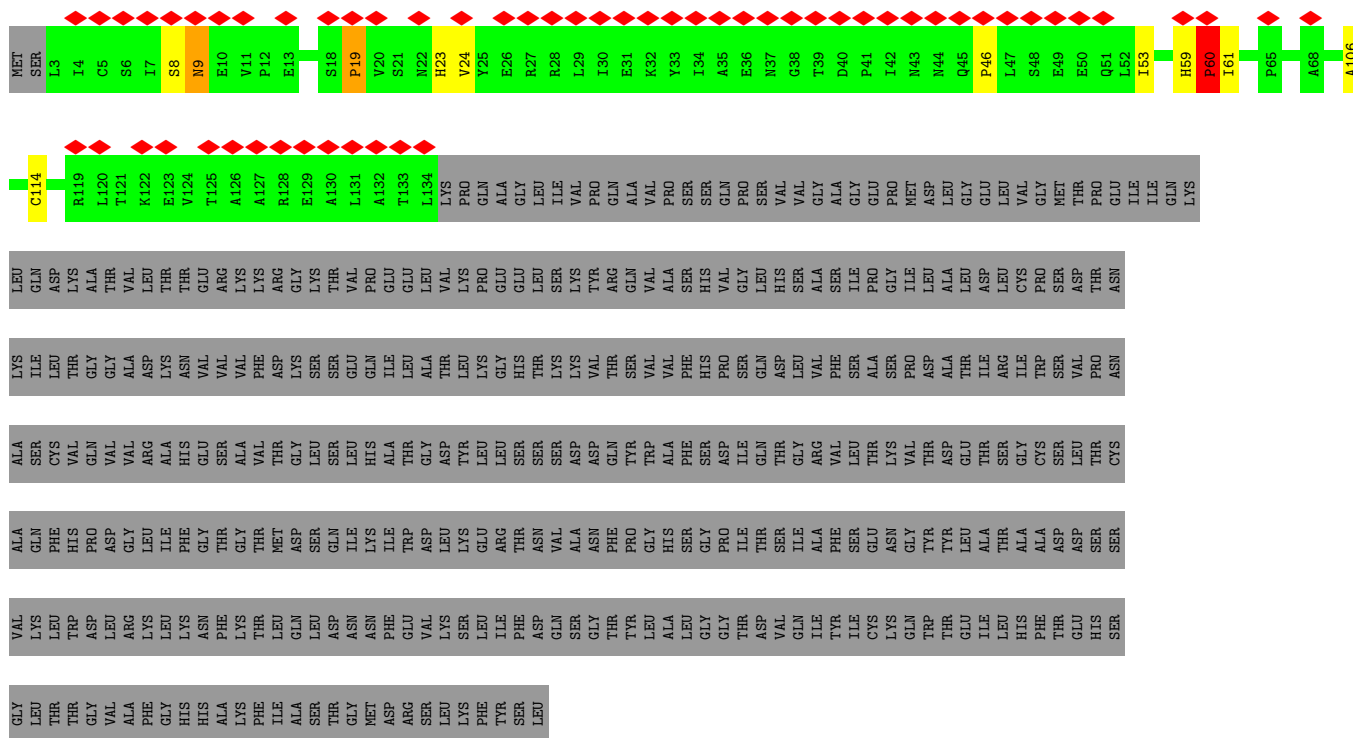


- Molecule 40: Protein CASC3

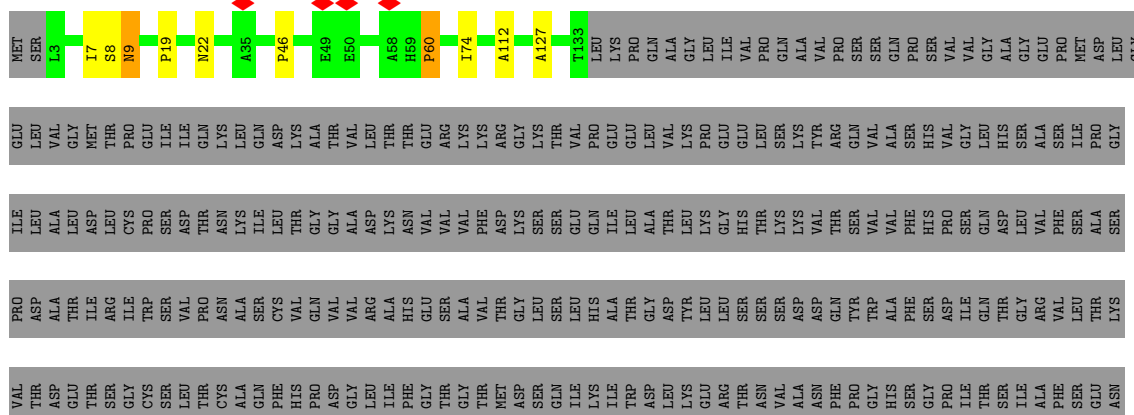
Chain x:  96%

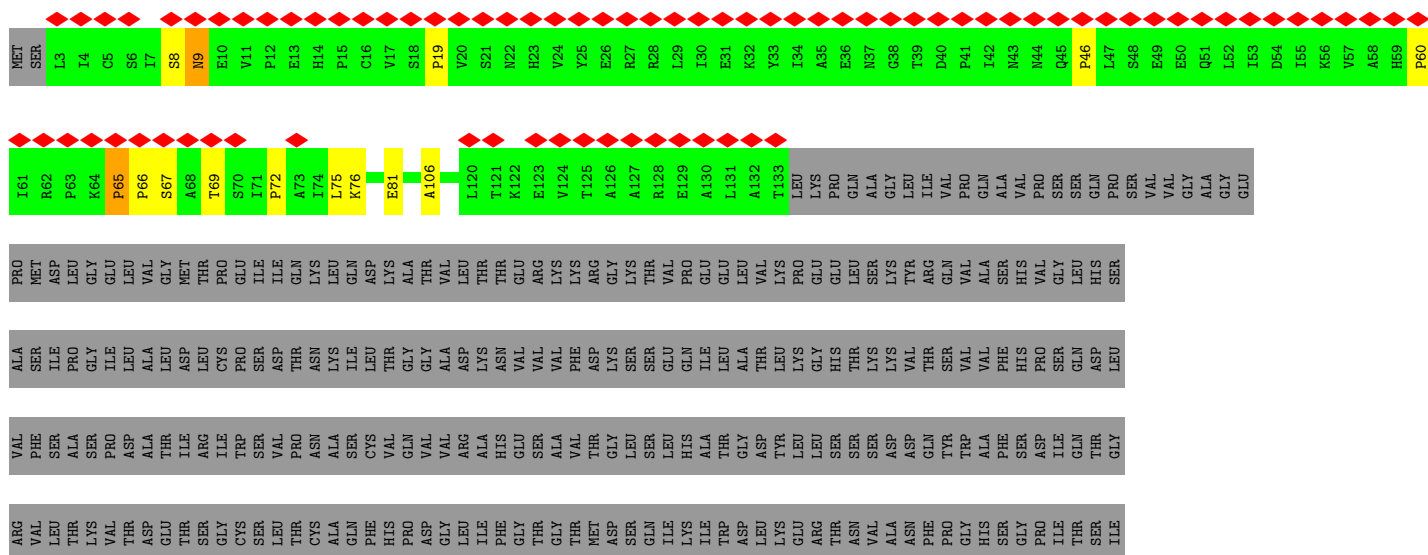


- Molecule 41: Pre-mRNA-processing factor 19

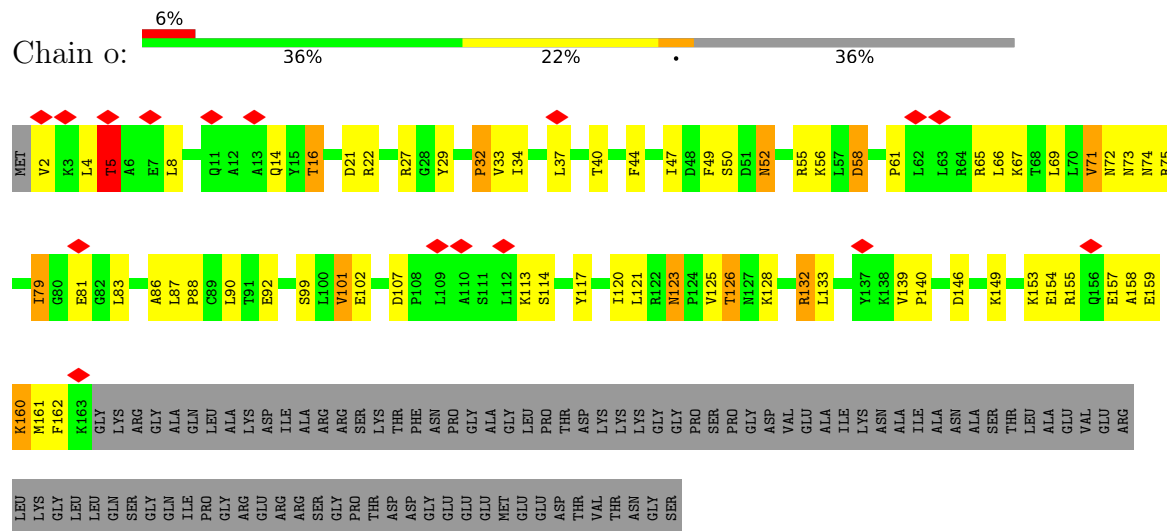


- Molecule 41: Pre-mRNA-processing factor 19

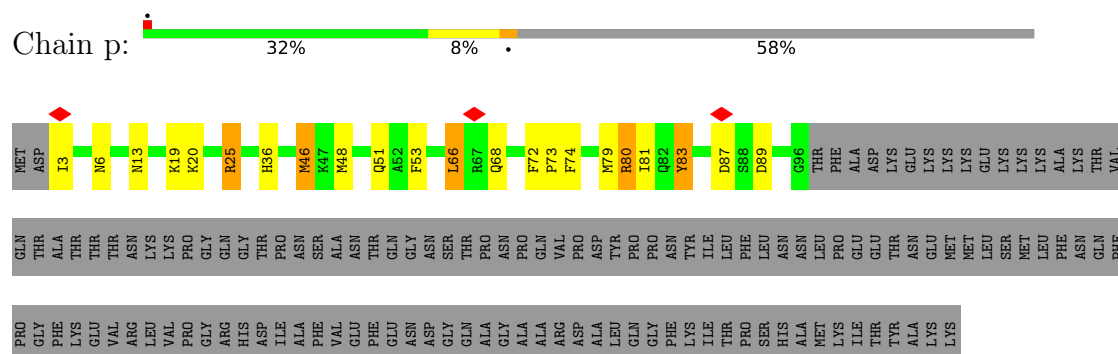




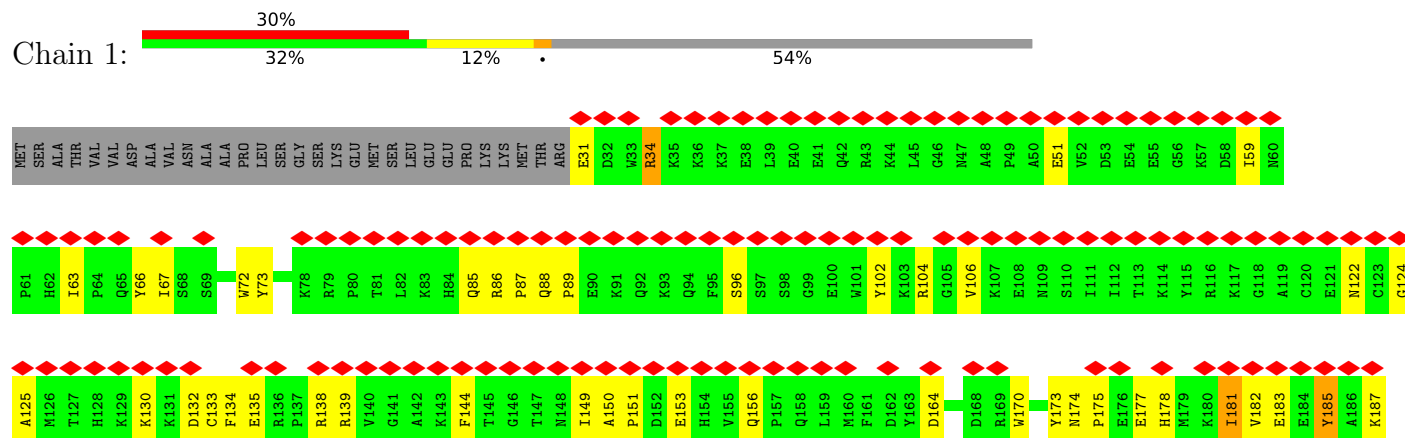
- Molecule 42: U2 small nuclear ribonucleoprotein A'



- Molecule 43: U2 small nuclear ribonucleoprotein B''



- Molecule 44: Pre-mRNA-splicing factor SLU7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	212224	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.505	Depositor
Minimum map value	-1.600	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.39	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.94	79/16897 (0.5%)	1.20	176/22917 (0.8%)
2	B	0.60	2/1970 (0.1%)	0.82	6/3060 (0.2%)
3	C	0.56	0/6942	0.85	11/9432 (0.1%)
4	E	0.53	0/2392	0.73	0/3242
5	F	0.48	0/2323	0.82	3/3619 (0.1%)
6	4	0.72	0/307	1.00	3/476 (0.6%)
7	G	0.62	2/1674 (0.1%)	1.41	35/2594 (1.3%)
8	H	0.85	26/3305 (0.8%)	1.41	60/5130 (1.2%)
9	I	0.65	0/3884	1.45	29/5301 (0.5%)
10	J	0.57	1/3851 (0.0%)	0.88	16/5227 (0.3%)
11	K	0.59	1/768 (0.1%)	0.98	2/1067 (0.2%)
12	L	0.53	0/3046	0.85	10/4115 (0.2%)
13	M	0.53	0/1119	0.90	6/1497 (0.4%)
14	N	0.66	0/1210	0.80	2/1622 (0.1%)
15	O	0.53	0/2344	0.80	2/3163 (0.1%)
16	P	0.74	1/967 (0.1%)	1.18	13/1285 (1.0%)
17	Q	0.40	0/6565	0.89	1/9143 (0.0%)
18	R	0.80	6/2091 (0.3%)	1.03	11/2809 (0.4%)
19	S	0.48	0/1268	0.75	1/1714 (0.1%)
20	T	0.78	0/2519	0.95	9/3433 (0.3%)
21	U	0.50	0/424	0.85	2/582 (0.3%)
22	V	0.43	0/2642	0.82	0/3602
23	W	0.43	0/4237	0.88	5/5723 (0.1%)
24	X	1.07	1/706 (0.1%)	2.08	23/941 (2.4%)
25	Y	1.00	1/3436 (0.0%)	1.52	24/4774 (0.5%)
26	Z	0.41	1/936 (0.1%)	0.76	0/1258
27	2	0.55	0/1030	1.16	10/1371 (0.7%)
28	z	0.94	2/513 (0.4%)	1.58	8/683 (1.2%)
29	b	0.77	0/797	1.05	4/1062 (0.4%)
29	i	0.72	0/700	1.03	4/933 (0.4%)
30	y	1.30	2/389 (0.5%)	1.65	5/540 (0.9%)
31	a	0.64	0/616	0.85	0/830

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	h	0.66	0/639	0.86	0/857
32	c	0.74	0/657	0.98	0/888
32	j	0.74	0/657	0.98	0/888
33	d	0.94	1/786 (0.1%)	1.10	2/1053 (0.2%)
33	k	0.95	0/696	1.07	1/935 (0.1%)
34	f	1.04	1/588 (0.2%)	1.08	0/795
34	m	1.05	1/584 (0.2%)	1.14	1/791 (0.1%)
35	e	0.84	0/660	1.06	1/886 (0.1%)
35	l	0.85	0/660	1.06	1/886 (0.1%)
36	g	0.71	0/584	0.95	1/779 (0.1%)
36	n	0.71	0/548	1.03	2/729 (0.3%)
37	v	0.47	0/710	1.03	3/987 (0.3%)
38	w	0.47	0/444	1.20	4/614 (0.7%)
39	u	0.51	0/1906	1.20	13/2653 (0.5%)
40	x	0.53	0/123	1.13	0/170
41	q	0.62	0/658	1.04	3/919 (0.3%)
41	r	0.57	0/653	1.00	3/912 (0.3%)
41	s	0.60	0/658	1.11	4/919 (0.4%)
41	t	0.62	0/653	0.94	3/912 (0.3%)
42	o	0.81	0/1299	2.06	56/1761 (3.2%)
43	p	0.78	0/774	1.71	12/1035 (1.2%)
44	l	0.40	0/2247	0.84	9/3024 (0.3%)
All	All	0.71	128/99052 (0.1%)	1.10	600/136538 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	21
3	C	0	9
4	E	0	1
9	I	0	7
10	J	0	5
14	N	0	4
15	O	0	1
16	P	0	3
18	R	0	7
20	T	0	3
23	W	0	2
27	2	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	d	0	1
33	k	0	1
All	All	0	66

All (128) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	y	38	PRO	N-CA	20.50	1.71	1.47
1	A	1724	PRO	N-CA	16.51	1.68	1.47
28	z	60	PRO	N-CA	16.09	1.68	1.47
1	A	1955	LYS	C-N	14.36	1.51	1.34
18	R	223	PRO	N-CA	13.60	1.67	1.47
25	Y	426	LEU	C-N	10.94	1.52	1.34
1	A	1534	PHE	C-O	-10.79	1.11	1.24
1	A	1535	THR	C-O	-10.34	1.11	1.24
1	A	1883	VAL	C-N	10.30	1.46	1.33
30	y	37	ILE	C-N	9.95	1.46	1.33
18	R	219	PRO	C-O	-9.88	1.11	1.23
18	R	222	PRO	C-O	-9.57	1.13	1.24
1	A	771	VAL	C-O	-9.52	1.13	1.24
1	A	1536	LEU	C-O	-9.44	1.13	1.24
1	A	1537	TRP	C-O	-9.29	1.13	1.24
1	A	776	LEU	C-O	-9.08	1.12	1.24
1	A	773	LYS	C-O	-8.74	1.13	1.24
1	A	854	SER	C-O	-8.34	1.14	1.23
1	A	244	GLN	C-O	-8.29	1.14	1.24
1	A	1745	GLU	C-O	-8.28	1.14	1.24
1	A	1552	GLN	C-O	-8.23	1.13	1.24
1	A	1574	ILE	C-O	-8.01	1.14	1.24
1	A	1572	SER	CA-CB	-7.98	1.40	1.53
1	A	1747	ILE	C-O	-7.98	1.15	1.24
1	A	1584	LYS	C-O	-7.95	1.14	1.24
1	A	1569	LEU	C-O	-7.77	1.14	1.24
8	H	142	C	C1'-N1	7.66	1.59	1.48
8	H	77	C	C1'-N1	7.65	1.59	1.48
1	A	775	ASN	C-O	-7.52	1.14	1.24
1	A	1163	ARG	C-O	-7.45	1.15	1.24
1	A	663	ARG	C-O	-7.44	1.14	1.23
1	A	1135	PRO	C-O	-7.41	1.14	1.24
2	B	103	G	C1'-N9	-7.25	1.37	1.48
8	H	55	U	C1'-N1	7.20	1.59	1.48
8	H	72	U	C1'-N1	7.20	1.59	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	54	U	C1'-N1	7.17	1.59	1.48
8	H	92	U	C1'-N1	7.16	1.59	1.48
8	H	74	U	C1'-N1	7.13	1.59	1.48
8	H	60	U	C1'-N1	7.10	1.59	1.48
8	H	89	U	C1'-N1	7.09	1.59	1.48
8	H	69	U	C1'-N1	7.09	1.59	1.48
8	H	58	U	C1'-N1	7.08	1.59	1.48
8	H	91	U	C1'-N1	7.06	1.59	1.48
8	H	182	U	C1'-N1	6.98	1.58	1.48
8	H	150	U	C1'-N1	6.98	1.58	1.48
1	A	1563	HIS	C-O	-6.95	1.15	1.23
1	A	1587	GLU	C-O	-6.85	1.16	1.24
7	G	21	A	O3'-P	-6.74	1.51	1.61
16	P	11	PRO	C-O	-6.72	1.16	1.23
1	A	1459	ARG	C-O	-6.72	1.15	1.24
8	H	151	C	C1'-N1	6.69	1.58	1.48
8	H	97	G	C1'-N9	-6.67	1.38	1.48
8	H	73	C	C1'-N1	6.67	1.58	1.48
1	A	772	CYS	C-O	-6.66	1.16	1.24
1	A	1568	THR	C-O	-6.65	1.15	1.24
8	H	141	C	C1'-N1	6.63	1.58	1.48
1	A	1740	LEU	C-O	-6.63	1.16	1.24
8	H	184	C	C1'-N1	6.59	1.58	1.48
8	H	67	C	C1'-N1	6.57	1.58	1.48
8	H	71	C	C1'-N1	6.54	1.58	1.48
8	H	148	C	C1'-N1	6.53	1.58	1.48
1	A	864	LEU	C-O	-6.50	1.16	1.24
8	H	70	C	C1'-N1	6.48	1.58	1.48
8	H	78	C	C1'-N1	6.47	1.58	1.48
8	H	84	C	C1'-N1	6.47	1.58	1.48
1	A	1570	LYS	C-O	-6.43	1.16	1.24
1	A	1880	PRO	C-O	-6.41	1.16	1.23
1	A	168	PRO	C-O	-6.39	1.15	1.24
1	A	1730	MET	C-O	-6.37	1.16	1.24
1	A	860	GLN	C-O	-6.30	1.16	1.24
26	Z	714	PRO	C-N	6.24	1.39	1.33
18	R	226	PRO	C-O	-6.23	1.16	1.23
1	A	1521	ALA	C-O	6.20	1.32	1.24
1	A	1558	THR	C-O	-6.17	1.16	1.23
1	A	863	GLU	C-O	-6.12	1.17	1.24
1	A	167	PRO	C-O	-6.09	1.17	1.24
1	A	1809	ILE	C-O	-6.05	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	859	SER	C-O	-6.03	1.17	1.24
1	A	1741	TYR	C-O	-6.01	1.17	1.24
1	A	1892	PRO	C-O	-6.00	1.16	1.24
1	A	167	PRO	N-CD	-5.96	1.39	1.47
1	A	861	ARG	C-O	-5.94	1.17	1.24
7	G	98	U	O3'-P	-5.82	1.52	1.61
1	A	1562	MET	C-O	-5.79	1.17	1.24
24	X	76	LYS	C-O	-5.76	1.17	1.24
1	A	1592	ASP	C-O	-5.74	1.17	1.24
1	A	669	ALA	C-O	-5.69	1.16	1.24
1	A	1532	ARG	C-O	-5.65	1.17	1.24
1	A	1748	ARG	C-O	-5.63	1.16	1.24
1	A	1726	ILE	C-O	-5.62	1.17	1.24
1	A	1583	GLN	C-O	-5.58	1.17	1.24
1	A	1744	ARG	C-O	-5.56	1.17	1.24
1	A	1576	ILE	C-O	-5.55	1.17	1.24
8	H	110	A	C1'-N9	-5.50	1.39	1.48
1	A	862	GLU	C-O	-5.49	1.17	1.24
18	R	222	PRO	C-N	5.46	1.43	1.34
1	A	821	ARG	C-O	-5.44	1.15	1.23
1	A	1595	GLN	C-O	-5.43	1.17	1.24
1	A	1743	LEU	C-O	-5.41	1.17	1.24
1	A	1738	PRO	C-O	-5.41	1.17	1.24
1	A	1573	LEU	C-O	-5.37	1.17	1.24
1	A	1861	ILE	C-O	-5.37	1.18	1.24
1	A	668	VAL	C-O	-5.37	1.17	1.24
11	K	162	ASP	CA-CB	-5.34	1.44	1.53
10	J	551	PRO	C-O	-5.32	1.17	1.24
1	A	1753	LEU	C-O	-5.32	1.17	1.24
1	A	165	ARG	C-O	-5.30	1.17	1.23
1	A	866	LEU	C-O	-5.28	1.17	1.24
1	A	859	SER	CA-CB	-5.26	1.45	1.53
1	A	1529	ILE	CA-CB	-5.23	1.51	1.54
1	A	1858	PRO	C-O	-5.19	1.18	1.23
1	A	1882	ILE	C-O	-5.17	1.18	1.24
1	A	1579	ALA	C-O	-5.16	1.16	1.23
18	R	220	ARG	C-O	-5.16	1.17	1.23
28	z	60	PRO	C-O	-5.14	1.17	1.24
1	A	1811	ASN	C-O	-5.12	1.18	1.24
34	f	14	LEU	CA-C	5.11	1.59	1.52
1	A	1746	ARG	C-O	-5.11	1.18	1.24
1	A	1554	GLN	C-O	-5.10	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	774	LYS	C-O	-5.10	1.18	1.24
1	A	1494	TYR	C-O	-5.10	1.17	1.24
1	A	1553	VAL	C-O	-5.09	1.18	1.24
1	A	1526	LEU	C-O	5.07	1.30	1.24
1	A	1560	ILE	C-O	-5.05	1.18	1.24
34	m	14	LEU	CA-C	5.04	1.59	1.52
1	A	1531	ASN	C-O	-5.02	1.18	1.24
2	B	96	A	C1'-N9	-5.02	1.40	1.48
33	d	73	MET	CA-C	-5.02	1.46	1.52

All (600) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	y	37	ILE	CA-C-N	18.84	139.11	119.90
30	y	37	ILE	C-N-CA	18.84	139.11	119.90
1	A	1883	VAL	CA-C-N	-18.75	98.16	123.10
1	A	1883	VAL	C-N-CA	-18.75	98.16	123.10
7	G	1	G	C1'-C2'-O2'	-16.54	86.99	111.80
28	z	59	THR	CA-C-N	15.96	139.79	119.84
28	z	59	THR	C-N-CA	15.96	139.79	119.84
1	A	1741	TYR	CB-CA-C	-14.93	86.00	110.79
1	A	775	ASN	CA-CB-CG	-14.38	98.22	112.60
1	A	1534	PHE	CB-CA-C	-13.60	88.22	110.79
42	o	55	ARG	CD-NE-CZ	13.16	142.82	124.40
1	A	1723	LYS	CA-C-N	13.11	136.22	119.84
1	A	1723	LYS	C-N-CA	13.11	136.22	119.84
1	A	1874	VAL	O-C-N	13.04	133.58	121.98
1	A	1571	ILE	CB-CA-C	-12.89	95.47	111.97
27	2	29	GLU	CB-CA-C	12.83	132.66	110.85
1	A	1515	TRP	N-CA-C	-12.81	97.30	111.14
7	G	130	G	C4'-C3'-O3'	12.59	131.89	113.00
7	G	84	U	C2'-C3'-O3'	-12.12	95.52	113.70
1	A	1587	GLU	CB-CA-C	-12.09	91.90	110.88
9	I	84	HIS	O-C-N	-12.04	109.67	122.07
9	I	83	LYS	O-C-N	-12.03	109.68	122.07
9	I	311	MET	O-C-N	-12.02	109.69	122.07
9	I	310	LYS	O-C-N	-12.00	109.71	122.07
9	I	309	ALA	O-C-N	-11.89	109.83	122.07
1	A	1584	LYS	CB-CA-C	-11.65	91.04	110.85
1	A	1561	PHE	CB-CA-C	-11.63	89.84	109.50
1	A	167	PRO	CA-N-CD	-11.62	95.73	112.00
24	X	107	GLU	CB-CA-C	-11.60	92.67	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	o	49	PHE	CA-CB-CG	11.43	125.23	113.80
24	X	115	TYR	CB-CA-C	11.42	130.26	110.85
24	X	96	GLN	CB-CA-C	-11.33	91.98	110.79
18	R	226	PRO	CB-CA-C	-11.14	97.08	111.46
25	Y	420	ASP	CB-CA-C	-11.13	90.92	110.95
1	A	1744	ARG	CB-CA-C	-11.05	92.44	110.79
1	A	772	CYS	CA-CB-SG	-11.01	89.08	114.40
1	A	1620	TYR	CA-C-N	-10.78	105.26	122.73
1	A	1620	TYR	C-N-CA	-10.78	105.26	122.73
39	u	37	THR	CA-C-N	10.62	130.39	119.56
39	u	37	THR	C-N-CA	10.62	130.39	119.56
1	A	1530	PRO	CA-N-CD	-10.59	97.17	112.00
1	A	1744	ARG	CB-CG-CD	-10.55	87.02	111.30
38	w	114	LYS	N-CA-C	-10.44	93.71	110.20
1	A	1535	THR	CB-CA-C	-10.13	93.62	110.85
7	G	98	U	C3'-C2'-O2'	10.00	125.70	110.70
1	A	1955	LYS	CA-C-N	9.96	129.62	119.56
1	A	1955	LYS	C-N-CA	9.96	129.62	119.56
2	B	104	C	C2'-C3'-O3'	-9.95	94.57	109.50
1	A	1497	THR	CA-CB-OG1	-9.93	94.71	109.60
1	A	1883	VAL	CA-C-O	-9.92	109.73	121.04
9	I	458	LYS	O-C-N	9.78	132.14	122.07
1	A	1878	ASP	N-CA-C	-9.77	100.59	111.14
9	I	459	ALA	O-C-N	9.66	132.02	122.07
9	I	457	ARG	O-C-N	9.56	131.92	122.07
7	G	124	G	C2'-C3'-O3'	9.55	123.83	109.50
27	2	63	PHE	CB-CA-C	-9.47	96.79	110.62
1	A	1724	PRO	N-CA-C	-9.46	92.97	112.47
41	s	46	PRO	N-CA-CB	9.43	111.19	103.36
7	G	98	U	C2'-C3'-O3'	-9.31	99.73	113.70
1	A	1535	THR	CA-CB-OG1	-9.30	95.65	109.60
7	G	127	G	C4'-C3'-O3'	9.28	126.91	113.00
42	o	58	ASP	CA-CB-CG	9.10	121.70	112.60
1	A	166	PHE	CA-CB-CG	-9.09	104.71	113.80
1	A	383	PHE	N-CA-C	-8.98	102.91	114.04
25	Y	425	ILE	N-CA-C	8.97	119.78	110.72
1	A	1754	TYR	CB-CA-C	-8.96	93.61	111.17
1	A	342	THR	CB-CA-C	-8.91	94.94	109.72
12	L	124	LYS	N-CA-C	8.90	124.28	112.35
28	z	64	ALA	CA-C-O	-8.88	111.13	120.55
7	G	125	C	C4'-C3'-O3'	8.83	122.65	109.40
2	B	12	U	C4'-C3'-O3'	8.79	122.58	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	458	LYS	CA-C-O	-8.77	111.61	120.82
1	A	167	PRO	N-CA-C	-8.76	100.02	110.70
44	1	272	ALA	CA-C-N	8.75	132.34	120.44
44	1	272	ALA	C-N-CA	8.75	132.34	120.44
25	Y	687	ALA	CA-C-N	8.75	133.94	120.82
25	Y	687	ALA	C-N-CA	8.75	133.94	120.82
28	z	60	PRO	CA-N-CD	-8.72	99.80	112.00
41	r	46	PRO	N-CA-CB	8.72	111.11	103.27
8	H	82	G	O3'-P-O5'	-8.69	90.96	104.00
8	H	183	G	O3'-P-O5'	-8.67	91.00	104.00
8	H	77	C	O3'-P-O5'	-8.63	91.05	104.00
8	H	59	A	O3'-P-O5'	-8.63	91.05	104.00
8	H	68	G	O3'-P-O5'	-8.63	91.05	104.00
8	H	141	C	O3'-P-O5'	-8.63	91.05	104.00
8	H	113	G	O3'-P-O5'	-8.63	91.06	104.00
8	H	56	A	O3'-P-O5'	-8.62	91.07	104.00
8	H	91	U	O3'-P-O5'	-8.62	91.07	104.00
8	H	78	C	O3'-P-O5'	-8.62	91.07	104.00
9	I	459	ALA	CA-C-O	-8.61	111.78	120.82
8	H	150	U	O3'-P-O5'	-8.61	91.09	104.00
8	H	148	C	O3'-P-O5'	-8.61	91.09	104.00
8	H	54	U	O3'-P-O5'	-8.60	91.10	104.00
8	H	73	C	O3'-P-O5'	-8.60	91.10	104.00
8	H	182	U	O3'-P-O5'	-8.60	91.10	104.00
8	H	74	U	O3'-P-O5'	-8.60	91.10	104.00
8	H	180	G	O3'-P-O5'	-8.60	91.10	104.00
8	H	57	A	O3'-P-O5'	-8.59	91.12	104.00
8	H	90	A	O3'-P-O5'	-8.59	91.12	104.00
8	H	181	G	O3'-P-O5'	-8.59	91.12	104.00
8	H	93	A	O3'-P-O5'	-8.58	91.12	104.00
7	G	130	G	N9-C1'-C2'	-8.58	99.13	112.00
8	H	81	G	O3'-P-O5'	-8.58	91.13	104.00
8	H	72	U	O3'-P-O5'	-8.58	91.14	104.00
9	I	457	ARG	CA-C-O	-8.58	111.81	120.82
8	H	69	U	O3'-P-O5'	-8.57	91.14	104.00
8	H	89	U	O3'-P-O5'	-8.57	91.14	104.00
8	H	55	U	O3'-P-O5'	-8.57	91.15	104.00
8	H	79	G	O3'-P-O5'	-8.57	91.15	104.00
8	H	80	A	O3'-P-O5'	-8.56	91.16	104.00
8	H	149	A	O3'-P-O5'	-8.56	91.16	104.00
8	H	84	C	O3'-P-O5'	-8.56	91.17	104.00
8	H	58	U	O3'-P-O5'	-8.55	91.17	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	67	C	O3'-P-O5'	-8.55	91.17	104.00
8	H	92	U	O3'-P-O5'	-8.55	91.17	104.00
8	H	71	C	O3'-P-O5'	-8.54	91.18	104.00
8	H	83	A	O3'-P-O5'	-8.53	91.20	104.00
8	H	114	A	O3'-P-O5'	-8.53	91.20	104.00
8	H	88	A	O3'-P-O5'	-8.53	91.20	104.00
42	o	5	THR	N-CA-CB	-8.53	98.26	111.05
1	A	1583	GLN	CB-CA-C	-8.52	96.64	110.79
12	L	9	GLY	CA-C-N	8.52	137.31	121.97
12	L	9	GLY	C-N-CA	8.52	137.31	121.97
8	H	70	C	O3'-P-O5'	-8.50	91.25	104.00
41	q	46	PRO	N-CA-CB	8.49	111.24	103.34
7	G	124	G	C3'-C2'-O2'	8.48	127.32	114.60
1	A	1502	PHE	CA-C-N	8.40	137.58	121.54
1	A	1502	PHE	C-N-CA	8.40	137.58	121.54
36	n	10	LYS	CB-CA-C	8.36	126.10	110.63
27	2	110	GLN	CB-CA-C	-8.33	97.80	110.88
43	p	80	ARG	CD-NE-CZ	8.28	135.99	124.40
7	G	1	G	C4'-C3'-O3'	8.26	121.80	109.40
24	X	108	GLU	CB-CA-C	-8.26	97.91	110.88
6	4	-12	G	N9-C1'-C2'	-8.23	99.66	112.00
28	z	64	ALA	CA-C-N	-8.19	106.57	120.58
28	z	64	ALA	C-N-CA	-8.19	106.57	120.58
1	A	166	PHE	CA-C-N	8.18	128.81	120.38
1	A	166	PHE	C-N-CA	8.18	128.81	120.38
44	l	273	LYS	CB-CA-C	-8.17	97.99	110.90
41	s	60	PRO	N-CA-CB	8.17	111.83	103.25
1	A	1530	PRO	N-CA-CB	8.16	112.20	103.39
25	Y	1040	GLY	N-CA-C	8.15	122.82	111.25
7	G	1	G	N9-C1'-C2'	-8.11	101.84	114.00
42	o	16	THR	CA-C-O	-8.05	111.75	120.36
24	X	66	GLN	CB-CA-C	-7.92	98.45	110.88
24	X	103	GLN	CB-CA-C	-7.92	98.45	110.88
1	A	861	ARG	CG-CD-NE	-7.91	94.59	112.00
42	o	99	SER	N-CA-C	7.89	122.68	112.26
1	A	1533	ARG	CB-CG-CD	7.89	129.45	111.30
42	o	47	ILE	N-CA-CB	7.89	123.04	111.52
1	A	1532	ARG	CA-C-O	-7.88	112.19	120.55
20	T	187	LYS	CA-C-N	7.88	129.69	119.84
20	T	187	LYS	C-N-CA	7.88	129.69	119.84
12	L	54	LEU	N-CA-C	7.88	119.86	111.28
1	A	1537	TRP	CB-CA-C	7.86	123.07	110.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	7	PRO	CA-C-N	7.86	136.55	121.54
16	P	7	PRO	C-N-CA	7.86	136.55	121.54
7	G	21	A	O3'-P-O5'	7.80	115.71	104.00
1	A	1874	VAL	CA-C-N	7.79	130.71	120.28
1	A	1874	VAL	C-N-CA	7.79	130.71	120.28
42	o	117	TYR	CA-C-O	7.69	128.48	120.40
17	Q	1379	TYR	N-CA-C	7.68	122.74	112.30
7	G	130	G	C1'-C2'-O2'	-7.66	96.91	108.40
13	M	120	PRO	CB-CA-C	-7.65	99.43	110.75
1	A	1574	ILE	CA-C-O	-7.59	113.06	120.95
8	H	168	A	P-O5'-C5'	-7.59	109.52	120.90
18	R	223	PRO	CA-N-CD	-7.57	101.40	112.00
24	X	89	PHE	CA-CB-CG	-7.54	106.26	113.80
1	A	1875	HIS	CA-CB-CG	-7.54	106.26	113.80
1	A	162	LYS	CB-CA-C	-7.52	97.86	109.89
6	4	-12	G	C4'-C3'-O3'	7.52	124.28	113.00
1	A	1514	LYS	CA-C-N	-7.51	110.22	120.44
1	A	1514	LYS	C-N-CA	-7.51	110.22	120.44
41	q	60	PRO	N-CA-CB	7.45	111.07	103.25
1	A	866	LEU	CA-C-N	7.44	132.45	120.55
1	A	866	LEU	C-N-CA	7.44	132.45	120.55
9	I	723	MET	N-CA-C	-7.43	103.19	111.28
3	C	823	ALA	N-CA-C	7.42	120.50	108.34
1	A	1879	PHE	CB-CA-C	-7.40	102.85	110.17
1	A	664	HIS	CA-CB-CG	-7.38	106.42	113.80
2	B	20	G	N9-C1'-C2'	7.38	125.06	114.00
1	A	1898	LYS	N-CA-C	-7.36	103.87	112.92
1	A	863	GLU	CB-CG-CD	-7.35	100.10	112.60
1	A	167	PRO	CB-CA-C	7.35	119.88	110.92
11	K	90	PRO	N-CA-CB	7.34	111.07	103.00
7	G	124	G	C1'-C2'-O2'	7.29	122.74	111.80
8	H	22	U	C2'-C3'-O3'	-7.29	102.76	113.70
7	G	119	A	C2'-C3'-O3'	-7.27	98.60	109.50
1	A	1954	LEU	CA-C-N	-7.26	114.75	122.89
1	A	1954	LEU	C-N-CA	-7.26	114.75	122.89
8	H	167	U	O3'-P-O5'	-7.25	93.12	104.00
11	K	78	PRO	N-CA-CB	7.25	110.87	103.25
42	o	71	VAL	CA-C-N	7.22	131.65	120.75
42	o	71	VAL	C-N-CA	7.22	131.65	120.75
8	H	31	G	N9-C1'-C2'	-7.21	101.18	112.00
41	t	60	PRO	N-CA-CB	7.17	111.33	103.30
7	G	129	U	C3'-C2'-O2'	7.16	121.44	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	663	ARG	CG-CD-NE	-7.16	96.26	112.00
1	A	158	ARG	CB-CA-C	-7.12	98.79	109.90
39	u	77	ASP	N-CA-C	-7.12	99.74	110.28
42	o	21	ASP	CA-CB-CG	7.12	119.72	112.60
7	G	120	G	C2'-C3'-O3'	7.07	120.10	109.50
1	A	1881	ASN	CA-CB-CG	-7.00	105.60	112.60
8	H	170	C	C3'-C2'-O2'	-7.00	104.10	114.60
16	P	8	THR	CA-CB-OG1	-7.00	99.10	109.60
42	o	72	ASN	OD1-CG-ND2	7.00	129.60	122.60
42	o	107	ASP	CA-CB-CG	6.96	119.56	112.60
25	Y	685	ASP	CA-C-N	6.93	134.78	121.54
25	Y	685	ASP	C-N-CA	6.93	134.78	121.54
1	A	343	GLU	CB-CA-C	6.93	123.62	109.55
7	G	120	G	O4'-C1'-N9	-6.92	97.81	108.20
42	o	4	LEU	N-CA-C	-6.91	97.96	108.67
42	o	121	LEU	CA-C-O	6.87	128.86	121.44
1	A	1528	GLN	CB-CG-CD	-6.85	100.96	112.60
7	G	130	G	C2'-C3'-O3'	-6.84	103.44	113.70
42	o	75	ARG	NE-CZ-NH1	-6.83	114.67	121.50
41	t	46	PRO	N-CA-CB	6.82	110.41	103.25
20	T	309	ASP	O-C-N	6.79	131.15	122.39
10	J	675	PRO	N-CA-CB	6.78	110.37	103.25
7	G	121	C	C1'-C2'-O2'	-6.78	98.23	108.40
1	A	1520	ASN	O-C-N	-6.77	114.53	122.32
25	Y	686	GLU	CA-C-N	6.76	134.46	121.54
25	Y	686	GLU	C-N-CA	6.76	134.46	121.54
43	p	53	PHE	CA-C-O	-6.76	112.89	120.32
9	I	697	PRO	CA-C-N	6.75	134.44	121.54
9	I	697	PRO	C-N-CA	6.75	134.44	121.54
10	J	604	PRO	N-CA-CB	6.75	110.33	103.25
16	P	10	GLU	CB-CA-C	6.74	121.65	111.14
42	o	58	ASP	N-CA-CB	-6.73	100.60	111.24
1	A	1499	GLU	N-CA-CB	-6.72	99.93	109.94
1	A	1753	LEU	N-CA-CB	-6.70	99.90	110.69
1	A	1528	GLN	CA-C-N	-6.69	114.98	120.33
1	A	1528	GLN	C-N-CA	-6.69	114.98	120.33
7	G	127	G	C1'-C2'-O2'	-6.69	98.37	108.40
41	q	19	PRO	N-CA-CB	6.68	110.27	103.25
44	l	287	PRO	CB-CA-C	-6.68	102.43	113.06
8	H	164	C	C5'-C4'-O4'	-6.68	99.08	109.10
1	A	1883	VAL	O-C-N	6.68	129.95	122.67
41	r	19	PRO	N-CA-CB	6.68	110.24	102.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	2	28	ALA	CA-C-N	-6.67	110.82	120.29
27	2	28	ALA	C-N-CA	-6.67	110.82	120.29
1	A	1740	LEU	N-CA-C	-6.66	104.03	111.28
1	A	1537	TRP	N-CA-C	6.62	118.19	110.97
25	Y	689	GLU	N-CA-C	-6.61	97.28	108.26
7	G	80	U	C2'-C3'-O3'	-6.59	103.82	113.70
39	u	38	PRO	N-CA-C	6.57	122.39	113.84
1	A	1615	HIS	N-CA-C	-6.57	98.08	109.58
1	A	1967	ILE	CA-C-O	-6.54	114.39	120.34
18	R	219	PRO	CB-CA-C	-6.51	103.44	111.64
1	A	663	ARG	CB-CA-C	-6.51	98.52	109.65
10	J	239	ARG	CA-C-N	6.51	133.97	121.54
10	J	239	ARG	C-N-CA	6.51	133.97	121.54
1	A	1681	ARG	CA-C-O	-6.50	113.61	120.63
1	A	1806	ALA	O-C-N	-6.50	116.47	123.42
27	2	97	ASP	CB-CA-C	-6.49	100.15	110.86
41	t	19	PRO	N-CA-CB	6.49	110.07	103.25
10	J	637	PRO	N-CA-CB	6.49	110.39	103.52
1	A	1745	GLU	CB-CA-C	-6.48	100.04	110.79
28	z	72	ARG	N-CA-C	-6.48	103.81	112.94
7	G	22	C	C4'-C3'-O3'	-6.46	103.30	113.00
2	B	12	U	C2'-C3'-O3'	-6.46	99.81	109.50
42	o	87	LEU	CA-C-N	6.44	126.20	119.05
42	o	87	LEU	C-N-CA	6.44	126.20	119.05
7	G	119	A	C3'-C2'-O2'	6.43	124.25	114.60
1	A	1810	PHE	CA-C-O	-6.43	113.19	120.32
1	A	244	GLN	CB-CG-CD	-6.42	101.68	112.60
1	A	1586	HIS	CA-CB-CG	-6.42	107.39	113.80
13	M	121	ASP	CA-CB-CG	-6.41	106.19	112.60
1	A	775	ASN	CB-CA-C	-6.40	96.93	110.31
1	A	776	LEU	N-CA-C	-6.39	104.97	112.89
41	s	19	PRO	N-CA-CB	6.38	109.95	103.25
10	J	187	VAL	CA-C-N	6.37	133.70	121.54
10	J	187	VAL	C-N-CA	6.37	133.70	121.54
42	o	55	ARG	NE-CZ-NH1	6.35	127.85	121.50
1	A	1518	LEU	N-CA-C	-6.34	100.01	109.15
18	R	222	PRO	CB-CA-C	-6.34	103.19	110.92
1	A	1529	ILE	CA-C-O	-6.32	114.46	118.69
1	A	774	LYS	CB-CA-C	-6.31	100.92	110.90
42	o	40	THR	CA-C-N	6.31	131.55	122.40
42	o	40	THR	C-N-CA	6.31	131.55	122.40
16	P	7	PRO	CB-CA-C	-6.30	101.17	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	1	275	LEU	CA-C-N	-6.29	111.84	120.28
44	1	275	LEU	C-N-CA	-6.29	111.84	120.28
41	r	60	PRO	N-CA-CB	6.29	109.86	103.25
24	X	89	PHE	CB-CA-C	-6.29	101.01	110.88
18	R	124	VAL	CA-C-N	6.29	133.54	121.54
18	R	124	VAL	C-N-CA	6.29	133.54	121.54
9	I	725	ARG	CB-CA-C	-6.27	100.99	110.90
7	G	97	A	C2'-C3'-O3'	6.27	118.90	109.50
8	H	168	A	C5'-C4'-C3'	-6.26	106.61	116.00
1	A	1618	LYS	CB-CA-C	-6.25	97.71	109.72
39	u	68	ALA	N-CA-C	6.25	119.38	111.69
24	X	106	GLU	CA-C-N	-6.25	112.31	120.44
24	X	106	GLU	C-N-CA	-6.25	112.31	120.44
1	A	1922	ASP	CA-CB-CG	-6.25	106.35	112.60
7	G	1	G	C2'-C3'-O3'	6.25	118.87	109.50
10	J	670	PRO	N-CA-CB	6.25	110.44	103.44
7	G	121	C	C3'-C2'-O2'	6.24	120.06	110.70
1	A	1537	TRP	CA-C-O	-6.24	114.45	121.00
2	B	26	A	P-O5'-C5'	-6.24	111.55	120.90
8	H	169	C	P-O3'-C3'	6.23	129.55	120.20
1	A	1864	THR	CB-CA-C	6.23	119.48	109.02
16	P	9	PHE	CA-C-N	-6.22	115.62	123.15
16	P	9	PHE	C-N-CA	-6.22	115.62	123.15
8	H	31	G	C4'-C3'-O3'	6.22	122.33	113.00
24	X	85	ASP	CA-CB-CG	-6.21	106.39	112.60
24	X	29	GLN	N-CA-C	-6.18	104.54	111.28
14	N	40	LYS	CA-C-N	6.18	133.34	121.54
14	N	40	LYS	C-N-CA	6.18	133.34	121.54
10	J	412	ASP	CA-C-N	6.17	128.87	120.54
10	J	412	ASP	C-N-CA	6.17	128.87	120.54
1	A	1249	MET	N-CA-C	-6.17	103.71	111.11
1	A	2011	ILE	N-CA-C	-6.17	104.50	110.42
1	A	1967	ILE	N-CA-C	-6.16	106.94	112.12
1	A	1875	HIS	CA-C-N	-6.14	112.85	122.73
1	A	1875	HIS	C-N-CA	-6.14	112.85	122.73
39	u	339	ARG	N-CA-C	6.14	119.71	109.95
27	2	70	SER	N-CA-C	-6.13	104.52	112.68
1	A	1554	GLN	CB-CG-CD	-6.13	102.18	112.60
1	A	1613	THR	CA-CB-OG1	-6.13	100.41	109.60
1	A	1860	GLN	CB-CA-C	-6.13	96.94	109.38
42	o	73	ASN	N-CA-C	6.13	119.81	111.17
24	X	68	GLU	CA-C-O	-6.11	114.03	120.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	3	A	N9-C1'-C2'	-6.09	102.86	112.00
24	X	68	GLU	CA-C-N	-6.09	110.53	120.71
24	X	68	GLU	C-N-CA	-6.09	110.53	120.71
27	2	32	LYS	N-CA-C	-6.09	104.72	111.36
1	A	1575	GLN	CB-CA-C	-6.09	100.68	110.79
37	v	142	LYS	N-CA-C	6.09	118.56	109.25
9	I	377	THR	CB-CA-C	-6.07	101.35	110.88
10	J	566	PRO	N-CA-CB	6.07	110.24	103.44
1	A	1570	LYS	CA-C-O	-6.07	114.12	120.55
1	A	1736	ALA	CA-C-O	-6.07	112.71	119.08
1	A	1192	PHE	N-CA-C	6.06	119.04	110.50
18	R	226	PRO	N-CD-CG	-6.06	94.11	103.20
42	o	52	ASN	CA-CB-CG	6.03	118.63	112.60
1	A	1616	PRO	CA-C-O	-6.00	114.58	121.36
1	A	1880	PRO	CB-CA-C	-6.00	103.28	110.00
16	P	5	ALA	N-CA-C	-6.00	104.67	111.14
43	p	89	ASP	CA-CB-CG	5.99	118.59	112.60
44	l	274	TYR	N-CA-C	-5.99	104.67	111.14
42	o	79	ILE	CA-C-N	5.99	125.79	120.10
42	o	79	ILE	C-N-CA	5.99	125.79	120.10
1	A	771	VAL	CA-C-O	-5.98	114.73	120.95
39	u	178	THR	N-CA-C	5.98	120.71	113.17
1	A	348	PRO	N-CA-CB	-5.98	99.23	103.23
24	X	85	ASP	CA-C-O	-5.97	112.74	119.79
12	L	214	ILE	N-CA-C	-5.97	102.45	108.96
42	o	75	ARG	N-CA-CB	-5.97	102.68	111.51
1	A	1556	ASP	CA-C-O	-5.95	114.25	120.55
36	n	67	ILE	CB-CA-C	-5.95	104.81	111.23
12	L	134	THR	N-CA-C	5.94	117.84	111.36
27	2	33	LEU	CA-C-O	-5.94	112.01	120.51
9	I	481	TYR	N-CA-C	5.94	118.71	111.82
24	X	98	GLU	CB-CA-C	-5.92	100.95	110.79
1	A	1508	GLY	CA-C-O	-5.92	114.61	121.00
8	H	163	G	O3'-P-O5'	-5.92	95.12	104.00
20	T	401	PRO	CA-C-N	5.92	136.62	126.32
20	T	401	PRO	C-N-CA	5.92	136.62	126.32
9	I	726	ILE	CA-C-N	-5.92	111.89	120.29
9	I	726	ILE	C-N-CA	-5.92	111.89	120.29
44	l	185	TYR	CB-CA-C	5.91	122.02	110.67
42	o	27	ARG	CB-CA-C	-5.91	98.67	109.54
7	G	125	C	P-O3'-C3'	5.90	129.06	120.20
1	A	1536	LEU	CA-C-O	-5.90	114.30	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	p	46	MET	N-CA-C	-5.90	104.76	111.07
21	U	83	GLU	CA-C-N	5.89	132.80	121.54
21	U	83	GLU	C-N-CA	5.89	132.80	121.54
36	g	67	ILE	CB-CA-C	-5.89	104.87	111.23
42	o	123	ASN	OD1-CG-ND2	5.88	128.48	122.60
30	y	47	ARG	CB-CA-C	-5.88	101.03	110.79
30	y	38	PRO	N-CA-CB	5.87	108.41	103.25
1	A	1747	ILE	CA-C-O	-5.86	114.96	121.17
10	J	413	GLU	N-CA-C	5.86	118.14	111.11
34	m	5	LEU	N-CA-C	-5.85	100.46	109.76
1	A	1532	ARG	CB-CG-CD	-5.85	97.85	111.30
24	X	106	GLU	CA-C-O	-5.85	113.75	120.24
1	A	1568	THR	CA-CB-OG1	-5.84	100.84	109.60
42	o	50	SER	CA-C-O	5.83	127.73	121.55
1	A	1534	PHE	CA-C-O	-5.82	114.38	120.55
1	A	1533	ARG	CB-CA-C	-5.80	101.17	110.79
1	A	773	LYS	CA-C-O	-5.78	114.43	120.55
5	F	73	A	C2'-C3'-O3'	-5.75	100.87	109.50
39	u	336	VAL	N-CA-C	-5.74	104.00	112.04
1	A	1733	ILE	CB-CA-C	-5.73	104.40	112.14
5	F	50	A	C1'-C2'-O2'	5.70	116.95	108.40
1	A	1528	GLN	CB-CA-C	5.70	122.23	110.31
9	I	457	ARG	N-CA-C	5.70	117.17	111.07
13	M	121	ASP	CA-C-N	5.70	132.15	122.12
13	M	121	ASP	C-N-CA	5.70	132.15	122.12
18	R	217	LYS	CB-CA-C	-5.70	99.87	109.72
1	A	1732	LYS	CB-CA-C	-5.69	101.94	110.88
42	o	27	ARG	CA-C-N	5.69	128.70	120.11
42	o	27	ARG	C-N-CA	5.69	128.70	120.11
1	A	1813	ARG	CB-CA-C	5.66	119.72	110.95
8	H	164	C	P-O3'-C3'	5.66	128.69	120.20
29	i	52	LYS	CA-C-N	-5.64	114.12	119.76
29	i	52	LYS	C-N-CA	-5.64	114.12	119.76
42	o	71	VAL	O-C-N	-5.64	115.52	122.57
37	v	114	LYS	N-CA-C	-5.63	100.50	109.96
42	o	149	LYS	CB-CA-C	-5.63	102.05	110.16
7	G	127	G	C2'-C3'-O3'	-5.63	105.26	113.70
1	A	1813	ARG	CA-C-O	-5.62	115.11	120.90
1	A	1499	GLU	CB-CG-CD	5.59	122.10	112.60
12	L	7	LYS	CA-C-N	5.58	130.44	121.17
12	L	7	LYS	C-N-CA	5.58	130.44	121.17
5	F	73	A	C3'-C2'-O2'	5.57	122.96	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	157	G	P-O5'-C5'	-5.57	112.54	120.90
1	A	1743	LEU	CA-C-O	-5.57	114.98	120.82
1	A	1054	GLY	N-CA-C	-5.56	106.06	112.29
1	A	1537	TRP	CA-C-N	5.56	132.16	121.54
1	A	1537	TRP	C-N-CA	5.56	132.16	121.54
42	o	16	THR	O-C-N	5.56	129.56	123.22
12	L	9	GLY	O-C-N	5.55	129.33	122.78
42	o	159	GLU	N-CA-C	-5.54	104.87	111.69
1	A	1741	TYR	CA-C-O	-5.54	114.68	120.55
16	P	5	ALA	CA-C-O	-5.54	114.99	120.70
39	u	384	ASP	N-CA-C	5.54	117.76	111.11
8	H	168	A	O4'-C1'-C2'	-5.53	102.07	107.60
42	o	32	PRO	CA-C-N	5.53	130.68	122.99
42	o	32	PRO	C-N-CA	5.53	130.68	122.99
8	H	165	A	N9-C1'-C2'	5.53	120.30	112.00
1	A	1617	ARG	N-CA-C	-5.53	105.83	112.58
29	b	5	LYS	N-CA-C	5.53	118.23	111.82
3	C	560	VAL	CA-C-N	5.53	129.98	121.19
3	C	560	VAL	C-N-CA	5.53	129.98	121.19
1	A	1779	PHE	CB-CA-C	-5.52	99.61	109.71
16	P	12	ALA	CA-C-O	-5.51	115.71	121.55
1	A	158	ARG	CG-CD-NE	-5.50	99.89	112.00
42	o	34	ILE	CA-C-O	-5.50	114.25	120.74
1	A	663	ARG	CA-C-O	-5.50	115.00	121.16
42	o	40	THR	N-CA-C	-5.49	106.08	112.89
1	A	1092	ILE	N-CA-C	5.49	120.76	109.34
1	A	1530	PRO	CA-CB-CG	-5.49	94.07	104.50
25	Y	680	ALA	N-CA-C	-5.49	104.82	112.45
3	C	800	PRO	CA-C-N	5.49	132.02	121.54
3	C	800	PRO	C-N-CA	5.49	132.02	121.54
29	i	5	LYS	N-CA-C	5.48	118.18	111.82
25	Y	688	HIS	CA-C-N	5.48	130.50	122.39
25	Y	688	HIS	C-N-CA	5.48	130.50	122.39
1	A	1736	ALA	CA-C-N	-5.47	113.16	121.92
1	A	1736	ALA	C-N-CA	-5.47	113.16	121.92
8	H	160	A	P-O5'-C5'	-5.47	112.69	120.90
20	T	190	TRP	N-CA-C	5.46	122.44	110.80
1	A	1955	LYS	N-CA-C	-5.46	101.05	109.79
42	o	132	ARG	CD-NE-CZ	5.46	132.04	124.40
1	A	1577	PHE	CA-CB-CG	-5.45	108.35	113.80
29	b	52	LYS	CA-C-N	-5.45	114.31	119.76
29	b	52	LYS	C-N-CA	-5.45	114.31	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	698	ARG	N-CA-CB	5.45	119.70	110.49
25	Y	1183	VAL	N-CA-C	5.45	114.21	106.53
38	w	115	GLY	N-CA-C	5.44	126.07	113.18
3	C	534	VAL	N-CA-C	-5.44	101.89	109.45
1	A	1519	THR	CB-CA-C	-5.41	108.64	116.54
20	T	389	SER	CA-C-N	-5.41	118.45	122.18
20	T	389	SER	C-N-CA	-5.41	118.45	122.18
16	P	4	ALA	N-CA-C	-5.39	106.28	112.92
1	A	1860	GLN	CA-C-N	-5.39	116.13	122.93
1	A	1860	GLN	C-N-CA	-5.39	116.13	122.93
23	W	204	ASP	CA-C-N	5.39	130.19	121.95
23	W	204	ASP	C-N-CA	5.39	130.19	121.95
25	Y	425	ILE	CA-C-O	-5.38	115.15	120.85
1	A	344	ASP	CB-CA-C	-5.37	100.06	108.91
1	A	1944	HIS	CB-CA-C	5.36	118.66	109.65
27	2	63	PHE	CA-CB-CG	5.36	119.16	113.80
1	A	1780	VAL	N-CA-CB	-5.36	105.97	112.07
3	C	515	THR	CA-C-N	5.36	127.77	120.54
3	C	515	THR	C-N-CA	5.36	127.77	120.54
23	W	266	ARG	CA-C-N	5.36	128.45	120.90
23	W	266	ARG	C-N-CA	5.36	128.45	120.90
28	z	68	MET	N-CA-CB	5.35	119.27	110.39
30	y	38	PRO	N-CA-C	-5.34	102.70	111.15
25	Y	975	ARG	CA-C-N	5.34	127.39	120.44
25	Y	975	ARG	C-N-CA	5.34	127.39	120.44
1	A	1535	THR	CA-C-O	-5.34	114.76	120.42
10	J	356	TYR	CA-C-N	-5.34	111.34	121.54
10	J	356	TYR	C-N-CA	-5.34	111.34	121.54
7	G	122	U	N1-C1'-C2'	-5.34	103.99	112.00
25	Y	1169	ASP	N-CA-C	-5.34	100.93	109.04
29	b	65	ARG	CB-CG-CD	5.34	123.58	111.30
24	X	76	LYS	CB-CA-C	-5.33	101.78	110.85
42	o	146	ASP	CA-C-N	5.33	130.13	122.40
42	o	146	ASP	C-N-CA	5.33	130.13	122.40
1	A	1737	ASN	CB-CA-C	5.33	121.58	110.50
6	4	-13	C	C4'-C3'-O3'	5.33	117.39	109.40
43	p	25	ARG	CD-NE-CZ	5.33	131.86	124.40
15	O	30	GLU	CA-C-N	-5.33	114.21	121.61
15	O	30	GLU	C-N-CA	-5.33	114.21	121.61
1	A	1856	GLU	N-CA-C	5.32	120.43	113.30
25	Y	841	ILE	N-CA-CB	5.32	117.77	110.54
1	A	1730	MET	CA-C-O	-5.32	114.91	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	o	125	VAL	CA-C-N	5.32	127.94	120.28
42	o	125	VAL	C-N-CA	5.32	127.94	120.28
3	C	824	THR	N-CA-C	5.32	123.40	112.40
42	o	33	VAL	N-CA-CB	-5.31	103.77	111.52
29	i	65	ARG	CB-CG-CD	5.30	123.50	111.30
43	p	6	ASN	N-CA-CB	-5.30	101.66	111.53
19	S	130	GLY	N-CA-C	5.30	118.86	110.96
41	s	54	ASP	N-CA-CB	-5.29	102.25	110.46
1	A	1723	LYS	N-CA-C	-5.29	105.56	112.75
1	A	862	GLU	CA-C-O	-5.28	114.95	120.55
1	A	862	GLU	O-C-N	5.27	127.71	122.12
25	Y	421	GLU	N-CA-C	-5.27	105.61	111.36
1	A	1553	VAL	CA-C-O	-5.26	114.96	120.27
24	X	59	GLN	CB-CA-C	5.26	119.79	110.85
1	A	1560	ILE	CA-C-O	-5.25	114.86	120.59
3	C	852	ARG	CB-CG-CD	-5.24	99.24	111.30
1	A	1742	VAL	CA-C-O	-5.24	115.50	120.95
8	H	171	U	C2'-C3'-O3'	-5.24	105.84	113.70
42	o	113	LYS	N-CA-C	5.24	118.45	111.75
16	P	11	PRO	CB-CA-C	-5.23	104.71	111.46
1	A	1724	PRO	CA-N-CD	-5.23	104.68	112.00
1	A	1921	ASP	O-C-N	5.22	127.67	122.03
8	H	156	U	C4'-C3'-C2'	5.22	107.82	102.60
9	I	231	ASN	O-C-N	5.22	125.13	120.48
1	A	1556	ASP	N-CA-C	5.22	116.97	111.28
1	A	1533	ARG	N-CA-CB	5.21	117.78	110.12
16	P	5	ALA	O-C-N	5.21	127.72	122.09
43	p	20	LYS	N-CA-C	5.21	117.36	111.11
43	p	68	GLN	OE1-CD-NE2	5.21	127.81	122.60
1	A	1596	VAL	CA-C-N	-5.20	113.68	120.44
1	A	1596	VAL	C-N-CA	-5.20	113.68	120.44
42	o	88	PRO	CB-CA-C	-5.20	104.05	112.62
12	L	52	GLU	N-CA-C	5.19	117.02	111.36
39	u	163	THR	N-CA-C	-5.19	103.65	110.39
1	A	1066	GLN	CB-CA-C	-5.18	102.04	110.85
3	C	359	LYS	CA-CB-CG	5.18	124.46	114.10
43	p	51	GLN	N-CA-C	5.18	117.55	109.52
24	X	96	GLN	CB-CG-CD	-5.17	103.80	112.60
25	Y	619	ARG	CA-C-N	5.17	127.53	120.54
25	Y	619	ARG	C-N-CA	5.17	127.53	120.54
25	Y	1052	TRP	CA-C-N	5.17	127.17	120.44
25	Y	1052	TRP	C-N-CA	5.17	127.17	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	p	36	HIS	CA-CB-CG	-5.17	108.63	113.80
44	l	289	THR	CA-CB-OG1	-5.17	101.85	109.60
38	w	148	TRP	N-CA-C	-5.16	103.22	110.50
1	A	1563	HIS	CA-CB-CG	-5.16	108.64	113.80
1	A	1616	PRO	O-C-N	5.15	129.44	122.89
24	X	63	ASP	CB-CA-C	-5.15	102.24	110.79
39	u	342	ASP	N-CA-C	5.15	117.10	107.99
9	I	22	LEU	O-C-N	5.14	125.06	120.48
43	p	48	MET	N-CA-C	5.14	119.56	113.28
39	u	367	ARG	N-CA-C	-5.14	106.27	112.54
2	B	21	A	C2'-C3'-O3'	-5.13	106.00	113.70
42	o	55	ARG	NE-CZ-NH2	-5.13	114.58	119.20
1	A	168	PRO	CB-CA-C	5.13	120.83	112.26
42	o	90	LEU	CA-C-O	-5.13	113.17	120.51
1	A	1531	ASN	CA-CB-CG	-5.12	107.47	112.60
42	o	83	LEU	N-CA-C	5.12	117.53	111.33
9	I	487	TRP	N-CA-C	5.12	116.94	111.36
39	u	210	PRO	N-CA-C	5.11	121.37	113.75
33	d	99	MET	N-CA-C	5.11	116.84	108.76
33	d	88	LYS	CG-CD-CE	-5.10	99.56	111.30
33	k	99	MET	N-CA-C	5.10	116.82	108.76
38	w	107	ASP	N-CA-C	-5.10	102.09	109.59
7	G	125	C	C3'-C2'-O2'	5.10	122.25	114.60
9	I	149	TRP	O-C-N	5.10	125.02	120.48
23	W	79	VAL	N-CA-C	5.09	114.11	106.42
8	H	22	U	C1'-C2'-O2'	-5.09	100.76	108.40
43	p	83	TYR	CA-C-O	-5.09	115.25	121.05
37	v	141	PHE	N-CA-C	5.07	120.12	113.88
1	A	1596	VAL	CA-C-O	-5.07	115.68	120.95
1	A	1522	GLN	CB-CA-C	5.07	119.20	110.79
8	H	155	C	P-O3'-C3'	5.07	127.80	120.20
13	M	124	PHE	CA-C-N	5.07	129.25	121.19
13	M	124	PHE	C-N-CA	5.07	129.25	121.19
1	A	1779	PHE	CA-C-N	-5.06	116.85	122.27
1	A	1779	PHE	C-N-CA	-5.06	116.85	122.27
1	A	1738	PRO	N-CA-CB	-5.06	97.94	103.25
1	A	2003	THR	CB-CA-C	-5.06	102.47	114.16
8	H	160	A	C4'-C3'-C2'	-5.06	97.54	102.60
18	R	181	PRO	N-CA-C	5.06	120.42	113.84
20	T	495	ALA	N-CA-C	5.06	117.57	111.40
35	e	85	THR	N-CA-C	-5.06	105.95	112.68
42	o	90	LEU	O-C-N	5.05	129.31	122.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1519	THR	CA-C-N	-5.05	112.57	121.81
1	A	1519	THR	C-N-CA	-5.05	112.57	121.81
7	G	1	G	C3'-C2'-O2'	5.05	122.17	114.60
1	A	1855	GLU	CA-C-N	-5.05	114.67	122.49
1	A	1855	GLU	C-N-CA	-5.05	114.67	122.49
8	H	160	A	N9-C1'-C2'	5.04	119.56	112.00
9	I	728	ARG	CB-CG-CD	-5.04	99.70	111.30
35	l	85	THR	N-CA-C	-5.04	105.97	112.68
8	H	170	C	O4'-C1'-C2'	-5.03	100.77	105.80
42	o	139	VAL	CA-C-N	5.03	124.69	119.56
42	o	139	VAL	C-N-CA	5.03	124.69	119.56
18	R	70	ALA	CA-C-N	5.03	128.80	121.31
18	R	70	ALA	C-N-CA	5.03	128.80	121.31
1	A	772	CYS	CA-C-O	-5.02	115.10	120.42
7	G	21	A	P-O3'-C3'	-5.02	112.67	120.20
9	I	89	ASP	O-C-N	5.02	124.94	120.48
42	o	99	SER	N-CA-CB	-5.02	102.94	111.17
10	J	201	ARG	CA-C-N	5.01	129.48	122.36
10	J	201	ARG	C-N-CA	5.01	129.48	122.36
9	I	453	LEU	CA-C-N	5.01	126.99	120.28
9	I	453	LEU	C-N-CA	5.01	126.99	120.28
24	X	104	ARG	CA-C-O	-5.00	115.12	120.42
42	o	81	GLU	N-CA-C	5.00	118.53	112.23
1	A	1517	LYS	CA-C-N	-5.00	113.86	121.66
1	A	1517	LYS	C-N-CA	-5.00	113.86	121.66

There are no chirality outliers.

All (66) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
27	2	31	GLN	Mainchain
1	A	1019	TYR	Peptide
1	A	1201	ARG	Peptide
1	A	1210	LYS	Peptide
1	A	1338	SER	Peptide
1	A	1493	THR	Mainchain
1	A	1506	ALA	Mainchain
1	A	1520	ASN	Mainchain
1	A	1576	ILE	Mainchain
1	A	170	ASP	Mainchain
1	A	1717	ASN	Mainchain
1	A	1749	LYS	Mainchain

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Mol	Chain	Res	Type	Group
1	A	1806	ALA	Mainchain
1	A	1876	LEU	Mainchain
1	A	2010	ILE	Mainchain
1	A	377	GLU	Peptide
1	A	385	GLU	Peptide
1	A	55	ASP	Peptide
1	A	698	PRO	Peptide
1	A	73	HIS	Peptide
1	A	775	ASN	Sidechain
1	A	941	LYS	Peptide
3	C	308	CYS	Peptide
3	C	358	LYS	Peptide
3	C	360	ALA	Peptide
3	C	534	VAL	Peptide
3	C	799	GLU	Peptide
3	C	800	PRO	Peptide
3	C	902	HIS	Peptide
3	C	92	PRO	Peptide
3	C	93	ILE	Peptide
4	E	192	ASN	Peptide
9	I	309	ALA	Mainchain
9	I	310	LYS	Mainchain
9	I	311	MET	Mainchain
9	I	693	GLN	Mainchain
9	I	722	GLU	Mainchain
9	I	83	LYS	Mainchain
9	I	84	HIS	Mainchain
10	J	205	LEU	Peptide
10	J	215	THR	Peptide
10	J	216	ASP	Peptide
10	J	240	THR	Peptide
10	J	241	VAL	Peptide
14	N	136	HIS	Peptide
14	N	3	LYS	Peptide
14	N	36	PRO	Peptide
14	N	4	VAL	Peptide
15	O	63	MET	Peptide
16	P	204	GLN	Peptide
16	P	30	TYR	Peptide
16	P	48	GLN	Peptide
18	R	125	MET	Peptide
18	R	126	ASN	Peptide

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Mol	Chain	Res	Type	Group
18	R	183	GLN	Peptide
18	R	185	GLY	Peptide
18	R	212	PHE	Peptide
18	R	66	GLU	Peptide
18	R	94	GLY	Peptide
20	T	342	GLU	Peptide
20	T	400	PHE	Peptide
20	T	405	PHE	Peptide
23	W	257	ILE	Peptide
23	W	518	PRO	Peptide
33	d	112	ASN	Peptide
33	k	112	ASN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16449	0	16378	1202	0
2	B	1768	0	897	66	0
3	C	6791	0	6807	126	0
4	E	2338	0	2275	73	0
5	F	2075	0	1048	188	0
6	4	276	0	142	15	0
7	G	1510	0	760	217	0
8	H	2966	0	1505	292	0
9	I	3857	0	2738	157	0
10	J	3809	0	2900	42	0
11	K	772	0	342	19	0
12	L	3015	0	2570	90	0
13	M	1098	0	1082	39	0
14	N	1184	0	1190	27	0
15	O	2296	0	2284	77	0
16	P	953	0	939	37	0
17	Q	6562	0	2836	35	0
18	R	2073	0	2119	53	0
19	S	1236	0	1210	49	0
20	T	2454	0	2413	80	0
21	U	422	0	291	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	V	2632	0	1734	43	0
23	W	4129	0	4040	152	0
24	X	702	0	632	143	0
25	Y	3431	0	1662	41	0
26	Z	902	0	860	54	0
27	2	1013	0	1058	117	0
28	z	504	0	509	129	0
29	b	786	0	811	48	0
29	i	690	0	712	15	0
30	y	390	0	190	5	0
31	a	609	0	620	13	0
31	h	633	0	645	14	0
32	c	649	0	693	10	0
32	j	649	0	693	11	0
33	d	776	0	819	32	0
33	k	688	0	709	30	0
34	f	576	0	589	21	0
34	m	572	0	578	57	0
35	e	652	0	668	20	0
35	l	652	0	668	48	0
36	g	577	0	603	15	0
36	n	542	0	568	34	0
37	v	711	0	299	6	0
38	w	445	0	203	6	0
39	u	1907	0	845	3	0
40	x	124	0	51	0	0
41	q	659	0	296	19	0
41	r	654	0	294	9	0
41	s	659	0	296	20	0
41	t	654	0	294	16	0
42	o	1282	0	1305	30	0
43	p	760	0	783	12	0
44	1	2194	0	2137	321	0
45	A	36	0	6	9	0
46	C	32	0	12	2	0
47	C	1	0	0	0	0
47	F	6	0	0	0	0
47	Q	2	0	0	0	0
48	1	1	0	0	0	0
48	N	3	0	0	0	0
48	O	3	0	0	0	0
49	Q	31	0	12	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	96822	0	79620	3313	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 19.

All (3313) 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:1596:VAL:CG2	44:1:275:LEU:HD22	1.14	1.61
27:2:48:ILE:HG23	34:m:5:LEU:CD2	1.31	1.60
1:A:1556:ASP:HA	28:z:103:TYR:CD2	1.34	1.59
1:A:1701:VAL:CG2	1:A:1718:TRP:CH2	1.76	1.58
27:2:48:ILE:CG2	34:m:5:LEU:HD21	1.30	1.56
9:I:273:GLU:HA	17:Q:357:ALA:CB	1.33	1.52
30:y:38:PRO:N	30:y:38:PRO:CA	1.71	1.51
1:A:1701:VAL:HG23	1:A:1718:TRP:CZ3	1.49	1.48
28:z:60:PRO:CA	28:z:60:PRO:N	1.67	1.47
11:K:83:SER:HA	41:t:75:LEU:CB	1.46	1.45
1:A:1698:PRO:HG2	44:1:182:VAL:CA	1.43	1.44
1:A:1808:PHE:HE2	1:A:1893:PHE:CD1	1.35	1.44
9:I:273:GLU:CA	17:Q:357:ALA:HB2	1.46	1.43
7:G:82:G:H4'	23:W:541:LYS:NZ	1.27	1.41
1:A:1701:VAL:CG2	1:A:1718:TRP:CZ3	2.00	1.41
35:l:14:MET:HE1	36:n:10:LYS:CE	1.50	1.40
1:A:1991:TYR:HE1	26:Z:756:TYR:CE2	1.41	1.38
1:A:240:ARG:NH1	44:1:139:ARG:HB3	1.33	1.38
44:1:275:LEU:HD23	44:1:278:LEU:CD2	1.54	1.37
1:A:1701:VAL:HG23	1:A:1718:TRP:CH2	0.83	1.36
1:A:1596:VAL:CG2	44:1:275:LEU:CD2	2.04	1.36
1:A:1596:VAL:HG23	44:1:275:LEU:CD2	1.60	1.31
20:T:188:PRO:HB3	20:T:440:ASP:OD2	1.13	1.31
1:A:1724:PRO:N	1:A:1724:PRO:CA	1.68	1.31
1:A:1808:PHE:CE2	1:A:1893:PHE:HD1	1.47	1.30
44:1:275:LEU:CD2	44:1:278:LEU:HD21	1.60	1.30
27:2:48:ILE:CB	34:m:5:LEU:HD21	1.63	1.28
1:A:934:ARG:NH1	25:Y:425:ILE:HG21	1.49	1.26
1:A:1889:LEU:CD1	1:A:2012:LEU:HB3	1.64	1.26
1:A:1526:LEU:HD12	7:G:124:G:O6	1.31	1.26
1:A:1808:PHE:CE2	1:A:1893:PHE:CD1	2.22	1.26
7:G:73:G:O2'	7:G:74:G:O4'	1.54	1.26
23:W:72:LEU:HD11	23:W:83:PRO:CG	1.64	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:82:G:C4'	23:W:541:LYS:HZ3	1.47	1.25
9:I:704:TRP:CZ3	9:I:727:ARG:HG3	1.71	1.25
17:Q:801:GLN:O	49:Q:1501:ATP:N6	1.66	1.25
1:A:535:ARG:HH22	28:z:108:VAL:N	1.36	1.24
9:I:720:ILE:O	9:I:724:LEU:HB2	1.13	1.23
24:X:100:ILE:O	24:X:103:GLN:HB2	1.24	1.23
1:A:1790:ILE:HD13	27:2:76:SER:OG	1.38	1.23
7:G:82:G:C4'	23:W:541:LYS:NZ	2.01	1.23
1:A:1771:LEU:HA	1:A:1777:ILE:CD1	1.68	1.23
23:W:73:ASP:CB	23:W:74:PRO:HD3	1.66	1.23
23:W:83:PRO:HB3	23:W:87:THR:OG1	1.34	1.23
1:A:1770:GLU:OE1	44:1:316:ARG:HG3	1.36	1.22
1:A:1556:ASP:HA	28:z:103:TYR:CE2	1.73	1.22
23:W:73:ASP:HB3	23:W:74:PRO:CD	1.69	1.21
4:E:266:PRO:HG2	12:L:785:GLN:CB	1.71	1.21
1:A:1934:SER:OG	44:1:344:GLN:HA	1.37	1.21
20:T:185:MET:HG3	20:T:186:PRO:CD	1.69	1.21
1:A:584:HIS:HE1	45:A:3000:IHP:O26	1.21	1.21
20:T:185:MET:CG	20:T:186:PRO:HD3	1.72	1.20
1:A:537:LYS:HD2	5:F:37:C:N4	1.54	1.20
1:A:1737:ASN:OD1	1:A:1738:PRO:HD2	1.42	1.20
1:A:2009:ASP:O	1:A:2013:GLY:N	1.75	1.20
1:A:1772:PHE:HA	1:A:1813:ARG:CD	1.70	1.20
1:A:1772:PHE:CD1	1:A:1813:ARG:HG3	1.77	1.20
1:A:1715:TYR:C	1:A:1718:TRP:HZ2	1.48	1.20
1:A:1991:TYR:CE1	26:Z:756:TYR:CE2	2.29	1.19
28:z:54:GLY:O	44:1:174:ASN:ND2	1.74	1.18
1:A:1935:ARG:NH2	44:1:348:THR:HG21	1.59	1.17
1:A:1994:LYS:HB3	26:Z:756:TYR:HB2	1.23	1.17
23:W:72:LEU:CD1	23:W:83:PRO:HG3	1.72	1.17
1:A:1321:GLU:HB2	44:1:66:TYR:OH	1.42	1.17
1:A:1698:PRO:CG	44:1:182:VAL:HA	1.73	1.17
5:F:79:C:OP2	10:J:237:LYS:NZ	1.76	1.17
5:F:80:G:OP1	12:L:174:LYS:NZ	1.77	1.16
1:A:1705:ILE:HG21	1:A:1734:MET:CE	1.74	1.16
1:A:1889:LEU:HD11	1:A:2012:LEU:CG	1.75	1.16
9:I:265:TYR:CB	9:I:274:LYS:CB	2.24	1.16
1:A:196:ASP:OD2	1:A:199:GLU:HG2	1.42	1.16
1:A:535:ARG:HH12	28:z:108:VAL:HA	1.11	1.16
17:Q:801:GLN:C	49:Q:1501:ATP:HN62	1.53	1.15
1:A:1889:LEU:CD1	1:A:2012:LEU:HG	1.75	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:21:A:O2'	7:G:22:C:O5'	1.64	1.15
27:2:48:ILE:HA	34:m:5:LEU:CD2	1.76	1.15
3:C:818:SER:O	3:C:822:MET:HG2	1.43	1.15
27:2:48:ILE:CG2	34:m:5:LEU:CD2	2.02	1.15
1:A:1556:ASP:HB2	28:z:101:GLU:O	1.45	1.14
1:A:1705:ILE:HD13	1:A:1734:MET:HE2	1.23	1.14
1:A:1719:PHE:HB2	1:A:1720:PRO:HD2	1.25	1.14
1:A:1772:PHE:CA	1:A:1813:ARG:HD3	1.76	1.14
12:L:4:ILE:HD11	24:X:78:MET:HE3	1.26	1.14
1:A:1705:ILE:HG21	1:A:1734:MET:HE3	1.16	1.14
5:F:54:G:OP1	7:G:122:U:OP2	1.65	1.14
7:G:21:A:C1'	15:O:152:ARG:NH2	2.11	1.14
1:A:535:ARG:NH1	28:z:108:VAL:HA	1.63	1.14
1:A:1504:GLU:OE2	1:A:1754:TYR:CE2	2.01	1.14
1:A:535:ARG:HH22	28:z:108:VAL:CA	1.59	1.13
1:A:1556:ASP:CA	28:z:103:TYR:CD2	2.30	1.13
9:I:720:ILE:O	9:I:724:LEU:CB	1.95	1.13
9:I:661:ASP:HB2	9:I:694:ILE:HG21	1.30	1.13
20:T:188:PRO:CB	20:T:440:ASP:OD2	1.97	1.12
20:T:188:PRO:HG3	20:T:443:THR:OG1	1.47	1.11
8:H:36:G:H2'	8:H:37:U:H5'	1.31	1.11
23:W:73:ASP:HB3	23:W:74:PRO:HD3	1.17	1.11
34:m:2:SER:CB	35:l:48:ILE:HG23	1.79	1.11
1:A:1935:ARG:HH21	44:1:348:THR:HG21	0.96	1.11
35:l:14:MET:HE1	36:n:10:LYS:HE3	1.28	1.11
1:A:584:HIS:CE1	45:A:3000:IHP:O26	2.02	1.10
1:A:1471:ARG:HD3	44:1:66:TYR:CD1	1.86	1.10
1:A:1617:ARG:HD3	28:z:96:LEU:HB3	1.26	1.10
1:A:1698:PRO:HG2	44:1:182:VAL:CB	1.79	1.10
8:H:47:U:OP1	27:2:40:LYS:NZ	1.84	1.10
12:L:129:ASP:OD2	12:L:130:PRO:HD2	1.51	1.10
1:A:1715:TYR:O	1:A:1718:TRP:HZ2	1.35	1.10
1:A:1694:ILE:HD11	28:z:88:ARG:CD	1.81	1.10
4:E:93:TRP:HZ3	29:b:105:GLY:O	1.33	1.10
9:I:721:LYS:NZ	12:L:65:ARG:NH2	2.00	1.10
8:H:168:A:H1'	36:n:48:MET:HE1	1.19	1.10
9:I:84:HIS:CB	9:I:90:PRO:HA	1.82	1.10
1:A:1644:LEU:HD21	1:A:1681:ARG:HD2	1.26	1.09
17:Q:801:GLN:C	49:Q:1501:ATP:N6	2.08	1.09
27:2:128:ARG:O	27:2:132:GLN:HG2	1.50	1.09
1:A:1481:VAL:HG23	44:1:85:GLN:NE2	1.66	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:455:GLN:HG2	20:T:456:PRO:HD2	1.14	1.09
5:F:45:A:N6	7:G:2:U:O2	1.85	1.09
16:P:212:ASN:HB3	20:T:458:SER:N	1.67	1.09
1:A:1644:LEU:HD21	1:A:1681:ARG:CD	1.81	1.09
27:2:48:ILE:HA	34:m:5:LEU:HD22	1.23	1.09
1:A:1471:ARG:HD3	44:1:66:TYR:CE1	1.88	1.09
8:H:36:G:C2'	8:H:37:U:H5'	1.83	1.09
1:A:1556:ASP:CA	28:z:103:TYR:HD2	1.65	1.08
1:A:1889:LEU:HD13	1:A:2012:LEU:CB	1.81	1.08
1:A:1617:ARG:HG2	28:z:96:LEU:HD13	1.27	1.08
9:I:681:ILE:HG23	9:I:710:PHE:CZ	1.88	1.08
1:A:1617:ARG:CD	28:z:96:LEU:HB3	1.82	1.08
8:H:154:C:OP2	43:p:19:LYS:HG2	1.49	1.08
1:A:1793:THR:HG21	5:F:43:A:H5''	1.36	1.08
5:F:39:A:C2'	5:F:40:U:H5'	1.82	1.08
7:G:21:A:H1'	15:O:152:ARG:HH21	1.05	1.08
1:A:1494:TYR:OH	1:A:1735:LYS:HA	1.52	1.08
1:A:1889:LEU:CD1	1:A:2012:LEU:CB	2.30	1.07
1:A:1556:ASP:O	28:z:103:TYR:HE2	1.34	1.07
5:F:34:G:H2'	5:F:35:A:H5''	1.29	1.07
27:2:120:ALA:HB1	36:n:55:ASN:OD1	1.52	1.07
1:A:1135:PRO:HD2	1:A:1138:ALA:HB3	1.36	1.07
7:G:21:A:OP2	15:O:193:LEU:HD21	1.51	1.07
1:A:361:HIS:HE1	22:V:324:HIS:HA	1.20	1.07
1:A:1771:LEU:HA	1:A:1777:ILE:HD12	1.31	1.07
1:A:535:ARG:NH2	28:z:107:LYS:C	2.13	1.07
1:A:1872:LEU:O	1:A:1876:LEU:HG	1.51	1.07
8:H:156:U:H6	8:H:156:U:H5''	1.09	1.07
23:W:73:ASP:CG	23:W:74:PRO:HD3	1.79	1.06
7:G:82:G:C5'	23:W:541:LYS:HZ1	1.68	1.06
8:H:105:G:H2'	8:H:106:G:H5''	1.37	1.06
22:V:457:ARG:HH12	44:1:88:GLN:HG2	1.14	1.06
13:M:118:LYS:H	13:M:118:LYS:HD3	1.18	1.06
34:m:2:SER:HB3	35:l:48:ILE:HG23	1.38	1.06
1:A:1781:ASP:OD1	1:A:1783:THR:HB	1.56	1.05
27:2:48:ILE:CA	34:m:5:LEU:CD2	2.35	1.05
4:E:59:ILE:HD11	23:W:82:ASN:HD21	1.10	1.05
9:I:273:GLU:CB	17:Q:357:ALA:HB2	1.87	1.05
34:m:5:LEU:O	35:l:49:GLY:HA3	1.54	1.05
1:A:1134:TRP:HB3	1:A:1135:PRO:HD3	1.38	1.04
1:A:1701:VAL:HG21	1:A:1718:TRP:CZ3	1.85	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1930:TYR:HB2	44:1:324:MET:HE3	1.37	1.04
1:A:1935:ARG:HH21	44:1:348:THR:CG2	1.70	1.04
1:A:1889:LEU:HD11	1:A:2012:LEU:HG	1.09	1.04
1:A:1596:VAL:HG21	44:1:275:LEU:HD22	1.33	1.04
1:A:1849:ILE:HG23	1:A:1857:GLN:CG	1.85	1.04
23:W:79:VAL:HG21	29:b:114:ILE:HD11	1.05	1.04
41:q:60:PRO:CB	41:s:93:ARG:C	2.30	1.04
1:A:934:ARG:HH12	25:Y:425:ILE:HG21	0.90	1.03
1:A:1715:TYR:O	1:A:1718:TRP:CZ2	2.11	1.03
1:A:1778:TRP:CD2	1:A:1809:ILE:HG21	1.93	1.03
35:l:14:MET:CE	36:n:10:LYS:CE	2.36	1.03
8:H:151:C:OP2	27:2:131:ARG:NH1	1.91	1.03
41:s:71:ILE:CB	41:t:81:GLU:CB	2.35	1.03
1:A:535:ARG:HH22	28:z:107:LYS:C	1.67	1.03
1:A:1763:LEU:HG	1:A:1862:ILE:HG13	1.39	1.03
7:G:82:G:C5'	23:W:541:LYS:NZ	2.21	1.03
8:H:40:C:H4'	8:H:41:U:OP1	1.56	1.03
1:A:1694:ILE:HD11	28:z:88:ARG:HD3	1.06	1.02
1:A:1849:ILE:CG2	1:A:1857:GLN:HG2	1.88	1.02
3:C:756:LYS:HA	3:C:759:LEU:HB3	1.41	1.02
1:A:1889:LEU:CD1	1:A:2012:LEU:CG	2.32	1.02
7:G:100:C:H2'	7:G:101:U:C6	1.93	1.02
8:H:30:A:H1'	24:X:73:PHE:CE1	1.94	1.02
11:K:83:SER:CA	41:t:75:LEU:CB	2.37	1.02
1:A:1871:PRO:O	1:A:1875:HIS:HB2	1.59	1.02
27:2:48:ILE:HG23	34:m:5:LEU:HD23	1.39	1.02
8:H:30:A:H1'	24:X:73:PHE:HE1	1.23	1.02
9:I:698:ARG:HA	9:I:698:ARG:HE	1.23	1.02
1:A:1715:TYR:C	1:A:1718:TRP:CZ2	2.38	1.01
1:A:1596:VAL:HG21	44:1:275:LEU:CD2	1.82	1.01
8:H:39:U:H6	8:H:39:U:H5''	1.23	1.01
9:I:187:LEU:HA	9:I:196:ALA:HB1	1.38	1.01
27:2:48:ILE:HG13	34:m:5:LEU:HD11	1.39	1.01
1:A:1698:PRO:CG	44:1:182:VAL:CA	2.32	1.01
5:F:86:U:O2'	5:F:87:C:O5'	1.78	1.01
9:I:273:GLU:HA	17:Q:357:ALA:HB3	1.40	1.01
12:L:10:VAL:CG2	24:X:86:GLU:HG3	1.89	1.01
11:K:15:ALA:HB1	41:s:112:ALA:O	1.60	1.01
12:L:124:LYS:CE	12:L:129:ASP:OD2	2.08	1.01
27:2:48:ILE:CA	34:m:5:LEU:HD22	1.90	1.01
1:A:1772:PHE:HD1	1:A:1813:ARG:HG3	1.09	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:20:A:HO2'	15:O:193:LEU:HD21	1.20	1.00
27:2:51:LYS:HZ3	35:l:28:ARG:HD3	1.27	1.00
1:A:1778:TRP:CD2	1:A:1809:ILE:CG2	2.45	1.00
1:A:1873:GLU:HG3	44:1:290:ARG:HH21	1.21	1.00
5:F:8:C:H6	5:F:8:C:H5''	1.23	1.00
1:A:535:ARG:CZ	28:z:108:VAL:HA	1.92	1.00
1:A:106:MET:HE3	1:A:561:HIS:NE2	1.76	1.00
1:A:1859:LYS:HA	1:A:1859:LYS:HE2	1.40	1.00
1:A:2015:GLU:HG2	24:X:55:TYR:CZ	1.97	1.00
7:G:91:A:C2	8:H:39:U:O2	2.14	1.00
20:T:455:GLN:HG2	20:T:456:PRO:CD	1.91	1.00
1:A:887:THR:HB	12:L:122:LYS:HE2	1.43	1.00
27:2:52:MET:HB2	35:l:28:ARG:NH2	1.75	1.00
23:W:79:VAL:CG2	29:b:114:ILE:HD11	1.92	0.99
1:A:1930:TYR:CD2	44:1:324:MET:HG3	1.97	0.99
1:A:1258:LYS:CE	7:G:126:G:H4'	1.91	0.99
1:A:1617:ARG:CG	28:z:96:LEU:HD13	1.92	0.99
9:I:704:TRP:CE3	9:I:727:ARG:HG3	1.97	0.99
1:A:535:ARG:NH2	28:z:108:VAL:HA	1.78	0.99
1:A:1386:TRP:HB3	25:Y:410:VAL:CG2	1.92	0.99
1:A:1621:LYS:NZ	28:z:92:PHE:CZ	2.30	0.99
1:A:934:ARG:NH1	25:Y:425:ILE:CG2	2.25	0.99
1:A:1778:TRP:CE3	1:A:1809:ILE:HG21	1.97	0.99
18:R:106:GLN:NE2	18:R:225:PRO:HG2	1.77	0.98
1:A:1884:ILE:O	44:1:289:THR:HA	1.61	0.98
23:W:79:VAL:HG21	29:b:114:ILE:CD1	1.93	0.98
1:A:1526:LEU:CD1	7:G:124:G:O6	2.10	0.98
8:H:168:A:H5''	8:H:168:A:C8	1.98	0.98
5:F:41:A:N1	7:G:6:A:N1	2.11	0.98
9:I:721:LYS:HZ2	12:L:65:ARG:NH2	1.58	0.98
22:V:496:CYS:SG	44:1:72:TRP:HH2	1.85	0.98
37:v:29:ASP:CB	38:w:154:PRO:CB	2.42	0.98
1:A:1889:LEU:HD13	1:A:2012:LEU:HB3	1.01	0.98
7:G:21:A:H4'	7:G:22:C:OP1	1.60	0.98
5:F:34:G:C2'	5:F:35:A:H5''	1.94	0.98
1:A:361:HIS:CE1	22:V:324:HIS:HA	1.98	0.97
1:A:1617:ARG:HG2	28:z:96:LEU:CD1	1.94	0.97
7:G:21:A:H1'	15:O:152:ARG:NH2	1.73	0.97
1:A:1884:ILE:N	44:1:289:THR:O	1.96	0.97
7:G:82:G:H4'	23:W:541:LYS:CE	1.94	0.97
8:H:40:C:O2'	8:H:41:U:H5''	1.64	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1685:LEU:CD1	44:1:173:TYR:CD2	2.47	0.97
1:A:1698:PRO:HG2	44:1:182:VAL:HA	1.00	0.97
7:G:21:A:N9	15:O:152:ARG:NH2	2.11	0.97
1:A:2004:GLN:HB3	44:1:342:HIS:NE2	1.80	0.97
3:C:673:LYS:NZ	21:U:56:ASP:CB	2.28	0.96
1:A:1778:TRP:CZ2	1:A:1818:PHE:CE2	2.53	0.96
44:1:275:LEU:HD23	44:1:278:LEU:HD21	0.96	0.96
1:A:240:ARG:NH1	44:1:139:ARG:CB	2.28	0.96
1:A:1571:ILE:HD13	28:z:112:LYS:HE3	1.47	0.96
1:A:1889:LEU:HD12	1:A:1891:LEU:HD21	1.46	0.96
7:G:95:U:O2'	7:G:96:U:H5'	1.64	0.96
27:2:38:LEU:HD23	34:m:12:ASN:HD22	1.31	0.96
1:A:1861:ILE:HD11	1:A:1882:ILE:HG21	1.47	0.96
1:A:1688:THR:HB	44:1:181:ILE:HD13	1.47	0.96
5:F:39:A:H2'	5:F:40:U:H5'	1.46	0.96
1:A:1833:LEU:HD22	1:A:1833:LEU:H	1.28	0.95
22:V:457:ARG:HG3	44:1:73:TYR:CD2	2.01	0.95
1:A:1678:ARG:NH2	44:1:96:SER:O	1.99	0.95
22:V:450:ILE:CG1	44:1:89:PRO:HG2	1.96	0.95
41:q:60:PRO:C	41:s:93:ARG:CB	2.39	0.95
1:A:1386:TRP:HB3	25:Y:410:VAL:HG21	1.47	0.95
1:A:1873:GLU:HG3	44:1:290:ARG:NH2	1.82	0.95
1:A:1556:ASP:O	28:z:103:TYR:CE2	2.19	0.95
35:l:14:MET:HE1	36:n:10:LYS:CD	1.95	0.95
1:A:1681:ARG:NH2	1:A:1681:ARG:HB3	1.82	0.95
1:A:1760:GLU:H	44:1:289:THR:HG21	1.30	0.94
1:A:1694:ILE:CD1	28:z:88:ARG:HD3	1.97	0.94
34:m:2:SER:HB3	35:l:48:ILE:CG2	1.96	0.94
1:A:1504:GLU:OE2	1:A:1754:TYR:HE2	1.44	0.94
27:2:120:ALA:CB	36:n:55:ASN:OD1	2.14	0.94
8:H:156:U:H5''	8:H:156:U:C6	2.02	0.94
1:A:821:ARG:HH12	25:Y:426:LEU:HD11	1.30	0.94
9:I:721:LYS:HZ2	12:L:65:ARG:HH21	1.05	0.94
1:A:160:HIS:HE1	44:1:170:TRP:HA	1.31	0.94
1:A:1701:VAL:HG21	1:A:1718:TRP:HZ3	1.32	0.94
1:A:1861:ILE:HD11	1:A:1882:ILE:CG2	1.98	0.94
4:E:93:TRP:CZ3	29:b:105:GLY:O	2.20	0.94
12:L:124:LYS:HE2	12:L:129:ASP:OD2	1.68	0.94
1:A:1772:PHE:HA	1:A:1813:ARG:HD3	0.95	0.94
2:B:95:G:H5'	34:f:25:TRP:HH2	1.28	0.94
1:A:1258:LYS:HE2	7:G:126:G:H4'	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:120:G:H5'	7:G:120:G:H8	1.33	0.94
44:1:185:TYR:CE2	44:1:188:VAL:HG11	2.03	0.94
1:A:1716:GLY:O	1:A:1718:TRP:NE1	2.01	0.93
7:G:20:A:O2'	15:O:193:LEU:HD21	1.68	0.93
23:W:83:PRO:CB	23:W:87:THR:OG1	2.16	0.93
18:R:106:GLN:NE2	18:R:225:PRO:CG	2.31	0.93
1:A:537:LYS:CD	5:F:37:C:N4	2.30	0.93
1:A:934:ARG:HH12	25:Y:425:ILE:CG2	1.79	0.93
1:A:1134:TRP:HB3	1:A:1135:PRO:CD	1.98	0.93
1:A:1896:CYS:SG	1:A:1896:CYS:O	2.27	0.93
1:A:1471:ARG:CD	44:1:66:TYR:CD1	2.52	0.93
1:A:861:ARG:HH21	24:X:78:MET:CE	1.81	0.93
1:A:1994:LYS:HB3	26:Z:756:TYR:CB	1.99	0.93
8:H:40:C:O2'	8:H:41:U:C5'	2.16	0.93
28:z:92:PHE:HE2	28:z:96:LEU:HD11	1.34	0.93
1:A:1719:PHE:CB	1:A:1720:PRO:HD2	1.99	0.93
1:A:1790:ILE:HD13	27:2:76:SER:CB	1.98	0.93
7:G:27:U:O2'	7:G:28:A:O5'	1.84	0.93
7:G:100:C:H2'	7:G:101:U:H6	1.29	0.92
1:A:1994:LYS:CB	26:Z:756:TYR:HB2	1.97	0.92
1:A:1523:ARG:CB	7:G:124:G:C8	2.52	0.92
1:A:1772:PHE:HD1	1:A:1813:ARG:CG	1.81	0.92
1:A:1502:PHE:HE1	1:A:1754:TYR:HB2	1.33	0.92
1:A:1719:PHE:HB2	1:A:1720:PRO:CD	1.98	0.92
7:G:27:U:C2'	7:G:28:A:O5'	2.15	0.92
12:L:10:VAL:HG21	24:X:86:GLU:HG3	1.52	0.92
1:A:2008:ARG:O	1:A:2011:ILE:HB	1.70	0.92
1:A:1621:LYS:HD3	28:z:92:PHE:HZ	1.35	0.92
1:A:1793:THR:HG21	5:F:43:A:C5'	1.99	0.92
1:A:1781:ASP:OD1	1:A:1783:THR:CB	2.16	0.91
1:A:166:PHE:HB3	1:A:167:PRO:HD2	1.49	0.91
3:C:667:VAL:H	3:C:824:THR:HG23	1.35	0.91
11:K:15:ALA:CB	41:s:112:ALA:O	2.18	0.91
1:A:1597:PHE:O	1:A:1600:GLU:N	2.03	0.91
8:H:40:C:O2'	8:H:41:U:O4'	1.87	0.91
9:I:698:ARG:HA	9:I:698:ARG:NE	1.79	0.91
3:C:666:VAL:HG13	3:C:823:ALA:O	1.70	0.91
22:V:457:ARG:HH12	44:1:88:GLN:CG	1.84	0.91
35:l:14:MET:HE1	36:n:10:LYS:HE2	1.50	0.91
8:H:30:A:C1'	24:X:73:PHE:HE1	1.83	0.91
8:H:168:A:C1'	36:n:48:MET:HE1	2.01	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1705:ILE:CG2	1:A:1734:MET:HE3	2.01	0.91
1:A:1934:SER:HG	44:1:344:GLN:HA	1.18	0.91
26:Z:758:ARG:HB3	26:Z:758:ARG:HH11	1.35	0.91
1:A:535:ARG:NH2	28:z:108:VAL:N	2.17	0.91
17:Q:878:ARG:HA	17:Q:1036:ALA:O	1.69	0.90
1:A:152:ARG:O	44:1:134:PHE:CD1	2.24	0.90
24:X:113:LYS:HZ2	24:X:113:LYS:HA	1.36	0.90
1:A:1790:ILE:HD13	27:2:76:SER:HG	1.29	0.90
1:A:613:TYR:HE2	45:A:3000:IHP:O45	1.52	0.90
8:H:39:U:O2'	8:H:40:C:OP1	1.87	0.90
9:I:276:ARG:CB	17:Q:357:ALA:HB3	2.02	0.90
1:A:1502:PHE:CE1	1:A:1754:TYR:HB2	2.06	0.90
1:A:535:ARG:NH2	28:z:108:VAL:CA	2.34	0.90
12:L:5:MET:N	12:L:5:MET:SD	2.45	0.90
1:A:1521:ALA:HB3	7:G:119:A:HI'	1.52	0.90
1:A:1894:GLN:HA	1:A:1897:LEU:HD12	1.52	0.89
8:H:168:A:HI'	36:n:48:MET:CE	2.01	0.89
1:A:1681:ARG:HB3	1:A:1681:ARG:CZ	2.01	0.89
1:A:1861:ILE:CD1	1:A:1882:ILE:CG2	2.50	0.89
9:I:187:LEU:HA	9:I:196:ALA:CB	2.02	0.89
16:P:16:ARG:HH12	18:R:220:ARG:HA	1.37	0.89
1:A:1994:LYS:NZ	27:2:67:VAL:HG22	1.88	0.89
8:H:20:G:O4'	16:P:7:PRO:HB3	1.72	0.89
35:l:14:MET:CE	36:n:10:LYS:HD3	2.02	0.89
16:P:212:ASN:HB3	20:T:458:SER:H	1.31	0.89
1:A:1135:PRO:HD2	1:A:1138:ALA:CB	2.01	0.89
7:G:21:A:C1'	15:O:152:ARG:HH21	1.75	0.89
1:A:1771:LEU:CA	1:A:1777:ILE:HD12	2.02	0.89
7:G:95:U:H2'	7:G:96:U:C5	2.07	0.89
18:R:106:GLN:HE22	18:R:225:PRO:HG2	1.35	0.89
27:2:138:LYS:HE2	27:2:138:LYS:HA	1.55	0.89
1:A:2002:LEU:HD23	1:A:2002:LEU:H	1.38	0.89
7:G:20:A:O2'	7:G:21:A:OP2	1.91	0.89
27:2:48:ILE:CA	34:m:5:LEU:HD21	2.01	0.89
8:H:168:A:H5''	8:H:168:A:H8	1.37	0.88
1:A:1770:GLU:CD	44:1:316:ARG:HG3	1.98	0.88
8:H:39:U:H5''	8:H:39:U:C6	2.07	0.88
8:H:77:C:P	23:W:242:HIS:CE1	2.65	0.88
5:F:88:G:H5''	13:M:133:ARG:HH22	1.37	0.88
7:G:100:C:C2	7:G:101:U:C5	2.61	0.88
1:A:535:ARG:HH22	28:z:108:VAL:HA	1.33	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:124:G:N3	7:G:124:G:O2'	2.05	0.88
1:A:537:LYS:HD2	5:F:37:C:H42	1.39	0.88
1:A:1685:LEU:HD13	44:1:173:TYR:CD2	2.07	0.88
1:A:1737:ASN:OD1	1:A:1738:PRO:CD	2.20	0.88
17:Q:849:THR:HA	17:Q:1058:ASN:O	1.73	0.88
23:W:83:PRO:HB3	23:W:87:THR:HG1	1.09	0.88
1:A:1471:ARG:HD3	44:1:66:TYR:CG	2.08	0.88
1:A:1685:LEU:HD11	44:1:173:TYR:CD2	2.08	0.88
9:I:688:TYR:O	9:I:703:PHE:HZ	1.56	0.88
9:I:731:GLN:O	9:I:731:GLN:NE2	2.07	0.88
5:F:88:G:C5'	13:M:133:ARG:HH22	1.86	0.88
5:F:45:A:O2'	5:F:73:A:N3	2.05	0.88
1:A:775:ASN:O	1:A:775:ASN:ND2	2.07	0.88
1:A:2002:LEU:HA	1:A:2006:GLU:OE1	1.74	0.88
12:L:4:ILE:CD1	24:X:78:MET:HE3	2.02	0.87
2:B:95:G:H5''	33:d:47:ARG:HH22	1.38	0.87
28:z:68:MET:HE3	28:z:68:MET:C	1.99	0.87
1:A:857:ASN:N	1:A:857:ASN:OD1	2.06	0.87
1:A:1471:ARG:HD3	44:1:66:TYR:CZ	2.09	0.87
1:A:1615:HIS:NE2	1:A:1626:CYS:SG	2.47	0.87
1:A:1685:LEU:HD13	44:1:173:TYR:CG	2.09	0.87
1:A:1475:ILE:HD11	44:1:66:TYR:HE2	1.38	0.87
1:A:1945:VAL:O	27:2:67:VAL:HG11	1.75	0.87
1:A:1994:LYS:HZ3	27:2:67:VAL:HG22	1.38	0.87
3:C:750:LEU:HA	3:C:753:GLU:HB2	1.57	0.87
8:H:156:U:H6	8:H:156:U:C5'	1.88	0.87
9:I:273:GLU:CA	17:Q:357:ALA:CB	2.23	0.87
29:b:46:ASP:OD2	29:b:64:LYS:HE3	1.75	0.87
7:G:22:C:O2'	7:G:23:U:OP1	1.91	0.87
24:X:72:GLN:NE2	24:X:72:GLN:O	2.08	0.87
1:A:1502:PHE:HD1	1:A:1502:PHE:H	1.22	0.86
1:A:1772:PHE:CA	1:A:1813:ARG:CD	2.45	0.86
1:A:1889:LEU:HD11	1:A:2012:LEU:CB	2.02	0.86
7:G:120:G:H5'	7:G:120:G:C8	2.09	0.86
8:H:154:C:O2	8:H:176:G:N2	2.07	0.86
1:A:240:ARG:HH11	44:1:139:ARG:HB3	1.36	0.86
1:A:1471:ARG:CD	44:1:66:TYR:CG	2.58	0.86
3:C:818:SER:O	3:C:822:MET:CG	2.22	0.86
29:i:46:ASP:OD2	29:i:64:LYS:HE3	1.75	0.86
1:A:1849:ILE:HG23	1:A:1857:GLN:HG2	0.92	0.86
4:E:59:ILE:HD11	23:W:82:ASN:ND2	1.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:LYS:HE3	44:1:170:TRP:CH2	2.10	0.86
27:2:52:MET:HB2	35:l:28:ARG:HH21	1.35	0.86
35:l:14:MET:CE	36:n:10:LYS:HE2	2.04	0.86
1:A:1725:LEU:O	1:A:1725:LEU:HD12	1.74	0.86
1:A:1596:VAL:CG2	44:1:278:LEU:HD11	2.06	0.86
1:A:1701:VAL:HG23	1:A:1718:TRP:CZ2	2.00	0.86
1:A:2002:LEU:HB3	1:A:2006:GLU:OE1	1.75	0.86
19:S:85:GLU:O	19:S:127:THR:HG23	1.74	0.86
9:I:692:SER:HA	9:I:695:CYS:HB2	1.57	0.86
9:I:717:GLU:HB3	24:X:112:LEU:HD21	1.57	0.86
23:W:83:PRO:CB	23:W:87:THR:HG1	1.89	0.86
1:A:2015:GLU:HG2	24:X:55:TYR:CE2	2.11	0.86
1:A:1771:LEU:HA	1:A:1777:ILE:HD13	1.57	0.85
5:F:33:G:H5''	5:F:33:G:H8	1.41	0.85
10:J:198:ALA:O	10:J:201:ARG:HB2	1.76	0.85
1:A:1596:VAL:CG2	44:1:278:LEU:HD21	2.07	0.85
1:A:1621:LYS:CD	28:z:92:PHE:HZ	1.89	0.85
7:G:99:C:H2'	7:G:100:C:H5''	1.57	0.85
1:A:1724:PRO:N	1:A:1724:PRO:C	2.33	0.85
1:A:1523:ARG:CB	7:G:124:G:H8	1.89	0.85
1:A:1798:LEU:HB2	7:G:96:U:C4'	2.07	0.85
9:I:230:GLN:CB	9:I:240:VAL:CB	2.54	0.85
30:y:13:LEU:CB	30:y:48:GLY:O	2.25	0.85
1:A:1481:VAL:HG21	44:1:67:ILE:HG23	1.57	0.85
17:Q:851:ILE:HA	17:Q:1060:LEU:O	1.76	0.85
1:A:1556:ASP:CA	28:z:103:TYR:CE2	2.54	0.85
1:A:1896:CYS:HB2	1:A:1940:LEU:CD2	2.07	0.85
2:B:95:G:H4'	2:B:96:A:O4'	1.77	0.85
8:H:98:G:N2	34:m:66:CYS:SG	2.50	0.85
1:A:1778:TRP:CZ2	1:A:1818:PHE:HE2	1.92	0.84
1:A:2014:MET:N	1:A:2014:MET:SD	2.50	0.84
17:Q:820:MET:O	17:Q:1130:THR:HA	1.76	0.84
1:A:1991:TYR:HE1	26:Z:756:TYR:CD2	1.94	0.84
1:A:1759:THR:HG21	44:1:288:LYS:CD	2.06	0.84
19:S:37:LYS:NZ	19:S:37:LYS:HB2	1.92	0.84
1:A:1793:THR:CG2	5:F:43:A:H5''	2.07	0.84
1:A:158:ARG:HD2	1:A:161:PHE:CD1	2.12	0.84
9:I:187:LEU:CA	9:I:196:ALA:HB1	2.07	0.84
44:1:274:TYR:HD1	44:1:274:TYR:H	1.26	0.84
1:A:1760:GLU:OE2	1:A:1885:LYS:NZ	2.11	0.84
20:T:455:GLN:CG	20:T:456:PRO:HD2	2.05	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:154:C:OP2	43:p:19:LYS:CG	2.24	0.84
1:A:535:ARG:HH12	28:z:108:VAL:CA	1.90	0.84
8:H:18:U:OP2	13:M:221:LYS:NZ	2.10	0.84
1:A:861:ARG:HH21	24:X:78:MET:HE1	1.40	0.84
1:A:2004:GLN:HB3	44:1:342:HIS:HE2	1.42	0.84
17:Q:877:LEU:O	17:Q:1036:ALA:N	2.09	0.84
1:A:1883:VAL:HG22	44:1:291:ALA:HB2	1.60	0.83
1:A:1895:ALA:CB	1:A:1944:HIS:HB3	2.08	0.83
1:A:2007:ILE:O	1:A:2011:ILE:HD13	1.77	0.83
1:A:1644:LEU:CD2	1:A:1681:ARG:CD	2.56	0.83
2:B:18:C:O2'	2:B:19:A:O5'	1.96	0.83
1:A:1617:ARG:HD3	28:z:96:LEU:CB	2.08	0.83
1:A:1258:LYS:HE2	7:G:126:G:C4'	2.09	0.83
1:A:1808:PHE:CE1	1:A:1897:LEU:HD21	2.14	0.83
1:A:1569:LEU:HD12	1:A:1569:LEU:O	1.78	0.83
4:E:266:PRO:CG	12:L:785:GLN:CB	2.54	0.83
5:F:8:C:H5''	5:F:8:C:C6	2.11	0.83
13:M:118:LYS:HD3	13:M:118:LYS:N	1.87	0.83
1:A:1759:THR:HB	44:1:289:THR:HG23	1.61	0.83
1:A:1873:GLU:HA	44:1:290:ARG:NH2	1.94	0.83
3:C:751:PRO:HG2	21:U:63:LYS:CB	2.09	0.83
25:Y:426:LEU:HD23	25:Y:427:PRO:HD2	1.60	0.83
8:H:154:C:P	43:p:19:LYS:HD3	2.19	0.83
16:P:16:ARG:NH1	18:R:220:ARG:HA	1.94	0.83
1:A:1321:GLU:CB	44:1:66:TYR:OH	2.26	0.82
12:L:10:VAL:HG22	24:X:86:GLU:HG3	1.58	0.82
1:A:1793:THR:CG2	5:F:43:A:C5'	2.57	0.82
20:T:197:TYR:CD2	20:T:488:VAL:HG12	2.13	0.82
1:A:861:ARG:HB3	1:A:861:ARG:NH1	1.93	0.82
4:E:93:TRP:CH2	29:b:105:GLY:CA	2.63	0.82
8:H:105:G:C2'	8:H:106:G:H5''	2.10	0.82
9:I:727:ARG:HH21	9:I:727:ARG:CB	1.92	0.82
3:C:668:GLU:N	3:C:824:THR:HG21	1.94	0.82
8:H:40:C:O2'	8:H:41:U:C6	2.33	0.82
8:H:152:G:N2	8:H:153:A:N7	2.27	0.82
12:L:124:LYS:HE2	12:L:129:ASP:CG	2.04	0.82
17:Q:89:ALA:O	17:Q:93:SER:CB	2.28	0.82
1:A:361:HIS:HE1	22:V:324:HIS:CA	1.92	0.82
5:F:22:A:N7	23:W:130:ARG:HD3	1.94	0.82
1:A:165:ARG:H	1:A:165:ARG:HD3	1.42	0.82
1:A:1673:SER:HB2	44:1:164:ASP:OD2	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:727:GLU:HB2	26:Z:754:TYR:OH	1.79	0.82
28:z:65:PHE:CZ	28:z:69:GLN:NE2	2.48	0.82
8:H:152:G:OP2	27:2:127:ARG:HD3	1.79	0.82
8:H:152:G:H5''	8:H:153:A:OP2	1.80	0.82
9:I:84:HIS:CB	9:I:90:PRO:CA	2.56	0.82
9:I:704:TRP:CZ3	9:I:727:ARG:CG	2.62	0.82
9:I:728:ARG:NH2	12:L:62:GLU:OE2	2.12	0.82
1:A:1617:ARG:HH12	28:z:99:LEU:HD22	1.43	0.81
1:A:2002:LEU:CB	1:A:2006:GLU:OE1	2.28	0.81
1:A:532:THR:OG1	7:G:3:A:O5'	1.98	0.81
1:A:1808:PHE:CZ	1:A:1893:PHE:HD1	1.98	0.81
9:I:728:ARG:HH21	9:I:728:ARG:HG2	1.43	0.81
11:K:36:VAL:O	41:r:112:ALA:HB1	1.79	0.81
1:A:1895:ALA:HB2	1:A:1944:HIS:HB3	1.63	0.81
1:A:1993:LYS:HZ1	26:Z:726:ARG:HD3	1.45	0.81
7:G:126:G:H2'	7:G:126:G:N3	1.96	0.81
1:A:1578:ARG:CB	1:A:1578:ARG:HH11	1.92	0.81
1:A:1596:VAL:CG1	44:1:278:LEU:HD11	2.11	0.81
5:F:80:G:H5''	5:F:81:C:OP2	1.81	0.81
27:2:48:ILE:CG1	34:m:5:LEU:HD21	2.10	0.81
1:A:1133:CYS:SG	1:A:1234:ASP:OD2	2.38	0.81
35:l:14:MET:CE	36:n:10:LYS:CD	2.57	0.81
7:G:20:A:C2	15:O:187:THR:OG1	2.33	0.81
1:A:343:GLU:HA	1:A:343:GLU:OE2	1.81	0.81
7:G:120:G:H3'	7:G:120:G:OP2	1.81	0.81
8:H:40:C:C4'	8:H:41:U:OP1	2.27	0.81
1:A:1481:VAL:CG2	44:1:85:GLN:NE2	2.44	0.81
1:A:1896:CYS:HB2	1:A:1940:LEU:HD22	1.62	0.80
9:I:717:GLU:CB	24:X:112:LEU:HD21	2.11	0.80
23:W:264:ASN:OD1	23:W:264:ASN:N	2.12	0.80
23:W:84:THR:HG22	23:W:86:GLU:H	1.46	0.80
1:A:861:ARG:NH2	24:X:78:MET:HE1	1.95	0.80
1:A:1895:ALA:HB2	1:A:1944:HIS:CB	2.11	0.80
8:H:39:U:H3'	8:H:40:C:C5	2.16	0.80
24:X:68:GLU:OE2	24:X:68:GLU:HA	1.81	0.80
3:C:753:GLU:OE2	3:C:759:LEU:HD23	1.82	0.80
5:F:83:A:OP2	10:J:247:LYS:HD2	1.81	0.80
1:A:1617:ARG:NH1	28:z:99:LEU:HD22	1.95	0.80
5:F:45:A:N3	5:F:73:A:H1'	1.97	0.80
7:G:83:A:O2'	7:G:84:U:OP2	1.99	0.80
24:X:113:LYS:HA	24:X:113:LYS:NZ	1.96	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:116:ARG:CB	24:X:116:ARG:HH11	1.94	0.80
27:2:51:LYS:NZ	35:l:28:ARG:HD3	1.96	0.80
1:A:344:ASP:N	1:A:344:ASP:OD1	2.13	0.80
3:C:756:LYS:O	3:C:760:GLY:N	2.14	0.80
5:F:45:A:N6	7:G:120:G:C5	2.49	0.80
44:1:185:TYR:HE2	44:1:188:VAL:HG11	1.45	0.80
28:z:58:ARG:HH12	44:1:177:GLU:CD	1.89	0.80
9:I:681:ILE:HD13	9:I:714:HIS:HB3	1.63	0.80
26:Z:758:ARG:HH11	26:Z:758:ARG:CB	1.94	0.80
1:A:1774:ASN:ND2	44:1:318:THR:CG2	2.45	0.79
3:C:673:LYS:HZ2	21:U:56:ASP:CB	1.92	0.79
9:I:273:GLU:HA	17:Q:357:ALA:HB2	0.80	0.79
1:A:1688:THR:HB	44:1:181:ILE:CD1	2.12	0.79
9:I:724:LEU:CD1	24:X:108:GLU:HG2	2.12	0.79
1:A:1716:GLY:O	1:A:1718:TRP:CD1	2.36	0.79
1:A:1859:LYS:N	1:A:1859:LYS:HD2	1.96	0.79
1:A:1889:LEU:CD1	1:A:1891:LEU:HD21	2.12	0.79
8:H:40:C:H2'	8:H:41:U:C6	2.16	0.79
8:H:46:U:OP1	27:2:44:LYS:HE2	1.82	0.79
9:I:286:VAL:CB	9:I:348:VAL:HA	2.12	0.79
24:X:96:GLN:HA	24:X:96:GLN:HE21	1.47	0.79
1:A:240:ARG:HH12	44:1:139:ARG:HB3	1.41	0.79
5:F:43:A:H2	7:G:4:A:H61	1.31	0.79
35:e:20:LEU:HD22	35:e:24:TYR:CE2	2.18	0.79
34:m:2:SER:HB2	35:l:48:ILE:HG23	1.63	0.79
3:C:276:TYR:CE2	22:V:324:HIS:CB	2.66	0.79
7:G:21:A:OP2	15:O:193:LEU:CD2	2.30	0.79
20:T:197:TYR:CE2	20:T:488:VAL:HG11	2.18	0.79
1:A:1991:TYR:CE1	26:Z:756:TYR:CZ	2.71	0.79
5:F:86:U:HO2'	5:F:87:C:P	2.04	0.79
9:I:692:SER:HB2	9:I:703:PHE:CE2	2.17	0.79
12:L:124:LYS:HE3	12:L:129:ASP:OD2	1.83	0.79
8:H:101:U:H5''	8:H:102:U:H5'	1.64	0.78
24:X:101:GLU:OE2	24:X:104:ARG:HD2	1.84	0.78
1:A:613:TYR:CE2	45:A:3000:IHP:O45	2.35	0.78
28:z:92:PHE:CE2	28:z:96:LEU:HD11	2.18	0.78
34:m:4:PRO:HD3	35:l:25:LEU:HD21	1.64	0.78
1:A:1919:LEU:O	1:A:1919:LEU:HD13	1.82	0.78
8:H:153:A:H2'	8:H:154:C:H5'	1.65	0.78
16:P:212:ASN:HB3	20:T:458:SER:CA	2.13	0.78
1:A:156:ARG:NH1	44:1:134:PHE:CD2	2.52	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1861:ILE:CD1	1:A:1882:ILE:HG22	2.13	0.78
5:F:29:A:N6	7:G:16:G:O2'	2.16	0.78
9:I:720:ILE:HG21	24:X:112:LEU:HD23	1.63	0.78
35:l:20:LEU:HD22	35:l:24:TYR:CE2	2.18	0.78
8:H:177:A:H5''	8:H:178:A:OP1	1.84	0.78
1:A:620:PRO:HD2	44:1:134:PHE:CZ	2.19	0.78
1:A:1556:ASP:C	28:z:103:TYR:HE2	1.91	0.78
28:z:72:ARG:HG2	28:z:72:ARG:HH21	1.47	0.78
41:q:60:PRO:CB	41:s:93:ARG:O	2.32	0.78
31:h:47:THR:CB	42:o:65:ARG:NH2	2.47	0.78
1:A:1991:TYR:CE1	26:Z:756:TYR:CD2	2.71	0.78
16:P:16:ARG:HH21	16:P:16:ARG:HG3	1.49	0.78
41:t:8:SER:O	41:t:9:ASN:CB	2.32	0.78
1:A:106:MET:CE	1:A:561:HIS:NE2	2.47	0.77
41:q:106:ALA:HB1	41:t:106:ALA:CB	2.14	0.77
1:A:1807:ILE:O	1:A:1819:LEU:HD12	1.84	0.77
5:F:36:A:H2'	5:F:37:C:O5'	1.84	0.77
1:A:169:PHE:HE1	1:A:563:GLN:HE21	1.29	0.77
44:1:34:ARG:CB	44:1:34:ARG:HH11	1.97	0.77
27:2:51:LYS:NZ	35:l:28:ARG:CD	2.48	0.77
18:R:218:ILE:H	18:R:218:ILE:HD12	1.48	0.77
24:X:113:LYS:HA	24:X:113:LYS:CE	2.14	0.77
34:f:70:LEU:HD22	34:f:71:TYR:HD2	1.50	0.77
41:q:60:PRO:O	41:s:93:ARG:CB	2.32	0.77
1:A:1759:THR:CB	44:1:288:LYS:HE3	2.14	0.77
7:G:82:G:H4'	23:W:541:LYS:HZ3	0.66	0.77
24:X:58:LEU:HD22	24:X:58:LEU:C	2.10	0.77
22:V:460:TYR:CE1	44:1:72:TRP:HZ2	2.02	0.77
1:A:1993:LYS:NZ	26:Z:726:ARG:HD3	1.98	0.77
8:H:33:G:O2'	27:2:68:MET:HE3	1.85	0.77
1:A:1778:TRP:CE3	1:A:1809:ILE:CG2	2.66	0.77
9:I:231:ASN:O	9:I:267:ILE:CB	2.33	0.77
1:A:1132:LYS:HZ3	1:A:1132:LYS:HB2	1.50	0.77
24:X:72:GLN:HA	24:X:72:GLN:HE21	1.50	0.77
35:e:48:ILE:HD11	35:e:59:ASP:HB2	1.66	0.77
5:F:45:A:O2'	5:F:73:A:C2	2.38	0.76
1:A:160:HIS:CE1	44:1:170:TRP:HA	2.19	0.76
1:A:1701:VAL:HG22	1:A:1718:TRP:HH2	1.49	0.76
2:B:90:U:H5''	2:B:91:U:H5'	1.65	0.76
8:H:39:U:H2'	8:H:40:C:C6	2.20	0.76
9:I:109:MET:N	30:y:66:ASN:CB	2.49	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1759:THR:OG1	44:1:288:LYS:HE3	1.85	0.76
1:A:1774:ASN:HD21	44:1:318:THR:CG2	1.98	0.76
22:V:499:GLN:OE1	22:V:499:GLN:HA	1.85	0.76
31:h:45:ASN:OD1	42:o:16:THR:CB	2.34	0.76
1:A:159:ARG:HG2	44:1:104:ARG:HB2	1.67	0.76
4:E:266:PRO:HG2	12:L:785:GLN:CA	2.15	0.76
1:A:1772:PHE:O	1:A:1813:ARG:HD2	1.85	0.76
27:2:52:MET:HE2	34:m:3:LEU:HD13	1.65	0.76
41:q:106:ALA:HB1	41:t:106:ALA:HB1	1.64	0.76
1:A:347:LEU:N	1:A:347:LEU:HD23	2.01	0.76
5:F:22:A:C8	23:W:130:ARG:NE	2.53	0.76
12:L:49:ARG:NH1	12:L:133:GLU:O	2.19	0.76
27:2:68:MET:HG3	27:2:68:MET:O	1.85	0.76
34:m:70:LEU:HD22	34:m:71:TYR:HD2	1.49	0.76
8:H:98:G:H1	34:m:41:ASN:HD21	1.34	0.76
1:A:1578:ARG:HH11	1:A:1578:ARG:HB2	1.51	0.76
8:H:143:A:H3'	8:H:143:A:N3	2.00	0.76
33:d:50:LYS:HG2	33:d:74:TRP:HB3	1.68	0.76
41:q:8:SER:O	41:q:9:ASN:CB	2.34	0.76
3:C:670:SER:HA	3:C:823:ALA:HB2	1.66	0.76
36:g:35:ASP:HB2	36:g:36:PRO:HD2	1.68	0.76
35:l:48:ILE:HD11	35:l:59:ASP:HB2	1.66	0.76
7:G:21:A:C1'	15:O:152:ARG:HH22	1.97	0.75
1:A:1891:LEU:HD22	1:A:2012:LEU:HD12	1.69	0.75
24:X:113:LYS:C	24:X:113:LYS:HD3	2.11	0.75
1:A:861:ARG:NH2	24:X:78:MET:CE	2.50	0.75
1:A:1861:ILE:N	1:A:1861:ILE:HD12	2.00	0.75
7:G:100:C:C2'	7:G:101:U:H6	1.98	0.75
1:A:470:ARG:HH21	1:A:470:ARG:HG2	1.52	0.75
3:C:670:SER:HA	3:C:823:ALA:CB	2.16	0.75
17:Q:99:ASN:O	17:Q:103:ARG:CB	2.35	0.75
24:X:95:ARG:CZ	24:X:95:ARG:HB2	2.13	0.75
1:A:1578:ARG:HD3	1:A:1746:ARG:CZ	2.16	0.75
1:A:1694:ILE:CD1	28:z:88:ARG:CD	2.63	0.75
1:A:1701:VAL:CG2	1:A:1718:TRP:HH2	1.44	0.75
5:F:5:U:H3'	5:F:7:G:H5''	1.68	0.75
24:X:54:LEU:HD23	24:X:54:LEU:N	2.02	0.75
24:X:113:LYS:HZ2	24:X:113:LYS:CA	2.00	0.75
1:A:435:CYS:CB	6:4-11:G:H22	1.99	0.75
1:A:1770:GLU:CD	44:1:316:ARG:CG	2.60	0.75
1:A:1798:LEU:HD13	7:G:95:U:O2'	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2002:LEU:CA	1:A:2006:GLU:OE1	2.34	0.75
1:A:1596:VAL:HG22	44:1:278:LEU:HD11	1.67	0.75
1:A:1809:ILE:O	1:A:1817:LEU:HD12	1.87	0.75
44:1:273:LYS:CD	44:1:292:MET:HG3	2.17	0.75
9:I:329:LEU:CB	17:Q:353:LEU:HA	2.16	0.75
11:K:90:PRO:CB	11:K:109:ASN:CB	2.64	0.74
22:V:457:ARG:HG3	44:1:73:TYR:HD2	1.52	0.74
41:s:8:SER:O	41:s:9:ASN:CB	2.34	0.74
1:A:705:LYS:HG2	8:H:15:U:C5	2.22	0.74
1:A:1596:VAL:HG21	44:1:278:LEU:HD21	1.69	0.74
7:G:27:U:H2'	7:G:28:A:O5'	1.86	0.74
33:d:110:LEU:HD11	34:f:59:LEU:HB3	1.70	0.74
1:A:346:ASP:OD1	1:A:346:ASP:N	2.18	0.74
1:A:1774:ASN:OD1	44:1:318:THR:HG23	1.87	0.74
8:H:152:G:P	27:2:127:ARG:HD3	2.28	0.74
1:A:106:MET:HE1	1:A:578:LEU:HD13	1.69	0.74
1:A:1891:LEU:N	1:A:1891:LEU:HD23	2.02	0.74
1:A:1994:LYS:NZ	27:2:67:VAL:CG2	2.51	0.74
33:k:107:ILE:HG22	33:k:108:VAL:HG23	1.69	0.74
34:m:70:LEU:HD22	34:m:71:TYR:CD2	2.23	0.74
1:A:1578:ARG:HH11	1:A:1578:ARG:CG	2.01	0.74
8:H:30:A:H4'	24:X:73:PHE:HZ	1.52	0.74
9:I:726:ILE:HD13	9:I:729:SER:HB3	1.68	0.74
36:n:35:ASP:HB2	36:n:36:PRO:HD2	1.67	0.74
44:1:275:LEU:HD22	44:1:278:LEU:HD21	1.66	0.74
1:A:1617:ARG:CG	28:z:96:LEU:HB3	2.18	0.74
1:A:1759:THR:HG21	44:1:288:LYS:HD3	1.70	0.74
8:H:40:C:C2'	8:H:41:U:C6	2.71	0.74
9:I:721:LYS:HZ1	12:L:65:ARG:NH2	1.84	0.74
28:z:63:ALA:O	28:z:67:LYS:N	2.19	0.74
1:A:1526:LEU:HD12	7:G:124:G:C6	2.20	0.74
1:A:1774:ASN:HD21	44:1:318:THR:HG23	1.52	0.74
8:H:106:G:H4'	8:H:107:A:O4'	1.88	0.74
19:S:85:GLU:O	19:S:127:THR:CG2	2.36	0.74
1:A:1611:LYS:HA	1:A:1629:ILE:HG12	1.70	0.74
1:A:1759:THR:HA	44:1:286:ASP:OD2	1.88	0.74
2:B:19:A:O2'	2:B:20:G:OP1	2.04	0.74
7:G:26:U:H2'	7:G:27:U:H5''	1.69	0.74
1:A:1571:ILE:HD13	28:z:112:LYS:CE	2.18	0.73
1:A:1774:ASN:ND2	44:1:318:THR:HG23	2.03	0.73
1:A:2009:ASP:C	1:A:2013:GLY:H	1.96	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:k:50:LYS:HG2	33:k:74:TRP:HB3	1.68	0.73
1:A:1491:LYS:HD2	1:A:1709:TYR:HD1	1.52	0.73
4:E:93:TRP:CH2	29:b:105:GLY:HA3	2.23	0.73
9:I:728:ARG:O	9:I:731:GLN:HB3	1.88	0.73
27:2:140:LEU:C	27:2:140:LEU:HD12	2.13	0.73
7:G:99:C:C2'	7:G:100:C:H5'	2.19	0.73
16:P:16:ARG:HG3	16:P:16:ARG:NH2	2.02	0.73
33:d:107:ILE:HG22	33:d:108:VAL:HG23	1.69	0.73
2:B:46:U:O2	21:U:11:ARG:NH2	2.20	0.73
1:A:1642:PRO:HB2	44:1:175:PRO:HB3	1.71	0.73
1:A:1813:ARG:HB3	1:A:1813:ARG:NH1	2.03	0.73
9:I:661:ASP:HB2	9:I:694:ILE:CG2	2.13	0.73
33:k:110:LEU:HD11	34:m:59:LEU:HB3	1.70	0.73
1:A:821:ARG:CB	1:A:821:ARG:HH11	2.01	0.73
1:A:1615:HIS:HE2	1:A:1626:CYS:CB	2.00	0.73
1:A:1719:PHE:CD2	1:A:1720:PRO:HD2	2.24	0.73
1:A:1762:TYR:HB3	1:A:1886:GLY:O	1.88	0.73
5:F:57:U:O2'	16:P:8:THR:OG1	2.02	0.73
7:G:102:G:C2'	7:G:103:U:H5'	2.19	0.73
7:G:102:G:H2'	7:G:103:U:H5'	1.70	0.73
8:H:11:G:N7	13:M:198:ARG:NH2	2.36	0.73
8:H:179:C:H2'	8:H:180:G:H8	1.53	0.73
1:A:1740:LEU:HD13	1:A:1744:ARG:HH22	1.54	0.72
1:A:1764:SER:HA	1:A:1888:GLU:HB3	1.69	0.72
7:G:13:C:H2'	7:G:14:A:C8	2.24	0.72
7:G:100:C:H5'	7:G:100:C:H6	1.53	0.72
8:H:153:A:C2'	8:H:154:C:H5'	2.17	0.72
9:I:685:ARG:NE	9:I:711:GLU:OE2	2.19	0.72
26:Z:758:ARG:HH11	26:Z:758:ARG:CG	2.02	0.72
27:2:111:LYS:HA	27:2:114:GLU:HG2	1.70	0.72
31:h:47:THR:CB	42:o:65:ARG:HH22	2.02	0.72
5:F:28:A:O2'	14:N:39:GLY:CA	2.37	0.72
1:A:620:PRO:HD2	44:1:134:PHE:HZ	1.55	0.72
1:A:1980:GLU:OE2	44:1:348:THR:HG22	1.89	0.72
20:T:455:GLN:CG	20:T:456:PRO:CD	2.64	0.72
24:X:113:LYS:HD3	24:X:113:LYS:O	1.90	0.72
34:f:70:LEU:HD22	34:f:71:TYR:CD2	2.23	0.72
9:I:575:ARG:O	9:I:579:LEU:HB2	1.90	0.72
19:S:72:ARG:HD3	23:W:90:ALA:O	1.87	0.72
20:T:197:TYR:HD2	20:T:488:VAL:HG12	1.53	0.72
1:A:1571:ILE:CD1	28:z:112:LYS:HE3	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1774:ASN:OD1	1:A:1774:ASN:N	2.09	0.72
6:4:-12:G:O2'	6:4:-11:G:O5'	2.07	0.72
27:2:51:LYS:HZ3	35:l:28:ARG:CD	2.03	0.72
44:1:273:LYS:HD3	44:1:292:MET:HG3	1.69	0.72
1:A:1685:LEU:HD22	44:1:173:TYR:CZ	2.23	0.72
7:G:91:A:H2	8:H:39:U:O2	1.71	0.72
26:Z:758:ARG:HB3	26:Z:758:ARG:NH1	2.02	0.72
5:F:41:A:C2	7:G:6:A:C2	2.78	0.72
5:F:59:G:O2'	5:F:60:C:OP1	2.07	0.72
1:A:1617:ARG:NH2	28:z:99:LEU:HD22	2.05	0.72
8:H:30:A:C1'	24:X:73:PHE:CE1	2.65	0.72
23:W:82:ASN:N	23:W:83:PRO:HD2	2.05	0.72
1:A:1772:PHE:C	1:A:1813:ARG:HD3	2.13	0.72
8:H:40:C:O2'	8:H:41:U:H6	1.73	0.72
8:H:153:A:H2'	8:H:154:C:C5'	2.19	0.72
27:2:48:ILE:HG23	34:m:5:LEU:HD21	0.85	0.72
43:p:66:LEU:HD12	43:p:81:ILE:HG22	1.70	0.72
1:A:1833:LEU:HD22	1:A:1833:LEU:N	2.02	0.72
7:G:7:G:O2'	7:G:8:C:H5'	1.90	0.72
7:G:90:C:C5	7:G:90:C:OP2	2.43	0.72
1:A:609:LYS:NZ	45:A:3000:IHP:O31	2.23	0.71
5:F:31:U:C2'	5:F:32:U:H5'	2.19	0.71
5:F:36:A:C2'	5:F:37:C:O5'	2.38	0.71
12:L:6:ILE:HD13	12:L:6:ILE:C	2.15	0.71
20:T:282:ARG:HB2	20:T:320:LYS:HD3	1.72	0.71
1:A:1770:GLU:OE2	44:1:316:ARG:HG2	1.90	0.71
7:G:20:A:H2	15:O:187:THR:HG1	1.30	0.71
44:1:275:LEU:CD2	44:1:278:LEU:CD2	2.37	0.71
1:A:152:ARG:O	44:1:134:PHE:CE1	2.43	0.71
8:H:106:G:H21	8:H:107:A:N6	1.87	0.71
24:X:116:ARG:NH1	24:X:119:LEU:HD23	2.04	0.71
1:A:158:ARG:HD2	1:A:161:PHE:HD1	1.54	0.71
1:A:1705:ILE:CD1	1:A:1734:MET:HE2	2.14	0.71
7:G:21:A:C4	15:O:152:ARG:NH2	2.59	0.71
34:m:3:LEU:HG	34:m:4:PRO:HD2	1.70	0.71
7:G:20:A:HO2'	7:G:21:A:P	2.12	0.71
12:L:7:LYS:HB3	12:L:40:ARG:C	2.16	0.71
24:X:72:GLN:NE2	24:X:72:GLN:HA	2.05	0.71
1:A:1594:CYS:HB3	1:A:1629:ILE:HD11	1.72	0.71
5:F:45:A:H2	5:F:73:A:O4'	1.72	0.71
44:1:185:TYR:CD2	44:1:188:VAL:HB	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:981:PHE:CE2	1:A:1095:ILE:HD11	2.25	0.71
5:F:34:G:C5'	5:F:34:G:H8	2.03	0.71
5:F:35:A:C5'	5:F:35:A:H8	2.03	0.71
1:A:1501:LEU:N	1:A:1501:LEU:HD23	2.03	0.71
19:S:98:LEU:HB3	19:S:130:GLY:CA	2.20	0.71
25:Y:413:LYS:H	25:Y:413:LYS:HD2	1.55	0.71
26:Z:725:ASN:ND2	26:Z:725:ASN:O	2.23	0.71
5:F:84:A:N3	10:J:277:THR:HG21	2.06	0.71
9:I:727:ARG:HH21	9:I:727:ARG:CG	2.04	0.71
24:X:101:GLU:OE2	24:X:101:GLU:HA	1.91	0.71
27:2:137:LYS:HE3	27:2:140:LEU:HD21	1.72	0.71
1:A:1132:LYS:HB2	1:A:1132:LYS:NZ	2.06	0.71
5:F:45:A:C2	5:F:73:A:H1'	2.26	0.71
20:T:437:HIS:HD2	20:T:446:ASN:HD21	1.37	0.71
1:A:1596:VAL:HG13	44:1:278:LEU:HD11	1.73	0.70
1:A:1685:LEU:CD2	44:1:173:TYR:CE2	2.74	0.70
1:A:1776:ILE:HD13	1:A:1776:ILE:N	2.06	0.70
3:C:818:SER:HB3	3:C:822:MET:HE2	1.70	0.70
7:G:98:U:O2'	7:G:99:C:H6	1.73	0.70
24:X:96:GLN:HE21	24:X:96:GLN:CA	2.04	0.70
24:X:112:LEU:HD13	24:X:112:LEU:C	2.16	0.70
44:1:34:ARG:HH11	44:1:34:ARG:CA	2.04	0.70
1:A:1527:ASN:HD22	1:A:1527:ASN:H	1.38	0.70
12:L:4:ILE:O	12:L:4:ILE:HD13	1.90	0.70
5:F:41:A:H2	7:G:6:A:H2	1.38	0.70
8:H:151:C:P	27:2:131:ARG:NH1	2.65	0.70
27:2:48:ILE:CB	34:m:5:LEU:CD2	2.48	0.70
27:2:113:LEU:HD13	27:2:113:LEU:C	2.16	0.70
1:A:1471:ARG:HD3	44:1:66:TYR:CD2	2.26	0.70
1:A:1701:VAL:HG23	1:A:1718:TRP:HH2	0.93	0.70
1:A:163:ARG:NH2	45:A:3000:IHP:O35	2.22	0.70
1:A:2004:GLN:HB3	44:1:342:HIS:CD2	2.26	0.70
7:G:90:C:O2'	7:G:91:A:OP1	2.10	0.70
27:2:38:LEU:HD23	34:m:12:ASN:ND2	2.06	0.70
1:A:1873:GLU:HA	44:1:290:ARG:HH22	1.56	0.70
8:H:154:C:H2'	8:H:155:C:C6	2.27	0.70
12:L:7:LYS:CG	12:L:40:ARG:HA	2.22	0.70
1:A:684:GLU:HG2	20:T:308:ARG:HH12	1.56	0.70
1:A:1132:LYS:HG3	1:A:1139:ARG:HH12	1.55	0.70
1:A:1475:ILE:HD11	44:1:66:TYR:CE2	2.25	0.70
1:A:1771:LEU:CA	1:A:1777:ILE:CD1	2.59	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:106:G:C5'	33:k:47:ARG:HH22	2.05	0.70
1:A:1428:HIS:HB2	25:Y:396:ASP:HB3	1.73	0.70
1:A:1673:SER:HB2	44:1:164:ASP:CG	2.17	0.70
1:A:1873:GLU:CG	44:1:290:ARG:NH2	2.54	0.70
5:F:21:U:O2	23:W:168:PHE:CE1	2.44	0.70
34:m:2:SER:CB	35:l:48:ILE:CG2	2.60	0.70
7:G:98:U:O2'	7:G:99:C:C6	2.43	0.69
12:L:7:LYS:HB3	12:L:40:ARG:O	1.92	0.69
8:H:153:A:N6	8:H:177:A:C2	2.60	0.69
1:A:1617:ARG:HH22	28:z:99:LEU:HD22	1.57	0.69
3:C:666:VAL:CG1	3:C:823:ALA:O	2.39	0.69
5:F:31:U:O2'	5:F:32:U:H5'	1.92	0.69
9:I:187:LEU:CB	9:I:196:ALA:HB1	2.22	0.69
1:A:1698:PRO:CG	44:1:182:VAL:CB	2.66	0.69
1:A:1760:GLU:CD	1:A:1885:LYS:NZ	2.51	0.69
1:A:1882:ILE:HD13	1:A:1882:ILE:N	2.06	0.69
15:O:262:THR:HB	15:O:271:PHE:HB2	1.74	0.69
19:S:98:LEU:HD23	19:S:130:GLY:HA3	1.75	0.69
1:A:185:VAL:HG11	28:z:72:ARG:HH11	1.58	0.69
1:A:1556:ASP:HA	28:z:103:TYR:HD2	0.88	0.69
1:A:2002:LEU:HD23	1:A:2002:LEU:N	2.07	0.69
3:C:114:TYR:CB	31:a:79:ASN:HB3	2.23	0.69
5:F:42:C:H3'	5:F:43:A:C8	2.28	0.69
7:G:90:C:C5'	7:G:90:C:H6	2.04	0.69
8:H:150:U:H3	8:H:181:G:H1	1.41	0.69
1:A:1705:ILE:HD13	1:A:1734:MET:CE	2.14	0.69
1:A:1725:LEU:HD12	1:A:1725:LEU:C	2.15	0.69
1:A:1774:ASN:ND2	44:1:318:THR:HG21	2.08	0.69
1:A:1793:THR:CG2	5:F:43:A:H5'	2.21	0.69
1:A:1873:GLU:CA	44:1:290:ARG:HH22	2.05	0.69
7:G:90:C:O2'	7:G:91:A:P	2.50	0.69
8:H:10:C:N4	13:M:198:ARG:HH12	1.91	0.69
1:A:1596:VAL:HG23	44:1:275:LEU:HD22	0.70	0.69
1:A:1772:PHE:C	1:A:1813:ARG:CD	2.66	0.69
2:B:21:A:O3'	2:B:22:U:H4'	1.93	0.69
2:B:90:U:O4'	31:a:66:SER:HB3	1.92	0.69
5:F:85:U:H3'	5:F:86:U:H5'	1.75	0.69
24:X:58:LEU:HD22	24:X:58:LEU:O	1.92	0.69
1:A:1685:LEU:HD22	44:1:173:TYR:CE2	2.28	0.69
1:A:1698:PRO:HG3	44:1:181:ILE:HG13	1.75	0.69
1:A:1775:GLN:HE21	44:1:315:VAL:HB	1.55	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1778:TRP:HZ2	1:A:1818:PHE:CE2	2.04	0.69
3:C:853:ARG:HG2	3:C:879:ASP:HB3	1.74	0.69
5:F:7:G:H5'	5:F:7:G:H8	1.58	0.69
8:H:10:C:N4	13:M:198:ARG:NH1	2.40	0.69
12:L:6:ILE:HD13	12:L:6:ILE:O	1.93	0.69
19:S:37:LYS:HB2	19:S:37:LYS:HZ2	1.54	0.69
19:S:72:ARG:HG3	23:W:71:HIS:CE1	2.27	0.69
1:A:1774:ASN:CG	44:1:318:THR:HG23	2.18	0.69
1:A:1759:THR:HB	44:1:289:THR:CG2	2.23	0.69
8:H:101:U:O4'	31:h:66:SER:HB3	1.92	0.69
20:T:197:TYR:CE2	20:T:488:VAL:CG1	2.76	0.69
44:1:272:ALA:HB3	44:1:275:LEU:HB2	1.73	0.69
24:X:85:ASP:OD1	24:X:85:ASP:N	2.18	0.68
1:A:1527:ASN:HD22	1:A:1527:ASN:N	1.90	0.68
1:A:2011:ILE:HG22	1:A:2012:LEU:HD13	1.74	0.68
5:F:45:A:C6	7:G:120:G:C6	2.82	0.68
5:F:60:C:H5''	18:R:219:PRO:HD3	1.74	0.68
1:A:1615:HIS:HD2	28:z:89:VAL:HG22	1.58	0.68
1:A:1645:LEU:HD22	1:A:1713:SER:HA	1.74	0.68
9:I:720:ILE:HD13	9:I:723:MET:CE	2.23	0.68
44:1:268:ARG:HG2	44:1:268:ARG:O	1.92	0.68
5:F:24:A:C6	15:O:65:PHE:HE2	2.11	0.68
5:F:39:A:O2'	5:F:40:U:H5'	1.93	0.68
1:A:663:ARG:NH2	1:A:663:ARG:HG3	2.08	0.68
1:A:1774:ASN:CG	44:1:318:THR:CG2	2.66	0.68
1:A:1991:TYR:CD1	26:Z:756:TYR:CZ	2.82	0.68
1:A:156:ARG:NH1	44:1:153:GLU:OE2	2.27	0.68
1:A:1471:ARG:HD3	44:1:66:TYR:CE2	2.28	0.68
1:A:1503:TRP:HZ3	1:A:1533:ARG:CD	2.07	0.68
1:A:1751:LEU:N	1:A:1751:LEU:HD23	2.08	0.68
1:A:1829:GLY:HA3	5:F:40:U:OP1	1.94	0.68
19:S:71:GLY:C	19:S:111:GLN:HE22	2.00	0.68
28:z:72:ARG:HH21	28:z:72:ARG:CG	2.05	0.68
1:A:821:ARG:NH1	25:Y:426:LEU:HD11	2.05	0.68
3:C:750:LEU:HD23	3:C:750:LEU:C	2.18	0.68
9:I:727:ARG:HH21	9:I:727:ARG:HB3	1.58	0.68
25:Y:402:ILE:HG23	25:Y:411:LEU:HD11	1.75	0.68
1:A:162:LYS:CE	44:1:170:TRP:CH2	2.77	0.68
1:A:1135:PRO:CD	1:A:1138:ALA:HB3	2.19	0.68
1:A:1537:TRP:HE3	1:A:1751:LEU:HD13	1.57	0.68
5:F:88:G:C5'	13:M:133:ARG:NH2	2.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:40:C:H2'	8:H:41:U:C5	2.29	0.68
1:A:1621:LYS:HD3	28:z:92:PHE:CZ	2.25	0.68
8:H:143:A:H2'	8:H:144:C:H6	1.59	0.68
26:Z:756:TYR:CZ	26:Z:758:ARG:HA	2.28	0.68
1:A:105:ASN:HD22	1:A:129:VAL:HG11	1.59	0.68
1:A:1600:GLU:HG3	1:A:1725:LEU:CD2	2.24	0.68
5:F:45:A:C2	5:F:73:A:C1'	2.76	0.68
7:G:16:G:O2'	7:G:17:U:OP2	2.10	0.68
8:H:152:G:O3'	8:H:153:A:O4'	2.11	0.68
10:J:201:ARG:HG2	10:J:201:ARG:HH21	1.57	0.68
8:H:168:A:C8	8:H:168:A:C5'	2.76	0.67
26:Z:706:ALA:HB2	26:Z:725:ASN:HB2	1.75	0.67
1:A:1134:TRP:CB	1:A:1135:PRO:CD	2.70	0.67
1:A:1482:GLU:OE1	44:1:87:PRO:HD3	1.93	0.67
7:G:20:A:C2	15:O:187:THR:HG21	2.29	0.67
9:I:721:LYS:NZ	12:L:65:ARG:HH21	1.77	0.67
9:I:728:ARG:NH2	9:I:728:ARG:HG2	2.06	0.67
33:k:33:THR:HG22	33:k:37:LYS:HE2	1.76	0.67
1:A:1085:ILE:HG12	1:A:1099:PHE:HE1	1.59	0.67
1:A:1859:LYS:HA	1:A:1859:LYS:CE	2.15	0.67
3:C:673:LYS:HZ3	21:U:56:ASP:CB	2.05	0.67
41:q:53:ILE:CB	41:r:22:ASN:CB	2.73	0.67
1:A:1141:ARG:NH1	1:A:1183:PRO:HD2	2.09	0.67
19:S:98:LEU:HB3	19:S:130:GLY:HA3	1.76	0.67
1:A:1760:GLU:N	44:1:289:THR:HG21	2.06	0.67
10:J:179:VAL:HA	26:Z:738:CYS:O	1.93	0.67
29:b:18:ARG:NH1	29:b:52:LYS:HB2	2.09	0.67
41:q:60:PRO:CB	41:s:94:GLN:N	2.57	0.67
1:A:1526:LEU:CB	7:G:124:G:O6	2.43	0.67
1:A:1737:ASN:CG	1:A:1738:PRO:HD2	2.20	0.67
1:A:1890:GLN:HA	1:A:1890:GLN:NE2	2.09	0.67
5:F:79:C:C2	16:P:3:THR:HG23	2.29	0.67
1:A:1759:THR:HG22	44:1:286:ASP:OD2	1.94	0.67
1:A:1790:ILE:CD1	27:2:76:SER:OG	2.29	0.67
8:H:151:C:H2'	8:H:152:G:H8	1.60	0.67
21:U:23:LEU:H	22:V:474:HIS:HD2	1.42	0.67
1:A:1503:TRP:CZ3	1:A:1533:ARG:HD2	2.29	0.67
1:A:1741:TYR:HE2	44:1:288:LYS:HB2	1.58	0.67
1:A:1793:THR:HG22	5:F:43:A:H5'	1.76	0.67
5:F:21:U:O2	23:W:168:PHE:HE1	1.77	0.67
7:G:17:U:HI'	15:O:46:LYS:NZ	2.10	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:26:U:H2'	7:G:27:U:C5'	2.24	0.67
8:H:151:C:C2	8:H:152:G:C8	2.83	0.67
8:H:151:C:O2	8:H:152:G:C8	2.48	0.67
15:O:243:ILE:HG12	15:O:294:ASN:HD22	1.60	0.67
20:T:261:LEU:HB2	20:T:273:TRP:HB2	1.77	0.67
24:X:65:LYS:CB	26:Z:753:ARG:NH2	2.58	0.67
35:e:20:LEU:HD12	36:g:41:VAL:HG13	1.77	0.67
20:T:188:PRO:CG	20:T:443:THR:OG1	2.35	0.67
1:A:1471:ARG:HG2	44:1:66:TYR:CD2	2.30	0.66
1:A:1829:GLY:CA	5:F:40:U:OP1	2.43	0.66
23:W:73:ASP:OD2	23:W:74:PRO:HD3	1.94	0.66
42:o:5:THR:HG22	42:o:8:LEU:H	1.60	0.66
5:F:85:U:H3'	5:F:86:U:C5'	2.25	0.66
7:G:91:A:N1	8:H:39:U:O2	2.27	0.66
9:I:681:ILE:HG23	9:I:710:PHE:CE2	2.30	0.66
17:Q:88:LYS:O	17:Q:92:MET:N	2.23	0.66
1:A:698:PRO:HG2	1:A:701:ILE:HD13	1.75	0.66
1:A:1676:ILE:HD13	1:A:1706:ASP:HB2	1.77	0.66
5:F:33:G:H5''	5:F:33:G:C8	2.28	0.66
5:F:45:A:N6	7:G:120:G:N7	2.43	0.66
1:A:861:ARG:HH21	24:X:78:MET:HE2	1.57	0.66
1:A:1486:GLU:OE1	1:A:1674:HIS:NE2	2.29	0.66
1:A:1536:LEU:HD23	1:A:1536:LEU:O	1.96	0.66
1:A:1994:LYS:HD2	26:Z:756:TYR:HD1	1.58	0.66
7:G:95:U:H2'	7:G:96:U:C6	2.30	0.66
25:Y:402:ILE:HG23	25:Y:411:LEU:CD1	2.25	0.66
29:i:18:ARG:NH1	29:i:52:LYS:HB2	2.09	0.66
35:l:20:LEU:HD12	36:n:41:VAL:HG13	1.77	0.66
44:1:268:ARG:HG3	44:1:268:ARG:HH11	1.61	0.66
1:A:1532:ARG:HB3	1:A:1532:ARG:HH11	1.60	0.66
7:G:17:U:O2'	15:O:46:LYS:NZ	2.28	0.66
1:A:1611:LYS:O	1:A:1611:LYS:HG2	1.96	0.66
1:A:1617:ARG:CZ	28:z:99:LEU:HD22	2.24	0.66
8:H:30:A:H4'	24:X:73:PHE:CZ	2.31	0.66
8:H:67:C:H42	8:H:85:A:H61	1.44	0.66
24:X:64:ARG:NH1	24:X:64:ARG:HG3	2.11	0.66
24:X:116:ARG:N	24:X:116:ARG:HD2	2.09	0.66
30:y:38:PRO:N	30:y:38:PRO:C	2.53	0.66
1:A:1418:ARG:HE	1:A:1464:LEU:HD23	1.60	0.66
1:A:1569:LEU:HD12	1:A:1569:LEU:C	2.17	0.66
8:H:75:A:H61	8:H:77:C:H42	1.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:153:A:C3'	8:H:154:C:H5'	2.25	0.66
29:i:18:ARG:NH1	29:i:52:LYS:CB	2.58	0.66
1:A:2004:GLN:HE21	44:1:342:HIS:CD2	2.14	0.66
7:G:91:A:N1	8:H:39:U:C2	2.64	0.66
17:Q:100:GLU:O	17:Q:104:GLU:CB	2.43	0.66
1:A:109:PRO:HB2	1:A:191:ILE:HD12	1.77	0.66
1:A:166:PHE:HB3	1:A:167:PRO:CD	2.22	0.66
1:A:381:PRO:HD2	3:C:334:ILE:HG22	1.78	0.66
1:A:658:ARG:NH2	5:F:65:G:OP2	2.29	0.66
1:A:1780:VAL:CG2	1:A:1861:ILE:CG2	2.74	0.66
1:A:1849:ILE:CG2	1:A:1879:PHE:CE2	2.79	0.66
9:I:721:LYS:HZ1	12:L:65:ARG:HH22	1.44	0.66
15:O:223:LEU:HD22	15:O:285:GLU:HG2	1.78	0.66
27:2:109:PHE:HA	27:2:112:ARG:NH1	2.11	0.66
1:A:157:ASP:HB3	28:z:59:THR:HG22	1.77	0.66
1:A:1521:ALA:CB	7:G:119:A:H1'	2.23	0.66
8:H:41:U:H5''	8:H:41:U:H6	1.59	0.66
29:b:18:ARG:NH1	29:b:52:LYS:CB	2.58	0.66
1:A:1599:GLN:NE2	44:1:271:ILE:HD13	2.11	0.65
1:A:1759:THR:HG21	44:1:288:LYS:CG	2.24	0.65
2:B:95:G:H5'	34:f:25:TRP:CH2	2.21	0.65
5:F:45:A:C6	7:G:120:G:C5	2.85	0.65
1:A:1833:LEU:H	1:A:1833:LEU:CD2	2.02	0.65
1:A:2009:ASP:O	1:A:2013:GLY:O	2.14	0.65
7:G:17:U:H1'	15:O:46:LYS:HZ3	1.62	0.65
7:G:90:C:OP2	7:G:90:C:H5	1.78	0.65
8:H:40:C:O2'	8:H:41:U:C4'	2.44	0.65
8:H:114:A:H61	8:H:142:C:H42	1.44	0.65
1:A:199:GLU:HB3	44:1:139:ARG:HD2	1.77	0.65
1:A:1487:HIS:CE1	1:A:1671:TYR:CZ	2.85	0.65
5:F:6:C:OP2	5:F:6:C:H4'	1.95	0.65
18:R:64:PHE:O	18:R:71:GLN:NE2	2.29	0.65
18:R:136:ASP:HB3	18:R:138:GLU:H	1.60	0.65
24:X:100:ILE:O	24:X:103:GLN:CB	2.21	0.65
33:d:33:THR:HG22	33:d:37:LYS:HE2	1.76	0.65
1:A:525:LYS:HD3	28:z:100:THR:CG2	2.26	0.65
1:A:1556:ASP:C	28:z:103:TYR:CE2	2.72	0.65
1:A:1774:ASN:OD1	44:1:318:THR:CG2	2.43	0.65
3:C:476:CYS:HB3	3:C:565:ILE:HB	1.77	0.65
28:z:107:LYS:NZ	28:z:109:SER:OG	2.29	0.65
1:A:152:ARG:O	44:1:134:PHE:HD1	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1193:GLU:HB3	1:A:1231:ARG:HB3	1.79	0.65
1:A:1258:LYS:HE3	7:G:126:G:H4'	1.79	0.65
3:C:333:ASP:OD1	36:g:3:LYS:HB2	1.96	0.65
20:T:314:ILE:HD12	20:T:324:HIS:HB2	1.78	0.65
44:1:268:ARG:HG3	44:1:268:ARG:NH1	2.11	0.65
19:S:72:ARG:HG3	23:W:71:HIS:ND1	2.10	0.65
26:Z:756:TYR:CE2	26:Z:758:ARG:HA	2.32	0.65
1:A:1617:ARG:HG2	28:z:96:LEU:HB3	1.79	0.65
1:A:1739:ALA:HB2	1:A:1877:LEU:HD13	1.79	0.65
15:O:250:ASN:OD1	19:S:91:LYS:NZ	2.26	0.65
1:A:1600:GLU:HG3	1:A:1725:LEU:HD21	1.78	0.65
1:A:690:MET:HE1	16:P:9:PHE:HB3	1.79	0.65
1:A:1778:TRP:HZ2	1:A:1818:PHE:HE2	1.38	0.65
8:H:33:G:H1'	27:2:68:MET:HE1	1.79	0.65
27:2:48:ILE:C	34:m:5:LEU:HD22	2.21	0.65
27:2:138:LYS:HE2	27:2:138:LYS:CA	2.25	0.65
1:A:419:ARG:NH2	1:A:423:ASP:O	2.30	0.65
1:A:2004:GLN:O	1:A:2007:ILE:N	2.30	0.65
3:C:667:VAL:N	3:C:824:THR:HG23	2.09	0.65
7:G:82:G:C4'	23:W:541:LYS:CE	2.66	0.65
23:W:341:ASN:OD1	23:W:388:GLN:NE2	2.29	0.65
25:Y:413:LYS:HA	25:Y:416:PHE:CD2	2.32	0.65
1:A:537:LYS:HB2	5:F:37:C:H41	1.60	0.64
19:S:125:LYS:CB	19:S:126:HIS:CD2	2.80	0.64
1:A:1599:GLN:HE21	44:1:271:ILE:HD13	1.62	0.64
1:A:1935:ARG:NH2	44:1:348:THR:CG2	2.44	0.64
4:E:307:ARG:HH22	29:b:115:PRO:HB3	1.61	0.64
7:G:101:U:O2	7:G:101:U:H2'	1.95	0.64
8:H:153:A:H3'	8:H:154:C:H5'	1.79	0.64
1:A:1141:ARG:HB2	1:A:1182:ASN:OD1	1.98	0.64
1:A:1503:TRP:CZ3	1:A:1533:ARG:CD	2.80	0.64
1:A:2002:LEU:H	1:A:2002:LEU:CD2	2.01	0.64
5:F:45:A:C2	5:F:73:A:O4'	2.51	0.64
8:H:147:G:H2'	8:H:148:C:H6	1.63	0.64
9:I:720:ILE:CG2	24:X:112:LEU:HD23	2.26	0.64
9:I:724:LEU:HD22	9:I:724:LEU:C	2.22	0.64
9:I:725:ARG:HD2	9:I:725:ARG:C	2.22	0.64
1:A:152:ARG:HH12	44:1:132:ASP:C	2.05	0.64
1:A:1560:ILE:O	1:A:1560:ILE:HD12	1.97	0.64
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.79	0.64
5:F:28:A:H1'	14:N:39:GLY:O	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:d:32:LEU:HD22	33:d:65:MET:HE3	1.80	0.64
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.31	0.64
3:C:137:HIS:HD2	3:C:238:ASN:H	1.44	0.64
4:E:93:TRP:HH2	29:b:105:GLY:CA	2.10	0.64
8:H:41:U:H2'	8:H:42:G:C8	2.33	0.64
8:H:154:C:H2'	8:H:155:C:H6	1.63	0.64
1:A:166:PHE:HE1	1:A:581:ILE:HD11	1.63	0.64
1:A:1772:PHE:HE1	1:A:1812:PRO:O	1.81	0.64
5:F:22:A:H2'	23:W:130:ARG:HH21	1.62	0.64
2:B:23:C:O2'	2:B:24:G:O5'	2.15	0.64
5:F:88:G:H5'	13:M:133:ARG:NH2	2.13	0.64
8:H:164:C:H6	8:H:164:C:H5'	1.63	0.64
15:O:133:PRO:HG2	15:O:137:LEU:HB2	1.80	0.64
18:R:106:GLN:NE2	18:R:225:PRO:HG3	2.11	0.64
19:S:102:ASN:ND2	19:S:108:ASN:OD1	2.30	0.64
1:A:1835:GLN:OE1	1:A:1835:GLN:HA	1.97	0.64
7:G:100:C:C2	7:G:101:U:C6	2.86	0.64
9:I:681:ILE:HG23	9:I:710:PHE:HZ	1.56	0.64
9:I:704:TRP:CH2	9:I:727:ARG:HG3	2.32	0.64
22:V:544:LEU:HD11	22:V:578:SER:HB3	1.79	0.64
23:W:534:ILE:HD12	23:W:544:SER:HB3	1.79	0.64
33:k:32:LEU:HD22	33:k:65:MET:HE3	1.79	0.64
1:A:535:ARG:NH2	28:z:107:LYS:O	2.30	0.64
1:A:1503:TRP:CH2	1:A:1533:ARG:HD2	2.33	0.64
1:A:1930:TYR:CB	44:1:324:MET:HE3	2.21	0.64
5:F:42:C:H5''	5:F:43:A:OP2	1.97	0.64
8:H:39:U:H2'	8:H:40:C:C5	2.32	0.64
1:A:1596:VAL:HG21	44:1:278:LEU:CD2	2.28	0.63
4:E:93:TRP:HH2	29:b:105:GLY:HA2	1.63	0.63
9:I:276:ARG:CB	17:Q:357:ALA:CB	2.75	0.63
27:2:24:PRO:HB3	27:2:30:GLU:N	2.13	0.63
1:A:1935:ARG:N	44:1:347:PRO:HG3	2.12	0.63
7:G:21:A:OP2	15:O:193:LEU:HD11	1.98	0.63
27:2:48:ILE:CG2	34:m:5:LEU:HD23	2.05	0.63
41:r:8:SER:CB	41:s:86:MET:CB	2.77	0.63
1:A:165:ARG:HD3	1:A:165:ARG:N	2.11	0.63
1:A:1578:ARG:O	1:A:1578:ARG:HG2	1.96	0.63
1:A:1798:LEU:HB2	7:G:96:U:H4'	1.77	0.63
1:A:1958:LYS:HD3	27:2:96:MET:HB3	1.79	0.63
4:E:307:ARG:NH2	29:b:115:PRO:HB3	2.12	0.63
8:H:77:C:H5'	23:W:242:HIS:CE1	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:197:TYR:CD2	20:T:488:VAL:CG1	2.81	0.63
20:T:250:ARG:NH1	20:T:266:GLU:OE2	2.30	0.63
1:A:1471:ARG:HD2	44:1:66:TYR:CG	2.33	0.63
1:A:1813:ARG:HB3	1:A:1813:ARG:CZ	2.28	0.63
1:A:159:ARG:HA	44:1:104:ARG:HG3	1.80	0.63
5:F:29:A:N3	15:O:166:SER:OG	2.29	0.63
7:G:18:A:C2	15:O:196:GLN:O	2.52	0.63
23:W:70:VAL:HG22	23:W:71:HIS:CD2	2.34	0.63
1:A:1020:LYS:NZ	8:H:26:A:OP1	2.32	0.63
8:H:152:G:C2	8:H:153:A:C5	2.87	0.63
20:T:307:SER:OG	20:T:308:ARG:N	2.29	0.63
25:Y:413:LYS:HA	25:Y:416:PHE:HD2	1.64	0.63
1:A:1684:PHE:CE2	44:1:178:HIS:CD2	2.87	0.63
1:A:1716:GLY:C	1:A:1718:TRP:NE1	2.56	0.63
1:A:1764:SER:CA	1:A:1888:GLU:HB3	2.29	0.63
1:A:1778:TRP:CD1	1:A:1811:ASN:HB2	2.33	0.63
1:A:1849:ILE:HG21	1:A:1879:PHE:CE2	2.34	0.63
5:F:41:A:H2	7:G:6:A:C2	2.16	0.63
15:O:27:CYS:SG	15:O:83:THR:OG1	2.57	0.63
23:W:72:LEU:HD11	23:W:83:PRO:HG3	0.76	0.63
2:B:95:G:C5'	33:d:47:ARG:HH22	2.12	0.62
3:C:531:TRP:HB2	3:C:551:LEU:HB2	1.80	0.62
7:G:95:U:H4'	7:G:96:U:OP1	1.98	0.62
8:H:156:U:C6	8:H:156:U:C5'	2.72	0.62
1:A:1615:HIS:HE2	1:A:1626:CYS:HB2	1.62	0.62
1:A:1760:GLU:CD	1:A:1885:LYS:HZ3	2.06	0.62
1:A:1808:PHE:HE1	1:A:1897:LEU:HD21	1.64	0.62
1:A:2004:GLN:CB	44:1:342:HIS:HE2	2.10	0.62
3:C:668:GLU:H	3:C:824:THR:HG21	1.64	0.62
7:G:5:G:O5'	7:G:5:G:H8	1.81	0.62
8:H:33:G:O2'	27:2:68:MET:CE	2.46	0.62
7:G:73:G:C2'	7:G:74:G:O4'	2.46	0.62
10:J:242:ILE:HA	10:J:245:TRP:HD1	1.65	0.62
14:N:139:CYS:SG	14:N:140:ARG:N	2.72	0.62
19:S:125:LYS:HB3	19:S:126:HIS:CD2	2.33	0.62
1:A:165:ARG:NE	1:A:165:ARG:O	2.30	0.62
1:A:1502:PHE:CE1	1:A:1754:TYR:O	2.52	0.62
1:A:1768:TYR:OH	44:1:344:GLN:NE2	2.32	0.62
3:C:177:ARG:NH2	3:C:638:ASP:OD2	2.32	0.62
5:F:27:A:O2'	5:F:28:A:C8	2.51	0.62
7:G:100:C:H6	7:G:100:C:C5'	2.12	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:143:A:H2'	8:H:144:C:C6	2.35	0.62
8:H:157:G:H5''	8:H:157:G:H8	1.65	0.62
12:L:123:LEU:HD22	12:L:125:PRO:HD2	1.81	0.62
18:R:218:ILE:HD12	18:R:218:ILE:N	2.13	0.62
1:A:1854:VAL:CG2	44:1:270:ASP:OD1	2.47	0.62
7:G:20:A:H2	15:O:187:THR:HG21	1.64	0.62
9:I:725:ARG:HD2	9:I:725:ARG:O	1.99	0.62
44:1:51:GLU:HB2	44:1:59:ILE:HB	1.81	0.62
1:A:1798:LEU:HD13	7:G:96:U:H5'	1.82	0.62
1:A:1993:LYS:NZ	26:Z:726:ARG:CD	2.63	0.62
7:G:18:A:N1	15:O:196:GLN:O	2.32	0.62
20:T:187:LYS:N	20:T:188:PRO:CD	2.63	0.62
41:r:8:SER:O	41:r:9:ASN:CB	2.47	0.62
42:o:123:ASN:O	42:o:126:THR:HB	1.99	0.62
1:A:1771:LEU:C	1:A:1777:ILE:HD12	2.24	0.62
1:A:1809:ILE:HD12	1:A:1818:PHE:HB2	1.80	0.62
2:B:19:A:H2'	2:B:20:G:H5''	1.81	0.62
8:H:15:U:C2'	8:H:16:U:OP2	2.48	0.62
1:A:2009:ASP:O	1:A:2013:GLY:CA	2.48	0.62
8:H:151:C:OP2	27:2:131:ARG:CZ	2.47	0.62
12:L:106:LYS:CD	24:X:105:ARG:HH22	2.13	0.62
23:W:70:VAL:HG13	23:W:71:HIS:HD2	1.63	0.62
1:A:196:ASP:CG	1:A:199:GLU:HG2	2.23	0.62
3:C:506:PRO:HA	3:C:526:THR:HA	1.82	0.62
3:C:711:ARG:NH2	3:C:730:ARG:O	2.33	0.62
4:E:274:VAL:HG12	4:E:275:LYS:HG3	1.82	0.62
19:S:61:MET:HE2	19:S:63:GLN:HB2	1.82	0.62
23:W:253:SER:HB3	23:W:256:HIS:HB2	1.80	0.62
1:A:1532:ARG:HH11	1:A:1532:ARG:CB	2.12	0.61
1:A:1931:THR:HG23	44:1:347:PRO:HB2	1.82	0.61
1:A:2004:GLN:NE2	44:1:342:HIS:HD2	1.98	0.61
12:L:10:VAL:HG22	24:X:86:GLU:CG	2.30	0.61
23:W:73:ASP:CB	23:W:74:PRO:CD	2.38	0.61
24:X:60:GLU:OE1	24:X:60:GLU:HA	2.00	0.61
1:A:1433:ASP:OD1	1:A:1439:ARG:NH2	2.33	0.61
15:O:78:LYS:O	15:O:97:ARG:NH2	2.32	0.61
25:Y:401:GLU:O	25:Y:405:MET:HG2	2.00	0.61
1:A:1132:LYS:HA	1:A:1139:ARG:HH12	1.63	0.61
1:A:1770:GLU:OE1	44:1:316:ARG:CG	2.29	0.61
5:F:35:A:H5''	5:F:35:A:H8	1.64	0.61
5:F:43:A:O5'	5:F:43:A:H8	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:39:U:H6	8:H:39:U:C5'	2.07	0.61
27:2:33:LEU:O	27:2:36:GLU:N	2.33	0.61
2:B:12:U:O2'	2:B:13:C:O5'	2.19	0.61
15:O:26:THR:OG1	15:O:159:ARG:NH2	2.34	0.61
24:X:95:ARG:HB2	24:X:95:ARG:NH1	2.15	0.61
1:A:1258:LYS:CE	7:G:126:G:C4'	2.72	0.61
1:A:1475:ILE:CD1	44:1:66:TYR:HE2	2.12	0.61
1:A:1639:VAL:H	1:A:1656:THR:HA	1.65	0.61
1:A:1813:ARG:CG	1:A:1813:ARG:HH11	2.14	0.61
1:A:157:ASP:HB3	28:z:59:THR:CG2	2.30	0.61
4:E:104:THR:OG1	29:b:103:GLY:HA3	2.00	0.61
4:E:307:ARG:HH22	29:b:115:PRO:HG3	1.65	0.61
8:H:33:G:H2'	8:H:34:U:C6	2.35	0.61
8:H:106:G:H5'	33:k:47:ARG:HH22	1.66	0.61
12:L:4:ILE:O	12:L:4:ILE:HG23	1.99	0.61
12:L:6:ILE:O	12:L:6:ILE:HG23	2.00	0.61
24:X:116:ARG:HH11	24:X:116:ARG:HB3	1.64	0.61
1:A:1698:PRO:HG2	44:1:182:VAL:N	2.12	0.61
9:I:725:ARG:O	9:I:728:ARG:N	2.34	0.61
24:X:100:ILE:C	24:X:103:GLN:HB2	2.17	0.61
1:A:1620:TYR:N	1:A:1620:TYR:CD1	2.69	0.61
1:A:1719:PHE:HD2	1:A:1720:PRO:HD2	1.64	0.61
9:I:721:LYS:NZ	12:L:65:ARG:HH22	1.93	0.61
17:Q:823:GLY:O	17:Q:1096:ASP:CB	2.48	0.61
1:A:1475:ILE:CD1	44:1:66:TYR:CE2	2.83	0.61
6:4:-2:C:OP1	28:z:108:VAL:N	2.21	0.61
16:P:13:ARG:HG3	16:P:13:ARG:NH1	2.14	0.61
23:W:247:TYR:HB3	23:W:251:GLY:HA2	1.83	0.61
23:W:384:ASP:OD2	23:W:430:ASN:ND2	2.34	0.61
24:X:116:ARG:HH11	24:X:116:ARG:HA	1.66	0.61
1:A:1698:PRO:CG	44:1:182:VAL:N	2.63	0.61
3:C:779:LEU:HB3	3:C:934:MET:HE1	1.83	0.61
6:4:-2:C:OP1	28:z:108:VAL:HG23	2.01	0.61
8:H:112:G:H2'	8:H:113:G:H8	1.65	0.61
8:H:142:C:C2'	8:H:143:A:H5'	2.30	0.61
20:T:187:LYS:N	20:T:188:PRO:HD2	2.16	0.61
20:T:312:ALA:HB3	20:T:326:LEU:HB2	1.83	0.61
1:A:532:THR:HG1	7:G:3:A:P	2.24	0.60
1:A:1930:TYR:CE2	44:1:324:MET:HG3	2.36	0.60
4:E:162:ARG:HH21	4:E:203:ASP:HB3	1.66	0.60
7:G:13:C:H2'	7:G:14:A:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:153:A:N6	8:H:177:A:H2	1.98	0.60
23:W:565:LYS:HD2	23:W:577:LEU:HD21	1.83	0.60
35:e:74:LEU:HB3	35:e:77:ILE:HD11	1.81	0.60
7:G:21:A:O2'	7:G:22:C:P	2.59	0.60
25:Y:413:LYS:HB3	25:Y:425:ILE:HD11	1.83	0.60
35:l:74:LEU:HB3	35:l:77:ILE:HD11	1.81	0.60
1:A:525:LYS:HD3	28:z:100:THR:OG1	2.01	0.60
1:A:1132:LYS:CG	1:A:1139:ARG:HH12	2.15	0.60
1:A:1471:ARG:CD	44:1:66:TYR:CD2	2.85	0.60
3:C:693:GLU:H	3:C:696:LEU:HD12	1.65	0.60
9:I:608:LEU:HB2	9:I:611:HIS:HB2	1.83	0.60
19:S:98:LEU:HB3	19:S:130:GLY:C	2.26	0.60
24:X:116:ARG:HH12	24:X:119:LEU:HD23	1.63	0.60
44:1:272:ALA:HB3	44:1:275:LEU:HD12	1.82	0.60
1:A:1854:VAL:HG23	44:1:270:ASP:OD2	2.01	0.60
1:A:1873:GLU:C	44:1:290:ARG:HH22	2.09	0.60
1:A:1895:ALA:HB2	1:A:1944:HIS:HB2	1.83	0.60
3:C:668:GLU:H	3:C:824:THR:CG2	2.14	0.60
4:E:81:LEU:HB2	4:E:93:TRP:HB2	1.83	0.60
27:2:48:ILE:HG13	34:m:5:LEU:CD1	2.22	0.60
3:C:829:GLU:HB2	3:C:907:VAL:HG22	1.84	0.60
9:I:692:SER:HB2	9:I:703:PHE:HE2	1.65	0.60
22:V:457:ARG:HG3	44:1:73:TYR:CE2	2.36	0.60
44:1:34:ARG:HH11	44:1:34:ARG:CG	2.14	0.60
1:A:1526:LEU:CG	7:G:124:G:O6	2.50	0.60
1:A:1617:ARG:HH11	28:z:96:LEU:HD22	1.66	0.60
1:A:1941:ARG:NH1	1:A:2010:ILE:O	2.35	0.60
7:G:90:C:H6	7:G:90:C:O5'	1.85	0.60
20:T:188:PRO:HG3	20:T:443:THR:HG1	1.63	0.60
22:V:460:TYR:CE1	44:1:72:TRP:CZ2	2.88	0.60
23:W:354:ARG:NH1	23:W:373:ARG:O	2.35	0.60
28:z:60:PRO:N	28:z:60:PRO:C	2.55	0.60
1:A:1136:ARG:O	1:A:1139:ARG:HG2	2.02	0.60
1:A:1471:ARG:HD2	44:1:66:TYR:CD1	2.37	0.60
1:A:1741:TYR:CE2	44:1:288:LYS:HB2	2.37	0.60
1:A:1787:ARG:HH21	1:A:1805:GLY:HA2	1.67	0.60
3:C:221:ILE:HG23	3:C:495:ARG:HB2	1.82	0.60
1:A:252:ASP:O	1:A:332:TYR:OH	2.19	0.60
1:A:1535:THR:O	1:A:1535:THR:HG22	2.01	0.60
1:A:1759:THR:OG1	44:1:288:LYS:CE	2.48	0.60
1:A:1780:VAL:HG21	1:A:1861:ILE:HG21	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:277:LYS:NZ	3:C:864:PRO:O	2.35	0.60
7:G:83:A:O2'	7:G:84:U:P	2.60	0.60
20:T:197:TYR:HE2	20:T:488:VAL:HG11	1.64	0.60
28:z:68:MET:HE3	28:z:68:MET:O	2.02	0.60
1:A:435:CYS:HB3	6:4:-11:G:H22	1.65	0.60
1:A:1888:GLU:OE1	1:A:1888:GLU:HA	2.00	0.60
11:K:83:SER:O	41:t:76:LYS:HA	2.02	0.60
23:W:82:ASN:N	23:W:83:PRO:CD	2.65	0.60
5:F:34:G:C5'	5:F:34:G:C8	2.85	0.60
5:F:85:U:O2'	5:F:86:U:H5''	2.02	0.60
1:A:1592:ASP:OD2	44:1:275:LEU:CD1	2.50	0.59
20:T:339:GLN:NE2	20:T:342:GLU:O	2.35	0.59
26:Z:757:ARG:NE	27:2:68:MET:HB2	2.15	0.59
1:A:1861:ILE:HD12	1:A:1882:ILE:HG22	1.84	0.59
20:T:438:LEU:HD12	20:T:448:GLN:HB3	1.83	0.59
44:1:67:ILE:HG23	44:1:85:GLN:HE21	1.66	0.59
1:A:915:GLU:OE1	1:A:1012:LYS:NZ	2.36	0.59
1:A:1481:VAL:CG2	44:1:85:GLN:HE21	2.14	0.59
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.83	0.59
1:A:1873:GLU:CA	44:1:290:ARG:NH2	2.64	0.59
4:E:248:SER:HB3	4:E:265:ARG:HE	1.67	0.59
7:G:6:A:H2'	7:G:7:G:C8	2.37	0.59
7:G:23:U:C6	7:G:23:U:H5''	2.37	0.59
44:1:274:TYR:HD1	44:1:274:TYR:N	2.00	0.59
1:A:761:ILE:CD1	1:A:772:CYS:SG	2.90	0.59
1:A:2014:MET:HE2	1:A:2014:MET:O	2.02	0.59
3:C:667:VAL:H	3:C:824:THR:CG2	2.12	0.59
9:I:688:TYR:O	9:I:703:PHE:CZ	2.47	0.59
18:R:126:ASN:ND2	18:R:128:ASP:O	2.36	0.59
5:F:58:G:O2'	5:F:59:G:OP1	2.20	0.59
20:T:345:ILE:HB	20:T:357:TRP:HB2	1.82	0.59
20:T:399:LYS:HB3	20:T:404:SER:HB3	1.84	0.59
26:Z:682:TYR:HB3	26:Z:685:LEU:HD11	1.85	0.59
41:r:7:ILE:O	41:s:90:PHE:CB	2.50	0.59
1:A:58:LYS:NZ	1:A:477:LYS:O	2.35	0.59
7:G:19:G:H21	15:O:196:GLN:HG3	1.66	0.59
8:H:154:C:OP1	43:p:19:LYS:HD3	2.03	0.59
1:A:977:LEU:HB3	1:A:1097:ILE:HB	1.85	0.59
1:A:1772:PHE:HA	1:A:1813:ARG:CG	2.31	0.59
5:F:27:A:O2'	5:F:28:A:N7	2.35	0.59
5:F:35:A:C5'	5:F:35:A:C8	2.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:106:G:N2	8:H:107:A:C6	2.67	0.59
10:J:344:GLN:HG2	13:M:132:LEU:HD21	1.83	0.59
5:F:85:U:O2'	5:F:86:U:OP1	2.20	0.59
7:G:20:A:O2'	7:G:21:A:P	2.59	0.59
9:I:720:ILE:HD13	9:I:723:MET:HE3	1.84	0.59
9:I:731:GLN:NE2	9:I:731:GLN:HA	2.18	0.59
12:L:10:VAL:CG2	24:X:86:GLU:CG	2.75	0.59
23:W:347:PHE:HD2	23:W:359:TRP:HB2	1.68	0.59
1:A:1934:SER:HG	44:1:344:GLN:CA	2.06	0.59
7:G:87:U:C5'	7:G:88:G:OP2	2.51	0.59
9:I:696:ASP:HB3	9:I:699:THR:HB	1.85	0.59
13:M:120:PRO:O	13:M:120:PRO:HG2	2.03	0.59
24:X:79:VAL:O	24:X:79:VAL:HG22	2.02	0.59
1:A:1523:ARG:HA	7:G:124:G:N7	2.18	0.59
4:E:102:TYR:O	29:b:102:GLY:HA2	2.03	0.59
22:V:457:ARG:NH1	44:1:88:GLN:CG	2.62	0.59
30:y:38:PRO:N	30:y:38:PRO:CB	2.63	0.59
1:A:1132:LYS:HA	1:A:1139:ARG:NH1	2.18	0.58
1:A:1554:GLN:HA	1:A:1561:PHE:HA	1.84	0.58
1:A:1592:ASP:OD2	44:1:275:LEU:HD11	2.02	0.58
3:C:824:THR:HG23	3:C:824:THR:O	2.02	0.58
7:G:12:G:H2'	7:G:13:C:C5	2.38	0.58
12:L:4:ILE:HD11	24:X:78:MET:CE	2.17	0.58
20:T:244:GLY:O	20:T:271:LYS:NZ	2.34	0.58
22:V:503:TYR:HB2	22:V:546:ASN:HA	1.84	0.58
24:X:79:VAL:O	24:X:79:VAL:HG13	2.01	0.58
34:f:70:LEU:CD2	34:f:71:TYR:HD2	2.16	0.58
1:A:1617:ARG:HH12	28:z:99:LEU:HD13	1.69	0.58
1:A:1896:CYS:HB2	1:A:1940:LEU:HD21	1.83	0.58
3:C:196:LYS:HD2	31:a:14:GLU:OE1	2.02	0.58
16:P:2:THR:O	16:P:2:THR:HG22	2.02	0.58
24:X:116:ARG:NH1	24:X:119:LEU:CD2	2.66	0.58
44:1:274:TYR:N	44:1:274:TYR:CD1	2.71	0.58
1:A:864:LEU:C	1:A:864:LEU:HD23	2.27	0.58
1:A:1393:ARG:HH11	25:Y:405:MET:HE2	1.68	0.58
1:A:1770:GLU:OE2	44:1:316:ARG:CG	2.51	0.58
1:A:1937:ILE:HG21	1:A:2012:LEU:CD1	2.33	0.58
8:H:40:C:HO2'	8:H:41:U:C1'	2.16	0.58
9:I:721:LYS:O	9:I:724:LEU:HB3	2.02	0.58
9:I:726:ILE:O	9:I:726:ILE:HD12	2.03	0.58
1:A:864:LEU:HD23	1:A:864:LEU:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:22:C:O2	7:G:22:C:H2'	2.02	0.58
7:G:87:U:C5	7:G:88:G:N2	2.71	0.58
26:Z:756:TYR:OH	26:Z:758:ARG:HA	2.03	0.58
17:Q:828:GLY:HA2	49:Q:1501:ATP:O1B	2.04	0.58
27:2:28:ALA:HA	27:2:31:GLN:HB3	1.84	0.58
28:z:65:PHE:HZ	28:z:69:GLN:NE2	1.97	0.58
1:A:1490:PHE:HE1	1:A:1501:LEU:HD11	1.67	0.58
1:A:1596:VAL:CG1	44:1:278:LEU:CD1	2.80	0.58
1:A:1617:ARG:HG3	28:z:96:LEU:HD13	1.85	0.58
7:G:22:C:HO2'	7:G:23:U:P	2.27	0.58
8:H:152:G:OP1	27:2:127:ARG:CD	2.52	0.58
20:T:186:PRO:HG2	20:T:188:PRO:HD3	1.84	0.58
26:Z:706:ALA:CB	26:Z:725:ASN:HB2	2.33	0.58
27:2:48:ILE:HG23	34:m:5:LEU:CG	2.27	0.58
3:C:224:GLY:HA3	3:C:438:ILE:HD12	1.84	0.58
4:E:93:TRP:CH2	29:b:105:GLY:HA2	2.38	0.58
20:T:185:MET:HG3	20:T:186:PRO:HD3	0.76	0.58
25:Y:405:MET:HB3	25:Y:411:LEU:HG	1.84	0.58
34:m:70:LEU:CD2	34:m:71:TYR:HD2	2.16	0.58
1:A:955:TRP:CD1	1:A:1189:MET:HE1	2.39	0.58
1:A:1553:VAL:HG13	1:A:1553:VAL:O	2.03	0.58
1:A:1762:TYR:CB	1:A:1886:GLY:O	2.51	0.58
1:A:1938:LEU:HD11	44:1:345:ALA:O	2.03	0.58
12:L:135:LYS:HD2	12:L:135:LYS:N	2.17	0.58
15:O:276:THR:HG23	15:O:279:ALA:H	1.67	0.58
1:A:1601:LEU:HA	1:A:1606:ILE:HD12	1.86	0.58
1:A:1705:ILE:HG21	1:A:1734:MET:HE2	1.78	0.58
3:C:776:GLU:OE1	3:C:813:ARG:NH2	2.37	0.58
10:J:266:GLU:OE2	10:J:301:ARG:NH1	2.31	0.58
19:S:83:GLU:HA	19:S:106:ASP:HB2	1.84	0.58
1:A:300:ASN:HB3	3:C:939:ARG:HH22	1.69	0.58
1:A:1136:ARG:HA	1:A:1139:ARG:HE	1.69	0.58
1:A:1471:ARG:CD	44:1:66:TYR:CE1	2.78	0.58
5:F:77:C:H2'	5:F:78:A:H5'	1.86	0.58
8:H:10:C:C4	13:M:198:ARG:NH2	2.72	0.58
8:H:24:A:H3'	8:H:25:G:H5''	1.86	0.58
10:J:285:MET:O	10:J:289:ASN:ND2	2.37	0.58
12:L:5:MET:HE2	12:L:39:HIS:ND1	2.19	0.58
15:O:239:LEU:O	15:O:296:ARG:NH1	2.34	0.58
31:h:45:ASN:HB3	42:o:22:ARG:NH1	2.18	0.58
1:A:73:HIS:ND1	1:A:88:TYR:OH	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ARG:NH1	1:A:573:GLN:HE21	2.01	0.57
1:A:873:ASN:ND2	1:A:876:GLU:OE1	2.37	0.57
1:A:1553:VAL:O	1:A:1553:VAL:HG22	2.04	0.57
11:K:110:SER:CB	12:L:699:ASN:CB	2.81	0.57
15:O:84:CYS:SG	15:O:159:ARG:NH2	2.77	0.57
17:Q:828:GLY:CA	49:Q:1501:ATP:O1B	2.52	0.57
22:V:608:LEU:HB3	22:V:611:PHE:HB3	1.86	0.57
42:o:133:LEU:HD12	42:o:158:ALA:HB2	1.84	0.57
1:A:1895:ALA:CB	1:A:1944:HIS:CB	2.75	0.57
4:E:209:ILE:HG12	4:E:219:VAL:HG22	1.85	0.57
5:F:39:A:C3'	5:F:40:U:H5'	2.34	0.57
1:A:2015:GLU:CG	24:X:55:TYR:CE2	2.87	0.57
28:z:68:MET:HE1	28:z:72:ARG:HD3	1.85	0.57
1:A:1253:SER:O	1:A:1253:SER:OG	2.07	0.57
9:I:724:LEU:HD22	9:I:724:LEU:O	2.05	0.57
23:W:404:ASP:OD2	23:W:406:ARG:NH1	2.38	0.57
1:A:1322:LEU:HD21	44:l:67:ILE:CD1	2.34	0.57
15:O:76:LYS:HG2	23:W:111:LEU:HD22	1.85	0.57
20:T:223:SER:OG	20:T:224:ALA:N	2.37	0.57
24:X:116:ARG:HH11	24:X:116:ARG:CA	2.16	0.57
1:A:415:SER:OG	1:A:416:GLY:N	2.37	0.57
1:A:861:ARG:HB3	1:A:861:ARG:HH11	1.70	0.57
8:H:179:C:H2'	8:H:180:G:C8	2.38	0.57
22:V:457:ARG:NH1	44:l:88:GLN:CD	2.62	0.57
23:W:72:LEU:CD1	23:W:83:PRO:CG	2.55	0.57
1:A:1614:ILE:HD11	1:A:1616:PRO:HA	1.86	0.57
1:A:1644:LEU:CD2	1:A:1681:ARG:CG	2.83	0.57
1:A:1810:PHE:C	1:A:1810:PHE:CD2	2.83	0.57
5:F:28:A:HO2'	14:N:39:GLY:CA	2.17	0.57
7:G:80:U:H4'	23:W:545:ARG:HH22	1.68	0.57
42:o:2:VAL:HG11	42:o:29:TYR:O	2.05	0.57
42:o:101:VAL:HG23	42:o:102:GLU:HG3	1.86	0.57
1:A:348:PRO:O	1:A:350:PHE:N	2.38	0.57
1:A:1490:PHE:HZ	1:A:1498:TRP:N	2.03	0.57
1:A:1584:LYS:NZ	1:A:1874:VAL:HG12	2.20	0.57
5:F:39:A:H2'	5:F:40:U:C5'	2.29	0.57
5:F:45:A:C5	7:G:120:G:C6	2.93	0.57
7:G:89:U:OP2	7:G:89:U:H6	1.88	0.57
8:H:36:G:O2'	8:H:37:U:H5'	2.04	0.57
8:H:71:C:H2'	8:H:72:U:H6	1.70	0.57
11:K:117:GLN:CB	12:L:706:GLU:CB	2.83	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:181:MET:O	11:K:185:TRP:N	2.36	0.57
12:L:256:GLU:OE2	12:L:260:ARG:NH2	2.38	0.57
24:X:57:ARG:HG3	24:X:61:GLN:HE21	1.70	0.57
1:A:1532:ARG:NH1	1:A:1532:ARG:HB2	2.20	0.57
1:A:1930:TYR:HB2	44:1:324:MET:CE	2.23	0.57
1:A:480:LYS:NZ	14:N:112:ASN:OD1	2.37	0.57
1:A:1813:ARG:HH11	1:A:1813:ARG:HG2	1.67	0.57
8:H:141:C:C2	8:H:142:C:C5	2.93	0.57
8:H:152:G:P	27:2:127:ARG:CD	2.93	0.57
10:J:180:LYS:HE3	12:L:145:ASP:HB3	1.86	0.57
18:R:106:GLN:HE22	18:R:225:PRO:CG	2.05	0.57
44:1:273:LYS:HD2	44:1:292:MET:HG3	1.86	0.57
1:A:852:VAL:O	1:A:852:VAL:HG12	2.05	0.56
1:A:1502:PHE:HE1	1:A:1754:TYR:C	2.12	0.56
5:F:38:G:H2'	5:F:39:A:C8	2.40	0.56
5:F:60:C:O4'	18:R:219:PRO:HD3	2.05	0.56
8:H:39:U:C3'	8:H:40:C:C5	2.87	0.56
8:H:73:C:H2'	8:H:74:U:H6	1.70	0.56
20:T:343:PRO:HD3	20:T:401:PRO:HB3	1.86	0.56
1:A:1719:PHE:CB	1:A:1720:PRO:CD	2.65	0.56
1:A:1943:LEU:HD23	1:A:1950:ALA:CB	2.35	0.56
4:E:324:PRO:O	29:b:112:ARG:NH1	2.38	0.56
7:G:83:A:HO2'	7:G:84:U:P	2.28	0.56
8:H:77:C:P	23:W:242:HIS:HE1	2.27	0.56
8:H:152:G:N2	8:H:153:A:C5	2.73	0.56
8:H:154:C:O2'	8:H:155:C:H5'	2.04	0.56
9:I:720:ILE:HD13	9:I:723:MET:HE1	1.87	0.56
19:S:11:PRO:O	19:S:29:TRP:NE1	2.36	0.56
28:z:67:LYS:HA	28:z:70:GLU:HG3	1.85	0.56
1:A:166:PHE:CB	1:A:167:PRO:HD2	2.28	0.56
1:A:623:LYS:HB3	45:A:3000:IHP:P4	2.45	0.56
1:A:761:ILE:HD13	1:A:772:CYS:SG	2.45	0.56
1:A:978:GLU:OE2	1:A:1188:ASN:N	2.36	0.56
1:A:1644:LEU:CD2	1:A:1681:ARG:HG2	2.35	0.56
1:A:1741:TYR:CZ	1:A:1745:GLU:OE1	2.58	0.56
1:A:1771:LEU:HD23	1:A:1777:ILE:HG21	1.87	0.56
1:A:1780:VAL:HG23	1:A:1861:ILE:CG2	2.35	0.56
1:A:1994:LYS:HD2	26:Z:756:TYR:CD1	2.39	0.56
1:A:1994:LYS:CD	26:Z:756:TYR:HD1	2.17	0.56
2:B:47:A:O2'	2:B:48:A:H5''	2.06	0.56
4:E:91:LEU:HD22	4:E:101:ASN:HD21	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:307:ARG:HH22	29:b:115:PRO:CB	2.17	0.56
22:V:457:ARG:NH1	44:1:88:GLN:HG2	2.00	0.56
34:f:11:LEU:CD1	34:f:40:MET:HE2	2.35	0.56
29:i:52:LYS:HE3	32:j:53:VAL:HG21	1.88	0.56
34:m:11:LEU:CD1	34:m:40:MET:HE2	2.35	0.56
36:n:19:LEU:O	36:n:26:HIS:HD2	1.88	0.56
7:G:124:G:N3	7:G:124:G:C2'	2.68	0.56
8:H:54:U:H2'	8:H:55:U:H6	1.70	0.56
8:H:68:G:H2'	8:H:69:U:H6	1.71	0.56
8:H:69:U:H2'	8:H:70:C:H6	1.71	0.56
8:H:72:U:H2'	8:H:73:C:H6	1.71	0.56
8:H:149:A:H2'	8:H:150:U:H6	1.71	0.56
35:l:20:LEU:HD22	35:l:24:TYR:CZ	2.40	0.56
5:F:45:A:H5'	5:F:46:G:OP2	2.05	0.56
8:H:40:C:H5''	8:H:41:U:OP1	2.05	0.56
12:L:106:LYS:HD3	24:X:105:ARG:HH22	1.69	0.56
19:S:66:ASP:CG	19:S:73:GLY:O	2.48	0.56
1:A:1768:TYR:OH	44:1:344:GLN:CD	2.47	0.56
8:H:77:C:C2	8:H:78:C:C5	2.93	0.56
16:P:16:ARG:HH12	18:R:220:ARG:CA	2.16	0.56
1:A:537:LYS:CB	5:F:37:C:H41	2.19	0.56
1:A:1502:PHE:HE1	1:A:1754:TYR:CB	2.12	0.56
4:E:268:ALA:HB2	4:E:272:ARG:HH21	1.69	0.56
7:G:20:A:H2	15:O:187:THR:CB	2.19	0.56
8:H:57:A:H2'	8:H:58:U:H6	1.71	0.56
8:H:181:G:H2'	8:H:182:U:H6	1.71	0.56
22:V:496:CYS:SG	44:1:72:TRP:CH2	2.74	0.56
23:W:532:LEU:HD11	23:W:568:THR:HG21	1.87	0.56
29:b:52:LYS:HE3	32:c:53:VAL:HG21	1.88	0.56
1:A:162:LYS:HE2	44:1:170:TRP:CZ2	2.39	0.56
1:A:425:PRO:HD3	2:B:26:A:H5'	1.86	0.56
1:A:1328:LEU:HB3	1:A:1368:LEU:HD11	1.88	0.56
1:A:1810:PHE:HA	1:A:1817:LEU:HD12	1.86	0.56
1:A:1991:TYR:HD1	26:Z:756:TYR:CE1	2.24	0.56
3:C:196:LYS:HE3	31:a:14:GLU:HB2	1.87	0.56
8:H:77:C:H2'	8:H:78:C:H6	1.71	0.56
10:J:213:LYS:HZ1	23:W:529:ASN:HA	1.70	0.56
25:Y:686:GLU:HA	25:Y:716:THR:O	2.05	0.56
36:g:19:LEU:O	36:g:26:HIS:HD2	1.88	0.56
1:A:1994:LYS:HD3	26:Z:756:TYR:HB2	1.87	0.56
8:H:70:C:C2	8:H:71:C:C5	2.93	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:88:A:H2'	8:H:89:U:H6	1.70	0.56
8:H:141:C:H2'	8:H:142:C:H6	1.71	0.56
24:X:57:ARG:HG3	24:X:61:GLN:NE2	2.21	0.56
24:X:84:GLU:HA	24:X:84:GLU:OE2	2.05	0.56
28:z:63:ALA:O	28:z:67:LYS:CB	2.53	0.56
35:e:20:LEU:HD22	35:e:24:TYR:CZ	2.40	0.56
1:A:1685:LEU:CD1	44:1:173:TYR:CE2	2.88	0.56
1:A:1894:GLN:OE1	1:A:1894:GLN:N	2.39	0.56
1:A:1979:VAL:HA	1:A:1982:GLN:HB2	1.86	0.56
5:F:34:G:H8	5:F:34:G:O5'	1.89	0.56
8:H:71:C:C2	8:H:72:U:C5	2.94	0.56
8:H:91:U:H2'	8:H:92:U:H6	1.70	0.56
8:H:152:G:N2	8:H:153:A:C8	2.73	0.56
8:H:183:G:C4	8:H:184:C:C5	2.94	0.56
8:H:183:G:H2'	8:H:184:C:H6	1.71	0.56
19:S:54:HIS:CD2	19:S:71:GLY:HA3	2.41	0.56
23:W:70:VAL:HG13	23:W:71:HIS:CD2	2.41	0.56
33:k:50:LYS:HG2	33:k:74:TRP:CB	2.36	0.56
44:1:185:TYR:HD2	44:1:188:VAL:HB	1.69	0.56
1:A:1502:PHE:CD1	1:A:1502:PHE:N	2.72	0.55
1:A:1930:TYR:CG	44:1:324:MET:HG3	2.40	0.55
3:C:62:ASP:OD1	3:C:62:ASP:N	2.35	0.55
4:E:101:ASN:HD22	29:b:104:PRO:C	2.13	0.55
4:E:307:ARG:HH22	29:b:115:PRO:CG	2.18	0.55
8:H:69:U:C2	8:H:70:C:C5	2.94	0.55
8:H:70:C:H2'	8:H:71:C:H6	1.71	0.55
8:H:72:U:C2	8:H:73:C:C5	2.94	0.55
8:H:147:G:C4	8:H:148:C:C5	2.94	0.55
24:X:55:TYR:CD1	24:X:55:TYR:C	2.83	0.55
44:1:185:TYR:CE2	44:1:188:VAL:CG1	2.86	0.55
44:1:189:ASP:HA	44:1:192:LYS:HB2	1.88	0.55
1:A:774:LYS:HD2	8:H:23:A:N7	2.21	0.55
4:E:101:ASN:ND2	29:b:104:PRO:O	2.39	0.55
8:H:54:U:C2	8:H:55:U:C5	2.94	0.55
8:H:90:A:H2'	8:H:91:U:H6	1.71	0.55
28:z:80:LYS:HA	28:z:88:ARG:HH22	1.72	0.55
41:r:127:ALA:HB1	41:s:127:ALA:HB3	1.87	0.55
1:A:1617:ARG:NH1	28:z:99:LEU:HD13	2.21	0.55
2:B:94:U:H2'	2:B:95:G:H5''	1.89	0.55
3:C:233:GLU:OE1	3:C:837:GLN:NE2	2.39	0.55
8:H:68:G:C4	8:H:69:U:C5	2.95	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:73:C:C2	8:H:74:U:C5	2.94	0.55
29:b:56:SER:HB2	29:b:59:ALA:O	2.07	0.55
1:A:865:GLY:O	1:A:868:GLU:N	2.38	0.55
1:A:1504:GLU:OE2	1:A:1754:TYR:CD2	2.56	0.55
1:A:1614:ILE:HD13	1:A:1614:ILE:O	2.06	0.55
1:A:1829:GLY:N	5:F:40:U:OP1	2.40	0.55
3:C:677:GLU:OE1	3:C:681:LYS:NZ	2.38	0.55
7:G:82:G:C4'	23:W:541:LYS:HE2	2.36	0.55
15:O:34:ILE:HB	18:R:197:ILE:HG12	1.89	0.55
33:d:94:ARG:HE	33:d:96:ILE:HD11	1.72	0.55
1:A:377:GLU:O	3:C:342:ARG:NH2	2.38	0.55
1:A:1540:PRO:HB3	1:A:1670:ASP:HA	1.88	0.55
1:A:1776:ILE:HB	1:A:1858:PRO:HA	1.89	0.55
5:F:25:C:H4'	5:F:26:U:O5'	2.05	0.55
5:F:41:A:N1	7:G:6:A:C2	2.75	0.55
8:H:59:A:C4	8:H:60:U:C5	2.95	0.55
8:H:83:A:C4	8:H:84:C:C5	2.95	0.55
15:O:45:CYS:SG	15:O:48:CYS:N	2.76	0.55
33:d:50:LYS:HG2	33:d:74:TRP:CB	2.36	0.55
33:k:94:ARG:HE	33:k:96:ILE:HD11	1.72	0.55
35:l:14:MET:HE3	36:n:10:LYS:HE2	1.88	0.55
42:o:14:GLN:HG2	42:o:22:ARG:NH2	2.21	0.55
44:1:34:ARG:HH11	44:1:34:ARG:HA	1.70	0.55
1:A:537:LYS:CD	5:F:37:C:H41	2.17	0.55
1:A:1523:ARG:HA	7:G:124:G:C8	2.42	0.55
1:A:1781:ASP:C	1:A:1783:THR:H	2.15	0.55
10:J:222:ASP:O	10:J:226:ARG:NH1	2.39	0.55
10:J:502:GLU:O	10:J:506:GLU:N	2.39	0.55
12:L:124:LYS:N	12:L:125:PRO:HD2	2.21	0.55
19:S:84:ASP:OD1	19:S:108:ASN:ND2	2.38	0.55
1:A:470:ARG:HG2	1:A:470:ARG:NH2	2.20	0.55
1:A:603:ARG:NH2	6:4:-6:C:O2	2.38	0.55
1:A:861:ARG:CB	1:A:861:ARG:CZ	2.84	0.55
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.40	0.55
1:A:1482:GLU:HB2	44:1:85:GLN:O	2.07	0.55
5:F:45:A:N3	5:F:73:A:C1'	2.68	0.55
8:H:59:A:H2'	8:H:60:U:H6	1.71	0.55
8:H:150:U:H2'	8:H:151:C:H6	1.71	0.55
22:V:450:ILE:CB	44:1:89:PRO:HG2	2.36	0.55
1:A:762:ARG:HH22	16:P:226:LYS:HZ3	1.55	0.55
1:A:981:PHE:CZ	1:A:1095:ILE:HD11	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1523:ARG:CA	7:G:124:G:C8	2.90	0.55
1:A:1719:PHE:CG	1:A:1720:PRO:HD2	2.41	0.55
1:A:1770:GLU:OE2	44:1:317:TYR:CE1	2.60	0.55
1:A:1994:LYS:HZ1	27:2:67:VAL:CG2	2.18	0.55
5:F:81:C:H4'	5:F:82:A:OP2	2.07	0.55
7:G:120:G:C8	7:G:120:G:C5'	2.87	0.55
9:I:724:LEU:HD11	24:X:108:GLU:HG2	1.87	0.55
18:R:97:LYS:NZ	19:S:146:GLU:OE1	2.40	0.55
20:T:188:PRO:HG3	20:T:443:THR:CB	2.34	0.55
20:T:354:ILE:HB	20:T:368:LEU:HB2	1.88	0.55
24:X:119:LEU:HG	24:X:120:LYS:HE3	1.88	0.55
44:1:273:LYS:HD3	44:1:292:MET:CG	2.37	0.55
1:A:36:LYS:NZ	23:W:163:GLN:O	2.40	0.55
1:A:776:LEU:HD12	1:A:776:LEU:O	2.07	0.55
27:2:120:ALA:HB2	36:n:55:ASN:OD1	2.06	0.55
34:f:70:LEU:HD23	34:f:70:LEU:C	2.31	0.55
3:C:561:LYS:NZ	3:C:614:TYR:O	2.40	0.55
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.88	0.55
8:H:57:A:C4	8:H:58:U:C5	2.95	0.55
8:H:91:U:C2	8:H:92:U:C5	2.95	0.55
8:H:150:U:C2	8:H:151:C:C5	2.94	0.55
1:A:1275:ARG:NH2	1:A:1464:LEU:O	2.38	0.54
1:A:1501:LEU:HD23	1:A:1501:LEU:H	1.71	0.54
1:A:1771:LEU:O	1:A:1777:ILE:HD12	2.07	0.54
1:A:1937:ILE:HG21	1:A:2012:LEU:HD13	1.89	0.54
7:G:22:C:O2'	7:G:23:U:P	2.66	0.54
8:H:105:G:C6	32:j:20:LYS:HD3	2.42	0.54
23:W:71:HIS:H	23:W:87:THR:HG22	1.72	0.54
27:2:51:LYS:HZ2	35:l:28:ARG:CD	2.18	0.54
27:2:140:LEU:HD12	27:2:140:LEU:O	2.07	0.54
29:i:56:SER:HB2	29:i:59:ALA:O	2.07	0.54
34:m:5:LEU:O	35:l:49:GLY:CA	2.42	0.54
34:m:70:LEU:HD23	34:m:70:LEU:C	2.31	0.54
1:A:461:HIS:NE2	2:B:26:A:N6	2.55	0.54
1:A:579:GLN:HG3	1:A:629:PHE:H	1.73	0.54
1:A:939:TRP:NE1	1:A:1049:ASP:OD2	2.39	0.54
1:A:1479:GLY:C	44:1:88:GLN:NE2	2.66	0.54
1:A:244:GLN:NE2	1:A:244:GLN:CA	2.69	0.54
1:A:1827:TRP:HZ3	1:A:1836:LEU:HB3	1.72	0.54
1:A:1879:PHE:CD1	1:A:1879:PHE:N	2.74	0.54
3:C:136:GLY:O	3:C:142:LYS:NZ	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:145:LYS:NZ	4:E:181:ILE:O	2.39	0.54
5:F:22:A:C2	14:N:126:LEU:CD2	2.90	0.54
5:F:34:G:H8	5:F:34:G:H5''	1.70	0.54
8:H:90:A:C4	8:H:91:U:C5	2.95	0.54
8:H:149:A:C4	8:H:150:U:C5	2.95	0.54
9:I:704:TRP:CH2	9:I:727:ARG:CG	2.90	0.54
20:T:210:ILE:HG12	20:T:221:THR:HG22	1.89	0.54
1:A:105:ASN:HD22	1:A:129:VAL:CG1	2.20	0.54
1:A:156:ARG:HH22	44:1:134:PHE:HB2	1.71	0.54
1:A:453:TYR:O	1:A:457:ASN:ND2	2.40	0.54
1:A:714:SER:O	1:A:718:ARG:NH1	2.40	0.54
1:A:1252:GLY:HA3	7:G:122:U:O4	2.06	0.54
1:A:1838:LYS:HG2	1:A:1871:PRO:HG2	1.88	0.54
5:F:88:G:H5'	13:M:133:ARG:NH1	2.23	0.54
9:I:704:TRP:CE3	9:I:727:ARG:CG	2.83	0.54
10:J:201:ARG:HG2	10:J:201:ARG:NH2	2.21	0.54
20:T:353:THR:HG22	20:T:369:THR:HG22	1.90	0.54
24:X:64:ARG:CG	24:X:64:ARG:HH11	2.19	0.54
1:A:1532:ARG:CB	1:A:1532:ARG:NH1	2.70	0.54
7:G:17:U:O2	15:O:198:ILE:HD11	2.07	0.54
8:H:88:A:C4	8:H:89:U:C5	2.95	0.54
9:I:624:GLU:O	9:I:628:GLN:N	2.41	0.54
23:W:341:ASN:ND2	23:W:345:THR:OG1	2.37	0.54
26:Z:739:GLN:NE2	26:Z:746:GLN:OE1	2.40	0.54
1:A:1716:GLY:N	1:A:1718:TRP:HE1	2.06	0.54
1:A:1859:LYS:HE2	1:A:1859:LYS:CA	2.26	0.54
4:E:155:ASN:ND2	4:E:172:ASP:OD1	2.40	0.54
5:F:28:A:HO2'	14:N:39:GLY:C	2.16	0.54
7:G:21:A:O2'	7:G:22:C:C5'	2.55	0.54
8:H:10:C:H41	13:M:198:ARG:HH12	1.54	0.54
8:H:83:A:H2'	8:H:84:C:H6	1.71	0.54
23:W:73:ASP:CG	23:W:74:PRO:CD	2.69	0.54
23:W:326:ARG:NH1	23:W:363:THR:O	2.40	0.54
34:f:8:LYS:HB3	34:f:9:PRO:HD3	1.88	0.54
1:A:108:MET:HB3	1:A:109:PRO:HD2	1.90	0.54
1:A:199:GLU:HB3	1:A:240:ARG:HH22	1.73	0.54
1:A:572:PHE:HE2	28:z:61:ALA:CB	2.21	0.54
1:A:1555:LEU:HD11	1:A:1570:LYS:HE3	1.88	0.54
8:H:181:G:C4	8:H:182:U:C5	2.95	0.54
9:I:727:ARG:HB3	9:I:727:ARG:NH2	2.21	0.54
12:L:782:LYS:O	12:L:786:HIS:N	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:2:PRO:HG2	14:N:4:VAL:HA	1.90	0.54
24:X:72:GLN:NE2	24:X:72:GLN:CA	2.70	0.54
25:Y:402:ILE:O	25:Y:406:ILE:HD12	2.07	0.54
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.89	0.54
1:A:425:PRO:CD	2:B:26:A:H5'	2.38	0.54
1:A:1136:ARG:CG	1:A:1136:ARG:HH11	2.20	0.54
1:A:1502:PHE:CD1	1:A:1754:TYR:O	2.60	0.54
1:A:1787:ARG:NH2	1:A:1804:ASN:O	2.41	0.54
1:A:1813:ARG:CZ	1:A:1813:ARG:CB	2.85	0.54
1:A:1930:TYR:CZ	44:1:324:MET:HA	2.42	0.54
2:B:16:U:OP1	18:R:170:LYS:HE3	2.08	0.54
7:G:82:G:H5'	23:W:541:LYS:NZ	2.17	0.54
41:q:106:ALA:HB1	41:t:106:ALA:HB3	1.89	0.54
1:A:176:LEU:HB3	1:A:181:ASN:HD22	1.73	0.54
1:A:639:PHE:O	2:B:28:A:O2'	2.20	0.54
1:A:955:TRP:HE1	1:A:976:MET:HE1	1.73	0.54
1:A:1144:LYS:O	1:A:1148:ASN:ND2	2.41	0.54
1:A:1390:ALA:HB2	25:Y:410:VAL:CG1	2.38	0.54
3:C:704:VAL:HG23	3:C:705:VAL:HG13	1.89	0.54
4:E:62:LEU:HD23	29:b:107:GLY:HA2	1.88	0.54
12:L:264:LYS:O	12:L:268:LYS:N	2.36	0.54
33:d:88:LYS:HG3	33:d:89:PRO:HD2	1.89	0.54
1:A:1781:ASP:OD1	1:A:1783:THR:N	2.39	0.54
5:F:80:G:H5''	5:F:81:C:P	2.48	0.54
7:G:5:G:H2'	7:G:6:A:C8	2.43	0.54
19:S:70:THR:HG22	23:W:73:ASP:HA	1.90	0.54
35:l:14:MET:HE2	36:n:10:LYS:HD3	1.86	0.54
1:A:156:ARG:NH2	44:1:134:PHE:CB	2.71	0.53
1:A:1136:ARG:CG	1:A:1136:ARG:NH1	2.71	0.53
1:A:1481:VAL:HG21	44:1:67:ILE:CG2	2.35	0.53
4:E:128:SER:OG	4:E:129:THR:N	2.41	0.53
8:H:40:C:C5'	8:H:41:U:OP1	2.56	0.53
23:W:443:ARG:NH1	23:W:452:ASP:OD2	2.41	0.53
1:A:1685:LEU:CD1	44:1:173:TYR:CG	2.80	0.53
3:C:259:LYS:HG2	46:C:1500:GTP:C6	2.43	0.53
3:C:343:LEU:HD13	3:C:373:ILE:HD11	1.91	0.53
9:I:725:ARG:C	9:I:725:ARG:CD	2.81	0.53
21:U:77:MET:O	21:U:81:GLY:N	2.40	0.53
23:W:103:GLN:O	23:W:108:ARG:NH2	2.39	0.53
24:X:95:ARG:NH1	24:X:95:ARG:CB	2.72	0.53
27:2:113:LEU:HD13	27:2:113:LEU:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1632:PHE:HE1	1:A:1659:LYS:HG2	1.73	0.53
7:G:100:C:N1	7:G:101:U:C5	2.77	0.53
8:H:153:A:C3'	8:H:154:C:C5'	2.85	0.53
19:S:126:HIS:CD2	19:S:126:HIS:N	2.76	0.53
23:W:465:PRO:HG2	23:W:481:MET:HE3	1.89	0.53
1:A:188:LEU:HD22	1:A:567:GLY:HA2	1.88	0.53
1:A:244:GLN:NE2	1:A:244:GLN:HA	2.23	0.53
1:A:1884:ILE:H	44:1:289:THR:C	2.12	0.53
20:T:185:MET:N	20:T:186:PRO:CD	2.71	0.53
24:X:114:GLU:N	24:X:114:GLU:OE2	2.41	0.53
27:2:111:LYS:CA	27:2:114:GLU:HG2	2.36	0.53
44:1:185:TYR:CD2	44:1:188:VAL:CB	2.90	0.53
1:A:1322:LEU:HD21	44:1:67:ILE:HD11	1.90	0.53
1:A:1890:GLN:NE2	1:A:1890:GLN:CA	2.71	0.53
3:C:137:HIS:HB2	3:C:239:THR:HG23	1.91	0.53
8:H:39:U:C2'	8:H:40:C:C6	2.92	0.53
9:I:310:LYS:O	9:I:311:MET:C	2.51	0.53
9:I:721:LYS:CE	12:L:65:ARG:NH2	2.70	0.53
11:K:83:SER:CB	41:t:75:LEU:CB	2.86	0.53
23:W:449:ILE:HG22	23:W:451:VAL:H	1.74	0.53
23:W:453:PHE:HA	27:2:79:PHE:HE2	1.72	0.53
24:X:57:ARG:C	24:X:61:GLN:HE21	2.16	0.53
32:j:68:PHE:HB2	33:k:100:PHE:HB3	1.91	0.53
1:A:1087:LEU:HB2	1:A:1098:PHE:HB3	1.89	0.53
1:A:1664:ILE:HD13	1:A:1703:ILE:HB	1.90	0.53
4:E:133:VAL:HG21	4:E:169:THR:HG21	1.90	0.53
8:H:15:U:H2'	8:H:16:U:OP2	2.08	0.53
8:H:153:A:H3'	8:H:154:C:C5'	2.38	0.53
15:O:81:CYS:HB3	15:O:84:CYS:HB2	1.90	0.53
24:X:86:GLU:OE1	24:X:86:GLU:N	2.42	0.53
1:A:762:ARG:NH2	16:P:227:TYR:OH	2.42	0.53
1:A:1258:LYS:HE2	7:G:126:G:C3'	2.38	0.53
12:L:569:GLN:HA	41:q:114:CYS:O	2.07	0.53
16:P:13:ARG:HG3	16:P:13:ARG:HH11	1.72	0.53
26:Z:756:TYR:CD2	26:Z:756:TYR:C	2.87	0.53
28:z:91:ASP:OD1	28:z:94:ARG:NH2	2.41	0.53
36:n:17:LEU:HD23	36:n:72:ALA:HA	1.91	0.53
1:A:1491:LYS:HD2	1:A:1709:TYR:CD1	2.37	0.53
4:E:243:LEU:HD23	4:E:250:LEU:HD12	1.91	0.53
5:F:58:G:O2'	5:F:59:G:P	2.66	0.53
7:G:130:G:C2'	7:G:130:G:N3	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:225:PRO:HG2	18:R:225:PRO:O	2.09	0.53
19:S:70:THR:HA	23:W:73:ASP:OD1	2.09	0.53
20:T:270:VAL:HG21	20:T:305:THR:HG21	1.89	0.53
23:W:209:SER:O	23:W:213:GLN:N	2.41	0.53
24:X:116:ARG:N	24:X:116:ARG:CD	2.72	0.53
1:A:974:ASN:HD22	1:A:1178:TYR:HD2	1.57	0.53
1:A:1861:ILE:CD1	1:A:1882:ILE:HG21	2.19	0.53
27:2:32:LYS:N	27:2:32:LYS:HZ3	2.06	0.53
1:A:1854:VAL:HG22	44:1:270:ASP:OD1	2.09	0.53
5:F:40:U:H2'	5:F:41:A:C8	2.44	0.53
7:G:95:U:O2'	7:G:96:U:C5'	2.49	0.53
8:H:39:U:C4	8:H:40:C:N4	2.77	0.53
8:H:154:C:OP2	43:p:19:LYS:CD	2.56	0.53
8:H:154:C:OP2	43:p:19:LYS:HD3	2.09	0.53
9:I:727:ARG:CG	9:I:727:ARG:NH2	2.70	0.53
18:R:60:ASP:N	18:R:60:ASP:OD1	2.42	0.53
19:S:125:LYS:C	19:S:126:HIS:CD2	2.87	0.53
1:A:1686:ASP:O	1:A:1690:ASP:HB2	2.09	0.52
1:A:1703:ILE:HG21	1:A:1730:MET:HE2	1.91	0.52
1:A:1762:TYR:CG	1:A:1886:GLY:O	2.61	0.52
5:F:42:C:H2'	5:F:43:A:C1'	2.39	0.52
1:A:1532:ARG:NH2	1:A:1571:ILE:HD12	2.23	0.52
9:I:84:HIS:O	9:I:85:ARG:C	2.51	0.52
24:X:64:ARG:HG3	24:X:64:ARG:HH11	1.74	0.52
1:A:1251:SER:O	1:A:1298:ARG:NH2	2.41	0.52
4:E:171:SER:OG	4:E:173:ASP:OD1	2.26	0.52
5:F:26:U:O2'	5:F:27:A:P	2.67	0.52
9:I:592:ALA:HB3	9:I:623:VAL:HG12	1.91	0.52
19:S:72:ARG:CG	23:W:71:HIS:ND1	2.72	0.52
27:2:24:PRO:HA	27:2:29:GLU:HB3	1.90	0.52
27:2:123:GLN:O	27:2:127:ARG:NH1	2.42	0.52
44:1:122:ASN:ND2	44:1:133:CYS:SG	2.71	0.52
1:A:300:ASN:HB3	3:C:939:ARG:HH12	1.74	0.52
1:A:623:LYS:O	45:A:3000:IHP:O24	2.26	0.52
1:A:1618:LYS:C	1:A:1618:LYS:HD3	2.35	0.52
1:A:1621:LYS:CD	28:z:92:PHE:CZ	2.81	0.52
1:A:1861:ILE:HD12	1:A:1861:ILE:H	1.72	0.52
5:F:58:G:H2'	5:F:59:G:C8	2.44	0.52
22:V:584:LYS:HG3	22:V:634:ILE:HG12	1.91	0.52
24:X:113:LYS:HZ2	24:X:113:LYS:CB	2.23	0.52
44:1:272:ALA:HB1	44:1:274:TYR:CE1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:TYR:HB2	18:R:207:MET:HE1	1.91	0.52
1:A:1644:LEU:HD21	1:A:1681:ARG:HD3	1.83	0.52
1:A:1681:ARG:CZ	1:A:1681:ARG:CB	2.82	0.52
1:A:1684:PHE:HE2	44:1:178:HIS:CD2	2.28	0.52
7:G:20:A:O2'	15:O:193:LEU:CD2	2.50	0.52
8:H:39:U:H3'	8:H:40:C:H5	1.72	0.52
8:H:164:C:H5'	8:H:164:C:C6	2.44	0.52
8:H:177:A:C8	27:2:134:LEU:HD13	2.45	0.52
9:I:696:ASP:OD1	9:I:697:PRO:HD2	2.09	0.52
18:R:223:PRO:O	18:R:223:PRO:HG2	2.09	0.52
24:X:114:GLU:HB2	24:X:115:TYR:CD2	2.44	0.52
44:1:34:ARG:CG	44:1:34:ARG:NH1	2.73	0.52
1:A:1481:VAL:HG23	44:1:85:GLN:HE21	1.65	0.52
2:B:27:U:O2'	2:B:28:A:O5'	2.25	0.52
7:G:20:A:H2	15:O:187:THR:CG2	2.21	0.52
8:H:33:G:H3'	8:H:33:G:OP2	2.10	0.52
9:I:309:ALA:O	9:I:310:LYS:C	2.52	0.52
9:I:723:MET:HA	9:I:726:ILE:HG22	1.91	0.52
27:2:24:PRO:HA	27:2:29:GLU:CB	2.40	0.52
27:2:90:TYR:O	27:2:94:ASP:N	2.42	0.52
28:z:54:GLY:C	44:1:174:ASN:HD21	2.15	0.52
44:1:282:SER:OG	44:1:283:ALA:N	2.42	0.52
1:A:1616:PRO:O	28:z:96:LEU:HD12	2.08	0.52
1:A:1644:LEU:CD2	1:A:1681:ARG:HD3	2.39	0.52
1:A:1723:LYS:N	1:A:1724:PRO:CD	2.73	0.52
1:A:1772:PHE:C	1:A:1813:ARG:HD2	2.33	0.52
1:A:1854:VAL:CG2	44:1:270:ASP:CG	2.83	0.52
3:C:938:ARG:O	3:C:942:GLY:N	2.42	0.52
9:I:681:ILE:HD11	9:I:714:HIS:ND1	2.25	0.52
12:L:7:LYS:CB	12:L:40:ARG:HA	2.39	0.52
18:R:226:PRO:HG2	18:R:226:PRO:O	2.10	0.52
19:S:15:TYR:HB3	19:S:163:TYR:HB2	1.91	0.52
20:T:185:MET:N	20:T:186:PRO:HD2	2.25	0.52
23:W:243:VAL:HG13	23:W:245:GLU:H	1.74	0.52
27:2:52:MET:HB2	35:l:28:ARG:HH22	1.71	0.52
35:l:87:LEU:HB2	36:n:61:VAL:HB	1.92	0.52
1:A:158:ARG:HH12	1:A:573:GLN:HE21	1.55	0.52
1:A:863:GLU:C	1:A:863:GLU:CD	2.78	0.52
1:A:1471:ARG:CG	44:1:66:TYR:CD2	2.92	0.52
1:A:1556:ASP:N	1:A:1556:ASP:OD1	2.40	0.52
1:A:1615:HIS:CD2	28:z:89:VAL:HG22	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:79:C:O2	16:P:3:THR:HG23	2.10	0.52
7:G:21:A:HO2'	7:G:22:C:P	2.32	0.52
7:G:81:U:O2'	7:G:82:G:OP2	2.24	0.52
20:T:294:LEU:HD12	20:T:303:LEU:HD11	1.92	0.52
23:W:305:LEU:HD21	23:W:313:ILE:HG23	1.92	0.52
32:c:68:PHE:HB2	33:d:100:PHE:HB3	1.90	0.52
1:A:776:LEU:HD22	1:A:900:ASP:HB2	1.92	0.52
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.43	0.52
1:A:1533:ARG:CB	1:A:1533:ARG:NH1	2.73	0.52
2:B:22:U:O2	2:B:22:U:H2'	2.09	0.52
26:Z:758:ARG:HH11	26:Z:758:ARG:HG2	1.75	0.52
35:e:87:LEU:HB2	36:g:61:VAL:HB	1.92	0.52
37:v:53:HIS:CB	38:w:149:CYS:O	2.58	0.52
1:A:1354:ARG:HG3	21:U:19:VAL:HG22	1.92	0.52
1:A:1565:LYS:HG2	1:A:1565:LYS:O	2.08	0.52
1:A:1876:LEU:HD12	1:A:1884:ILE:HD11	1.91	0.52
2:B:18:C:C2'	2:B:19:A:O5'	2.58	0.52
3:C:207:GLY:O	3:C:238:ASN:ND2	2.42	0.52
5:F:5:U:H5'	5:F:6:C:OP2	2.10	0.52
5:F:88:G:H5'	13:M:133:ARG:CZ	2.40	0.52
7:G:100:C:C6	7:G:101:U:H5	2.28	0.52
13:M:236:ASN:ND2	13:M:242:ALA:O	2.43	0.52
16:P:10:GLU:HG2	16:P:10:GLU:O	2.09	0.52
22:V:590:LEU:HD22	22:V:599:LEU:HD13	1.90	0.52
22:V:620:ASN:HB3	22:V:623:ASN:HB2	1.92	0.52
36:g:17:LEU:HD23	36:g:72:ALA:HA	1.91	0.52
1:A:159:ARG:HD2	28:z:56:ASP:CG	2.35	0.51
1:A:1493:THR:C	1:A:1495:PHE:N	2.66	0.51
1:A:1862:ILE:O	1:A:1862:ILE:HG22	2.09	0.51
2:B:89:U:O2'	31:a:64:ARG:NH2	2.43	0.51
3:C:749:THR:HG23	3:C:749:THR:O	2.10	0.51
4:E:93:TRP:CZ3	29:b:105:GLY:C	2.87	0.51
8:H:147:G:H2'	8:H:148:C:C6	2.43	0.51
9:I:512:ASP:OD2	10:J:427:LYS:HE2	2.10	0.51
16:P:66:ARG:O	16:P:69:ALA:N	2.43	0.51
22:V:549:LYS:O	22:V:553:HIS:ND1	2.43	0.51
27:2:93:GLN:O	27:2:97:ASP:OD2	2.28	0.51
1:A:821:ARG:HH12	25:Y:426:LEU:CD1	2.15	0.51
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.92	0.51
1:A:1681:ARG:NH1	44:1:170:TRP:O	2.43	0.51
1:A:2011:ILE:N	1:A:2011:ILE:CD1	2.72	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:43:A:C6	5:F:44:G:O6	2.64	0.51
5:F:77:C:C2'	5:F:78:A:H5'	2.40	0.51
7:G:89:U:OP2	7:G:89:U:C6	2.61	0.51
12:L:222:LEU:HD12	18:R:84:ASN:HB3	1.92	0.51
17:Q:809:ALA:HB2	17:Q:1131:VAL:CB	2.40	0.51
33:d:85:LYS:HG2	33:d:85:LYS:O	2.09	0.51
1:A:620:PRO:HD2	44:1:134:PHE:CE2	2.46	0.51
1:A:977:LEU:HD23	1:A:1097:ILE:HD12	1.91	0.51
1:A:1413:ASP:O	1:A:1418:ARG:NH1	2.42	0.51
1:A:1571:ILE:HG12	28:z:110:TRP:CH2	2.45	0.51
1:A:1813:ARG:CG	1:A:1813:ARG:NH1	2.72	0.51
1:A:1977:ILE:HG12	44:1:349:LYS:HB2	1.93	0.51
8:H:14:C:N4	13:M:224:ARG:HD2	2.24	0.51
9:I:720:ILE:CD1	9:I:723:MET:HE1	2.40	0.51
9:I:731:GLN:NE2	9:I:731:GLN:CA	2.71	0.51
22:V:460:TYR:CD1	44:1:72:TRP:CZ2	2.98	0.51
1:A:1778:TRP:HD1	1:A:1811:ASN:HB2	1.75	0.51
1:A:1993:LYS:HZ1	26:Z:726:ARG:CD	2.21	0.51
20:T:418:THR:HG21	20:T:468:CYS:H	1.75	0.51
31:h:55:VAL:HG21	42:o:67:LYS:NZ	2.25	0.51
42:o:5:THR:CG2	42:o:8:LEU:H	2.23	0.51
42:o:102:GLU:HG2	42:o:128:LYS:HZ1	1.76	0.51
1:A:312:TYR:OH	3:C:886:ASP:OD2	2.27	0.51
1:A:1070:ASP:OD1	1:A:1073:SER:OG	2.24	0.51
1:A:1775:GLN:NE2	44:1:315:VAL:HB	2.23	0.51
7:G:100:C:C2'	7:G:101:U:C6	2.77	0.51
9:I:83:LYS:O	9:I:84:HIS:C	2.51	0.51
11:K:36:VAL:O	41:r:112:ALA:CB	2.55	0.51
19:S:25:LEU:HD23	19:S:98:LEU:HD22	1.93	0.51
24:X:54:LEU:N	24:X:54:LEU:CD2	2.73	0.51
24:X:115:TYR:CD2	24:X:115:TYR:N	2.78	0.51
1:A:461:HIS:CD2	2:B:26:A:N6	2.78	0.51
1:A:1321:GLU:HG3	44:1:66:TYR:HE1	1.75	0.51
1:A:1740:LEU:HB3	1:A:1744:ARG:CZ	2.41	0.51
1:A:1778:TRP:CG	1:A:1809:ILE:CG2	2.92	0.51
3:C:756:LYS:O	3:C:759:LEU:N	2.43	0.51
11:K:15:ALA:CB	41:s:112:ALA:C	2.82	0.51
17:Q:100:GLU:O	17:Q:104:GLU:N	2.44	0.51
18:R:312:MET:HE3	18:R:315:LYS:HG3	1.93	0.51
41:q:106:ALA:CB	41:t:106:ALA:CB	2.87	0.51
1:A:888:GLN:O	1:A:889:ARG:NH1	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1479:GLY:HA2	44:1:88:GLN:NE2	2.25	0.51
1:A:1596:VAL:CG2	44:1:278:LEU:CD1	2.86	0.51
1:A:1994:LYS:CD	26:Z:756:TYR:HB2	2.41	0.51
11:K:90:PRO:CB	11:K:109:ASN:C	2.83	0.51
22:V:570:LEU:HD13	22:V:611:PHE:HA	1.93	0.51
25:Y:426:LEU:HD23	25:Y:427:PRO:CD	2.36	0.51
1:A:361:HIS:HE1	22:V:324:HIS:CB	2.24	0.51
1:A:1793:THR:HG22	5:F:43:A:C5'	2.34	0.51
3:C:476:CYS:SG	3:C:477:HIS:N	2.83	0.51
5:F:28:A:O2'	14:N:39:GLY:C	2.53	0.51
7:G:130:G:N3	7:G:130:G:H2'	2.22	0.51
22:V:457:ARG:HH12	44:1:88:GLN:CD	2.19	0.51
23:W:453:PHE:CB	27:2:79:PHE:HE2	2.23	0.51
28:z:107:LYS:O	28:z:110:TRP:HB3	2.11	0.51
1:A:1581:LEU:O	1:A:1581:LEU:HD12	2.11	0.51
1:A:1739:ALA:CB	1:A:1877:LEU:HD13	2.40	0.51
1:A:1930:TYR:CE1	44:1:324:MET:HB2	2.46	0.51
2:B:94:U:H5	33:d:104:ASP:O	1.94	0.51
15:O:235:TYR:HB3	15:O:301:LYS:HB2	1.93	0.51
23:W:446:GLU:OE2	27:2:83:ARG:HD2	2.11	0.51
27:2:33:LEU:CD2	27:2:33:LEU:N	2.74	0.51
1:A:172:GLU:OE1	28:z:98:THR:OG1	2.19	0.51
1:A:1312:PRO:HG2	1:A:1314:VAL:HG12	1.93	0.51
1:A:1518:LEU:CB	7:G:124:G:H2'	2.41	0.51
1:A:1521:ALA:HB2	7:G:120:G:H5''	1.92	0.51
1:A:1828:ALA:C	5:F:40:U:OP1	2.54	0.51
1:A:1884:ILE:HD12	44:1:290:ARG:HD3	1.92	0.51
9:I:727:ARG:HH21	9:I:727:ARG:C	2.18	0.51
15:O:50:ARG:NH1	15:O:122:GLU:OE1	2.44	0.51
16:P:16:ARG:NH1	18:R:220:ARG:CA	2.72	0.51
16:P:38:HIS:HB3	20:T:282:ARG:HH21	1.75	0.51
22:V:535:THR:HA	22:V:538:ARG:HB2	1.92	0.51
33:k:41:GLN:H	33:k:115:ILE:HB	1.76	0.51
1:A:641:MET:HA	1:A:644:ILE:HG22	1.93	0.50
1:A:864:LEU:C	1:A:864:LEU:CD2	2.84	0.50
1:A:1090:ARG:HG3	1:A:1090:ARG:O	2.11	0.50
1:A:1501:LEU:H	1:A:1501:LEU:CD2	2.24	0.50
1:A:1526:LEU:HD23	1:A:1526:LEU:N	2.26	0.50
1:A:1813:ARG:NH1	1:A:1813:ARG:CB	2.73	0.50
1:A:1891:LEU:CD2	1:A:2012:LEU:HD12	2.39	0.50
1:A:2008:ARG:HD2	1:A:2012:LEU:HD23	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:124:LEU:HB3	4:E:136:TRP:HB2	1.94	0.50
8:H:100:U:O2'	31:h:64:ARG:NH2	2.43	0.50
1:A:1536:LEU:C	1:A:1536:LEU:CD2	2.85	0.50
1:A:1563:HIS:ND1	1:A:1563:HIS:N	2.59	0.50
1:A:1586:HIS:NE2	1:A:1664:ILE:HB	2.26	0.50
1:A:1617:ARG:HH12	28:z:99:LEU:CD2	2.18	0.50
1:A:1778:TRP:CE2	1:A:1809:ILE:HG21	2.46	0.50
5:F:50:A:O2'	5:F:51:U:P	2.69	0.50
7:G:7:G:H2'	7:G:8:C:C6	2.46	0.50
27:2:32:LYS:O	27:2:36:GLU:HG2	2.10	0.50
28:z:63:ALA:O	28:z:67:LYS:HB2	2.11	0.50
1:A:266:SER:OG	1:A:271:MET:O	2.28	0.50
1:A:618:THR:HG21	44:1:132:ASP:OD2	2.11	0.50
1:A:861:ARG:NH1	1:A:861:ARG:CB	2.71	0.50
1:A:1778:TRP:CE3	1:A:1858:PRO:HG2	2.45	0.50
3:C:300:LEU:HA	3:C:306:ASN:HD22	1.76	0.50
5:F:22:A:N7	23:W:130:ARG:CD	2.72	0.50
5:F:85:U:C3'	5:F:86:U:C5'	2.90	0.50
7:G:98:U:H2'	7:G:99:C:C6	2.45	0.50
8:H:111:G:O3'	8:H:112:G:O4'	2.29	0.50
14:N:51:ARG:NH2	23:W:192:PHE:O	2.45	0.50
19:S:55:ARG:HH21	19:S:57:ILE:HD11	1.76	0.50
24:X:96:GLN:CA	24:X:96:GLN:NE2	2.72	0.50
25:Y:405:MET:HE1	25:Y:410:VAL:HG11	1.93	0.50
25:Y:413:LYS:H	25:Y:413:LYS:CD	2.18	0.50
27:2:27:ALA:HB3	35:l:53:TYR:CE1	2.46	0.50
44:1:34:ARG:HA	44:1:34:ARG:NH1	2.27	0.50
1:A:766:THR:HG1	2:B:39:C:N4	2.09	0.50
1:A:1700:GLY:H	1:A:1717:ASN:HB2	1.77	0.50
1:A:1994:LYS:HZ1	27:2:67:VAL:HG22	1.73	0.50
4:E:93:TRP:CZ3	29:b:105:GLY:HA3	2.46	0.50
5:F:41:A:C2	7:G:6:A:H2	2.16	0.50
5:F:45:A:C6	7:G:2:U:O2	2.61	0.50
7:G:20:A:C2	15:O:187:THR:CG2	2.94	0.50
11:K:18:TYR:CB	11:K:171:GLN:CB	2.90	0.50
20:T:289:SER:OG	20:T:308:ARG:NH2	2.44	0.50
1:A:159:ARG:HG2	44:1:104:ARG:CB	2.39	0.50
1:A:343:GLU:HB3	44:1:144:PHE:CZ	2.46	0.50
1:A:1568:THR:HA	1:A:1571:ILE:HG13	1.93	0.50
1:A:1798:LEU:HB2	7:G:96:U:O4'	2.10	0.50
1:A:1854:VAL:CG2	44:1:270:ASP:OD2	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:107:A:C6	8:H:108:G:C5	2.99	0.50
9:I:511:LEU:HD12	9:I:543:ARG:HD2	1.92	0.50
20:T:347:THR:HG21	20:T:357:TRP:HE1	1.76	0.50
23:W:70:VAL:HG22	23:W:71:HIS:HD2	1.74	0.50
24:X:27:ARG:O	24:X:31:GLU:N	2.43	0.50
24:X:113:LYS:C	24:X:113:LYS:CD	2.85	0.50
24:X:116:ARG:HH11	24:X:116:ARG:CG	2.24	0.50
29:b:50:LYS:HG2	29:b:51:ILE:HG13	1.93	0.50
35:l:15:VAL:O	36:n:33:GLY:HA3	2.12	0.50
1:A:92:LEU:HG	1:A:652:LEU:HD13	1.93	0.50
1:A:139:VAL:O	1:A:143:GLN:N	2.40	0.50
1:A:705:LYS:HG2	8:H:15:U:C4	2.46	0.50
1:A:1214:TRP:NE1	1:A:1276:GLU:OE1	2.45	0.50
1:A:1921:ASP:HB3	1:A:1966:HIS:CG	2.47	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.47	0.50
3:C:607:LEU:O	3:C:611:ASN:ND2	2.45	0.50
7:G:21:A:OP2	15:O:193:LEU:CG	2.58	0.50
8:H:33:G:O2'	8:H:34:U:O4'	2.23	0.50
34:f:20:MET:HE2	34:f:30:LYS:HB2	1.94	0.50
1:A:1476:GLN:NE2	44:1:85:GLN:OE1	2.44	0.50
1:A:2004:GLN:HE21	44:1:342:HIS:HD2	1.54	0.50
3:C:183:SER:OG	3:C:480:LYS:NZ	2.44	0.50
3:C:210:ASN:HB3	3:C:636:TYR:HB2	1.93	0.50
9:I:717:GLU:CD	24:X:116:ARG:HG3	2.36	0.50
28:z:111:THR:O	28:z:112:LYS:OXT	2.30	0.50
1:A:658:ARG:HD3	5:F:67:G:OP1	2.12	0.50
1:A:1066:GLN:OE1	1:A:1066:GLN:HA	2.12	0.50
1:A:1475:ILE:HD12	44:1:66:TYR:CD2	2.46	0.50
1:A:1521:ALA:HB3	7:G:119:A:C1'	2.35	0.50
1:A:1778:TRP:CZ3	1:A:1809:ILE:HG21	2.45	0.50
1:A:1945:VAL:O	27:2:67:VAL:CG1	2.53	0.50
3:C:700:ILE:O	3:C:740:THR:OG1	2.28	0.50
5:F:22:A:C5	23:W:130:ARG:HD3	2.46	0.50
5:F:43:A:N6	5:F:44:G:O6	2.44	0.50
5:F:45:A:H1'	5:F:73:A:C2	2.47	0.50
12:L:145:ASP:OD1	12:L:145:ASP:N	2.40	0.50
15:O:116:TYR:O	15:O:120:ASN:ND2	2.45	0.50
28:z:92:PHE:CE2	28:z:96:LEU:CD1	2.94	0.50
1:A:861:ARG:NH2	24:X:78:MET:HE2	2.25	0.50
1:A:1536:LEU:HD13	1:A:1751:LEU:CD2	2.41	0.50
1:A:1998:ASN:HD21	1:A:2001:SER:H	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:8:C:H2'	7:G:9:C:C6	2.46	0.50
9:I:724:LEU:C	9:I:724:LEU:CD2	2.84	0.50
10:J:440:LEU:HG	10:J:445:LYS:HD2	1.93	0.50
23:W:392:VAL:HG12	23:W:424:ILE:HD13	1.92	0.50
27:2:111:LYS:HA	27:2:114:GLU:CG	2.39	0.50
44:1:31:GLU:O	44:1:34:ARG:HG3	2.12	0.50
1:A:1479:GLY:HA2	44:1:88:GLN:HE22	1.77	0.49
1:A:1596:VAL:HG23	44:1:275:LEU:CG	2.37	0.49
1:A:1617:ARG:HG2	28:z:96:LEU:CB	2.41	0.49
1:A:1618:LYS:C	1:A:1618:LYS:CD	2.85	0.49
1:A:1716:GLY:N	1:A:1718:TRP:CZ2	2.80	0.49
1:A:1780:VAL:HG21	1:A:1861:ILE:CG2	2.42	0.49
2:B:20:G:OP1	2:B:20:G:H4'	2.12	0.49
2:B:23:C:O2'	2:B:24:G:H3'	2.11	0.49
7:G:121:C:H3'	7:G:121:C:OP2	2.12	0.49
8:H:106:G:H5'	34:m:25:TRP:HH2	1.76	0.49
9:I:311:MET:O	9:I:312:GLU:C	2.51	0.49
12:L:699:ASN:O	12:L:703:MET:N	2.45	0.49
23:W:73:ASP:HB3	23:W:74:PRO:HD2	1.81	0.49
23:W:445:TRP:HE1	23:W:452:ASP:HB3	1.77	0.49
27:2:111:LYS:HA	27:2:114:GLU:OE2	2.12	0.49
36:n:10:LYS:HG2	36:n:34:PHE:HE2	1.77	0.49
1:A:435:CYS:HB3	6:4:-11:G:N2	2.27	0.49
1:A:855:ARG:NH2	8:H:29:A:H5''	2.27	0.49
1:A:1685:LEU:HD13	44:1:173:TYR:CE2	2.45	0.49
1:A:1719:PHE:CD2	1:A:1720:PRO:CD	2.95	0.49
4:E:107:GLY:O	4:E:143:ARG:NH1	2.45	0.49
4:E:253:ASN:HD21	4:E:302:ALA:HB1	1.76	0.49
7:G:21:A:OP2	15:O:193:LEU:CD1	2.60	0.49
7:G:100:C:N1	7:G:101:U:H5	2.10	0.49
27:2:123:GLN:HB3	27:2:127:ARG:HH12	1.77	0.49
28:z:65:PHE:CZ	28:z:69:GLN:CD	2.91	0.49
34:f:51:ILE:HG22	34:f:56:SER:HB2	1.93	0.49
1:A:409:ARG:NH1	2:B:25:C:C6	2.81	0.49
1:A:467:GLN:CG	2:B:19:A:C5	2.95	0.49
1:A:790:ARG:NH1	1:A:986:GLU:O	2.44	0.49
1:A:821:ARG:CB	1:A:821:ARG:NH1	2.73	0.49
1:A:880:ARG:HG3	1:A:884:HIS:CD2	2.47	0.49
1:A:1386:TRP:CB	25:Y:410:VAL:CG2	2.80	0.49
1:A:1554:GLN:HA	1:A:1561:PHE:HB3	1.94	0.49
1:A:1849:ILE:HG22	1:A:1879:PHE:CZ	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:340:PRO:HB2	4:E:356:ILE:HB	1.93	0.49
5:F:83:A:OP2	10:J:247:LYS:CD	2.58	0.49
7:G:90:C:C5'	7:G:90:C:C6	2.90	0.49
8:H:98:G:H2'	34:m:39:TYR:CE2	2.47	0.49
8:H:104:U:O2'	34:m:65:ARG:NH2	2.45	0.49
12:L:176:LEU:HD22	23:W:440:LYS:HE3	1.95	0.49
23:W:527:ASP:OD1	23:W:531:LYS:N	2.44	0.49
24:X:77:ASN:N	24:X:77:ASN:OD1	2.45	0.49
26:Z:694:TYR:HA	26:Z:709:ARG:O	2.13	0.49
27:2:31:GLN:HG3	27:2:31:GLN:O	2.12	0.49
27:2:48:ILE:C	34:m:5:LEU:CD2	2.82	0.49
27:2:113:LEU:C	27:2:113:LEU:CD1	2.85	0.49
35:e:15:VAL:O	36:g:33:GLY:HA3	2.12	0.49
35:e:20:LEU:HD13	36:g:61:VAL:CG2	2.43	0.49
31:h:75:ASP:O	31:h:78:LYS:HG2	2.12	0.49
44:1:125:ALA:HB2	44:1:150:ALA:HB3	1.94	0.49
1:A:1596:VAL:CG2	44:1:278:LEU:CD2	2.86	0.49
1:A:1778:TRP:CH2	1:A:1818:PHE:CE2	2.98	0.49
1:A:1958:LYS:HE2	27:2:97:ASP:HA	1.95	0.49
3:C:673:LYS:HG3	3:C:686:THR:HG23	1.95	0.49
7:G:20:A:HO2'	15:O:193:LEU:CD2	2.09	0.49
15:O:22:ILE:HD13	23:W:111:LEU:HD23	1.94	0.49
15:O:132:ARG:HD3	15:O:133:PRO:HD2	1.95	0.49
25:Y:397:PRO:O	25:Y:400:TRP:HB3	2.13	0.49
28:z:72:ARG:CG	28:z:72:ARG:NH2	2.71	0.49
29:i:50:LYS:HG2	29:i:51:ILE:HG13	1.93	0.49
1:A:425:PRO:HG3	2:B:26:A:H5''	1.94	0.49
1:A:1286:ASP:OD1	1:A:1354:ARG:NH2	2.45	0.49
1:A:1499:GLU:HA	44:1:63:ILE:HG12	1.95	0.49
8:H:153:A:C2'	8:H:154:C:C5'	2.86	0.49
9:I:681:ILE:CD1	9:I:714:HIS:ND1	2.76	0.49
9:I:696:ASP:HB3	9:I:699:THR:CG2	2.43	0.49
15:O:68:THR:HA	15:O:83:THR:HG22	1.93	0.49
20:T:392:PRO:HG3	20:T:415:ILE:HA	1.93	0.49
27:2:89:GLU:O	27:2:93:GLN:N	2.40	0.49
33:d:41:GLN:H	33:d:115:ILE:HB	1.76	0.49
44:1:102:TYR:HB3	44:1:156:GLN:HE21	1.77	0.49
1:A:209:ASP:HB3	1:A:212:PRO:HA	1.93	0.49
2:B:87:A:H2'	34:f:39:TYR:CE2	2.47	0.49
2:B:93:U:O2'	34:f:65:ARG:NH2	2.45	0.49
3:C:682:LYS:HB3	3:C:797:ALA:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:8:C:C6	5:F:8:C:C5'	2.91	0.49
5:F:45:A:H2	5:F:73:A:C1'	2.20	0.49
10:J:263:SER:O	10:J:267:ARG:N	2.45	0.49
16:P:3:THR:O	16:P:3:THR:OG1	2.23	0.49
23:W:103:GLN:NE2	23:W:111:LEU:O	2.46	0.49
41:q:60:PRO:CB	41:s:93:ARG:CB	2.91	0.49
1:A:1252:GLY:O	7:G:123:C:N4	2.46	0.49
1:A:1728:GLN:HE21	1:A:1728:GLN:C	2.20	0.49
2:B:57:G:H2'	2:B:58:U:H5'	1.95	0.49
5:F:39:A:H61	7:G:8:C:H42	1.59	0.49
5:F:42:C:H2'	5:F:43:A:H1'	1.94	0.49
5:F:79:C:P	10:J:237:LYS:NZ	2.84	0.49
7:G:7:G:OP2	7:G:7:G:H8	1.94	0.49
7:G:100:C:C2	7:G:101:U:H5	2.22	0.49
7:G:102:G:N3	24:X:66:GLN:NE2	2.60	0.49
9:I:724:LEU:HD11	24:X:108:GLU:CG	2.43	0.49
23:W:82:ASN:H	23:W:83:PRO:HD2	1.76	0.49
23:W:547:LYS:HE2	23:W:547:LYS:O	2.13	0.49
28:z:65:PHE:CE2	28:z:69:GLN:NE2	2.80	0.49
1:A:66:VAL:HG11	1:A:487:LEU:HD11	1.94	0.49
1:A:609:LYS:CE	45:A:3000:IHP:O31	2.61	0.49
1:A:1685:LEU:HD21	44:1:173:TYR:CE2	2.48	0.49
1:A:1790:ILE:CD1	27:2:76:SER:HG	2.13	0.49
5:F:34:G:C8	5:F:34:G:H5''	2.47	0.49
12:L:569:GLN:CB	41:q:114:CYS:C	2.86	0.49
26:Z:742:ASN:HB2	26:Z:744:ILE:HD12	1.94	0.49
42:o:66:LEU:HD21	42:o:69:LEU:HG	1.95	0.49
1:A:435:CYS:SG	6:4:-11:G:N2	2.78	0.49
1:A:1011:ALA:HB2	12:L:80:THR:HB	1.95	0.49
1:A:1201:ARG:O	1:A:1203:SER:N	2.45	0.49
1:A:1321:GLU:HG3	44:1:66:TYR:CE1	2.48	0.49
1:A:2015:GLU:HG2	24:X:55:TYR:CE1	2.46	0.49
4:E:214:ASP:OD1	4:E:214:ASP:N	2.46	0.49
4:E:215:ASN:O	4:E:232:ARG:NH1	2.46	0.49
5:F:37:C:H3'	5:F:37:C:H6	1.77	0.49
5:F:45:A:N6	7:G:120:G:C6	2.80	0.49
8:H:77:C:C5'	23:W:242:HIS:CE1	2.95	0.49
11:K:81:LEU:CB	41:t:72:PRO:CB	2.90	0.49
12:L:51:TYR:O	12:L:58:ILE:HD11	2.12	0.49
22:V:528:ILE:HA	22:V:531:GLU:HB2	1.93	0.49
24:X:56:GLU:CD	24:X:56:GLU:N	2.71	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:59:GLN:O	24:X:62:LYS:HB3	2.12	0.49
31:a:75:ASP:O	31:a:78:LYS:HG2	2.12	0.49
33:d:107:ILE:HG22	33:d:108:VAL:CG2	2.39	0.49
1:A:156:ARG:HH22	44:1:134:PHE:CB	2.25	0.49
1:A:1275:ARG:HD2	1:A:1375:TRP:CE2	2.47	0.49
1:A:1495:PHE:HD2	1:A:1501:LEU:HD13	1.78	0.49
1:A:1798:LEU:HB2	7:G:96:U:C5'	2.43	0.49
19:S:20:MET:HE2	19:S:141:ARG:HB3	1.95	0.49
22:V:620:ASN:O	22:V:624:THR:N	2.43	0.49
25:Y:412:SER:OG	25:Y:415:GLU:HG3	2.13	0.49
34:m:51:ILE:HG22	34:m:56:SER:HB2	1.93	0.49
1:A:642:ARG:NE	2:B:55:C:O2	2.31	0.48
1:A:1456:THR:OG1	1:A:1457:HIS:N	2.46	0.48
1:A:1493:THR:C	1:A:1495:PHE:H	2.20	0.48
1:A:1596:VAL:HG13	44:1:278:LEU:CD1	2.43	0.48
1:A:1873:GLU:HG2	1:A:1873:GLU:O	2.13	0.48
1:A:1901:LYS:HD3	1:A:1967:ILE:HD11	1.95	0.48
1:A:2009:ASP:O	1:A:2013:GLY:C	2.56	0.48
3:C:259:LYS:HD2	3:C:262:ARG:HD2	1.93	0.48
3:C:440:SER:HB2	3:C:443:VAL:H	1.77	0.48
8:H:77:C:O5'	23:W:242:HIS:HE1	1.95	0.48
16:P:212:ASN:CB	20:T:458:SER:H	2.13	0.48
26:Z:757:ARG:HE	27:2:68:MET:HB2	1.76	0.48
27:2:32:LYS:N	27:2:32:LYS:NZ	2.60	0.48
1:A:1275:ARG:NH1	1:A:1373:GLN:O	2.40	0.48
1:A:1694:ILE:CD1	28:z:88:ARG:CB	2.91	0.48
9:I:717:GLU:HB2	24:X:112:LEU:HD21	1.94	0.48
12:L:192:ARG:NH2	12:L:198:ILE:O	2.46	0.48
15:O:229:LYS:HD3	15:O:277:ARG:HH12	1.78	0.48
34:m:20:MET:HE2	34:m:30:LYS:HB2	1.94	0.48
1:A:1890:GLN:CA	1:A:1890:GLN:HE21	2.26	0.48
4:E:60:MET:HA	29:b:109:ALA:HA	1.94	0.48
5:F:50:A:O2'	5:F:51:U:OP1	2.27	0.48
6:4:-2:C:OP1	28:z:108:VAL:CB	2.61	0.48
8:H:24:A:H2	12:L:29:ASN:HB3	1.78	0.48
20:T:247:SER:OG	20:T:248:THR:N	2.46	0.48
24:X:114:GLU:HB2	24:X:115:TYR:CE2	2.48	0.48
35:l:20:LEU:HD13	36:n:61:VAL:CG2	2.43	0.48
1:A:1699:THR:HA	1:A:1717:ASN:HD22	1.78	0.48
1:A:1701:VAL:CB	1:A:1718:TRP:CZ3	2.88	0.48
1:A:1894:GLN:HG2	1:A:1898:LYS:NZ	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:427:LEU:HB3	20:T:439:TRP:HB2	1.95	0.48
24:X:100:ILE:HA	24:X:103:GLN:HG3	1.95	0.48
44:1:135:GLU:OE1	44:1:138:ARG:NH1	2.46	0.48
44:1:275:LEU:HA	44:1:278:LEU:CD2	2.44	0.48
1:A:1533:ARG:HB2	1:A:1533:ARG:HH11	1.79	0.48
1:A:2004:GLN:NE2	44:1:342:HIS:CD2	2.76	0.48
3:C:560:VAL:HG12	3:C:561:LYS:H	1.79	0.48
4:E:93:TRP:CZ3	29:b:105:GLY:CA	2.97	0.48
5:F:31:U:H2'	5:F:32:U:H5'	1.95	0.48
5:F:41:A:C2	7:G:6:A:N1	2.79	0.48
7:G:12:G:H2'	7:G:13:C:C6	2.49	0.48
9:I:681:ILE:CG2	9:I:710:PHE:CZ	2.80	0.48
12:L:55:ASP:HB3	12:L:58:ILE:HG13	1.95	0.48
16:P:13:ARG:HH11	16:P:13:ARG:CG	2.26	0.48
1:A:152:ARG:C	44:1:134:PHE:HD1	2.20	0.48
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.96	0.48
1:A:1533:ARG:CB	1:A:1533:ARG:HH11	2.26	0.48
1:A:1685:LEU:HD13	44:1:173:TYR:CD1	2.48	0.48
1:A:1728:GLN:C	1:A:1728:GLN:NE2	2.71	0.48
1:A:2008:ARG:O	1:A:2012:LEU:HD22	2.13	0.48
5:F:22:A:C2	14:N:126:LEU:HD23	2.48	0.48
7:G:90:C:OP2	7:G:90:C:C6	2.66	0.48
12:L:18:ILE:O	12:L:22:ALA:N	2.47	0.48
15:O:245:GLU:OE1	15:O:249:ARG:NH1	2.46	0.48
1:A:532:THR:CB	7:G:3:A:O5'	2.61	0.48
1:A:668:VAL:O	1:A:668:VAL:HG12	2.14	0.48
1:A:1578:ARG:HG2	1:A:1746:ARG:NH1	2.28	0.48
1:A:2015:GLU:CD	24:X:55:TYR:CE2	2.91	0.48
4:E:78:GLY:O	4:E:336:HIS:NE2	2.45	0.48
8:H:143:A:N3	8:H:143:A:C3'	2.73	0.48
9:I:727:ARG:NH2	9:I:727:ARG:C	2.71	0.48
9:I:728:ARG:O	9:I:731:GLN:CB	2.61	0.48
27:2:38:LEU:CD2	34:m:12:ASN:HD22	2.13	0.48
27:2:114:GLU:HG3	27:2:115:LYS:N	2.29	0.48
1:A:702:LYS:NZ	13:M:127:TYR:OH	2.47	0.48
1:A:1131:LYS:HZ1	1:A:1188:ASN:HB2	1.78	0.48
1:A:1476:GLN:HG3	44:1:73:TYR:OH	2.14	0.48
2:B:92:U:O4	29:b:38:MET:HG3	2.14	0.48
4:E:75:HIS:ND1	4:E:77:ASN:OD1	2.46	0.48
8:H:39:U:C2'	8:H:40:C:C5	2.97	0.48
8:H:107:A:C2	8:H:108:G:C4	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:457:ARG:CG	44:1:73:TYR:HD2	2.24	0.48
37:v:140:HIS:O	38:w:70:VAL:CB	2.62	0.48
5:F:43:A:C6	5:F:44:G:C6	3.02	0.48
8:H:44:U:H2'	8:H:45:C:C6	2.48	0.48
9:I:661:ASP:HA	9:I:664:ALA:HB3	1.95	0.48
10:J:183:ALA:HB3	12:L:142:ILE:HG12	1.96	0.48
12:L:6:ILE:C	12:L:6:ILE:CD1	2.82	0.48
36:g:35:ASP:HB2	36:g:36:PRO:CD	2.42	0.48
41:q:60:PRO:CB	41:s:94:GLN:HA	2.43	0.48
1:A:342:THR:HG22	1:A:351:TYR:CE1	2.49	0.48
1:A:681:PHE:HE2	1:A:746:LYS:HG3	1.78	0.48
1:A:1135:PRO:HD2	1:A:1135:PRO:O	2.14	0.48
1:A:1501:LEU:CD1	1:A:1753:LEU:HD11	2.44	0.48
1:A:1502:PHE:HD1	1:A:1502:PHE:N	2.00	0.48
1:A:1596:VAL:HG11	44:1:278:LEU:CD1	2.43	0.48
3:C:818:SER:HB3	3:C:822:MET:CE	2.41	0.48
7:G:19:G:H21	15:O:196:GLN:CG	2.27	0.48
9:I:661:ASP:CB	9:I:694:ILE:HG21	2.20	0.48
10:J:201:ARG:NH2	10:J:201:ARG:CG	2.73	0.48
15:O:147:LEU:O	15:O:151:ALA:N	2.47	0.48
18:R:265:ASP:N	18:R:265:ASP:OD1	2.45	0.48
24:X:72:GLN:NE2	24:X:72:GLN:C	2.72	0.48
24:X:112:LEU:C	24:X:112:LEU:CD1	2.87	0.48
28:z:58:ARG:NH1	44:1:177:GLU:OE1	2.45	0.48
41:r:127:ALA:HB1	41:s:127:ALA:CB	2.44	0.48
33:k:107:ILE:HG22	33:k:108:VAL:CG2	2.39	0.48
34:m:10:PHE:CE2	35:l:78:MET:HB2	2.48	0.48
1:A:2015:GLU:O	1:A:2015:GLU:HG3	2.14	0.47
4:E:294:SER:HB3	4:E:299:LYS:HB2	1.96	0.47
17:Q:936:PHE:CB	17:Q:1005:PHE:CB	2.92	0.47
20:T:471:ASP:OD1	20:T:471:ASP:N	2.46	0.47
23:W:256:HIS:HB3	23:W:257:ILE:HD12	1.96	0.47
23:W:453:PHE:CB	27:2:79:PHE:CE2	2.97	0.47
41:q:61:ILE:N	41:s:93:ARG:CB	2.75	0.47
1:A:80:LYS:HD3	14:N:37:HIS:HE2	1.79	0.47
1:A:1617:ARG:HG3	1:A:1617:ARG:O	2.14	0.47
5:F:50:A:HO2'	5:F:51:U:P	2.36	0.47
5:F:60:C:H5''	18:R:219:PRO:CD	2.40	0.47
8:H:77:C:H2'	8:H:78:C:C6	2.49	0.47
8:H:151:C:C2	8:H:152:G:N7	2.82	0.47
9:I:555:ASP:OD1	9:I:555:ASP:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:593:LYS:HE2	9:I:631:MET:HG3	1.95	0.47
14:N:51:ARG:HH21	23:W:193:LEU:HD23	1.78	0.47
20:T:267:ASP:OD2	20:T:269:GLN:NE2	2.47	0.47
24:X:116:ARG:NH1	24:X:116:ARG:CG	2.73	0.47
1:A:280:GLU:HG2	2:B:48:A:O4'	2.14	0.47
1:A:824:PRO:O	1:A:933:ARG:NH1	2.45	0.47
1:A:1248:LEU:HD21	1:A:1295:ILE:HG22	1.95	0.47
1:A:1386:TRP:HB3	25:Y:410:VAL:HG23	1.88	0.47
1:A:1775:GLN:HE21	44:1:315:VAL:CB	2.23	0.47
8:H:42:G:H8	8:H:42:G:O5'	1.98	0.47
9:I:329:LEU:CB	17:Q:353:LEU:CA	2.90	0.47
15:O:88:LEU:O	18:R:183:GLN:NE2	2.47	0.47
24:X:80:ARG:HD2	24:X:80:ARG:O	2.14	0.47
24:X:100:ILE:HA	24:X:103:GLN:CG	2.44	0.47
1:A:200:ASP:OD1	1:A:240:ARG:NH2	2.48	0.47
1:A:467:GLN:HG2	2:B:19:A:C5	2.49	0.47
1:A:761:ILE:HD11	1:A:772:CYS:SG	2.54	0.47
1:A:1684:PHE:HB3	1:A:1715:TYR:CD2	2.50	0.47
5:F:8:C:H6	5:F:8:C:C5'	2.09	0.47
7:G:102:G:C2	24:X:66:GLN:NE2	2.82	0.47
8:H:69:U:H2'	8:H:70:C:C6	2.49	0.47
20:T:349:SER:OG	20:T:351:ASP:OD1	2.29	0.47
34:f:10:PHE:CE2	35:e:78:MET:HB2	2.49	0.47
37:v:24:PHE:HA	37:v:33:ARG:O	2.14	0.47
1:A:53:PHE:HE2	1:A:55:ASP:HB3	1.79	0.47
1:A:589:THR:OG1	1:A:590:GLY:N	2.46	0.47
1:A:1689:THR:OG1	44:1:170:TRP:HH2	1.97	0.47
1:A:1998:ASN:ND2	1:A:1998:ASN:C	2.73	0.47
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.49	0.47
5:F:22:A:N1	14:N:126:LEU:HD23	2.29	0.47
8:H:60:U:O2'	8:H:67:C:N4	2.47	0.47
9:I:727:ARG:HH21	9:I:727:ARG:HG2	1.76	0.47
12:L:15:GLU:HG2	12:L:151:MET:HE1	1.96	0.47
25:Y:644:TYR:HA	25:Y:660:TYR:O	2.14	0.47
34:m:36:VAL:HG12	34:m:37:ASP:N	2.29	0.47
1:A:165:ARG:HE	1:A:165:ARG:C	2.22	0.47
1:A:1482:GLU:OE1	44:1:86:ARG:HA	2.15	0.47
1:A:1560:ILE:H	1:A:1560:ILE:HG13	1.46	0.47
1:A:2004:GLN:CD	1:A:2004:GLN:N	2.71	0.47
2:B:20:G:H1'	2:B:21:A:OP1	2.14	0.47
4:E:176:VAL:HB	4:E:190:PHE:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:17:U:O2	15:O:198:ILE:CD1	2.63	0.47
8:H:153:A:C8	8:H:154:C:H5'	2.50	0.47
9:I:720:ILE:O	9:I:724:LEU:N	2.45	0.47
10:J:181:ASN:HA	26:Z:740:PHE:O	2.15	0.47
25:Y:413:LYS:CB	25:Y:425:ILE:HD11	2.44	0.47
32:c:20:LYS:HE2	32:c:63:ASN:O	2.15	0.47
42:o:153:LYS:O	42:o:157:GLU:HG3	2.14	0.47
1:A:704:ASN:ND2	8:H:16:U:OP2	2.48	0.47
1:A:711:GLN:HE22	8:H:18:U:H3'	1.79	0.47
1:A:1108:ASP:OD2	1:A:1112:ARG:NH1	2.48	0.47
1:A:1578:ARG:HH11	1:A:1578:ARG:HG3	1.78	0.47
1:A:1942:ALA:C	1:A:1944:HIS:N	2.69	0.47
4:E:69:VAL:O	4:E:331:ASN:ND2	2.38	0.47
5:F:25:C:O4'	5:F:26:U:OP2	2.33	0.47
5:F:28:A:O2'	14:N:39:GLY:HA2	2.13	0.47
8:H:30:A:O4'	24:X:73:PHE:HE1	1.96	0.47
8:H:39:U:C3'	8:H:40:C:C6	2.97	0.47
8:H:59:A:H2'	8:H:60:U:C6	2.50	0.47
8:H:103:U:O4	29:i:38:MET:HG3	2.14	0.47
8:H:141:C:H2'	8:H:142:C:C6	2.50	0.47
8:H:149:A:H2'	8:H:150:U:C6	2.50	0.47
13:M:211:ILE:HD12	13:M:212:ASN:HB2	1.95	0.47
22:V:457:ARG:CG	44:1:73:TYR:CD2	2.88	0.47
23:W:523:VAL:HB	23:W:535:TRP:HB2	1.96	0.47
27:2:28:ALA:HA	27:2:31:GLN:CB	2.44	0.47
31:h:45:ASN:HB3	42:o:22:ARG:HH11	1.79	0.47
32:j:6:PHE:CD1	32:j:6:PHE:C	2.93	0.47
1:A:127:SER:OG	1:A:495:GLN:NE2	2.45	0.47
1:A:439:GLN:O	1:A:444:ARG:NH1	2.48	0.47
1:A:1741:TYR:CD2	44:1:287:PRO:HB2	2.50	0.47
8:H:54:U:H2'	8:H:55:U:C6	2.50	0.47
8:H:57:A:H2'	8:H:58:U:C6	2.50	0.47
8:H:71:C:H2'	8:H:72:U:C6	2.50	0.47
9:I:139:ALA:HB2	9:I:147:ARG:CB	2.45	0.47
20:T:335:THR:OG1	20:T:336:VAL:N	2.47	0.47
33:d:108:VAL:CG1	34:f:62:VAL:HG13	2.44	0.47
32:j:61:ARG:HB3	32:j:64:ASN:HD22	1.80	0.47
42:o:14:GLN:HG3	42:o:44:PHE:HE1	1.80	0.47
1:A:158:ARG:NH2	1:A:570:ASP:OD2	2.40	0.47
1:A:1034:LEU:HB2	1:A:1037:ALA:HB2	1.97	0.47
1:A:1765:SER:HB2	1:A:1889:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1809:ILE:HB	1:A:1818:PHE:HB2	1.95	0.47
8:H:150:U:H2'	8:H:151:C:C6	2.50	0.47
12:L:7:LYS:HG3	12:L:40:ARG:HA	1.96	0.47
12:L:54:LEU:O	12:L:55:ASP:C	2.58	0.47
15:O:196:GLN:HE21	15:O:208:PRO:HG2	1.80	0.47
31:a:24:THR:O	31:a:51:ARG:NH1	2.46	0.47
31:a:43:MET:HB3	31:a:46:ILE:HD11	1.97	0.47
36:g:64:GLY:HA2	36:g:67:ILE:HD12	1.97	0.47
35:l:68:THR:HG22	35:l:68:THR:O	2.15	0.47
36:n:64:GLY:HA2	36:n:67:ILE:HD12	1.97	0.47
1:A:162:LYS:CE	44:1:170:TRP:CZ2	2.98	0.47
1:A:1070:ASP:OD1	1:A:1070:ASP:N	2.39	0.47
1:A:1991:TYR:CD1	26:Z:756:TYR:CE1	3.03	0.47
5:F:24:A:C6	15:O:65:PHE:CE2	2.97	0.47
7:G:27:U:HO2'	7:G:28:A:C4'	2.27	0.47
8:H:70:C:H2'	8:H:71:C:C6	2.50	0.47
9:I:723:MET:O	9:I:727:ARG:N	2.46	0.47
12:L:123:LEU:HD22	12:L:125:PRO:CD	2.44	0.47
12:L:135:LYS:N	12:L:135:LYS:CD	2.78	0.47
19:S:72:ARG:HD3	23:W:90:ALA:HB3	1.97	0.47
19:S:97:ILE:CG2	19:S:128:ILE:HG23	2.45	0.47
32:j:20:LYS:HE2	32:j:63:ASN:O	2.15	0.47
42:o:2:VAL:O	42:o:2:VAL:HG13	2.13	0.47
1:A:702:LYS:HD2	13:M:124:PHE:HE2	1.80	0.46
1:A:1566:ILE:H	1:A:1566:ILE:HG12	1.47	0.46
1:A:1640:SER:CB	1:A:1718:TRP:O	2.63	0.46
1:A:1724:PRO:N	1:A:1725:LEU:N	2.63	0.46
1:A:1808:PHE:CD2	1:A:1808:PHE:O	2.69	0.46
8:H:72:U:H2'	8:H:73:C:C6	2.49	0.46
8:H:73:C:H2'	8:H:74:U:C6	2.50	0.46
8:H:90:A:H2'	8:H:91:U:C6	2.50	0.46
19:S:125:LYS:HB2	19:S:126:HIS:CD2	2.49	0.46
24:X:95:ARG:CZ	24:X:95:ARG:CB	2.88	0.46
26:Z:757:ARG:CZ	27:2:68:MET:HB2	2.01	0.46
32:c:6:PHE:CD1	32:c:6:PHE:C	2.93	0.46
34:f:36:VAL:HG12	34:f:37:ASP:N	2.29	0.46
33:k:108:VAL:CG1	34:m:62:VAL:HG13	2.45	0.46
34:m:3:LEU:HG	34:m:4:PRO:CD	2.41	0.46
34:m:5:LEU:HB3	35:l:48:ILE:HG22	1.96	0.46
42:o:56:LYS:HG2	42:o:58:ASP:HB2	1.97	0.46
1:A:58:LYS:HB2	1:A:477:LYS:HE2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:ARG:HD2	28:z:56:ASP:CB	2.45	0.46
1:A:1661:TRP:CZ2	1:A:1684:PHE:CE1	3.03	0.46
1:A:1772:PHE:CA	1:A:1813:ARG:HD2	2.43	0.46
1:A:1861:ILE:CD1	1:A:1861:ILE:N	2.72	0.46
3:C:785:ARG:HG2	3:C:786:ASN:HB2	1.97	0.46
3:C:852:ARG:NH2	6:4:-13:C:H2'	2.30	0.46
4:E:266:PRO:CB	12:L:788:TYR:CB	2.92	0.46
7:G:98:U:C2'	7:G:99:C:C6	2.98	0.46
8:H:30:A:C4'	24:X:73:PHE:CZ	2.98	0.46
9:I:728:ARG:NH2	9:I:728:ARG:CG	2.72	0.46
10:J:523:PRO:O	10:J:527:LYS:N	2.46	0.46
18:R:123:GLU:HG3	18:R:124:VAL:HG12	1.96	0.46
18:R:147:THR:HG23	20:T:360:VAL:HG12	1.96	0.46
19:S:66:ASP:OD1	19:S:73:GLY:O	2.32	0.46
35:e:18:ILE:HA	35:e:21:ILE:HD12	1.98	0.46
41:s:65:PRO:O	41:s:66:PRO:C	2.58	0.46
42:o:61:PRO:O	42:o:86:ALA:HB1	2.15	0.46
1:A:663:ARG:NH1	5:F:64:U:OP2	2.49	0.46
1:A:832:TYR:HD2	1:A:835:ASP:HB3	1.79	0.46
1:A:1575:GLN:O	1:A:1578:ARG:HD2	2.16	0.46
1:A:1944:HIS:C	1:A:1944:HIS:ND1	2.72	0.46
3:C:843:VAL:HG13	3:C:871:ILE:HD11	1.97	0.46
4:E:114:GLU:OE2	4:E:116:HIS:NE2	2.43	0.46
7:G:7:G:H2'	7:G:8:C:H6	1.80	0.46
8:H:83:A:H2'	8:H:84:C:C6	2.50	0.46
10:J:195:LEU:HD22	12:L:24:MET:HE1	1.96	0.46
10:J:454:ASN:O	10:J:458:PHE:N	2.46	0.46
27:2:138:LYS:O	27:2:142:LYS:HG2	2.15	0.46
28:z:58:ARG:NH2	44:1:177:GLU:OE1	2.43	0.46
44:1:34:ARG:CA	44:1:34:ARG:NH1	2.76	0.46
1:A:53:PHE:CE1	2:B:65:G:C5'	2.98	0.46
1:A:372:PRO:HG2	3:C:342:ARG:HG2	1.97	0.46
1:A:1772:PHE:CE1	1:A:1812:PRO:C	2.94	0.46
1:A:1798:LEU:HD22	7:G:96:U:O4'	2.16	0.46
1:A:1877:LEU:HD23	1:A:1877:LEU:HA	1.67	0.46
3:C:174:GLU:OE2	3:C:182:LYS:N	2.44	0.46
5:F:36:A:O2'	5:F:37:C:P	2.74	0.46
10:J:224:LYS:HE2	10:J:255:LEU:HD13	1.96	0.46
1:A:435:CYS:CB	6:4:-11:G:N2	2.74	0.46
1:A:467:GLN:NE2	2:B:19:A:C6	2.84	0.46
1:A:1698:PRO:CG	44:1:181:ILE:HG13	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1759:THR:HG21	44:1:288:LYS:CE	2.46	0.46
3:C:221:ILE:O	3:C:495:ARG:NH1	2.48	0.46
3:C:856:HIS:O	3:C:856:HIS:CG	2.68	0.46
6:4:-2:C:OP1	28:z:108:VAL:HB	2.15	0.46
8:H:183:G:H2'	8:H:184:C:C6	2.50	0.46
9:I:624:GLU:HB3	9:I:627:GLN:HB2	1.97	0.46
10:J:196:ARG:HA	13:M:208:ILE:HD11	1.98	0.46
28:z:54:GLY:C	44:1:174:ASN:ND2	2.66	0.46
1:A:244:GLN:CA	1:A:244:GLN:HE21	2.29	0.46
1:A:1620:TYR:CG	1:A:1620:TYR:O	2.68	0.46
1:A:1860:GLN:CB	1:A:1883:VAL:HB	2.45	0.46
1:A:1980:GLU:CD	44:1:348:THR:HG22	2.40	0.46
8:H:10:C:H41	13:M:198:ARG:NH1	2.10	0.46
22:V:498:ALA:HB1	22:V:543:LYS:HB3	1.97	0.46
32:c:61:ARG:HB3	32:c:64:ASN:HD22	1.80	0.46
33:k:46:CYS:HB3	33:k:48:ASN:OD1	2.15	0.46
35:l:18:ILE:HA	35:l:21:ILE:HD12	1.98	0.46
44:1:124:GLY:HA3	44:1:149:ILE:HG23	1.97	0.46
1:A:182:ILE:HD11	1:A:562:VAL:HG13	1.97	0.46
1:A:1908:LYS:HZ2	23:W:448:ASP:HB3	1.81	0.46
1:A:1942:ALA:C	1:A:1944:HIS:H	2.24	0.46
5:F:88:G:H5'	13:M:133:ARG:HH12	1.81	0.46
8:H:68:G:H2'	8:H:69:U:C6	2.50	0.46
8:H:182:U:H2'	8:H:183:G:H8	1.81	0.46
12:L:77:LEU:HD22	18:R:285:ALA:HA	1.98	0.46
17:Q:88:LYS:O	17:Q:92:MET:CB	2.64	0.46
20:T:210:ILE:HG13	20:T:480:ALA:HB2	1.97	0.46
27:2:29:GLU:OE1	27:2:29:GLU:HA	2.12	0.46
28:z:58:ARG:NH1	44:1:177:GLU:OE2	2.43	0.46
35:e:16:GLN:HB3	35:e:19:ASN:OD1	2.16	0.46
1:A:524:LEU:HD23	28:z:105:ILE:HD11	1.97	0.46
1:A:1536:LEU:HD23	1:A:1536:LEU:C	2.39	0.46
1:A:1620:TYR:O	1:A:1620:TYR:CD2	2.69	0.46
1:A:1700:GLY:O	1:A:1717:ASN:N	2.49	0.46
1:A:1797:ASN:OD1	7:G:96:U:H5''	2.16	0.46
1:A:1842:ALA:HB3	1:A:1875:HIS:CD2	2.51	0.46
1:A:1889:LEU:HD22	1:A:1889:LEU:HA	1.67	0.46
1:A:1998:ASN:ND2	1:A:1998:ASN:O	2.48	0.46
3:C:508:LYS:HA	3:C:524:ILE:HG22	1.98	0.46
8:H:107:A:C6	8:H:108:G:C6	3.04	0.46
12:L:5:MET:HE2	12:L:39:HIS:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:420:ALA:O	23:W:438:ASP:N	2.48	0.46
24:X:55:TYR:CD1	24:X:55:TYR:O	2.69	0.46
24:X:71:GLU:C	24:X:71:GLU:CD	2.84	0.46
24:X:116:ARG:CB	24:X:116:ARG:NH1	2.72	0.46
31:h:24:THR:O	31:h:51:ARG:NH1	2.46	0.46
1:A:464:PRO:HD2	2:B:20:G:O2'	2.16	0.46
1:A:821:ARG:HH11	1:A:821:ARG:HB3	1.79	0.46
1:A:829:PRO:HG2	1:A:832:TYR:HB2	1.96	0.46
1:A:1684:PHE:CE2	44:1:178:HIS:NE2	2.84	0.46
1:A:1930:TYR:CD1	44:1:324:MET:HB2	2.51	0.46
6:4:-2:C:OP1	28:z:108:VAL:CG2	2.63	0.46
8:H:39:U:N3	8:H:40:C:N4	2.63	0.46
8:H:152:G:O2'	8:H:153:A:H1'	2.16	0.46
9:I:516:ALA:HA	9:I:520:ILE:HD11	1.98	0.46
16:P:77:ASP:O	16:P:78:ARG:NE	2.47	0.46
19:S:125:LYS:HB2	19:S:126:HIS:HD2	1.80	0.46
20:T:193:PRO:HD2	20:T:495:ALA:HB1	1.98	0.46
28:z:65:PHE:CD1	28:z:65:PHE:O	2.69	0.46
35:e:68:THR:O	35:e:68:THR:HG22	2.15	0.46
31:h:43:MET:HB3	31:h:46:ILE:HD11	1.97	0.46
1:A:244:GLN:HE21	1:A:244:GLN:N	2.14	0.46
1:A:1640:SER:HB2	1:A:1650:ASP:HB3	1.98	0.46
1:A:1884:ILE:H	44:1:290:ARG:HG2	1.81	0.46
1:A:1892:PRO:HG3	1:A:1941:ARG:HE	1.81	0.46
2:B:93:U:O4	33:d:64:ASN:ND2	2.42	0.46
4:E:90:ILE:HB	4:E:105:LEU:HB2	1.98	0.46
8:H:114:A:H2'	8:H:115:G:H8	1.81	0.46
26:Z:752:LYS:HD2	26:Z:754:TYR:HE2	1.81	0.46
27:2:52:MET:SD	34:m:3:LEU:HB2	2.56	0.46
42:o:120:ILE:HG22	42:o:120:ILE:O	2.16	0.46
44:1:102:TYR:HD1	44:1:156:GLN:HB3	1.81	0.46
1:A:773:LYS:HB3	8:H:23:A:N3	2.31	0.45
1:A:843:LEU:HD22	1:A:867:ILE:HG23	1.98	0.45
1:A:1251:SER:OG	1:A:1259:ILE:HD11	2.16	0.45
1:A:1705:ILE:HD11	1:A:1730:MET:CE	2.46	0.45
1:A:1705:ILE:HD11	1:A:1730:MET:HE3	1.97	0.45
1:A:1801:LYS:HD2	5:F:42:C:OP1	2.16	0.45
1:A:1827:TRP:CE3	1:A:1833:LEU:HD12	2.51	0.45
1:A:1849:ILE:HB	1:A:1879:PHE:CE2	2.51	0.45
1:A:1892:PRO:HA	27:2:70:SER:O	2.16	0.45
15:O:131:THR:HG23	23:W:111:LEU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:233:PRO:HB2	18:R:234:SER:H	1.62	0.45
20:T:404:SER:OG	20:T:405:PHE:N	2.48	0.45
29:b:17:MET:HE1	29:b:82:VAL:HG22	1.99	0.45
33:d:46:CYS:HB3	33:d:48:ASN:OD1	2.15	0.45
1:A:80:LYS:NZ	14:N:38:GLU:O	2.49	0.45
1:A:572:PHE:HE2	28:z:61:ALA:HB1	1.79	0.45
1:A:1116:GLU:OE2	16:P:196:ASN:ND2	2.48	0.45
1:A:1479:GLY:HA2	44:1:88:GLN:OE1	2.16	0.45
1:A:1697:SER:OG	1:A:1699:THR:O	2.31	0.45
2:B:23:C:HO2'	2:B:24:G:P	2.38	0.45
7:G:87:U:H5''	7:G:88:G:OP2	2.15	0.45
8:H:78:C:H2'	8:H:79:G:H8	1.81	0.45
8:H:79:G:H2'	8:H:80:A:H8	1.81	0.45
8:H:181:G:H2'	8:H:182:U:C6	2.50	0.45
19:S:142:VAL:HG13	19:S:157:VAL:HG11	1.99	0.45
41:t:65:PRO:O	41:t:66:PRO:C	2.58	0.45
36:n:38:MET:HE2	36:n:67:ILE:HG21	1.98	0.45
44:1:275:LEU:HA	44:1:278:LEU:HD23	1.98	0.45
1:A:53:PHE:CE1	2:B:65:G:H5''	2.52	0.45
1:A:537:LYS:HB2	5:F:37:C:N4	2.30	0.45
1:A:803:ALA:HB2	18:R:287:LEU:HA	1.98	0.45
5:F:36:A:HO2'	5:F:37:C:P	2.40	0.45
8:H:58:U:H2'	8:H:59:A:H8	1.82	0.45
8:H:81:G:H2'	8:H:82:G:H8	1.81	0.45
8:H:113:G:H2'	8:H:114:A:H8	1.82	0.45
13:M:125:SER:HB3	18:R:239:VAL:HG22	1.97	0.45
22:V:460:TYR:CD1	44:1:72:TRP:HZ2	2.33	0.45
26:Z:756:TYR:CD2	26:Z:756:TYR:O	2.69	0.45
29:i:17:MET:HE1	29:i:82:VAL:HG22	1.99	0.45
33:k:72:GLU:HG2	33:k:74:TRP:CE3	2.51	0.45
42:o:92:GLU:OE1	43:p:25:ARG:NE	2.39	0.45
44:1:268:ARG:HH11	44:1:268:ARG:CG	2.23	0.45
1:A:159:ARG:HD2	28:z:56:ASP:HB3	1.99	0.45
8:H:80:A:H2'	8:H:81:G:H8	1.81	0.45
8:H:180:G:H2'	8:H:181:G:H8	1.81	0.45
9:I:599:TYR:HA	9:I:602:LEU:HG	1.99	0.45
23:W:453:PHE:CA	27:2:79:PHE:HE2	2.30	0.45
23:W:525:SER:OG	23:W:526:GLY:N	2.49	0.45
24:X:92:GLU:C	24:X:92:GLU:CD	2.84	0.45
1:A:240:ARG:HH12	44:1:139:ARG:CB	2.16	0.45
1:A:540:PHE:HB3	1:A:544:PHE:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1430:LEU:HB2	25:Y:400:TRP:CZ3	2.52	0.45
1:A:1487:HIS:NE2	1:A:1671:TYR:CZ	2.84	0.45
1:A:1894:GLN:HG2	1:A:1898:LYS:HZ1	1.82	0.45
3:C:725:ASP:HB3	3:C:728:ALA:HB3	1.98	0.45
7:G:90:C:O2'	7:G:91:A:O5'	2.35	0.45
7:G:94:C:H2'	7:G:95:U:C6	2.51	0.45
9:I:242:ALA:HB1	17:Q:528:GLY:HA3	1.97	0.45
10:J:197:GLU:O	10:J:201:ARG:HG2	2.17	0.45
10:J:267:ARG:HH11	12:L:216:PHE:HB2	1.82	0.45
11:K:83:SER:O	41:t:76:LYS:CA	2.63	0.45
20:T:339:GLN:NE2	20:T:343:PRO:O	2.42	0.45
23:W:70:VAL:CG1	23:W:71:HIS:HD2	2.29	0.45
23:W:79:VAL:CG2	29:b:114:ILE:CD1	2.72	0.45
33:d:22:GLU:OE1	33:d:22:GLU:HA	2.17	0.45
33:d:72:GLU:HG2	33:d:74:TRP:CE3	2.51	0.45
35:l:16:GLN:HB3	35:l:19:ASN:OD1	2.16	0.45
1:A:26:SER:H	1:A:29:LYS:HD2	1.81	0.45
1:A:1321:GLU:CG	44:1:66:TYR:OH	2.65	0.45
1:A:1554:GLN:HA	1:A:1561:PHE:CA	2.46	0.45
1:A:1689:THR:OG1	44:1:170:TRP:CH2	2.70	0.45
1:A:2004:GLN:CB	44:1:342:HIS:NE2	2.67	0.45
1:A:2015:GLU:CD	1:A:2015:GLU:C	2.85	0.45
8:H:14:C:N4	13:M:224:ARG:CD	2.79	0.45
8:H:82:G:H2'	8:H:83:A:H8	1.81	0.45
8:H:89:U:H2'	8:H:90:A:H8	1.82	0.45
8:H:168:A:C2'	36:n:48:MET:HE1	2.46	0.45
10:J:308:ARG:HH21	10:J:339:TRP:HE3	1.64	0.45
15:O:258:ILE:HD13	15:O:261:ILE:HD11	1.99	0.45
18:R:62:GLY:N	19:S:132:VAL:O	2.41	0.45
20:T:477:LEU:HB3	20:T:489:TYR:HB2	1.98	0.45
23:W:436:THR:HG21	23:W:464:MET:HB2	1.98	0.45
24:X:54:LEU:HD11	24:X:56:GLU:HB2	1.99	0.45
31:a:77:LEU:HD12	31:a:77:LEU:N	2.32	0.45
36:g:38:MET:HE2	36:g:67:ILE:HG21	1.98	0.45
41:s:65:PRO:O	41:s:67:SER:N	2.49	0.45
1:A:53:PHE:HE1	2:B:65:G:H5''	1.81	0.45
1:A:1475:ILE:HD12	44:1:66:TYR:HD2	1.82	0.45
1:A:1771:LEU:HD22	1:A:1812:PRO:HG2	1.99	0.45
7:G:27:U:HO2'	7:G:28:A:C5'	2.26	0.45
8:H:148:C:H2'	8:H:149:A:H8	1.82	0.45
36:n:32:ARG:HG3	36:n:43:ASP:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:HIS:HD1	1:A:88:TYR:HH	1.53	0.45
1:A:299:ILE:HG12	1:A:1346:THR:HG21	1.99	0.45
1:A:1146:ASP:OD2	1:A:1182:ASN:ND2	2.50	0.45
1:A:1921:ASP:HB3	1:A:1966:HIS:CD2	2.51	0.45
3:C:121:ASP:OD2	31:a:76:MET:SD	2.75	0.45
3:C:348:TYR:HE1	3:C:367:ARG:HG2	1.82	0.45
5:F:12:G:H2'	5:F:13:G:O4'	2.17	0.45
5:F:28:A:HO2'	14:N:39:GLY:HA3	1.82	0.45
7:G:23:U:H5''	7:G:23:U:H6	1.82	0.45
8:H:67:C:H2'	8:H:68:G:H8	1.81	0.45
8:H:93:A:H2'	8:H:94:A:H8	1.82	0.45
13:M:148:THR:HA	13:M:151:ARG:HB2	1.99	0.45
16:P:41:ILE:HD11	20:T:318:ARG:HB3	1.99	0.45
20:T:190:TRP:CE3	20:T:190:TRP:O	2.70	0.45
33:k:48:ASN:O	33:k:49:ASN:HB2	2.17	0.45
1:A:211:GLN:OE1	1:A:214:ARG:NH1	2.48	0.45
1:A:1490:PHE:CZ	1:A:1498:TRP:HA	2.51	0.45
1:A:1719:PHE:HD2	1:A:1720:PRO:CD	2.28	0.45
8:H:74:U:H2'	8:H:75:A:H8	1.82	0.45
8:H:84:C:H2'	8:H:85:A:H8	1.82	0.45
8:H:142:C:H2'	8:H:143:A:H5'	1.97	0.45
12:L:6:ILE:HD12	24:X:80:ARG:HG2	1.99	0.45
20:T:197:TYR:O	20:T:197:TYR:CD1	2.70	0.45
29:b:37:HIS:O	29:b:38:MET:HB2	2.17	0.45
1:A:984:MET:HG3	1:A:1048:MET:HE1	1.99	0.45
1:A:1772:PHE:CE1	1:A:1812:PRO:O	2.66	0.45
3:C:663:CYS:HB2	3:C:828:MET:HB2	1.98	0.45
3:C:682:LYS:HG3	3:C:803:ARG:HD3	1.99	0.45
4:E:62:LEU:HB2	4:E:351:LEU:HB2	1.97	0.45
8:H:56:A:H2'	8:H:57:A:H8	1.82	0.45
8:H:152:G:OP2	27:2:127:ARG:CD	2.57	0.45
9:I:707:TRP:CZ2	9:I:723:MET:HB2	2.52	0.45
15:O:229:LYS:HA	15:O:277:ARG:HH12	1.82	0.45
18:R:224:SEP:HB3	18:R:225:PRO:HD2	1.97	0.45
23:W:341:ASN:HB3	23:W:345:THR:H	1.81	0.45
24:X:90:LEU:N	24:X:90:LEU:HD23	2.31	0.45
27:2:138:LYS:HE2	27:2:138:LYS:O	2.17	0.45
33:d:48:ASN:O	33:d:49:ASN:HB2	2.17	0.45
36:n:35:ASP:HB2	36:n:36:PRO:CD	2.42	0.45
1:A:53:PHE:CE2	1:A:55:ASP:HB3	2.52	0.44
1:A:525:LYS:HB3	28:z:100:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1594:CYS:SG	44:1:268:ARG:NH1	2.83	0.44
1:A:1596:VAL:HG21	44:1:278:LEU:HD11	1.96	0.44
1:A:1716:GLY:N	1:A:1718:TRP:NE1	2.65	0.44
1:A:1949:ARG:HG2	1:A:1986:LEU:HD11	1.99	0.44
2:B:12:U:H3	2:B:65:G:H1	1.63	0.44
3:C:856:HIS:O	3:C:856:HIS:CD2	2.70	0.44
4:E:70:TYR:HE2	4:E:86:PHE:HB2	1.81	0.44
17:Q:929:CYS:CB	17:Q:1012:ARG:HA	2.47	0.44
19:S:41:GLU:OE2	19:S:44:ARG:NH2	2.38	0.44
23:W:84:THR:O	23:W:87:THR:N	2.50	0.44
23:W:313:ILE:HB	23:W:328:PHE:HB2	1.99	0.44
23:W:453:PHE:CD2	27:2:83:ARG:CD	3.00	0.44
33:d:43:LEU:HD11	33:d:51:LYS:HB3	1.99	0.44
1:A:165:ARG:O	1:A:165:ARG:CD	2.66	0.44
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.34	0.44
1:A:1306:LYS:NZ	2:B:38:C:O2'	2.49	0.44
1:A:1416:ILE:HD13	1:A:1416:ILE:HA	1.76	0.44
1:A:1781:ASP:OD1	1:A:1783:THR:OG1	2.34	0.44
1:A:1860:GLN:HG2	1:A:1883:VAL:CG2	2.47	0.44
1:A:1882:ILE:O	44:1:290:ARG:HG3	2.18	0.44
3:C:323:PHE:CD2	3:C:373:ILE:HG12	2.53	0.44
5:F:34:G:C3'	5:F:35:A:H5''	2.46	0.44
8:H:88:A:H2'	8:H:89:U:C6	2.50	0.44
8:H:92:U:H2'	8:H:93:A:H8	1.82	0.44
9:I:692:SER:HA	9:I:695:CYS:H	1.82	0.44
9:I:728:ARG:NH2	24:X:104:ARG:HG2	2.32	0.44
18:R:185:GLY:O	18:R:187:ALA:N	2.51	0.44
19:S:35:THR:HG22	19:S:82:PHE:HE2	1.82	0.44
33:k:33:THR:CG2	33:k:37:LYS:HE2	2.45	0.44
1:A:1686:ASP:HA	44:1:170:TRP:CZ2	2.53	0.44
1:A:1860:GLN:HB3	1:A:1883:VAL:HB	2.00	0.44
3:C:834:VAL:HG11	3:C:883:PHE:HE2	1.82	0.44
5:F:28:A:O2'	14:N:39:GLY:O	2.32	0.44
7:G:73:G:O2'	7:G:74:G:C1'	2.59	0.44
7:G:98:U:H2'	7:G:99:C:C5	2.52	0.44
9:I:649:ARG:HG2	9:I:674:MET:HE1	2.00	0.44
13:M:218:PHE:HE2	18:R:262:ILE:HD11	1.81	0.44
23:W:82:ASN:N	23:W:82:ASN:HD22	2.15	0.44
25:Y:413:LYS:HD2	25:Y:413:LYS:N	2.27	0.44
35:e:25:LEU:C	35:e:25:LEU:HD23	2.42	0.44
39:u:82:SER:O	39:u:219:ALA:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:h:5:VAL:HB	31:h:6:PRO:HD3	2.00	0.44
35:l:25:LEU:HD23	35:l:25:LEU:C	2.42	0.44
1:A:318:TYR:O	3:C:645:ARG:NH1	2.49	0.44
1:A:535:ARG:HH21	28:z:107:LYS:C	2.20	0.44
3:C:605:ASP:OD1	3:C:608:ARG:NH1	2.41	0.44
5:F:35:A:H5''	5:F:35:A:C8	2.50	0.44
8:H:19:G:H21	16:P:8:THR:HA	1.82	0.44
8:H:153:A:H2'	8:H:154:C:H5''	1.99	0.44
9:I:231:ASN:HA	9:I:264:ASP:HA	1.98	0.44
9:I:697:PRO:HD2	9:I:734:TYR:HD2	1.82	0.44
20:T:399:LYS:HB2	20:T:406:ILE:HD11	1.99	0.44
25:Y:426:LEU:C	25:Y:426:LEU:CD2	2.90	0.44
28:z:79:LYS:O	28:z:88:ARG:NH2	2.50	0.44
31:h:77:LEU:N	31:h:77:LEU:HD12	2.32	0.44
1:A:162:LYS:HE3	44:l:170:TRP:HH2	1.77	0.44
1:A:1125:ILE:HG22	1:A:1147:VAL:HG21	1.99	0.44
1:A:1317:TYR:HB3	1:A:1474:MET:HE3	1.98	0.44
1:A:1607:GLU:HB3	1:A:1632:PHE:HB3	1.99	0.44
1:A:1869:LEU:O	1:A:1873:GLU:HB2	2.18	0.44
3:C:130:ARG:HE	3:C:435:VAL:HA	1.83	0.44
5:F:58:G:O3'	16:P:12:ALA:HB2	2.17	0.44
8:H:106:G:H5''	33:k:47:ARG:HH22	1.82	0.44
8:H:112:G:H2'	8:H:113:G:C8	2.50	0.44
18:R:74:LEU:HD12	19:S:136:ILE:HG23	1.99	0.44
29:b:18:ARG:NH1	29:b:52:LYS:HB3	2.31	0.44
29:b:52:LYS:HG3	29:b:52:LYS:O	2.18	0.44
35:e:20:LEU:CD2	35:e:24:TYR:CZ	3.00	0.44
33:k:22:GLU:OE1	33:k:22:GLU:HA	2.16	0.44
33:k:43:LEU:HD11	33:k:51:LYS:HB3	1.99	0.44
44:l:346:ASP:N	44:l:346:ASP:OD1	2.50	0.44
1:A:57:GLN:NE2	2:B:13:C:O2'	2.51	0.44
1:A:80:LYS:HD3	14:N:37:HIS:NE2	2.33	0.44
1:A:197:PRO:HA	1:A:204:LEU:HD13	1.99	0.44
1:A:488:ASP:OD1	1:A:489:TRP:N	2.51	0.44
1:A:1621:LYS:CE	28:z:92:PHE:HZ	2.28	0.44
4:E:266:PRO:CD	12:L:785:GLN:CB	2.96	0.44
5:F:22:A:O4'	14:N:121:VAL:HG21	2.18	0.44
7:G:26:U:C2'	7:G:27:U:H5''	2.43	0.44
9:I:725:ARG:O	9:I:728:ARG:HB3	2.18	0.44
1:A:701:ILE:O	1:A:703:GLN:NE2	2.50	0.44
1:A:1614:ILE:HG12	1:A:1615:HIS:C	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:99:C:H2'	2:B:100:C:C6	2.53	0.44
5:F:40:U:O4	5:F:41:A:N6	2.50	0.44
5:F:58:G:HO2'	5:F:59:G:P	2.35	0.44
9:I:651:ILE:HD12	9:I:654:LYS:HE2	2.00	0.44
12:L:56:PRO:HG2	18:R:268:LEU:HD11	1.98	0.44
19:S:37:LYS:HB2	19:S:37:LYS:HZ3	1.78	0.44
23:W:79:VAL:HG23	29:b:114:ILE:HG12	2.00	0.44
23:W:453:PHE:CD2	27:2:83:ARG:NE	2.86	0.44
26:Z:643:PRO:HD2	26:Z:719:ILE:HD11	1.99	0.44
29:i:18:ARG:NH1	29:i:52:LYS:HB3	2.31	0.44
1:A:1501:LEU:HD12	1:A:1753:LEU:HD11	1.98	0.44
1:A:1562:MET:HG3	1:A:1562:MET:O	2.18	0.44
1:A:1640:SER:OG	1:A:1718:TRP:O	2.31	0.44
1:A:1792:LYS:HG2	1:A:1798:LEU:HG	1.99	0.44
3:C:115:GLU:O	3:C:119:LEU:N	2.50	0.44
3:C:818:SER:O	3:C:822:MET:HE2	2.18	0.44
4:E:150:HIS:CG	4:E:171:SER:HG	2.34	0.44
9:I:548:PHE:HD1	9:I:553:VAL:HG22	1.82	0.44
10:J:506:GLU:O	10:J:510:VAL:N	2.47	0.44
14:N:115:THR:OG1	14:N:116:ASN:N	2.51	0.44
15:O:261:ILE:HG23	15:O:272:ILE:HG13	1.99	0.44
20:T:248:THR:HB	20:T:266:GLU:HG3	2.00	0.44
20:T:270:VAL:HB	20:T:284:TYR:HB2	1.98	0.44
23:W:79:VAL:CG2	29:b:114:ILE:CG1	2.96	0.44
23:W:475:TRP:HA	23:W:490:ALA:H	1.82	0.44
23:W:497:ASN:OD1	23:W:497:ASN:N	2.49	0.44
23:W:547:LYS:O	23:W:547:LYS:HD2	2.18	0.44
24:X:112:LEU:HD13	24:X:116:ARG:HG2	2.00	0.44
31:a:5:VAL:HB	31:a:6:PRO:HD3	2.00	0.44
1:A:1135:PRO:CD	1:A:1138:ALA:CB	2.86	0.44
5:F:25:C:C4'	5:F:26:U:OP2	2.65	0.44
5:F:87:C:OP1	13:M:137:ARG:NH2	2.42	0.44
7:G:5:G:C5'	7:G:5:G:C8	3.01	0.44
23:W:391:PHE:HB2	23:W:403:TRP:HB2	1.99	0.44
29:i:37:HIS:O	29:i:38:MET:HB2	2.17	0.44
35:l:34:TRP:CD1	35:l:34:TRP:N	2.86	0.44
44:1:275:LEU:HD23	44:1:278:LEU:HD23	1.78	0.44
1:A:644:ILE:HD12	1:A:644:ILE:HA	1.90	0.43
2:B:27:U:HO2'	2:B:28:A:P	2.41	0.43
3:C:532:ILE:HD13	3:C:532:ILE:HA	1.87	0.43
4:E:94:ASN:HB3	4:E:100:ASP:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:26:U:H4'	5:F:27:A:OP2	2.18	0.43
7:G:7:G:C8	7:G:7:G:OP2	2.71	0.43
8:H:55:U:H2'	8:H:56:A:H8	1.82	0.43
8:H:143:A:OP2	8:H:143:A:C2	2.71	0.43
18:R:95:LYS:H	18:R:95:LYS:HD2	1.82	0.43
18:R:158:LYS:NZ	20:T:322:SER:O	2.51	0.43
23:W:338:ILE:HG22	23:W:349:SER:HA	1.99	0.43
1:A:1133:CYS:SG	1:A:1234:ASP:CG	3.00	0.43
1:A:1192:PHE:CD2	1:A:1192:PHE:N	2.86	0.43
3:C:94:ILE:H	3:C:94:ILE:HG13	1.59	0.43
9:I:509:ARG:HD3	9:I:509:ARG:HA	1.79	0.43
29:b:18:ARG:HB2	29:b:83:GLU:HG2	1.99	0.43
37:v:53:HIS:N	38:w:149:CYS:O	2.34	0.43
1:A:766:THR:OG1	2:B:39:C:N4	2.51	0.43
1:A:821:ARG:NH1	1:A:821:ARG:CG	2.79	0.43
1:A:1502:PHE:CZ	1:A:1754:TYR:HB2	2.52	0.43
5:F:7:G:H5'	5:F:7:G:C8	2.44	0.43
8:H:142:C:O2'	8:H:143:A:H5'	2.18	0.43
8:H:157:G:H2'	8:H:158:G:O4'	2.19	0.43
15:O:254:GLN:NE2	19:S:120:GLN:OE1	2.51	0.43
18:R:123:GLU:HG3	18:R:124:VAL:H	1.84	0.43
18:R:218:ILE:CD1	18:R:218:ILE:O	2.67	0.43
24:X:116:ARG:NH1	24:X:116:ARG:HB3	2.30	0.43
26:Z:752:LYS:HB3	26:Z:754:TYR:CE2	2.53	0.43
28:z:92:PHE:HE2	28:z:96:LEU:CD1	2.17	0.43
36:g:32:ARG:HG3	36:g:43:ASP:HB2	1.99	0.43
29:i:18:ARG:HB2	29:i:83:GLU:HG2	1.99	0.43
42:o:37:LEU:HB2	42:o:61:PRO:HD3	2.00	0.43
1:A:157:ASP:CB	28:z:59:THR:HG21	2.47	0.43
1:A:1187:PHE:CD2	1:A:1189:MET:HE3	2.53	0.43
1:A:1536:LEU:HD13	1:A:1751:LEU:HD23	2.00	0.43
1:A:1895:ALA:HB1	1:A:1944:HIS:HB3	1.94	0.43
4:E:99:CYS:O	29:b:107:GLY:HA3	2.18	0.43
4:E:259:VAL:HB	4:E:277:PHE:HB2	1.99	0.43
5:F:35:A:H8	5:F:35:A:H5'	1.82	0.43
9:I:518:PRO:HA	9:I:521:VAL:HG12	2.00	0.43
12:L:7:LYS:HB3	12:L:40:ARG:HA	2.00	0.43
15:O:239:LEU:HD22	15:O:270:ALA:HB2	2.00	0.43
20:T:407:GLN:HE22	20:T:443:THR:HA	1.83	0.43
23:W:417:HIS:ND1	23:W:437:SER:HB3	2.34	0.43
32:c:67:TYR:HB2	33:d:100:PHE:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:20:LEU:HD13	36:g:61:VAL:HG22	2.00	0.43
1:A:1066:GLN:OE1	1:A:1066:GLN:CA	2.66	0.43
1:A:1681:ARG:HB3	1:A:1681:ARG:HH21	1.76	0.43
1:A:1943:LEU:HD23	1:A:1950:ALA:HB1	2.00	0.43
5:F:42:C:C5'	5:F:43:A:OP2	2.65	0.43
9:I:692:SER:C	9:I:694:ILE:N	2.75	0.43
12:L:646:GLY:O	12:L:650:GLY:N	2.52	0.43
20:T:216:ASN:HD21	20:T:473:SER:H	1.67	0.43
27:2:130:LYS:HB2	27:2:130:LYS:HE2	1.83	0.43
28:z:58:ARG:HD2	28:z:58:ARG:HA	1.77	0.43
1:A:1502:PHE:CE1	1:A:1754:TYR:C	2.94	0.43
1:A:1728:GLN:NE2	44:1:278:LEU:O	2.52	0.43
2:B:40:U:H6	2:B:40:U:O5'	2.01	0.43
5:F:39:A:H2'	5:F:40:U:O4'	2.18	0.43
5:F:45:A:C2'	5:F:73:A:C2	3.02	0.43
7:G:80:U:H4'	23:W:545:ARG:NH2	2.32	0.43
7:G:92:U:H2'	7:G:93:A:O4'	2.18	0.43
8:H:85:A:H2'	8:H:88:A:N6	2.33	0.43
8:H:154:C:O2'	8:H:155:C:C5'	2.66	0.43
26:Z:686:ILE:HG12	26:Z:715:PRO:HB3	1.99	0.43
28:z:93:ASN:ND2	28:z:93:ASN:C	2.73	0.43
35:l:20:LEU:CD2	35:l:24:TYR:CZ	3.00	0.43
44:1:106:VAL:HB	44:1:151:PRO:HB2	2.00	0.43
1:A:693:ILE:HD12	1:A:706:ALA:HA	2.01	0.43
1:A:1537:TRP:CE3	1:A:1751:LEU:HD13	2.45	0.43
1:A:1578:ARG:CB	1:A:1578:ARG:NH1	2.72	0.43
1:A:1751:LEU:N	1:A:1751:LEU:CD2	2.73	0.43
1:A:1764:SER:OG	1:A:1766:GLN:NE2	2.49	0.43
7:G:21:A:N6	15:O:91:GLY:O	2.51	0.43
9:I:673:ASP:OD1	9:I:677:LYS:HE3	2.19	0.43
9:I:717:GLU:CB	24:X:112:LEU:HD11	2.49	0.43
25:Y:412:SER:HG	25:Y:415:GLU:HG3	1.84	0.43
34:f:65:ARG:HH11	34:f:65:ARG:HG3	1.83	0.43
41:q:106:ALA:CB	41:t:106:ALA:HB1	2.43	0.43
32:j:67:TYR:HB2	33:k:100:PHE:O	2.19	0.43
42:o:161:MET:O	42:o:162:PHE:HB2	2.19	0.43
44:1:271:ILE:HG22	44:1:276:ARG:HD3	2.01	0.43
1:A:856:LEU:N	8:H:29:A:N7	2.61	0.43
1:A:1093:ASP:OD1	1:A:1093:ASP:N	2.51	0.43
1:A:1502:PHE:HE1	1:A:1754:TYR:O	1.97	0.43
3:C:501:ILE:HG22	3:C:530:LEU:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:847:TYR:HE1	3:C:857:VAL:HG11	1.82	0.43
4:E:266:PRO:HB3	12:L:788:TYR:CB	2.49	0.43
9:I:685:ARG:HH21	9:I:711:GLU:CD	2.26	0.43
23:W:84:THR:N	23:W:87:THR:OG1	2.52	0.43
23:W:551:LYS:HB3	23:W:572:ASP:HB3	1.99	0.43
1:A:331:TRP:HZ3	3:C:179:VAL:HG11	1.83	0.43
1:A:1811:ASN:HA	1:A:1812:PRO:HD3	1.90	0.43
1:A:1919:LEU:HD11	1:A:1936:LEU:HD11	2.01	0.43
4:E:346:SER:OG	4:E:348:ASP:OD1	2.31	0.43
8:H:91:U:H2'	8:H:92:U:C6	2.50	0.43
8:H:178:A:N3	8:H:178:A:H2'	2.33	0.43
27:2:125:ALA:HA	27:2:128:ARG:HB2	2.00	0.43
28:z:65:PHE:O	28:z:65:PHE:CG	2.69	0.43
37:v:51:TYR:CB	38:w:151:VAL:O	2.66	0.43
41:q:106:ALA:CB	41:t:106:ALA:HB3	2.48	0.43
42:o:132:ARG:NE	42:o:154:GLU:OE1	2.43	0.43
1:A:1393:ARG:NH1	25:Y:405:MET:HG3	2.33	0.43
1:A:1584:LYS:NZ	1:A:1874:VAL:CG1	2.81	0.43
3:C:668:GLU:N	3:C:824:THR:CG2	2.70	0.43
8:H:33:G:OP2	8:H:33:G:H8	2.01	0.43
8:H:98:G:H5'	8:H:104:U:OP2	2.19	0.43
9:I:286:VAL:CB	9:I:348:VAL:CA	2.92	0.43
9:I:717:GLU:HB2	24:X:112:LEU:CG	2.48	0.43
9:I:726:ILE:HD13	9:I:726:ILE:HA	1.65	0.43
12:L:126:GLY:HA2	24:X:82:LEU:O	2.19	0.43
19:S:72:ARG:CD	23:W:90:ALA:O	2.62	0.43
23:W:266:ARG:HD3	35:l:14:MET:N	2.34	0.43
23:W:416:ARG:HB3	23:W:443:ARG:HH12	1.84	0.43
24:X:101:GLU:C	24:X:103:GLN:N	2.76	0.43
1:A:99:VAL:HG13	1:A:554:THR:HG21	1.99	0.42
1:A:369:GLU:O	1:A:371:LEU:N	2.51	0.42
1:A:1124:ASN:ND2	1:A:1148:ASN:OD1	2.52	0.42
1:A:1468:ASN:OD1	7:G:130:G:H5'	2.19	0.42
1:A:1482:GLU:OE1	44:1:86:ARG:HD3	2.19	0.42
1:A:1642:PRO:CB	44:1:175:PRO:HB3	2.46	0.42
1:A:1889:LEU:HD12	1:A:2012:LEU:HG	1.88	0.42
2:B:94:U:O2'	2:B:95:G:H3'	2.19	0.42
3:C:769:GLY:O	3:C:773:GLY:N	2.52	0.42
7:G:124:G:N3	7:G:124:G:H2'	2.32	0.42
10:J:486:ALA:O	10:J:490:ASN:N	2.52	0.42
12:L:6:ILE:HD11	24:X:80:ARG:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:826:GLY:O	17:Q:1136:GLN:HA	2.18	0.42
18:R:311:LYS:O	18:R:315:LYS:N	2.51	0.42
22:V:450:ILE:CG1	44:1:89:PRO:CG	2.82	0.42
29:i:52:LYS:HG3	29:i:52:LYS:O	2.18	0.42
44:1:305:ASP:OD1	44:1:305:ASP:N	2.52	0.42
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	2.01	0.42
1:A:1698:PRO:HG3	44:1:181:ILE:C	2.44	0.42
1:A:1759:THR:CG2	44:1:286:ASP:OD2	2.65	0.42
1:A:1849:ILE:CG2	1:A:1879:PHE:CZ	3.03	0.42
1:A:1856:GLU:OE1	1:A:1856:GLU:HA	2.11	0.42
1:A:2014:MET:N	26:Z:758:ARG:HD3	2.34	0.42
3:C:750:LEU:N	3:C:751:PRO:CD	2.83	0.42
4:E:307:ARG:HH12	29:b:115:PRO:CG	2.32	0.42
8:H:43:U:H2'	8:H:44:U:C6	2.54	0.42
8:H:77:C:H5'	23:W:242:HIS:ND1	2.33	0.42
10:J:206:LEU:HD23	10:J:206:LEU:HA	1.92	0.42
13:M:118:LYS:O	13:M:118:LYS:HE3	2.18	0.42
23:W:341:ASN:HB2	23:W:346:GLN:H	1.84	0.42
23:W:398:LYS:HG2	23:W:419:GLY:H	1.84	0.42
24:X:61:GLN:HA	24:X:64:ARG:HG2	2.00	0.42
1:A:166:PHE:CE1	1:A:581:ILE:CG1	3.03	0.42
1:A:331:TRP:CZ3	3:C:179:VAL:HG21	2.54	0.42
1:A:1490:PHE:CZ	1:A:1498:TRP:CA	3.03	0.42
1:A:1618:LYS:HE2	1:A:1618:LYS:O	2.18	0.42
1:A:1740:LEU:HB3	1:A:1744:ARG:NH1	2.34	0.42
3:C:566:THR:OG1	3:C:567:GLU:N	2.51	0.42
10:J:526:GLU:O	10:J:530:TRP:N	2.48	0.42
18:R:218:ILE:HD12	18:R:218:ILE:O	2.20	0.42
18:R:222:PRO:O	18:R:222:PRO:CG	2.68	0.42
20:T:465:ILE:HG12	20:T:481:GLU:HG2	2.01	0.42
23:W:248:ASP:HB2	23:W:252:ARG:HG2	2.00	0.42
23:W:552:VAL:HG13	23:W:571:TRP:CD1	2.54	0.42
28:z:55:LEU:CG	44:1:177:GLU:OE2	2.67	0.42
33:d:33:THR:CG2	33:d:37:LYS:HE2	2.46	0.42
42:o:160:LYS:O	42:o:161:MET:C	2.63	0.42
1:A:772:CYS:SG	1:A:1249:MET:HE1	2.60	0.42
1:A:1631:LEU:HB3	1:A:1637:TRP:HZ3	1.84	0.42
1:A:1811:ASN:OD1	1:A:1811:ASN:C	2.62	0.42
4:E:103:ALA:HA	29:b:101:ALA:O	2.20	0.42
7:G:87:U:H3'	7:G:88:G:H21	1.84	0.42
8:H:101:U:H4'	29:i:73:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:216:ASP:O	10:J:218:GLU:N	2.53	0.42
16:P:9:PHE:CD2	16:P:9:PHE:N	2.88	0.42
16:P:13:ARG:HA	20:T:309:ASP:O	2.19	0.42
26:Z:709:ARG:NH2	26:Z:718:ASP:OD2	2.51	0.42
29:b:9:MET:HE2	32:c:39:HIS:HE1	1.84	0.42
29:b:50:LYS:C	29:b:51:ILE:HG13	2.45	0.42
38:w:137:GLN:O	38:w:143:PRO:HA	2.19	0.42
34:m:65:ARG:HG3	34:m:65:ARG:HH11	1.83	0.42
1:A:1737:ASN:OD1	1:A:1738:PRO:N	2.51	0.42
1:A:1862:ILE:O	1:A:1862:ILE:CG2	2.68	0.42
1:A:1937:ILE:CG2	1:A:2011:ILE:HG23	2.50	0.42
2:B:57:G:C2'	2:B:58:U:H5'	2.49	0.42
2:B:95:G:C6	35:e:36:TYR:O	2.71	0.42
3:C:261:ASP:OD2	46:C:1500:GTP:N1	2.46	0.42
8:H:155:C:H2'	8:H:156:U:H5''	2.02	0.42
9:I:84:HIS:CB	9:I:90:PRO:CB	2.97	0.42
9:I:491:ALA:HB2	9:I:510:ILE:HD11	2.00	0.42
9:I:696:ASP:HB3	9:I:699:THR:CB	2.50	0.42
24:X:112:LEU:CD1	24:X:116:ARG:HG2	2.49	0.42
35:e:51:ASP:C	35:e:51:ASP:OD1	2.61	0.42
42:o:56:LYS:HE2	42:o:58:ASP:CG	2.45	0.42
1:A:343:GLU:HB3	44:1:144:PHE:HZ	1.83	0.42
1:A:1333:VAL:HG11	22:V:467:LEU:HD12	2.01	0.42
1:A:1567:PRO:O	1:A:1570:LYS:N	2.52	0.42
1:A:1578:ARG:CG	1:A:1578:ARG:NH1	2.71	0.42
1:A:1615:HIS:CD2	1:A:1626:CYS:SG	3.12	0.42
1:A:1810:PHE:HA	1:A:1817:LEU:CD1	2.50	0.42
1:A:2014:MET:SD	1:A:2014:MET:O	2.78	0.42
7:G:14:A:C8	7:G:14:A:OP2	2.72	0.42
8:H:107:A:N1	8:H:108:G:C5	2.88	0.42
9:I:727:ARG:NH2	9:I:727:ARG:HG2	2.33	0.42
9:I:728:ARG:HH12	24:X:104:ARG:HB3	1.85	0.42
11:K:83:SER:O	41:t:75:LEU:C	2.62	0.42
13:M:212:ASN:HB3	13:M:215:ASN:H	1.84	0.42
15:O:247:ASP:HA	15:O:250:ASN:HD22	1.84	0.42
22:V:495:ASP:O	22:V:499:GLN:HB2	2.20	0.42
23:W:84:THR:C	23:W:86:GLU:N	2.74	0.42
23:W:504:GLY:H	23:W:535:TRP:HZ2	1.65	0.42
32:c:63:ASN:HA	33:d:102:ARG:CZ	2.50	0.42
32:c:66:ARG:CZ	33:d:48:ASN:HB3	2.49	0.42
39:u:254:PHE:HA	39:u:401:ASP:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:k:68:GLU:HA	33:k:97:SER:O	2.19	0.42
34:m:65:ARG:HG3	34:m:65:ARG:NH1	2.35	0.42
35:l:51:ASP:C	35:l:51:ASP:OD1	2.61	0.42
1:A:310:THR:OG1	21:U:2:TYR:O	2.37	0.42
1:A:451:LEU:HD23	1:A:451:LEU:HA	1.84	0.42
1:A:663:ARG:HG3	1:A:663:ARG:HH21	1.81	0.42
1:A:1573:LEU:HA	1:A:1573:LEU:HD23	1.58	0.42
1:A:1631:LEU:HD23	1:A:1631:LEU:HA	1.85	0.42
1:A:1781:ASP:C	1:A:1783:THR:N	2.76	0.42
3:C:264:ILE:HG12	3:C:378:TYR:CE1	2.55	0.42
3:C:534:VAL:HB	3:C:537:TYR:HB2	2.00	0.42
3:C:667:VAL:N	3:C:824:THR:CG2	2.78	0.42
5:F:43:A:O2'	5:F:44:G:H5'	2.19	0.42
7:G:100:C:N3	7:G:101:U:C5	2.88	0.42
8:H:77:C:C5'	23:W:242:HIS:HE1	2.33	0.42
8:H:157:G:H5''	8:H:157:G:C8	2.50	0.42
9:I:590:LYS:HA	9:I:590:LYS:HD3	1.84	0.42
12:L:5:MET:SD	12:L:5:MET:O	2.78	0.42
14:N:117:CYS:SG	14:N:119:CYS:HB3	2.60	0.42
23:W:265:LEU:HD12	23:W:300:SER:HB2	2.02	0.42
26:Z:710:PHE:HE1	26:Z:747:LEU:HD13	1.84	0.42
1:A:258:PHE:CE2	1:A:434:HIS:HA	2.55	0.42
1:A:342:THR:O	1:A:342:THR:OG1	2.28	0.42
1:A:881:ILE:HG23	1:A:918:THR:HG23	2.02	0.42
1:A:1479:GLY:HA2	44:1:88:GLN:CD	2.44	0.42
1:A:1498:TRP:CZ3	1:A:1501:LEU:HD12	2.55	0.42
1:A:1614:ILE:CD1	1:A:1616:PRO:HA	2.49	0.42
2:B:87:A:H5'	2:B:93:U:OP2	2.19	0.42
5:F:88:G:C4'	13:M:121:ASP:HB2	2.50	0.42
8:H:43:U:OP2	8:H:43:U:C6	2.73	0.42
12:L:7:LYS:HB3	12:L:40:ARG:CA	2.49	0.42
13:M:182:MET:HE2	13:M:182:MET:HB3	1.97	0.42
20:T:418:THR:OG1	20:T:466:PHE:O	2.38	0.42
27:2:111:LYS:HG2	27:2:114:GLU:OE2	2.19	0.42
32:j:63:ASN:HA	33:k:102:ARG:CZ	2.50	0.42
35:l:20:LEU:HD13	36:n:61:VAL:HG22	2.00	0.42
1:A:185:VAL:CG1	28:z:72:ARG:HH11	2.28	0.42
1:A:773:LYS:HA	1:A:773:LYS:HD2	1.67	0.42
1:A:975:VAL:HG22	1:A:1177:VAL:HG22	2.01	0.42
1:A:1160:ARG:HD3	16:P:192:VAL:HG11	2.01	0.42
1:A:1618:LYS:O	1:A:1618:LYS:CG	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:589:LYS:HG3	3:C:628:VAL:HG13	2.01	0.42
4:E:266:PRO:HG2	12:L:785:GLN:HA	1.96	0.42
7:G:7:G:C2'	7:G:8:C:H5'	2.50	0.42
7:G:82:G:O4'	23:W:541:LYS:HE2	2.19	0.42
7:G:126:G:N3	7:G:126:G:C2'	2.72	0.42
9:I:731:GLN:NE2	9:I:731:GLN:C	2.74	0.42
10:J:313:TRP:CE3	10:J:336:TRP:HB2	2.55	0.42
23:W:553:CYS:HA	23:W:570:GLY:HA2	2.01	0.42
24:X:69:TYR:CD1	24:X:69:TYR:C	2.97	0.42
27:2:138:LYS:HA	27:2:138:LYS:CE	2.35	0.42
33:d:28:PRO:HD2	34:f:37:ASP:HB3	2.02	0.42
1:A:612:ILE:O	1:A:616:PHE:N	2.46	0.42
1:A:1430:LEU:CB	25:Y:400:TRP:CZ3	3.03	0.42
1:A:1660:TYR:OH	1:A:1717:ASN:O	2.30	0.42
8:H:177:A:N7	27:2:134:LEU:HB2	2.34	0.42
12:L:633:GLN:O	12:L:637:VAL:N	2.50	0.42
23:W:462:HIS:ND1	23:W:482:ASP:HB3	2.35	0.42
35:e:34:TRP:N	35:e:34:TRP:CD1	2.86	0.42
31:h:58:LEU:HD22	36:n:71:GLU:CD	2.45	0.42
29:i:50:LYS:C	29:i:51:ILE:HG13	2.44	0.42
32:j:66:ARG:CZ	33:k:48:ASN:HB3	2.49	0.42
33:k:28:PRO:HD2	34:m:37:ASP:HB3	2.02	0.42
33:k:103:GLY:O	33:k:106:VAL:HG23	2.20	0.42
1:A:764:GLY:HA2	1:A:1245:ARG:NH1	2.35	0.41
1:A:1136:ARG:HA	1:A:1139:ARG:NE	2.33	0.41
5:F:23:U:C6	14:N:118:ILE:HG23	2.55	0.41
5:F:37:C:C3'	5:F:37:C:C6	3.02	0.41
7:G:82:G:C5'	23:W:541:LYS:HZ3	2.02	0.41
14:N:102:CYS:HB3	14:N:104:ARG:H	1.84	0.41
23:W:304:LEU:HD11	23:W:567:ILE:HG21	2.02	0.41
23:W:315:LEU:O	23:W:325:LEU:N	2.47	0.41
24:X:112:LEU:HD13	24:X:112:LEU:O	2.20	0.41
26:Z:758:ARG:CG	26:Z:758:ARG:O	2.69	0.41
28:z:55:LEU:HG	44:1:177:GLU:OE2	2.20	0.41
1:A:188:LEU:HD13	28:z:68:MET:HB3	2.02	0.41
1:A:1555:LEU:HA	1:A:1555:LEU:HD13	1.65	0.41
1:A:1745:GLU:CG	1:A:1749:LYS:HE3	2.49	0.41
1:A:1745:GLU:HG3	1:A:1749:LYS:HE3	2.02	0.41
1:A:1892:PRO:O	1:A:1892:PRO:CG	2.68	0.41
3:C:140:HIS:CD2	3:C:230:ASP:HB2	2.56	0.41
5:F:22:A:C8	23:W:130:ARG:CD	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:581:GLU:HA	9:I:584:LEU:HD12	2.01	0.41
10:J:527:LYS:O	10:J:531:LYS:N	2.48	0.41
13:M:138:LEU:HD23	13:M:138:LEU:HA	1.89	0.41
13:M:165:ASN:HB2	18:R:95:LYS:HA	2.02	0.41
33:d:68:GLU:HA	33:d:97:SER:O	2.19	0.41
29:i:9:MET:HE2	32:j:39:HIS:HE1	1.84	0.41
42:o:52:ASN:HB2	42:o:74:ASN:OD1	2.20	0.41
1:A:470:ARG:NH2	1:A:470:ARG:CG	2.81	0.41
1:A:1808:PHE:O	1:A:1808:PHE:CG	2.69	0.41
1:A:1976:TRP:HA	1:A:1979:VAL:HG22	2.00	0.41
2:B:90:U:H4'	29:b:73:ARG:NH2	2.35	0.41
4:E:61:LEU:O	29:b:108:ARG:O	2.38	0.41
5:F:25:C:N4	15:O:39:GLU:OE1	2.53	0.41
5:F:48:A:H61	12:L:30:GLN:HE22	1.68	0.41
8:H:24:A:C2	12:L:29:ASN:HB3	2.53	0.41
9:I:511:LEU:HD11	9:I:521:VAL:HG23	2.01	0.41
9:I:699:THR:CG2	9:I:699:THR:O	2.68	0.41
14:N:124:SER:OG	14:N:125:LYS:NZ	2.47	0.41
22:V:171:ASN:CB	39:u:277:ILE:HA	2.51	0.41
24:X:84:GLU:OE2	24:X:84:GLU:CA	2.68	0.41
41:q:60:PRO:CB	41:s:94:GLN:CA	2.97	0.41
1:A:599:MET:HE3	1:A:599:MET:HB3	1.89	0.41
1:A:1156:ASP:OD2	1:A:1160:ARG:NH2	2.53	0.41
1:A:1251:SER:OG	1:A:1259:ILE:HG12	2.20	0.41
1:A:1682:ALA:O	44:1:170:TRP:CD1	2.74	0.41
1:A:1883:VAL:HA	44:1:290:ARG:O	2.21	0.41
1:A:1977:ILE:HG21	44:1:349:LYS:HD2	2.02	0.41
1:A:2004:GLN:O	1:A:2007:ILE:HB	2.20	0.41
2:B:20:G:C1'	2:B:21:A:OP1	2.69	0.41
3:C:561:LYS:NZ	3:C:611:ASN:O	2.38	0.41
4:E:266:PRO:HB3	12:L:788:TYR:C	2.46	0.41
4:E:310:TYR:CE1	4:E:322:LYS:HE2	2.55	0.41
7:G:21:A:C8	15:O:152:ARG:NH2	2.86	0.41
8:H:39:U:C6	8:H:39:U:C5'	2.90	0.41
9:I:721:LYS:O	9:I:725:ARG:N	2.47	0.41
9:I:729:SER:C	9:I:731:GLN:N	2.77	0.41
14:N:132:ILE:HD13	14:N:132:ILE:HA	1.88	0.41
24:X:58:LEU:C	24:X:58:LEU:CD2	2.83	0.41
28:z:107:LYS:O	28:z:110:TRP:CB	2.69	0.41
32:j:3:LEU:O	32:j:6:PHE:HB3	2.21	0.41
36:n:10:LYS:HG2	36:n:34:PHE:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:PRO:HB3	6:4:-11:G:C8	2.56	0.41
1:A:467:GLN:HG2	2:B:19:A:C4	2.55	0.41
1:A:1565:LYS:HE3	1:A:1565:LYS:HB2	1.79	0.41
1:A:1587:GLU:CA	1:A:1587:GLU:OE1	2.67	0.41
1:A:1694:ILE:HD11	28:z:88:ARG:CG	2.47	0.41
1:A:1779:PHE:HE1	1:A:1891:LEU:HD12	1.86	0.41
1:A:1930:TYR:HA	1:A:1933:PHE:HB3	2.02	0.41
5:F:43:A:N1	5:F:44:G:C6	2.89	0.41
8:H:103:U:C3'	8:H:104:U:H5'	2.51	0.41
9:I:329:LEU:CB	17:Q:353:LEU:CB	2.98	0.41
16:P:72:ARG:O	16:P:76:ARG:N	2.53	0.41
18:R:99:ASP:OD2	18:R:103:ARG:NE	2.42	0.41
24:X:120:LYS:HD3	24:X:120:LYS:HA	1.88	0.41
26:Z:752:LYS:HD2	26:Z:754:TYR:CE2	2.55	0.41
35:e:24:TYR:CD1	35:e:31:ILE:HD11	2.56	0.41
34:m:65:ARG:HB3	34:m:68:ASN:HD22	1.85	0.41
1:A:591:MET:HE2	1:A:591:MET:HB3	1.84	0.41
1:A:858:GLN:C	1:A:858:GLN:CD	2.85	0.41
1:A:1618:LYS:CD	1:A:1618:LYS:O	2.68	0.41
2:B:92:U:C3'	2:B:93:U:H5'	2.50	0.41
3:C:307:VAL:HG12	3:C:308:CYS:O	2.20	0.41
7:G:100:C:C5'	7:G:100:C:C6	3.00	0.41
8:H:24:A:H3'	8:H:25:G:C5'	2.50	0.41
8:H:152:G:H2'	8:H:153:A:C1'	2.51	0.41
9:I:717:GLU:HA	9:I:720:ILE:HB	2.02	0.41
10:J:529:HIS:O	10:J:533:TYR:N	2.42	0.41
23:W:82:ASN:ND2	23:W:82:ASN:N	2.69	0.41
24:X:54:LEU:HG	24:X:56:GLU:H	1.85	0.41
33:d:39:ASN:OD1	33:d:55:ARG:HD3	2.20	0.41
44:1:183:GLU:O	44:1:187:LYS:NZ	2.43	0.41
1:A:779:LEU:HD23	1:A:782:LEU:HD12	2.02	0.41
1:A:1298:ARG:HA	1:A:1298:ARG:HD2	1.90	0.41
1:A:1501:LEU:HD13	1:A:1753:LEU:CD1	2.50	0.41
1:A:1529:ILE:N	1:A:1529:ILE:HD13	2.35	0.41
1:A:1536:LEU:O	1:A:1536:LEU:CD2	2.68	0.41
1:A:1615:HIS:CB	28:z:92:PHE:HB3	2.50	0.41
1:A:1951:LYS:O	1:A:1955:LYS:N	2.53	0.41
4:E:231:MET:HB3	4:E:262:TRP:CZ3	2.55	0.41
8:H:20:G:N7	16:P:5:ALA:HB1	2.35	0.41
9:I:699:THR:O	9:I:699:THR:HG23	2.21	0.41
15:O:250:ASN:HA	19:S:91:LYS:HZ3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:f:65:ARG:HB3	34:f:68:ASN:HD22	1.85	0.41
43:p:74:PHE:CG	43:p:79:MET:HE3	2.55	0.41
1:A:1134:TRP:HB3	1:A:1138:ALA:HB3	2.02	0.41
3:C:131:ASN:HA	3:C:201:ASN:HB2	2.03	0.41
3:C:666:VAL:CG1	3:C:824:THR:HG22	2.49	0.41
9:I:681:ILE:HA	9:I:710:PHE:HZ	1.86	0.41
10:J:258:ILE:O	10:J:262:ARG:N	2.51	0.41
16:P:10:GLU:HA	16:P:11:PRO:HD2	1.88	0.41
18:R:222:PRO:O	18:R:222:PRO:HG2	2.20	0.41
23:W:140:ASP:OD1	23:W:140:ASP:N	2.50	0.41
24:X:105:ARG:HA	24:X:108:GLU:OE1	2.20	0.41
24:X:114:GLU:OE2	24:X:114:GLU:CA	2.69	0.41
25:Y:413:LYS:HB3	25:Y:425:ILE:CD1	2.49	0.41
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.89	0.41
1:A:273:ILE:H	1:A:273:ILE:HG13	1.56	0.41
1:A:274:PRO:HG3	21:U:1:MET:HB3	2.02	0.41
1:A:461:HIS:CD2	2:B:26:A:H61	2.39	0.41
1:A:1596:VAL:HG21	44:1:278:LEU:CD1	2.50	0.41
1:A:1759:THR:HG21	44:1:288:LYS:HG2	2.01	0.41
1:A:1809:ILE:HD12	1:A:1818:PHE:CB	2.51	0.41
1:A:1890:GLN:HA	1:A:1890:GLN:HE21	1.82	0.41
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.53	0.41
3:C:366:GLN:HB3	3:C:370:VAL:HB	2.02	0.41
3:C:604:LEU:HD21	3:C:627:HIS:CE1	2.56	0.41
5:F:7:G:H4'	5:F:7:G:OP1	2.20	0.41
7:G:20:A:OP2	15:O:159:ARG:HG3	2.21	0.41
7:G:92:U:H3	8:H:38:A:H61	1.69	0.41
7:G:129:U:O2	7:G:129:U:C2'	2.67	0.41
8:H:30:A:O4'	24:X:73:PHE:CE1	2.74	0.41
8:H:106:G:H5'	33:k:47:ARG:NH2	2.34	0.41
8:H:152:G:H2'	8:H:152:G:N3	2.36	0.41
10:J:238:ASN:C	10:J:240:THR:H	2.28	0.41
13:M:165:ASN:OD1	13:M:166:SER:N	2.54	0.41
15:O:81:CYS:SG	15:O:82:GLN:N	2.94	0.41
15:O:292:ILE:HG12	15:O:297:ARG:HA	2.03	0.41
17:Q:875:HIS:O	17:Q:1034:ILE:N	2.49	0.41
19:S:11:PRO:HA	19:S:12:PRO:HD3	1.89	0.41
22:V:623:ASN:HA	22:V:626:PHE:HB3	2.03	0.41
23:W:79:VAL:HG21	29:b:114:ILE:CG1	2.49	0.41
23:W:458:GLU:HB3	23:W:460:SER:H	1.86	0.41
24:X:71:GLU:CD	24:X:71:GLU:O	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:z:57:LYS:HA	28:z:57:LYS:HD3	1.70	0.41
31:a:58:LEU:HD22	36:g:71:GLU:CD	2.46	0.41
33:d:103:GLY:O	33:d:106:VAL:HG23	2.20	0.41
34:f:65:ARG:HG3	34:f:65:ARG:NH1	2.35	0.41
35:e:21:ILE:HA	35:e:24:TYR:HD2	1.86	0.41
35:l:24:TYR:CD1	35:l:31:ILE:HD11	2.56	0.41
36:n:10:LYS:HA	36:n:13:MET:HG2	2.03	0.41
42:o:140:PRO:O	42:o:155:ARG:NH1	2.48	0.41
43:p:13:ASN:HB2	43:p:80:ARG:HH21	1.86	0.41
44:1:274:TYR:HB3	44:1:285:TYR:HD2	1.86	0.41
1:A:516:LEU:HD11	1:A:538:SER:HB2	2.03	0.41
1:A:572:PHE:CE2	28:z:61:ALA:CB	3.03	0.41
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.77	0.41
1:A:801:ILE:O	1:A:805:GLU:HB3	2.20	0.41
1:A:1199:LYS:NZ	1:A:1206:GLU:OE2	2.46	0.41
1:A:1757:GLU:HG3	1:A:1759:THR:H	1.86	0.41
1:A:1772:PHE:O	1:A:1813:ARG:CD	2.55	0.41
1:A:1919:LEU:HD22	1:A:1919:LEU:HA	1.67	0.41
1:A:1996:ASN:HB2	24:X:61:GLN:OE1	2.21	0.41
3:C:750:LEU:C	3:C:750:LEU:CD2	2.89	0.41
5:F:26:U:HO2'	5:F:27:A:P	2.42	0.41
8:H:40:C:C2'	8:H:41:U:H5''	2.47	0.41
9:I:631:MET:HA	9:I:634:ILE:HB	2.03	0.41
10:J:215:THR:OG1	10:J:216:ASP:N	2.47	0.41
13:M:118:LYS:O	13:M:118:LYS:CE	2.69	0.41
14:N:131:ILE:HG21	15:O:177:GLU:HG2	2.03	0.41
16:P:10:GLU:O	16:P:10:GLU:CG	2.69	0.41
19:S:70:THR:HG21	23:W:71:HIS:HB3	2.03	0.41
33:d:110:LEU:CD1	34:f:59:LEU:HB3	2.46	0.41
33:k:62:HIS:O	33:k:103:GLY:HA3	2.21	0.41
44:1:130:LYS:HB3	44:1:130:LYS:HE2	1.80	0.41
1:A:260:LEU:HA	1:A:260:LEU:HD23	1.91	0.40
1:A:496:VAL:O	1:A:500:GLY:N	2.52	0.40
1:A:1555:LEU:HD23	1:A:1560:ILE:CD1	2.50	0.40
1:A:1560:ILE:O	1:A:1560:ILE:CG1	2.69	0.40
1:A:1728:GLN:NE2	1:A:1728:GLN:O	2.53	0.40
1:A:1899:VAL:HB	1:A:1902:PHE:HD2	1.86	0.40
1:A:2011:ILE:HG22	1:A:2012:LEU:HD22	2.03	0.40
3:C:458:ASP:OD1	3:C:458:ASP:N	2.54	0.40
3:C:756:LYS:H	3:C:756:LYS:HG3	1.55	0.40
4:E:144:VAL:HG12	4:E:145:LYS:HG3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:118:LYS:O	13:M:118:LYS:CG	2.70	0.40
18:R:132:LEU:HB3	20:T:399:LYS:HE3	2.02	0.40
27:2:38:LEU:CD2	34:m:9:PRO:HA	2.51	0.40
27:2:111:LYS:HA	27:2:114:GLU:CD	2.47	0.40
35:l:18:ILE:H	35:l:18:ILE:HG13	1.70	0.40
43:p:3:ILE:HG22	43:p:83:TYR:HB2	2.02	0.40
1:A:156:ARG:NH1	44:1:134:PHE:CE2	2.87	0.40
1:A:169:PHE:CE1	1:A:563:GLN:NE2	2.71	0.40
1:A:821:ARG:HH11	1:A:821:ARG:CG	2.32	0.40
1:A:1495:PHE:HB3	1:A:1496:PRO:CD	2.51	0.40
1:A:1592:ASP:OD2	44:1:275:LEU:HD12	2.20	0.40
1:A:1596:VAL:HG21	44:1:275:LEU:HD21	1.90	0.40
1:A:1617:ARG:HH22	28:z:99:LEU:CD2	2.28	0.40
2:B:12:U:O2'	2:B:13:C:P	2.79	0.40
3:C:134:LEU:O	3:C:205:THR:OG1	2.29	0.40
3:C:935:ILE:HG22	3:C:939:ARG:HE	1.87	0.40
5:F:28:A:C2	15:O:174:LYS:HB2	2.55	0.40
5:F:33:G:O2'	5:F:34:G:P	2.79	0.40
8:H:168:A:C2	36:n:54:GLN:CB	3.04	0.40
8:H:171:U:H2'	8:H:172:C:O4'	2.21	0.40
8:H:183:G:C6	8:H:184:C:N4	2.89	0.40
11:K:84:MET:CB	41:r:74:ILE:CB	2.99	0.40
20:T:427:LEU:O	20:T:439:TRP:N	2.50	0.40
23:W:348:LEU:HD11	23:W:356:LEU:HD21	2.03	0.40
23:W:357:LYS:HE2	23:W:369:ARG:HD3	2.03	0.40
23:W:368:SER:OG	23:W:369:ARG:N	2.55	0.40
23:W:401:VAL:HG13	23:W:410:ILE:HG23	2.03	0.40
24:X:55:TYR:O	24:X:55:TYR:HD1	2.05	0.40
24:X:80:ARG:O	24:X:80:ARG:CG	2.69	0.40
32:c:20:LYS:O	32:c:66:ARG:NH2	2.55	0.40
33:k:39:ASN:OD1	33:k:55:ARG:HD3	2.21	0.40
33:k:110:LEU:CD1	34:m:59:LEU:HB3	2.46	0.40
1:A:91:ALA:HA	18:R:207:MET:HE3	2.04	0.40
1:A:192:GLN:H	1:A:192:GLN:HG2	1.73	0.40
1:A:1386:TRP:CD1	25:Y:408:ALA:HB1	2.56	0.40
1:A:1499:GLU:H	1:A:1499:GLU:HG3	1.52	0.40
1:A:1810:PHE:HB2	1:A:1817:LEU:CD1	2.51	0.40
5:F:45:A:H5'	12:L:169:ARG:HH22	1.85	0.40
6:4:-12:G:HO2'	6:4:-11:G:C5'	2.32	0.40
8:H:36:G:C3'	8:H:37:U:H5'	2.47	0.40
8:H:88:A:C6	8:H:89:U:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:521:VAL:HG21	9:I:544:GLY:HA3	2.03	0.40
19:S:71:GLY:O	19:S:111:GLN:NE2	2.50	0.40
24:X:57:ARG:O	24:X:61:GLN:HG3	2.20	0.40
25:Y:418:ASP:OD1	25:Y:418:ASP:N	2.55	0.40
31:a:63:ILE:HG12	36:g:69:MET:HG3	2.03	0.40
42:o:37:LEU:HB2	42:o:61:PRO:CD	2.51	0.40
43:p:72:PHE:HA	43:p:73:PRO:HD3	1.83	0.40
44:l:267:ILE:HA	44:l:267:ILE:HD12	1.72	0.40
1:A:165:ARG:N	1:A:165:ARG:CD	2.72	0.40
1:A:641:MET:HE3	1:A:641:MET:HB3	1.94	0.40
1:A:1392:LYS:NZ	1:A:1407:ASP:O	2.39	0.40
1:A:1614:ILE:O	1:A:1614:ILE:CD1	2.69	0.40
1:A:1618:LYS:O	1:A:1618:LYS:CE	2.70	0.40
1:A:1621:LYS:CE	28:z:92:PHE:CZ	3.03	0.40
1:A:1775:GLN:NE2	44:l:315:VAL:C	2.79	0.40
1:A:1963:GLU:OE1	1:A:1965:HIS:HE1	2.04	0.40
1:A:2013:GLY:C	26:Z:758:ARG:HD3	2.47	0.40
1:A:2015:GLU:OE2	24:X:55:TYR:CE2	2.74	0.40
3:C:756:LYS:C	3:C:759:LEU:H	2.29	0.40
4:E:167:VAL:HB	4:E:179:TRP:HB2	2.03	0.40
7:G:9:C:H2'	7:G:10:U:O4'	2.22	0.40
7:G:129:U:O2	7:G:129:U:O2'	2.30	0.40
8:H:33:G:OP2	8:H:33:G:C8	2.73	0.40
8:H:39:U:HO2'	8:H:40:C:P	2.28	0.40
13:M:118:LYS:O	13:M:118:LYS:CD	2.70	0.40
20:T:331:ASN:HB3	20:T:332:ALA:H	1.77	0.40
33:d:62:HIS:O	33:d:103:GLY:HA3	2.21	0.40
1:A:153:ARG:HG2	1:A:153:ARG:O	2.20	0.40
1:A:866:LEU:O	1:A:866:LEU:CD2	2.69	0.40
1:A:1136:ARG:NH1	1:A:1136:ARG:HG3	2.36	0.40
1:A:1284:LEU:HA	1:A:1284:LEU:HD23	1.89	0.40
1:A:1562:MET:O	1:A:1562:MET:CG	2.69	0.40
1:A:1617:ARG:CG	1:A:1617:ARG:O	2.70	0.40
1:A:1892:PRO:O	1:A:1892:PRO:CD	2.69	0.40
3:C:304:LEU:HD23	3:C:304:LEU:HA	1.90	0.40
4:E:305:ALA:HA	4:E:329:SER:HB2	2.04	0.40
5:F:37:C:H3'	5:F:37:C:C6	2.56	0.40
9:I:491:ALA:HA	9:I:506:VAL:HG11	2.03	0.40
17:Q:876:LEU:HA	17:Q:1034:ILE:O	2.22	0.40
23:W:101:THR:HG23	23:W:104:MET:H	1.86	0.40
24:X:120:LYS:HE3	24:X:120:LYS:CA	2.51	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	1980/2335 (85%)	1782 (90%)	181 (9%)	17 (1%)	14	46
3	C	856/972 (88%)	781 (91%)	71 (8%)	4 (0%)	24	57
4	E	297/357 (83%)	275 (93%)	22 (7%)	0	100	100
9	I	576/855 (67%)	557 (97%)	15 (3%)	4 (1%)	18	51
10	J	528/848 (62%)	487 (92%)	33 (6%)	8 (2%)	8	37
11	K	147/225 (65%)	137 (93%)	6 (4%)	4 (3%)	4	27
12	L	425/802 (53%)	408 (96%)	15 (4%)	2 (0%)	24	57
13	M	128/243 (53%)	117 (91%)	11 (9%)	0	100	100
14	N	141/144 (98%)	124 (88%)	16 (11%)	1 (1%)	18	51
15	O	283/420 (67%)	259 (92%)	23 (8%)	1 (0%)	30	61
16	P	107/229 (47%)	89 (83%)	15 (14%)	3 (3%)	4	26
17	Q	1308/1485 (88%)	1282 (98%)	26 (2%)	0	100	100
18	R	255/536 (48%)	228 (89%)	23 (9%)	4 (2%)	7	36
19	S	157/166 (95%)	147 (94%)	10 (6%)	0	100	100
20	T	310/514 (60%)	275 (89%)	29 (9%)	6 (2%)	6	33
21	U	68/2752 (2%)	60 (88%)	8 (12%)	0	100	100
22	V	444/908 (49%)	431 (97%)	12 (3%)	1 (0%)	43	72
23	W	507/579 (88%)	432 (85%)	69 (14%)	6 (1%)	10	41
24	X	83/254 (33%)	81 (98%)	2 (2%)	0	100	100
25	Y	667/1220 (55%)	642 (96%)	23 (3%)	2 (0%)	36	65
26	Z	97/758 (13%)	87 (90%)	10 (10%)	0	100	100
27	2	121/184 (66%)	113 (93%)	5 (4%)	3 (2%)	4	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	z	58/112 (52%)	55 (95%)	3 (5%)	0	100	100
29	b	98/240 (41%)	93 (95%)	2 (2%)	3 (3%)	3	25
29	i	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
30	y	77/301 (26%)	75 (97%)	2 (3%)	0	100	100
31	a	75/126 (60%)	74 (99%)	1 (1%)	0	100	100
31	h	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
32	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
32	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
33	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
33	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
34	f	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
34	m	72/86 (84%)	69 (96%)	2 (3%)	1 (1%)	9	38
35	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
35	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
36	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
36	n	65/76 (86%)	63 (97%)	2 (3%)	0	100	100
37	v	142/146 (97%)	138 (97%)	4 (3%)	0	100	100
38	w	89/174 (51%)	87 (98%)	1 (1%)	1 (1%)	11	43
39	u	384/411 (93%)	372 (97%)	9 (2%)	3 (1%)	16	49
40	x	23/703 (3%)	22 (96%)	1 (4%)	0	100	100
41	q	130/504 (26%)	117 (90%)	7 (5%)	6 (5%)	2	17
41	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	7	36
41	s	130/504 (26%)	115 (88%)	7 (5%)	8 (6%)	1	12
41	t	129/504 (26%)	116 (90%)	9 (7%)	4 (3%)	3	25
42	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	39
43	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
44	l	263/586 (45%)	244 (93%)	19 (7%)	0	100	100
All	All	12396/23429 (53%)	11559 (93%)	741 (6%)	96 (1%)	18	49

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	PRO

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Mol	Chain	Res	Type
1	A	1092	ILE
1	A	1136	ARG
1	A	1494	TYR
1	A	1503	TRP
1	A	1831	LYS
3	C	801	LEU
9	I	698	ARG
10	J	217	GLU
10	J	241	VAL
11	K	78	PRO
12	L	10	VAL
12	L	125	PRO
16	P	8	THR
18	R	233	PRO
20	T	187	LYS
20	T	188	PRO
20	T	190	TRP
23	W	73	ASP
23	W	74	PRO
23	W	82	ASN
23	W	83	PRO
27	2	76	SER
39	u	383	ASN
41	q	24	VAL
41	q	59	HIS
41	q	60	PRO
41	s	9	ASN
41	s	55	ILE
41	s	60	PRO
41	s	66	PRO
41	s	71	ILE
41	t	9	ASN
41	t	69	THR
34	m	4	PRO
1	A	349	ALA
3	C	94	ILE
3	C	439	PRO
9	I	532	LYS
10	J	709	VAL
20	T	406	ILE
25	Y	1185	ASP
27	2	33	LEU

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Mol	Chain	Res	Type
38	w	115	GLY
39	u	340	GLY
39	u	385	ASP
41	q	9	ASN
41	q	19	PRO
41	s	24	VAL
42	o	160	LYS
1	A	1538	TRP
1	A	1774	ASN
1	A	1782	ASP
9	I	699	THR
10	J	188	GLN
10	J	205	LEU
11	K	86	ARG
16	P	6	ARG
18	R	52	PRO
18	R	186	VAL
22	V	597	PRO
23	W	258	PRO
27	2	72	ALA
41	q	23	HIS
41	r	9	ASN
41	t	67	SER
1	A	570	ASP
1	A	1567	PRO
1	A	1598	ASP
3	C	83	GLU
10	J	341	PRO
10	J	604	PRO
11	K	65	ILE
14	N	41	ARG
16	P	205	LYS
18	R	73	PRO
25	Y	1182	LYS
41	t	65	PRO
42	o	32	PRO
1	A	364	SER
20	T	343	PRO
20	T	462	GLU
29	b	105	GLY
29	b	106	ILE
41	s	62	ARG

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Mol	Chain	Res	Type
9	I	372	ARG
10	J	216	ASP
15	O	20	PHE
29	b	115	PRO
1	A	1135	PRO
1	A	1419	ILE
11	K	17	PRO
23	W	271	PRO
1	A	1892	PRO
41	s	38	GLY
41	r	60	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1780/2108 (84%)	1674 (94%)	106 (6%)	17	45
3	C	760/866 (88%)	751 (99%)	9 (1%)	63	73
4	E	256/300 (85%)	255 (100%)	1 (0%)	84	81
9	I	199/749 (27%)	184 (92%)	15 (8%)	12	39
10	J	241/751 (32%)	239 (99%)	2 (1%)	73	77
12	L	218/709 (31%)	211 (97%)	7 (3%)	34	58
13	M	117/209 (56%)	115 (98%)	2 (2%)	53	69
14	N	130/130 (100%)	129 (99%)	1 (1%)	73	77
15	O	255/361 (71%)	253 (99%)	2 (1%)	73	77
16	P	101/203 (50%)	97 (96%)	4 (4%)	28	54
18	R	219/457 (48%)	216 (99%)	3 (1%)	59	71
19	S	129/134 (96%)	127 (98%)	2 (2%)	55	69
20	T	268/441 (61%)	264 (98%)	4 (2%)	57	70
21	U	21/2432 (1%)	19 (90%)	2 (10%)	8	32
22	V	98/838 (12%)	94 (96%)	4 (4%)	27	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	448/502 (89%)	440 (98%)	8 (2%)	51	68
24	X	67/230 (29%)	39 (58%)	28 (42%)	0	0
25	Y	32/1085 (3%)	28 (88%)	4 (12%)	4	22
26	Z	91/655 (14%)	87 (96%)	4 (4%)	25	52
27	2	106/157 (68%)	99 (93%)	7 (7%)	15	43
28	z	54/99 (54%)	47 (87%)	7 (13%)	4	21
29	b	83/177 (47%)	80 (96%)	3 (4%)	31	56
29	i	77/177 (44%)	74 (96%)	3 (4%)	28	54
31	a	68/101 (67%)	68 (100%)	0	100	100
31	h	70/101 (69%)	70 (100%)	0	100	100
32	c	77/101 (76%)	75 (97%)	2 (3%)	40	62
32	j	77/101 (76%)	75 (97%)	2 (3%)	40	62
33	d	90/110 (82%)	89 (99%)	1 (1%)	65	74
33	k	80/110 (73%)	79 (99%)	1 (1%)	61	72
34	f	63/74 (85%)	61 (97%)	2 (3%)	34	58
34	m	62/74 (84%)	58 (94%)	4 (6%)	15	43
35	e	74/84 (88%)	74 (100%)	0	100	100
35	l	74/84 (88%)	74 (100%)	0	100	100
36	g	64/66 (97%)	63 (98%)	1 (2%)	55	69
36	n	60/66 (91%)	59 (98%)	1 (2%)	53	69
42	o	139/218 (64%)	133 (96%)	6 (4%)	26	52
43	p	82/195 (42%)	79 (96%)	3 (4%)	30	56
44	1	233/520 (45%)	224 (96%)	9 (4%)	28	54
All	All	7063/15775 (45%)	6803 (96%)	260 (4%)	31	56

All (260) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	ARG
1	A	338	VAL
1	A	344	ASP
1	A	346	ASP
1	A	347	LEU
1	A	387	PHE

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Mol	Chain	Res	Type
1	A	413	LEU
1	A	664	HIS
1	A	666	LYS
1	A	701	ILE
1	A	771	VAL
1	A	773	LYS
1	A	774	LYS
1	A	821	ARG
1	A	850	TYR
1	A	853	LYS
1	A	857	ASN
1	A	861	ARG
1	A	866	LEU
1	A	880	ARG
1	A	1089	CYS
1	A	1132	LYS
1	A	1136	ARG
1	A	1189	MET
1	A	1249	MET
1	A	1251	SER
1	A	1416	ILE
1	A	1501	LEU
1	A	1502	PHE
1	A	1526	LEU
1	A	1527	ASN
1	A	1529	ILE
1	A	1530	PRO
1	A	1533	ARG
1	A	1536	LEU
1	A	1553	VAL
1	A	1555	LEU
1	A	1560	ILE
1	A	1561	PHE
1	A	1562	MET
1	A	1566	ILE
1	A	1569	LEU
1	A	1570	LYS
1	A	1571	ILE
1	A	1574	ILE
1	A	1576	ILE
1	A	1578	ARG
1	A	1581	LEU

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Mol	Chain	Res	Type
1	A	1587	GLU
1	A	1588	SER
1	A	1590	VAL
1	A	1593	LEU
1	A	1594	CYS
1	A	1596	VAL
1	A	1612	GLU
1	A	1614	ILE
1	A	1615	HIS
1	A	1618	LYS
1	A	1681	ARG
1	A	1722	SER
1	A	1723	LYS
1	A	1725	LEU
1	A	1726	ILE
1	A	1727	GLN
1	A	1728	GLN
1	A	1730	MET
1	A	1734	MET
1	A	1737	ASN
1	A	1738	PRO
1	A	1742	VAL
1	A	1744	ARG
1	A	1751	LEU
1	A	1752	GLN
1	A	1753	LEU
1	A	1755	SER
1	A	1763	LEU
1	A	1774	ASN
1	A	1776	ILE
1	A	1807	ILE
1	A	1813	ARG
1	A	1833	LEU
1	A	1856	GLU
1	A	1859	LYS
1	A	1862	ILE
1	A	1863	VAL
1	A	1864	THR
1	A	1875	HIS
1	A	1876	LEU
1	A	1879	PHE
1	A	1885	LYS

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Mol	Chain	Res	Type
1	A	1889	LEU
1	A	1891	LEU
1	A	1897	LEU
1	A	1919	LEU
1	A	1921	ASP
1	A	1922	ASP
1	A	1943	LEU
1	A	1944	HIS
1	A	1967	ILE
1	A	1993	LYS
1	A	1998	ASN
1	A	2002	LEU
1	A	2011	ILE
1	A	2012	LEU
1	A	2014	MET
1	A	2015	GLU
3	C	513	ASN
3	C	572	GLU
3	C	573	GLU
3	C	748	ASP
3	C	750	LEU
3	C	754	VAL
3	C	756	LYS
3	C	853	ARG
3	C	856	HIS
4	E	243	LEU
9	I	528	LEU
9	I	532	LYS
9	I	548	PHE
9	I	645	VAL
9	I	694	ILE
9	I	698	ARG
9	I	699	THR
9	I	723	MET
9	I	724	LEU
9	I	725	ARG
9	I	726	ILE
9	I	727	ARG
9	I	730	VAL
9	I	731	GLN
9	I	733	THR
10	J	201	ARG

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Mol	Chain	Res	Type
10	J	214	ILE
12	L	4	ILE
12	L	5	MET
12	L	6	ILE
12	L	7	LYS
12	L	10	VAL
12	L	123	LEU
12	L	133	GLU
13	M	118	LYS
13	M	152	LEU
14	N	119	CYS
15	O	150	LEU
15	O	272	ILE
16	P	3	THR
16	P	7	PRO
16	P	10	GLU
16	P	18	LYS
18	R	95	LYS
18	R	218	ILE
18	R	262	ILE
19	S	37	LYS
19	S	126	HIS
20	T	197	TYR
20	T	412	HIS
20	T	416	ILE
20	T	454	VAL
21	U	23	LEU
21	U	25	LEU
22	V	458	THR
22	V	499	GLN
22	V	535	THR
22	V	597	PRO
23	W	82	ASN
23	W	200	VAL
23	W	205	VAL
23	W	243	VAL
23	W	257	ILE
23	W	264	ASN
23	W	294	VAL
23	W	552	VAL
24	X	54	LEU
24	X	55	TYR

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Mol	Chain	Res	Type
24	X	56	GLU
24	X	58	LEU
24	X	59	GLN
24	X	63	ASP
24	X	64	ARG
24	X	67	GLN
24	X	68	GLU
24	X	72	GLN
24	X	78	MET
24	X	79	VAL
24	X	84	GLU
24	X	86	GLU
24	X	92	GLU
24	X	93	VAL
24	X	96	GLN
24	X	97	GLN
24	X	99	LEU
24	X	101	GLU
24	X	102	LYS
24	X	106	GLU
24	X	109	LEU
24	X	113	LYS
24	X	114	GLU
24	X	116	ARG
24	X	119	LEU
24	X	120	LYS
25	Y	413	LYS
25	Y	418	ASP
25	Y	421	GLU
25	Y	426	LEU
26	Z	725	ASN
26	Z	727	GLU
26	Z	751	PHE
26	Z	758	ARG
27	2	30	GLU
27	2	32	LYS
27	2	33	LEU
27	2	110	GLN
27	2	137	LYS
27	2	138	LYS
27	2	140	LEU
28	z	57	LYS

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Mol	Chain	Res	Type
28	z	60	PRO
28	z	62	GLN
28	z	68	MET
28	z	70	GLU
28	z	71	LYS
28	z	72	ARG
29	b	13	ILE
29	b	57	LYS
29	b	58	GLN
32	c	4	VAL
32	c	40	LEU
33	d	112	ASN
34	f	27	MET
34	f	55	LEU
36	g	65	ASN
29	i	13	ILE
29	i	57	LYS
29	i	58	GLN
32	j	4	VAL
32	j	40	LEU
33	k	112	ASN
34	m	4	PRO
34	m	5	LEU
34	m	27	MET
34	m	55	LEU
36	n	65	ASN
42	o	5	THR
42	o	71	VAL
42	o	79	ILE
42	o	101	VAL
42	o	114	SER
42	o	126	THR
43	p	46	MET
43	p	66	LEU
43	p	87	ASP
44	1	34	ARG
44	1	181	ILE
44	1	267	ILE
44	1	268	ARG
44	1	271	ILE
44	1	273	LYS
44	1	274	TYR

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Mol	Chain	Res	Type
44	1	290	ARG
44	1	315	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (140) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	78	ASN
1	A	105	ASN
1	A	181	ASN
1	A	244	GLN
1	A	321	ASN
1	A	361	HIS
1	A	368	GLN
1	A	457	ASN
1	A	467	GLN
1	A	573	GLN
1	A	584	HIS
1	A	703	GLN
1	A	711	GLN
1	A	834	HIS
1	A	904	HIS
1	A	974	ASN
1	A	994	ASN
1	A	1013	ASN
1	A	1014	ASN
1	A	1023	ASN
1	A	1024	HIS
1	A	1096	HIS
1	A	1117	HIS
1	A	1124	ASN
1	A	1359	HIS
1	A	1373	GLN
1	A	1460	HIS
1	A	1476	GLN
1	A	1487	HIS
1	A	1527	ASN
1	A	1528	GLN
1	A	1554	GLN
1	A	1599	GLN
1	A	1717	ASN
1	A	1727	GLN

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Mol	Chain	Res	Type
1	A	1728	GLN
1	A	1766	GLN
1	A	1775	GLN
1	A	1784	ASN
1	A	1830	GLN
1	A	1875	HIS
1	A	1890	GLN
1	A	1998	ASN
1	A	2004	GLN
3	C	137	HIS
3	C	154	HIS
3	C	208	HIS
3	C	245	HIS
3	C	280	HIS
3	C	297	ASN
3	C	411	ASN
3	C	451	HIS
3	C	513	ASN
3	C	538	HIS
3	C	702	ASN
3	C	892	GLN
4	E	101	ASN
4	E	188	GLN
4	E	253	ASN
9	I	531	HIS
9	I	601	GLN
9	I	705	GLN
10	J	212	GLN
10	J	221	ASN
10	J	238	ASN
10	J	250	GLN
10	J	259	GLN
10	J	373	HIS
12	L	186	GLN
12	L	245	GLN
12	L	266	HIS
13	M	212	ASN
15	O	113	ASN
15	O	120	ASN
15	O	196	GLN
15	O	251	HIS
15	O	294	ASN

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Mol	Chain	Res	Type
16	P	29	GLN
18	R	106	GLN
18	R	133	GLN
18	R	183	GLN
18	R	189	ASN
18	R	279	HIS
19	S	10	GLN
19	S	38	ASN
19	S	87	HIS
19	S	126	HIS
20	T	189	GLN
20	T	278	ASN
20	T	283	HIS
20	T	407	GLN
20	T	437	HIS
20	T	455	GLN
21	U	3	ASN
21	U	20	GLN
22	V	474	HIS
23	W	71	HIS
23	W	82	ASN
23	W	128	GLN
23	W	242	HIS
23	W	472	ASN
23	W	492	ASN
23	W	529	ASN
24	X	61	GLN
24	X	72	GLN
24	X	96	GLN
26	Z	725	ASN
27	2	31	GLN
27	2	110	GLN
27	2	116	ASN
28	z	62	GLN
28	z	69	GLN
28	z	93	ASN
28	z	95	HIS
29	b	22	GLN
29	b	76	ASN
31	a	60	GLN
32	c	64	ASN
33	d	34	GLN

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Mol	Chain	Res	Type
34	f	58	HIS
35	e	65	HIS
36	g	65	ASN
31	h	60	GLN
29	i	22	GLN
29	i	76	ASN
32	j	64	ASN
33	k	34	GLN
34	m	12	ASN
34	m	58	HIS
35	l	65	HIS
36	n	65	ASN
42	o	156	GLN
43	p	7	HIS
44	1	85	GLN
44	1	92	GLN
44	1	154	HIS
44	1	156	GLN
44	1	328	GLN
44	1	344	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	82/117 (70%)	17 (20%)	4 (4%)
5	F	96/107 (89%)	46 (47%)	16 (16%)
6	4	13/46 (28%)	8 (61%)	3 (23%)
7	G	80/174 (45%)	63 (78%)	20 (25%)
8	H	133/188 (70%)	34 (25%)	10 (7%)
All	All	404/632 (63%)	168 (41%)	53 (13%)

All (168) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C

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Mol	Chain	Res	Type
2	B	24	G
2	B	25	C
2	B	26	A
2	B	28	A
2	B	36	C
2	B	38	C
2	B	45	C
2	B	57	G
2	B	70	A
2	B	71	C
5	F	5	U
5	F	6	C
5	F	7	G
5	F	8	C
5	F	9	U
5	F	10	U
5	F	12	G
5	F	25	C
5	F	26	U
5	F	27	A
5	F	28	A
5	F	29	A
5	F	31	U
5	F	33	G
5	F	34	G
5	F	35	A
5	F	36	A
5	F	37	C
5	F	38	G
5	F	40	U
5	F	43	A
5	F	45	A
5	F	46	G
5	F	47	A
5	F	48	A
5	F	49	G
5	F	51	U
5	F	54	G
5	F	56	A
5	F	59	G
5	F	60	C
5	F	61	C

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Mol	Chain	Res	Type
5	F	62	C
5	F	68	C
5	F	73	A
5	F	74	U
5	F	78	A
5	F	79	C
5	F	80	G
5	F	81	C
5	F	82	A
5	F	83	A
5	F	84	A
5	F	85	U
5	F	86	U
5	F	87	C
6	4	-12	G
6	4	-11	G
6	4	-10	C
6	4	-9	C
6	4	-7	C
6	4	-6	C
6	4	-4	A
6	4	-1	G
7	G	2	U
7	G	3	A
7	G	5	G
7	G	6	A
7	G	7	G
7	G	8	C
7	G	10	U
7	G	11	A
7	G	12	G
7	G	13	C
7	G	14	A
7	G	17	U
7	G	21	A
7	G	22	C
7	G	23	U
7	G	24	G
7	G	25	G
7	G	26	U
7	G	27	U
7	G	28	A

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Mol	Chain	Res	Type
7	G	29	C
7	G	30	C
7	G	31	U
7	G	73	G
7	G	74	G
7	G	75	U
7	G	76	U
7	G	77	U
7	G	78	C
7	G	79	C
7	G	80	U
7	G	81	U
7	G	82	G
7	G	83	A
7	G	84	U
7	G	87	U
7	G	88	G
7	G	89	U
7	G	90	C
7	G	91	A
7	G	92	U
7	G	93	A
7	G	96	U
7	G	97	A
7	G	98	U
7	G	99	C
7	G	100	C
7	G	101	U
7	G	102	G
7	G	103	U
7	G	119	A
7	G	120	G
7	G	121	C
7	G	122	U
7	G	123	C
7	G	124	G
7	G	125	C
7	G	126	G
7	G	127	G
7	G	128	U
7	G	129	U
7	G	130	G

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Mol	Chain	Res	Type
7	G	132	G
8	H	13	C
8	H	14	C
8	H	15	U
8	H	16	U
8	H	17	U
8	H	19	G
8	H	24	A
8	H	25	G
8	H	28	C
8	H	29	A
8	H	30	A
8	H	31	G
8	H	33	G
8	H	37	U
8	H	39	U
8	H	40	C
8	H	41	U
8	H	42	G
8	H	43	U
8	H	112	G
8	H	143	A
8	H	147	G
8	H	152	G
8	H	153	A
8	H	154	C
8	H	156	U
8	H	157	G
8	H	164	C
8	H	165	A
8	H	168	A
8	H	169	C
8	H	177	A
8	H	178	A
8	H	179	C

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	18	C
2	B	19	A
2	B	20	G

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Mol	Chain	Res	Type
2	B	27	U
5	F	5	U
5	F	7	G
5	F	25	C
5	F	26	U
5	F	33	G
5	F	34	G
5	F	35	A
5	F	36	A
5	F	45	A
5	F	50	A
5	F	58	G
5	F	59	G
5	F	73	A
5	F	81	C
5	F	84	A
5	F	86	U
6	4	-13	C
6	4	-12	G
6	4	-11	G
7	G	1	G
7	G	16	G
7	G	20	A
7	G	21	A
7	G	22	C
7	G	23	U
7	G	90	C
7	G	95	U
7	G	96	U
7	G	97	A
7	G	98	U
7	G	100	C
7	G	119	A
7	G	120	G
7	G	121	C
7	G	124	G
7	G	125	C
7	G	126	G
7	G	128	U
7	G	129	U
8	H	15	U
8	H	28	C

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Mol	Chain	Res	Type
8	H	29	A
8	H	30	A
8	H	38	A
8	H	39	U
8	H	40	C
8	H	156	U
8	H	164	C
8	H	168	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
18	SEP	R	224	18	8,9,10	1.47	2 (25%)	7,12,14	1.71	1 (14%)
18	SEP	R	232	18	8,9,10	1.61	1 (12%)	7,12,14	1.00	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	SEP	R	224	18	-	0/6/8/10	-
18	SEP	R	232	18	-	2/6/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	R	232	SEP	P-O1P	3.55	1.61	1.50
18	R	224	SEP	P-O2P	-2.48	1.45	1.54
18	R	224	SEP	P-O3P	-2.28	1.46	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	224	SEP	OG-CB-CA	-3.55	104.69	108.14
18	R	232	SEP	OG-CB-CA	2.37	110.46	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	R	224	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 16 are monoatomic - leaving 3 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	$\# Z > 2$
45	IHP	A	3000	-	36,36,36	0.72	0	60,60,60	1.09	0
49	ATP	Q	1501	47	32,33,33	2.04	8 (25%)	48,52,52	1.87	16 (33%)
46	GTP	C	1500	47	33,34,34	1.08	2 (6%)	50,54,54	1.77	11 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	IHP	A	3000	-	-	3/30/54/54	0/1/1/1
49	ATP	Q	1501	47	-	4/22/38/38	0/3/3/3
46	GTP	C	1500	47	-	2/22/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	Q	1501	ATP	PB-O3B	7.24	1.67	1.59
49	Q	1501	ATP	C6-N6	4.70	1.46	1.34
49	Q	1501	ATP	C4-N3	3.20	1.40	1.34
49	Q	1501	ATP	C2'-C3'	-2.78	1.45	1.53
46	C	1500	GTP	C5-N7	-2.32	1.34	1.39
46	C	1500	GTP	O4'-C4'	-2.28	1.39	1.45
49	Q	1501	ATP	C8-N7	2.21	1.35	1.31
49	Q	1501	ATP	C3'-C4'	-2.18	1.47	1.53
49	Q	1501	ATP	O2'-C2'	-2.13	1.37	1.43
49	Q	1501	ATP	O3'-C3'	-2.06	1.37	1.43

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	C	1500	GTP	C5-C4-N3	-5.14	120.22	128.39
49	Q	1501	ATP	C5-C4-N3	-4.90	119.97	126.72
46	C	1500	GTP	C2-N3-C4	4.46	119.98	112.30
49	Q	1501	ATP	N3-C2-N1	-4.24	122.16	128.58
49	Q	1501	ATP	N3-C4-N9	3.74	133.53	127.17
46	C	1500	GTP	C2'-C1'-N9	-3.60	103.22	113.25
46	C	1500	GTP	N9-C4-N3	3.56	133.07	125.95
46	C	1500	GTP	C2-N1-C6	-3.53	118.71	125.11
49	Q	1501	ATP	N9-C8-N7	-3.42	109.08	113.94
49	Q	1501	ATP	C2-N3-C4	3.23	119.72	111.83
46	C	1500	GTP	N9-C8-N7	-2.99	107.85	113.40
49	Q	1501	ATP	C4-N9-C8	2.93	108.82	105.74
49	Q	1501	ATP	C5-N7-C8	2.93	108.05	103.45
46	C	1500	GTP	C5-C6-N1	2.85	120.52	113.25
49	Q	1501	ATP	C4-C5-N7	-2.66	107.54	110.58
49	Q	1501	ATP	O2A-PA-O1A	-2.54	100.64	112.44
46	C	1500	GTP	O2B-PB-O3B	2.47	113.95	107.27
49	Q	1501	ATP	O2G-PG-O1G	-2.46	101.23	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	C	1500	GTP	O6-C6-C5	-2.46	120.04	126.53
46	C	1500	GTP	C3'-C2'-C1'	2.31	105.83	101.46
46	C	1500	GTP	C8-N7-C5	2.31	108.37	104.26
49	Q	1501	ATP	O2A-PA-O3A	2.31	113.50	107.27
49	Q	1501	ATP	O2G-PG-O3B	2.26	112.20	104.64
49	Q	1501	ATP	O2B-PB-O1B	-2.25	101.96	112.44
49	Q	1501	ATP	O5'-C5'-C4'	2.09	116.11	108.99
49	Q	1501	ATP	O3G-PG-O3B	2.05	111.50	104.64
49	Q	1501	ATP	O4'-C1'-N9	2.03	111.99	108.09

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
49	Q	1501	ATP	C5'-O5'-PA-O1A
49	Q	1501	ATP	C5'-O5'-PA-O2A
49	Q	1501	ATP	C5'-O5'-PA-O3A
46	C	1500	GTP	O4'-C4'-C5'-O5'
46	C	1500	GTP	C5'-O5'-PA-O1A
45	A	3000	IHP	C3-O13-P3-O43
45	A	3000	IHP	C3-C4-O14-P4
45	A	3000	IHP	C4-O14-P4-O24
49	Q	1501	ATP	PB-O3A-PA-O2A

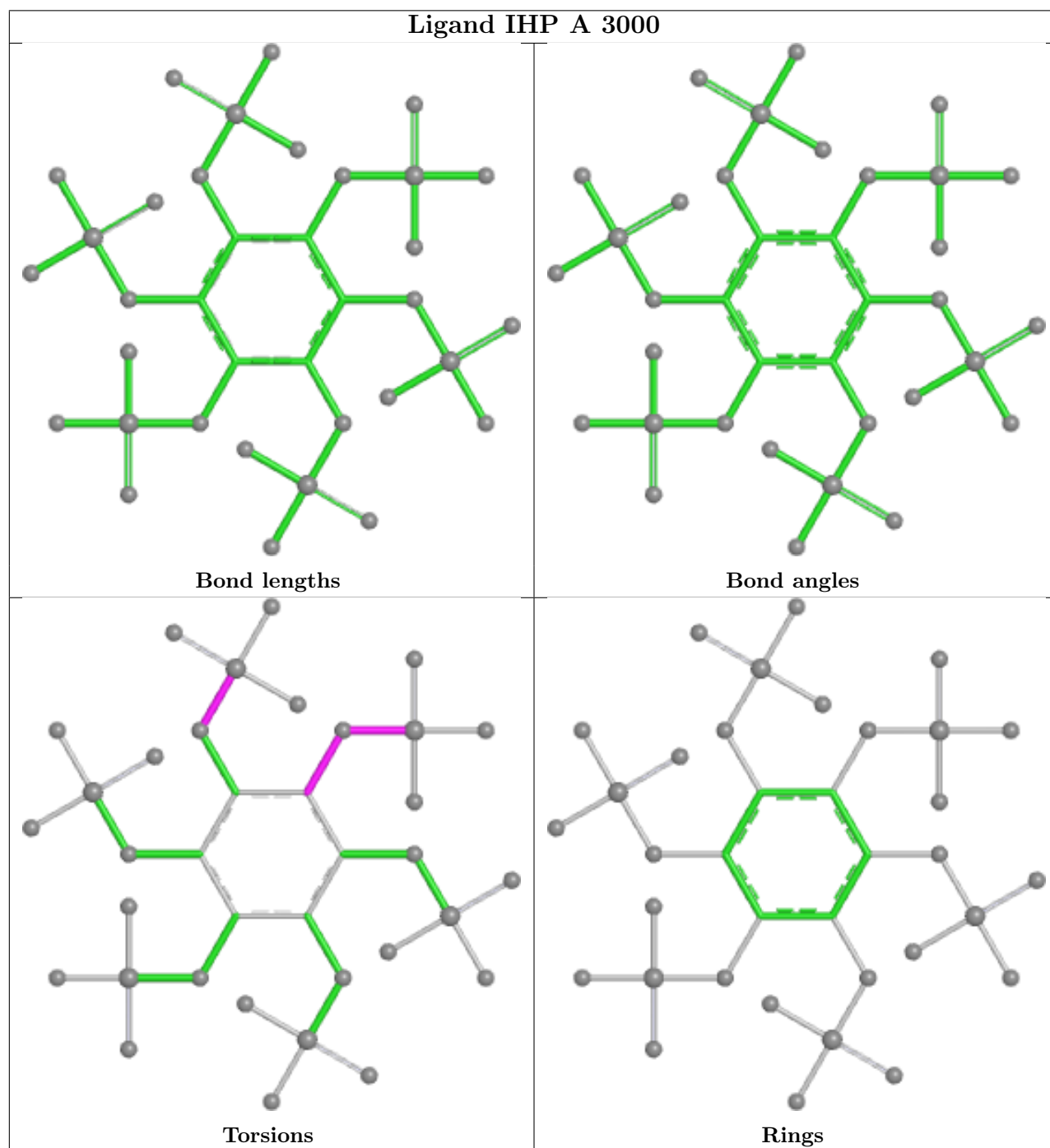
There are no ring outliers.

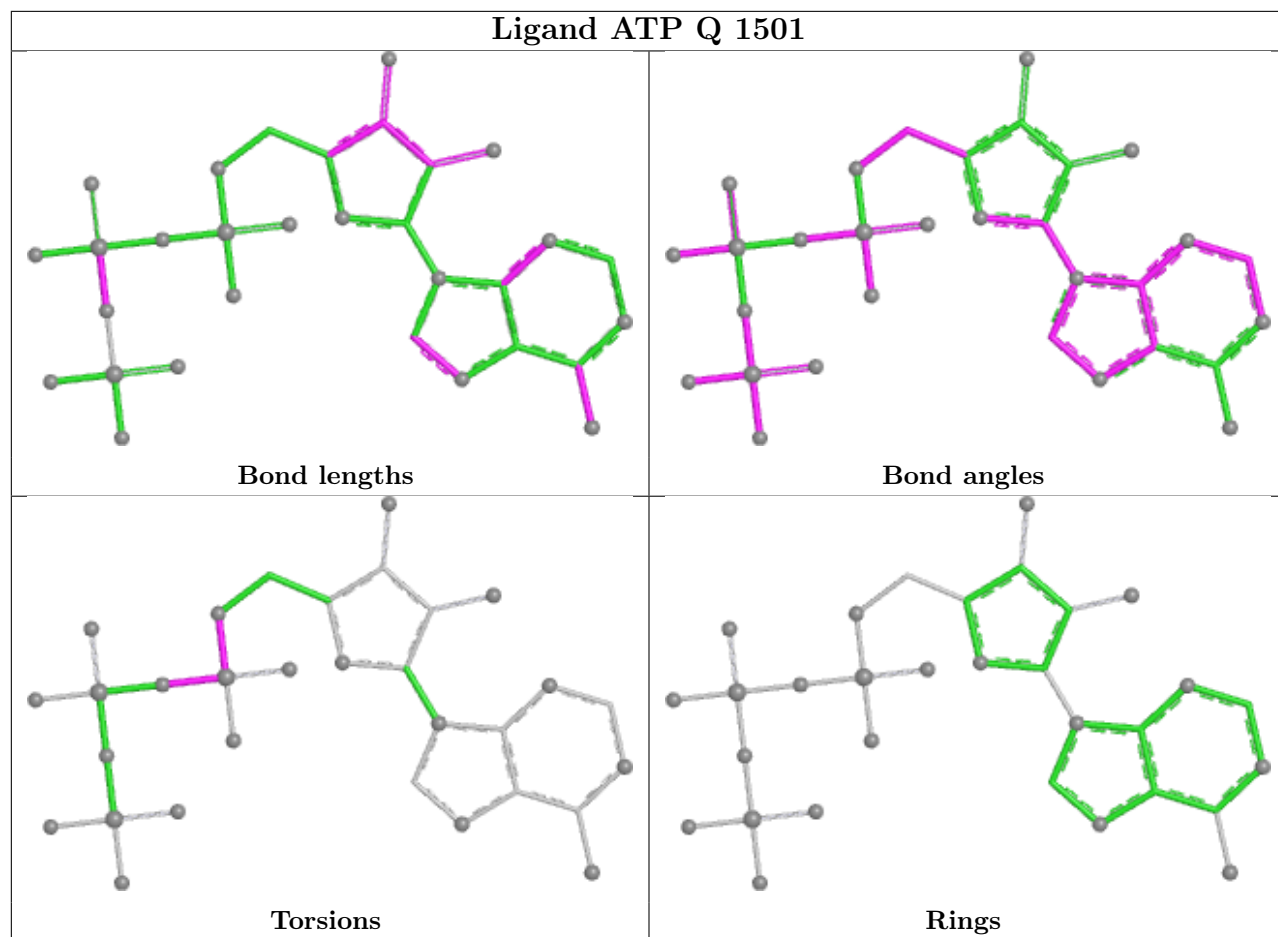
3 monomers are involved in 16 short contacts:

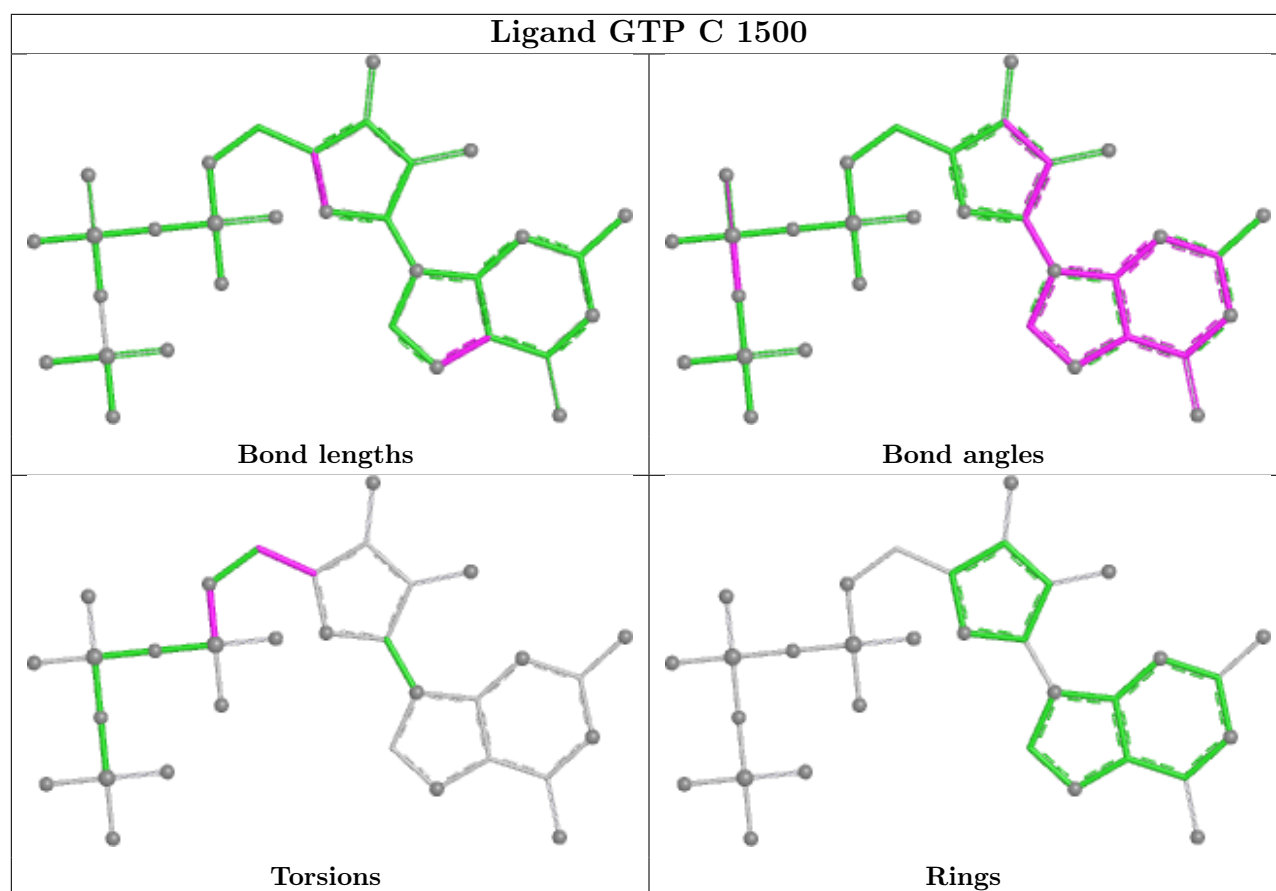
Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	A	3000	IHP	9	0
49	Q	1501	ATP	5	0
46	C	1500	GTP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

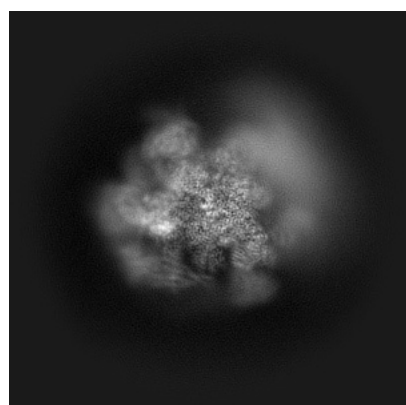
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32319. These allow visual inspection of the internal detail of the map and identification of artifacts.

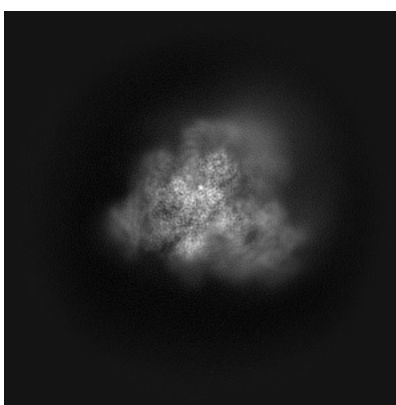
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

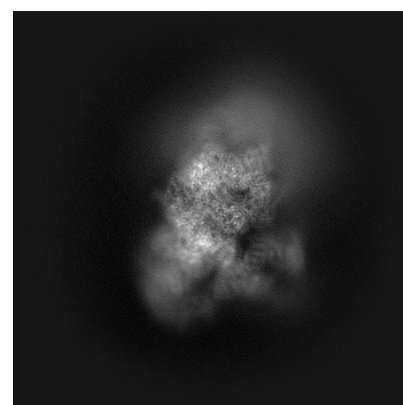
6.1.1 Primary map



X



Y

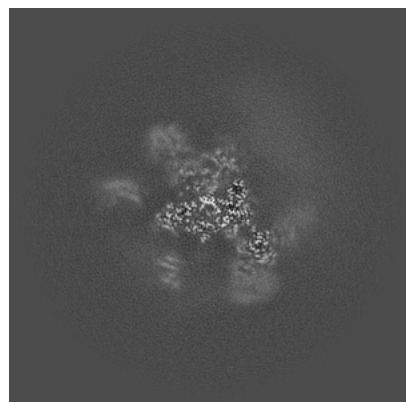


Z

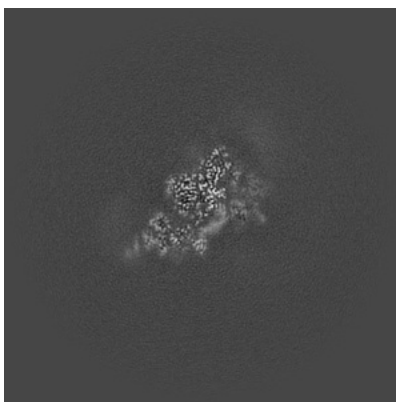
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

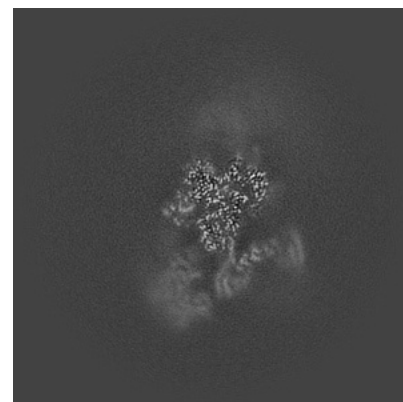
6.2.1 Primary map



X Index: 200



Y Index: 200

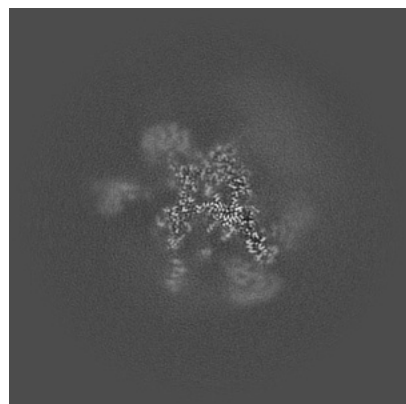


Z Index: 200

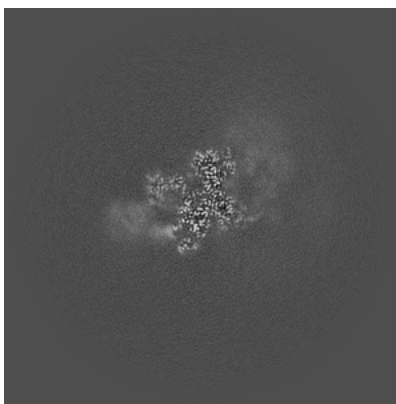
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

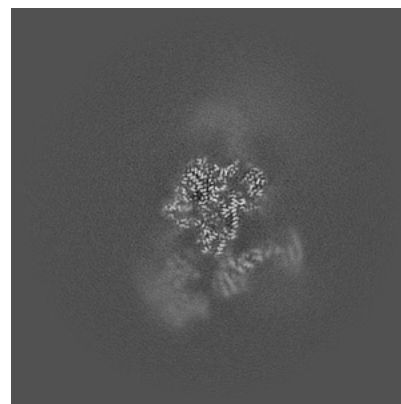
6.3.1 Primary map



X Index: 194



Y Index: 227

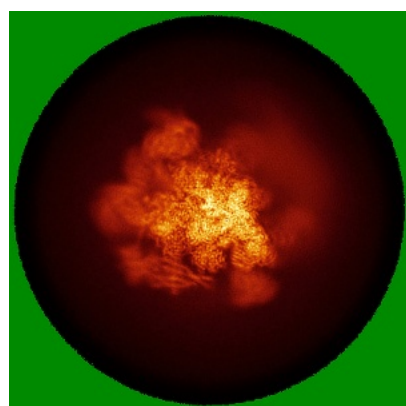


Z Index: 197

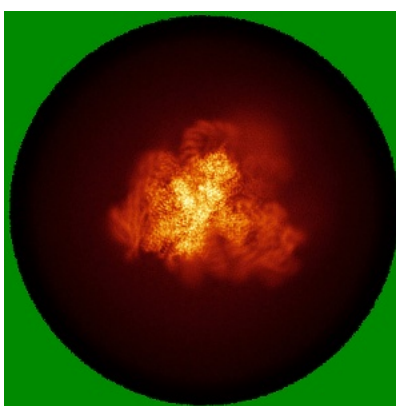
The images above show the largest variance slices of the map in three orthogonal directions.

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

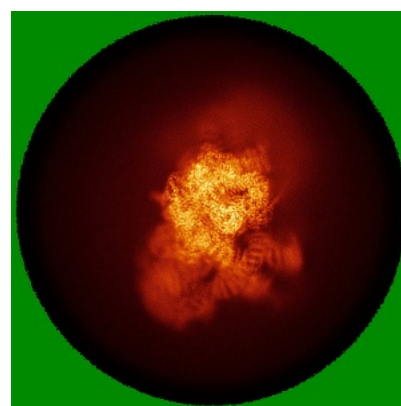
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.39. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

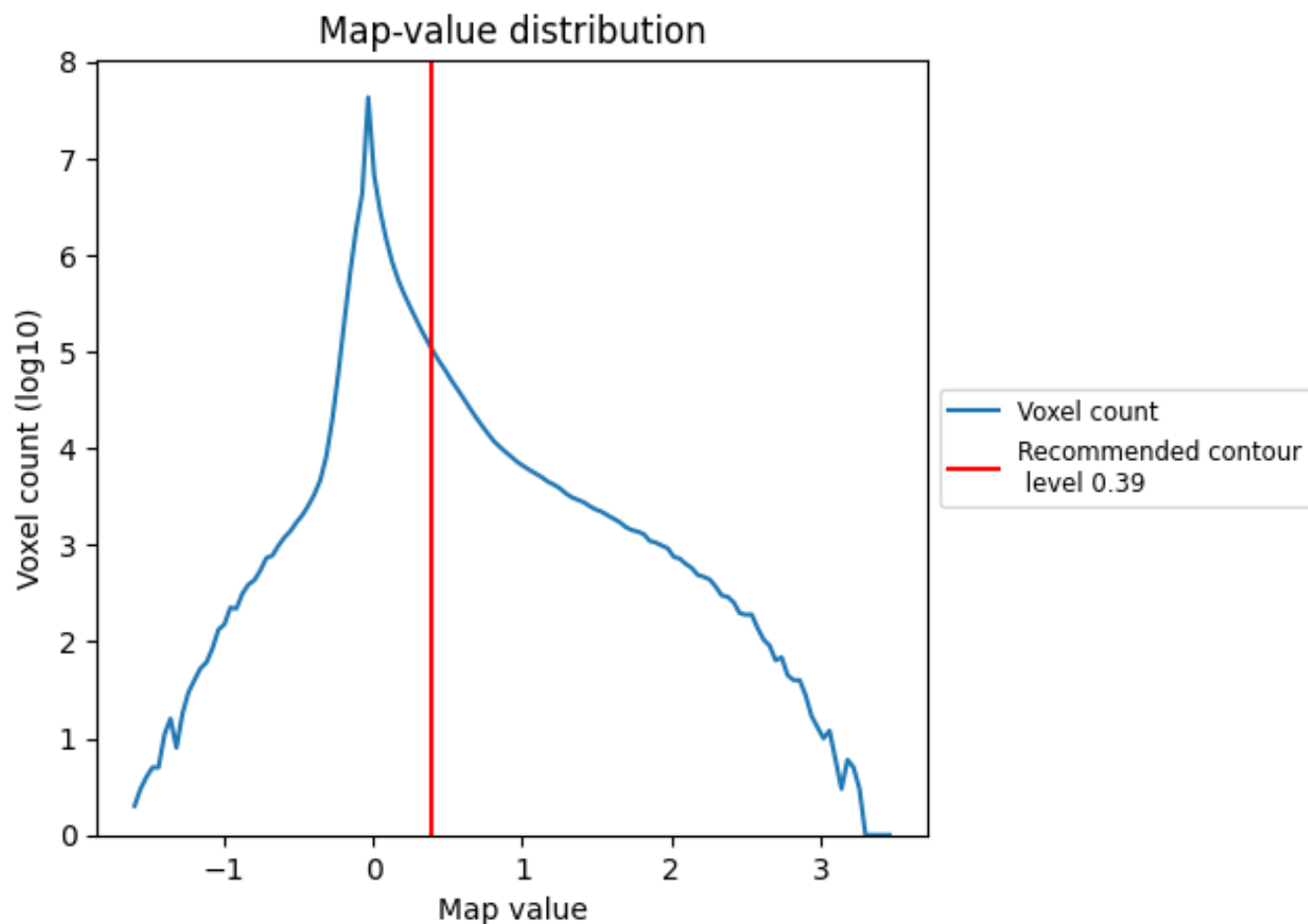
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

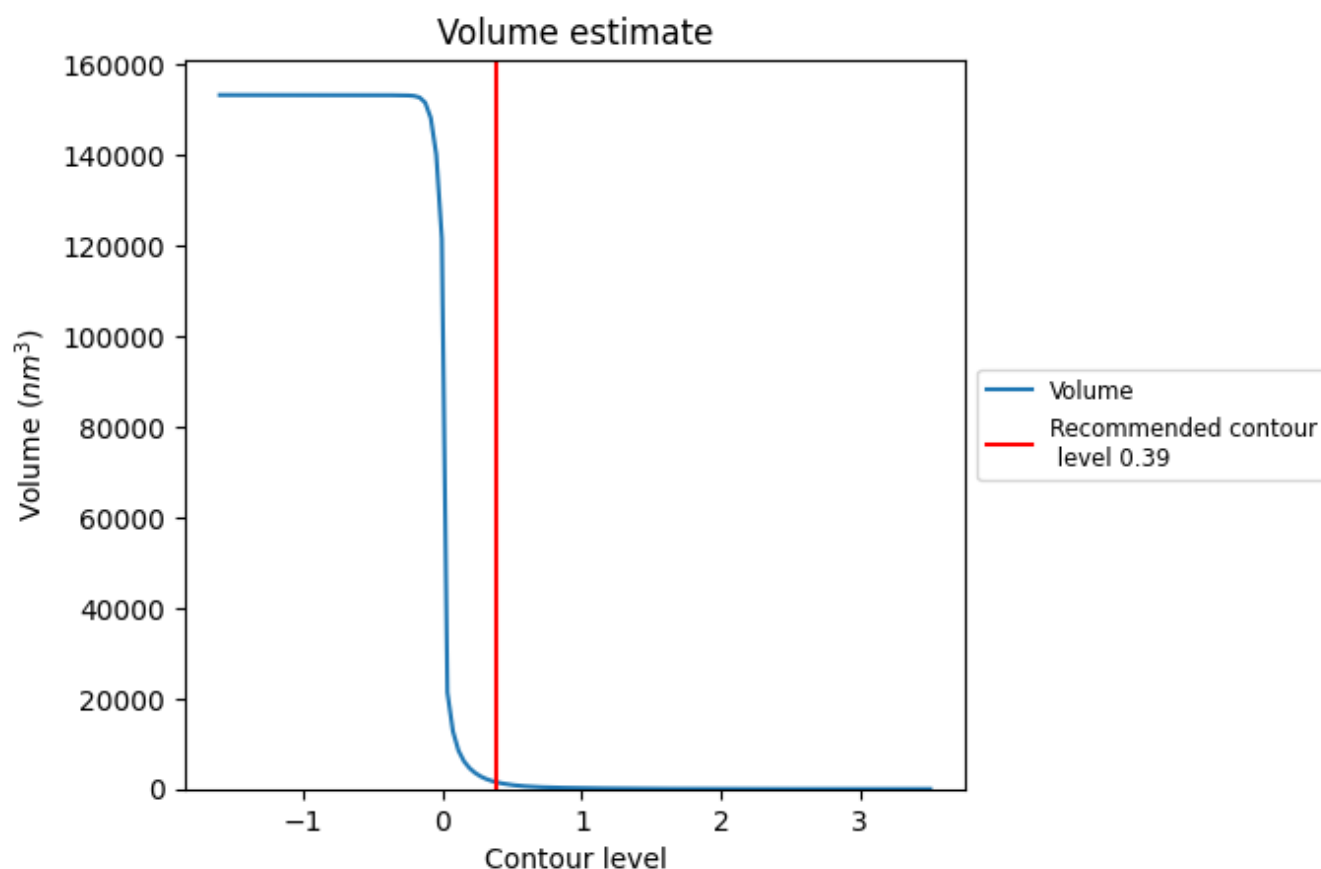
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

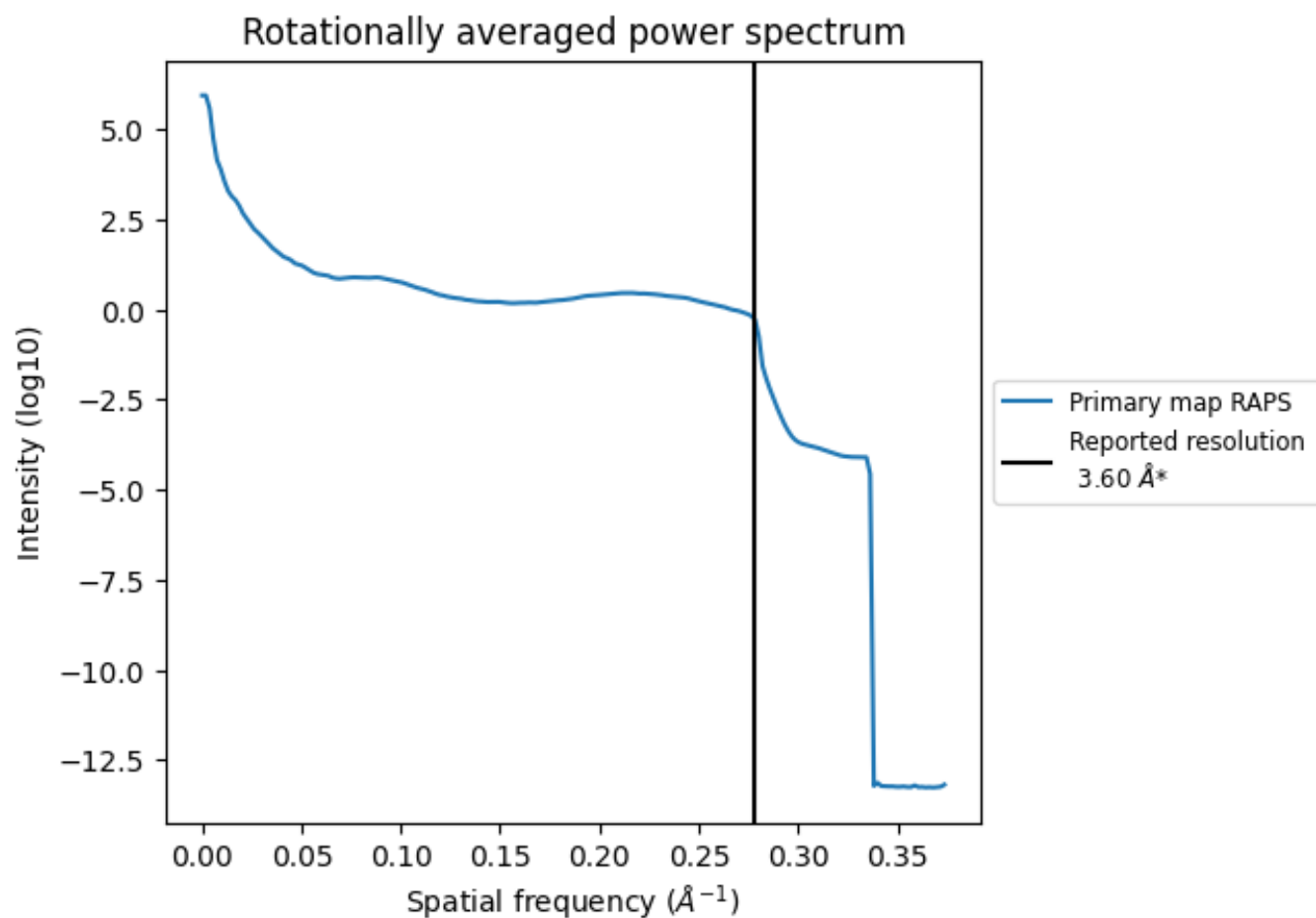
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1478 nm³; this corresponds to an approximate mass of 1335 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 0.278 Å⁻¹

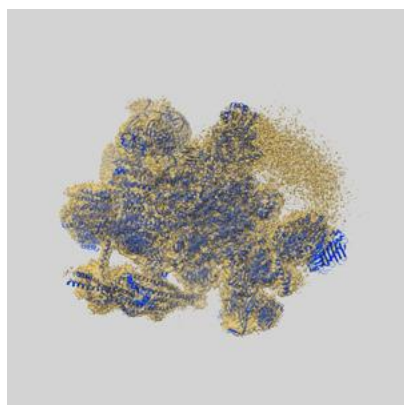
8 Fourier-Shell correlation

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

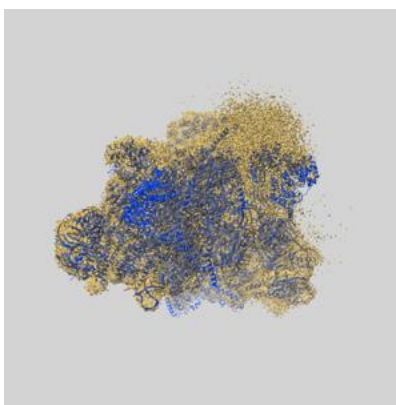
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32319 and PDB model 7W5A. Per-residue inclusion information can be found in section [3](#) on page [15](#).

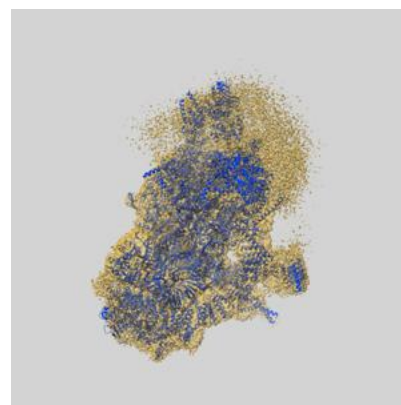
9.1 Map-model overlay [i](#)



X



Y



Z

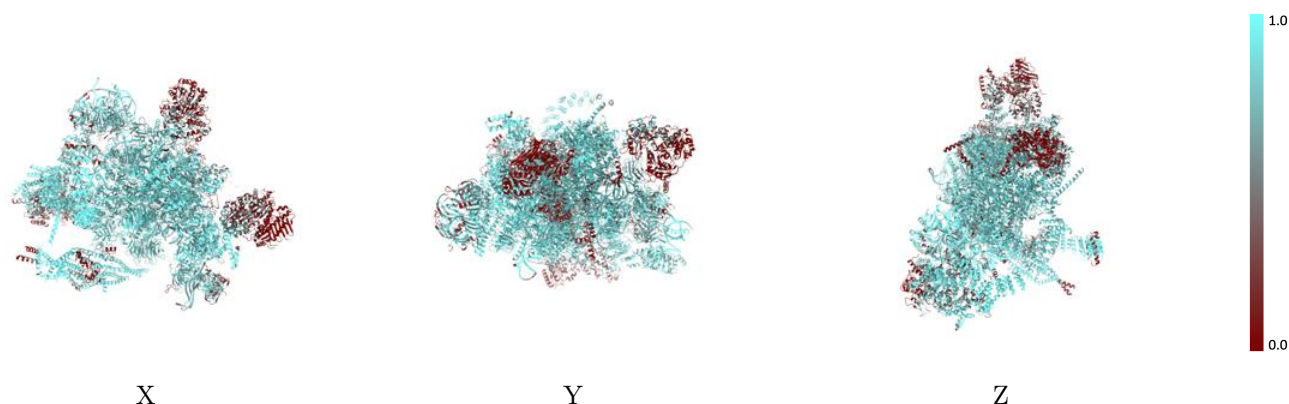
The images above show the 3D surface view of the map at the recommended contour level 0.39 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



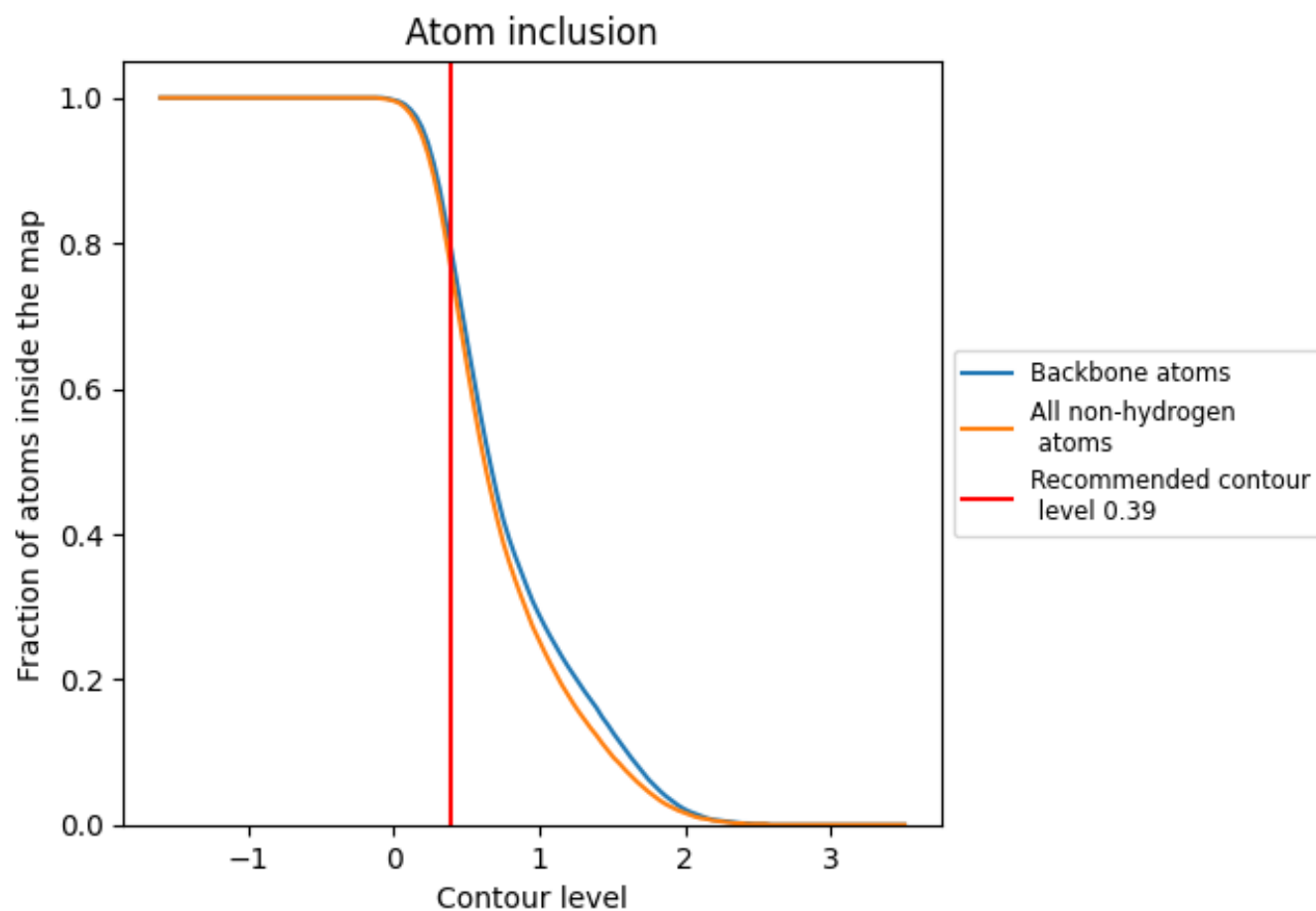
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.39).

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 (0.39) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7690	 0.2690
1	 0.2940	 0.2090
2	 0.7600	 0.2290
4	 0.9860	 0.4820
A	 0.9110	 0.4460
B	 0.9280	 0.3030
C	 0.8950	 0.3900
E	 0.9280	 0.4200
F	 0.9520	 0.3700
G	 0.7950	 0.2110
H	 0.9090	 0.1640
I	 0.9080	 0.2300
J	 0.8770	 0.3030
K	 0.9640	 0.2140
L	 0.8930	 0.3370
M	 0.8520	 0.3870
N	 0.9250	 0.4370
O	 0.8840	 0.3700
P	 0.8070	 0.3930
Q	 0.5250	 0.0520
R	 0.8550	 0.4010
S	 0.9260	 0.4110
T	 0.9550	 0.4950
U	 0.8850	 0.2950
V	 0.6440	 0.1890
W	 0.8190	 0.2890
X	 0.7270	 0.3180
Y	 0.2740	 0.0650
Z	 0.6840	 0.3220
a	 0.7370	 0.1700
b	 0.7180	 0.1150
c	 0.8310	 0.0590
d	 0.7320	 0.0270
e	 0.6020	 0.0550
f	 0.6110	 0.0080



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Chain	Atom inclusion	Q-score
g	 0.5610	 0.0960
h	 0.6810	 0.0850
i	 0.6090	 0.0580
j	 0.7920	 0.0500
k	 0.7260	 0.0950
l	 0.6630	 0.0860
m	 0.9060	 0.1440
n	 0.7140	 0.1320
o	 0.7790	 0.0570
p	 0.8830	 0.0900
q	 0.5660	 0.0450
r	 0.9270	 0.1650
s	 0.4870	 0.1010
t	 0.3980	 0.0490
u	 0.3010	 0.0250
v	 0.0110	 0.0060
w	 0.0130	 -0.0000
x	 0.0970	 0.0270
y	 0.8590	 0.1390
z	 0.1890	 0.1200