



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:03 PM UTC

PDB ID : 5GMK / pdb_00005gmk
EMDB ID : EMD-9525
Title : Cryo-EM structure of the Catalytic Step I spliceosome (C complex) at 3.4 angstrom resolution
Authors : Wan, R.; Yan, C.; Bai, R.; Huang, G.; Shi, Y.
Deposited on : 2016-07-14
Resolution : 3.40 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

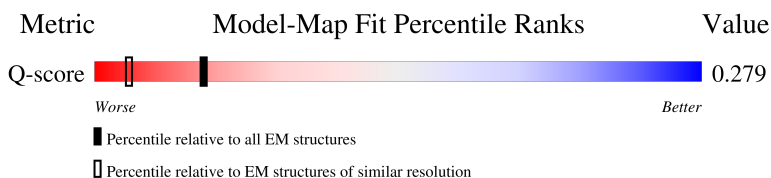
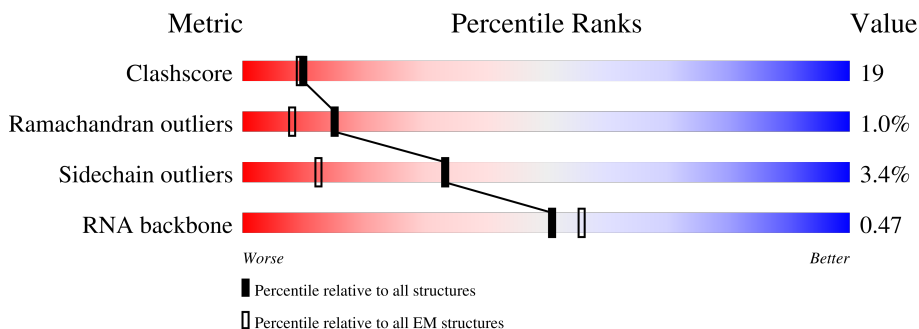
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 75273 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1910	Total	C	N	O	S	0	0
			15775	10142	2709	2867	57		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	878	Total	C	N	O	S	0	0
			7019	4529	1166	1295	29		

- Molecule 3 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 4 is a RNA chain called U6 snRNA.

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

- Molecule 5 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	127	Total	C	N	O	P	0	0
			2673	1197	445	904	127		

- Molecule 6 is a RNA chain called Intron_BPS.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	29	Total	C	N	O	P	0	0
			608	274	101	204	29		

- Molecule 7 is a RNA chain called 5'-Exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	13	Total	C	N	O	P	0	0
			275	124	47	91	13		

- Molecule 8 is a RNA chain called 5'-Splicing Site.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	15	Total	C	N	O	P	0	0
			312	140	45	112	15		

- Molecule 9 is a protein called Pre-mRNA-splicing factor CWC21.

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

- Molecule 10 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 11 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	201	Total	C	N	O	S	0	0
			1583	988	290	298	7		

- Molecule 12 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	185	Total	C	N	O	S	0	0
			1472	930	256	271	15		

- Molecule 13 is a protein called Pre-mRNA-splicing factor CWC2.

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

- Molecule 14 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	69	Total	C	N	O	S	0	0
			560	351	112	96	1		

- Molecule 15 is a protein called Pre-mRNA-splicing factor BUD31.

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

- Molecule 16 is a protein called Pre-mRNA-splicing factor CWC22.

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

- Molecule 17 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	c	436	Total	C	N	O	S	0	0
			2971	1841	549	573	8		

- Molecule 18 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	d	549	Total	C	N	O	S	0	0
			3590	2232	675	675	8		

- Molecule 19 is a protein called Protein CWC16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	F	115	Total	C	N	O	S	0	0
			937	592	167	169	9		

- Molecule 20 is a protein called Pre-mRNA-splicing factor CWC25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	G	41	Total	C	N	O	S	0	0
			342	215	63	63	1		

- Molecule 21 is a protein called Pre-mRNA-splicing factor ISY1.

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

- Molecule 22 is a protein called Pre-mRNA-splicing factor SYF2.

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

- Molecule 23 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	v	673	Total	C	N	O	S	0	0
			3580	2190	683	706	1		

- Molecule 24 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	n	299	Total	C	N	O	S	0	0
			1890	1175	340	369	6		

- Molecule 25 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		
25	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
25	q	387	Total	C	N	O	S	0	0
			2345	1471	402	464	8		
25	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 26 is a protein called Pre-mRNA-splicing factor SNT309.

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

- Molecule 27 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	k	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
27	s	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
28	u	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	70	Total	C	N	O	S	0	0
			554	355	98	100	1		
29	w	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	j	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
30	x	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	l	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
31	y	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
32	z	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
33	e	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

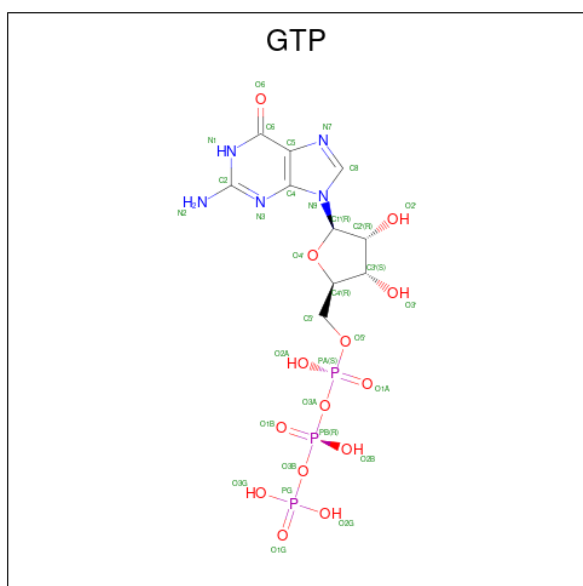
- Molecule 34 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	a	81	Total	C	N	O	0	0
			513	332	89	92		

- Molecule 35 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	b	135	Total	C	N	O	0	0
			841	538	142	161		

- Molecule 36 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	C	1	Total	Mg	0
			1	1	
37	E	5	Total	Mg	0
			5	5	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

SEQUENCE-PLOTS INFOmissingINFO

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	161066	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	4.7	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.240	Depositor
Minimum map value	-0.120	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0413	Depositor
Map size ($\text{\AA}$)	522.4, 522.4, 522.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3060001, 1.3060001, 1.3060001	Depositor

4 Model quality ⓘ

4.1 Standard geometry ⓘ

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

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	0.43	5/16178 (0.0%)	0.63	9/21929 (0.0%)
2	C	0.41	3/7168 (0.0%)	0.57	6/9707 (0.1%)
3	D	0.36	0/2747	0.38	0/4267
4	E	0.38	1/2452 (0.0%)	0.37	0/3817
5	L	0.87	32/2974 (1.1%)	1.30	47/4610 (1.0%)
6	M	0.40	1/678 (0.1%)	0.68	3/1051 (0.3%)
7	B	0.65	1/307 (0.3%)	0.34	0/475
8	N	0.66	1/346 (0.3%)	0.51	0/535
9	J	0.37	0/191	0.56	0/254
10	O	0.52	0/2704	0.67	3/3676 (0.1%)
11	P	0.37	1/1604 (0.1%)	0.62	2/2160 (0.1%)
12	Q	0.45	1/1496 (0.1%)	0.75	2/2014 (0.1%)
13	R	0.37	0/2135	0.58	0/2871
14	S	0.42	1/574 (0.2%)	0.57	0/766
15	T	0.41	0/1315	0.66	0/1759
16	Z	0.55	0/3712	1.10	15/5004 (0.3%)
17	c	0.40	1/2405 (0.0%)	0.72	1/3218 (0.0%)
18	d	0.42	0/2107	0.58	1/2852 (0.0%)
19	F	0.28	0/955	0.57	0/1277
20	G	0.21	0/346	0.58	0/462
21	H	0.26	0/826	0.69	0/1108
22	I	0.27	0/826	0.44	0/1097
23	v	0.87	9/905 (1.0%)	1.11	9/1214 (0.7%)
24	n	1.12	16/1900 (0.8%)	1.13	24/2537 (0.9%)
25	o	0.54	0/835	0.85	0/1126
25	p	0.53	0/848	0.91	0/1143
25	q	0.64	0/2342	0.93	2/3139 (0.1%)
25	r	0.53	0/828	0.86	0/1117
26	t	0.58	0/924	1.06	2/1244 (0.2%)
27	k	0.55	0/636	0.76	0/856
27	s	0.54	0/615	0.76	0/829
28	i	0.63	0/585	0.86	0/795

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	u	0.63	0/585	0.86	0/795
29	h	0.61	0/564	0.87	0/761
29	w	0.60	0/564	0.87	0/761
30	j	0.53	0/532	0.82	1/715 (0.1%)
30	x	0.53	0/532	0.82	1/715 (0.1%)
31	l	0.55	0/634	0.96	2/859 (0.2%)
31	y	0.55	0/634	0.96	2/859 (0.2%)
32	m	0.58	0/649	0.81	0/880
32	z	0.58	0/649	0.81	0/880
33	e	0.64	0/535	0.86	2/717 (0.3%)
33	g	0.65	0/753	0.96	2/1013 (0.2%)
34	a	1.00	2/514 (0.4%)	1.86	7/686 (1.0%)
35	b	1.24	6/839 (0.7%)	2.35	45/1127 (4.0%)
All	All	0.54	81/72448 (0.1%)	0.81	188/99677 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8
2	C	0	2
10	O	0	6
11	P	0	1
12	Q	0	3
16	Z	0	5
17	c	0	1
20	G	0	1
24	n	0	4
30	j	0	1
30	x	0	1
31	l	0	2
31	y	0	2
33	e	0	2
33	g	0	2
All	All	0	41

All (81) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	399	CYS	CB-SG	-12.11	1.41	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	444	CYS	CB-SG	-11.45	1.43	1.81
35	b	69	ASP	CA-CB	-10.58	1.38	1.53
24	n	454	CYS	CB-SG	-9.99	1.48	1.81
24	n	218	CYS	CB-SG	-9.77	1.49	1.81
7	B	98	A	O3'-P	-9.49	1.47	1.61
24	n	246	LEU	CA-CB	-9.48	1.37	1.53
24	n	352	CYS	CB-SG	-9.40	1.50	1.81
24	n	198	CYS	CB-SG	-8.81	1.52	1.81
23	v	712	CYS	CB-SG	-8.50	1.53	1.81
24	n	396	ARG	CA-CB	-8.43	1.44	1.54
5	L	1096	C	O3'-P	-7.98	1.49	1.61
24	n	250	PRO	CA-CB	-7.73	1.43	1.53
5	L	59	C	C1'-N1	7.71	1.60	1.48
5	L	1096	C	C1'-N1	7.70	1.59	1.48
5	L	71	C	C1'-N1	7.67	1.59	1.48
5	L	82	C	C1'-N1	7.63	1.59	1.48
5	L	84	C	C1'-N1	7.58	1.59	1.48
5	L	1118	U	C1'-N1	7.56	1.59	1.48
5	L	1120	G	C1'-N9	-7.55	1.36	1.48
8	N	102	A	O3'-P	-7.32	1.50	1.61
5	L	63	U	C1'-N1	7.15	1.59	1.48
5	L	97	U	C1'-N1	7.12	1.59	1.48
5	L	99	U	C1'-N1	7.11	1.59	1.48
5	L	98	U	C1'-N1	7.08	1.59	1.48
5	L	107	U	C1'-N1	7.07	1.59	1.48
5	L	101	U	C1'-N1	7.06	1.59	1.48
5	L	54	U	C1'-N1	7.05	1.59	1.48
5	L	56	U	C1'-N1	7.05	1.59	1.48
5	L	102	U	C1'-N1	7.00	1.58	1.48
5	L	68	U	C1'-N1	7.00	1.58	1.48
5	L	73	U	C1'-N1	6.99	1.58	1.48
5	L	1111	U	C1'-N1	6.99	1.58	1.48
5	L	1119	C	C1'-N1	6.98	1.58	1.48
5	L	83	U	C1'-N1	6.97	1.58	1.48
5	L	1101	C	C1'-N1	6.97	1.58	1.48
35	b	102	THR	CB-OG1	6.92	1.54	1.43
5	L	1109	C	C1'-N1	6.91	1.57	1.47
5	L	1115	G	C1'-N9	-6.84	1.37	1.48
24	n	325	ASN	CA-CB	-6.83	1.42	1.53
35	b	51	THR	CB-OG1	6.65	1.54	1.43
5	L	62	C	C1'-N1	6.53	1.58	1.48
5	L	104	C	C1'-N1	6.49	1.58	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	72	C	C1'-N1	6.45	1.58	1.48
5	L	74	C	C1'-N1	6.44	1.58	1.48
4	E	84	C	O3'-P	-6.42	1.51	1.61
24	n	291	HIS	CA-CB	-6.31	1.42	1.53
34	a	75	THR	CB-OG1	6.19	1.53	1.43
34	a	110	THR	CB-OG1	6.15	1.53	1.43
1	A	901	PRO	C-N	6.07	1.40	1.33
24	n	155	ILE	CB-CG1	-6.03	1.41	1.53
35	b	153	THR	CB-OG1	6.00	1.53	1.43
5	L	1112	G	C1'-N9	-5.94	1.39	1.48
35	b	38	THR	CB-OG1	5.88	1.53	1.43
5	L	121	C	C1'-N1	5.87	1.57	1.48
2	C	463	THR	C-N	5.74	1.41	1.33
35	b	160	THR	CB-OG1	5.72	1.52	1.43
23	v	718	SER	CB-OG	5.64	1.53	1.42
23	v	723	SER	CB-OG	5.58	1.53	1.42
1	A	898	ILE	C-N	5.55	1.41	1.33
24	n	430	THR	CB-OG1	5.52	1.52	1.43
5	L	26	G	O3'-P	-5.47	1.52	1.61
1	A	902	PRO	N-CD	5.43	1.55	1.47
12	Q	215	PRO	N-CD	5.42	1.55	1.47
1	A	899	PRO	N-CD	5.40	1.55	1.47
24	n	235	THR	CB-OG1	5.40	1.52	1.43
23	v	576	THR	CB-OG1	5.28	1.52	1.43
11	P	175	PRO	N-CD	5.24	1.55	1.47
17	c	202	LYS	C-N	-5.21	1.21	1.33
23	v	714	SER	CB-OG	5.21	1.52	1.42
14	S	7	PRO	N-CD	5.18	1.55	1.47
24	n	440	SER	CB-OG	5.17	1.52	1.42
23	v	719	THR	CB-OG1	5.16	1.52	1.43
2	C	464	PRO	N-CD	5.13	1.54	1.47
23	v	681	SER	CB-OG	5.11	1.52	1.42
24	n	342	LEU	CB-CG	-5.10	1.43	1.53
6	M	502	C	O3'-P	5.07	1.68	1.61
1	A	901	PRO	N-CD	5.06	1.54	1.47
2	C	459	PRO	N-CD	5.04	1.54	1.47
23	v	632	THR	CB-OG1	5.03	1.51	1.43
23	v	644	ILE	CB-CG1	-5.02	1.43	1.53

All (188) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	483	PRO	O-C-N	-33.46	77.47	122.64
6	M	502	C	O3'-P-O5'	-16.03	79.95	104.00
35	b	44	PRO	N-CA-CB	15.91	113.89	103.23
35	b	81	LEU	CA-C-N	12.08	131.57	120.10
35	b	81	LEU	C-N-CA	12.08	131.57	120.10
1	A	485	PRO	N-CA-C	-9.83	99.86	113.53
35	b	12	PRO	N-CA-CB	9.02	111.31	103.19
6	M	502	C	P-O3'-C3'	8.87	133.50	120.20
5	L	71	C	O3'-P-O5'	-8.62	91.08	104.00
5	L	70	A	O3'-P-O5'	-8.61	91.08	104.00
5	L	104	C	O3'-P-O5'	-8.61	91.08	104.00
5	L	54	U	O3'-P-O5'	-8.60	91.10	104.00
5	L	73	U	O3'-P-O5'	-8.60	91.10	104.00
5	L	78	G	O3'-P-O5'	-8.60	91.10	104.00
5	L	80	G	O3'-P-O5'	-8.60	91.10	104.00
5	L	106	A	O3'-P-O5'	-8.60	91.10	104.00
5	L	79	A	O3'-P-O5'	-8.60	91.10	104.00
5	L	81	G	O3'-P-O5'	-8.60	91.10	104.00
5	L	82	C	O3'-P-O5'	-8.59	91.11	104.00
5	L	83	U	O3'-P-O5'	-8.59	91.11	104.00
5	L	57	A	O3'-P-O5'	-8.59	91.12	104.00
5	L	58	A	O3'-P-O5'	-8.59	91.12	104.00
5	L	102	U	O3'-P-O5'	-8.59	91.12	104.00
5	L	67	A	O3'-P-O5'	-8.59	91.12	104.00
5	L	56	U	O3'-P-O5'	-8.58	91.12	104.00
5	L	66	A	O3'-P-O5'	-8.58	91.12	104.00
5	L	74	C	O3'-P-O5'	-8.58	91.12	104.00
5	L	99	U	O3'-P-O5'	-8.58	91.13	104.00
5	L	103	A	O3'-P-O5'	-8.58	91.13	104.00
5	L	72	C	O3'-P-O5'	-8.58	91.13	104.00
5	L	105	A	O3'-P-O5'	-8.58	91.13	104.00
5	L	96	A	O3'-P-O5'	-8.58	91.13	104.00
5	L	59	C	O3'-P-O5'	-8.58	91.13	104.00
5	L	98	U	O3'-P-O5'	-8.58	91.13	104.00
5	L	68	U	O3'-P-O5'	-8.57	91.14	104.00
5	L	101	U	O3'-P-O5'	-8.57	91.14	104.00
5	L	55	G	O3'-P-O5'	-8.57	91.14	104.00
5	L	97	U	O3'-P-O5'	-8.57	91.14	104.00
5	L	100	G	O3'-P-O5'	-8.57	91.14	104.00
5	L	61	A	O3'-P-O5'	-8.57	91.15	104.00
5	L	69	G	O3'-P-O5'	-8.57	91.15	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	62	C	O3'-P-O5'	-8.57	91.15	104.00
5	L	60	A	O3'-P-O5'	-8.56	91.16	104.00
1	A	486	PHE	N-CA-C	8.48	120.52	111.28
24	n	428	PRO	N-CA-CB	8.45	112.12	103.25
24	n	208	PRO	N-CA-CB	8.38	110.64	103.35
24	n	257	PRO	N-CA-CB	8.32	110.72	103.31
35	b	5	PRO	N-CA-CB	8.22	112.03	103.23
25	q	238	ASN	CA-C-N	8.13	130.00	119.84
25	q	238	ASN	C-N-CA	8.13	130.00	119.84
24	n	260	PRO	N-CA-CB	8.02	109.98	101.88
35	b	15	TYR	CA-C-O	-7.99	111.81	120.36
35	b	107	SER	N-CA-C	7.95	122.75	112.26
23	v	613	PRO	N-CA-CB	7.94	111.13	103.51
24	n	327	PRO	N-CA-CB	7.63	110.14	103.27
23	v	616	PRO	N-CA-CB	7.60	110.45	103.08
5	L	1111	U	P-O5'-C5'	-7.58	109.53	120.90
35	b	126	ASN	CA-C-O	7.54	128.32	120.40
5	L	1110	U	O3'-P-O5'	-7.34	92.99	104.00
24	n	424	PRO	N-CA-CB	7.30	110.52	103.51
35	b	57	LEU	N-CA-CB	7.26	123.01	110.81
34	a	65	PHE	CA-CB-CG	-7.24	106.56	113.80
35	b	33	ASP	CA-CB-CG	7.15	119.75	112.60
1	A	901	PRO	CA-C-N	-7.12	112.98	120.03
1	A	901	PRO	C-N-CA	-7.12	112.98	120.03
24	n	159	PRO	N-CA-CB	7.09	110.70	103.25
35	b	10	ASP	CA-CB-CG	7.08	119.68	112.60
24	n	373	PRO	N-CA-CB	7.06	110.67	103.25
23	v	722	PRO	N-CA-CB	7.05	111.09	103.33
35	b	42	SER	N-CA-CB	-7.04	99.64	110.42
5	L	1113	U	C3'-C2'-O2'	-7.03	104.05	114.60
35	b	7	ILE	CA-CB-CG1	7.00	122.31	110.40
35	b	3	PHE	N-CA-C	-6.85	98.06	108.67
34	a	73	PHE	CA-C-O	-6.84	112.80	120.32
2	C	463	THR	CA-C-N	-6.78	113.00	119.85
2	C	463	THR	C-N-CA	-6.78	113.00	119.85
23	v	617	PRO	CA-CB-CG	6.77	117.37	104.50
35	b	4	THR	N-CA-CB	-6.77	98.31	110.37
2	C	132	ARG	N-CA-C	6.75	118.71	111.36
1	A	488	ARG	N-CA-C	6.68	118.22	111.07
24	n	162	PRO	N-CA-CB	6.66	110.25	103.25
1	A	898	ILE	CA-C-N	-6.64	113.12	119.76
1	A	898	ILE	C-N-CA	-6.64	113.12	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1107	C	C5'-C4'-O4'	-6.62	99.18	109.10
16	Z	42	ARG	NE-CZ-NH2	6.60	125.14	119.20
33	e	82	LYS	N-CA-C	6.55	124.75	110.80
35	b	130	ILE	CA-C-O	6.53	128.95	120.78
33	g	82	LYS	N-CA-C	6.53	124.70	110.80
35	b	68	PRO	N-CA-CB	6.48	110.06	103.25
24	n	436	PRO	N-CA-CB	6.48	110.13	103.00
5	L	1112	G	P-O3'-C3'	6.31	129.66	120.20
35	b	50	LEU	CA-C-N	6.29	131.52	122.40
35	b	50	LEU	C-N-CA	6.29	131.52	122.40
18	d	60	ARG	N-CA-C	6.24	118.16	111.36
24	n	396	ARG	N-CA-CB	-6.22	107.88	114.10
5	L	1111	U	C5'-C4'-C3'	-6.22	106.67	116.00
16	Z	22	ARG	NE-CZ-NH2	6.19	124.77	119.20
35	b	83	ARG	N-CA-C	6.16	119.86	111.17
23	v	641	PRO	CA-CB-CG	6.14	116.16	104.50
24	n	178	ILE	CB-CA-C	-6.10	102.46	111.19
24	n	340	PRO	N-CA-CB	6.08	109.63	103.25
35	b	111	PHE	CA-CB-CG	6.08	119.88	113.80
35	b	62	ASN	CA-CB-CG	6.05	118.65	112.60
35	b	132	ASN	OD1-CG-ND2	6.04	128.64	122.60
35	b	85	ASN	N-CA-CB	-5.98	102.66	111.51
2	C	481	ALA	CB-CA-C	-5.96	109.69	116.54
35	b	127	LEU	CA-C-N	-5.96	114.37	122.77
35	b	127	LEU	C-N-CA	-5.96	114.37	122.77
24	n	373	PRO	CA-CB-CG	5.94	115.79	104.50
26	t	105	PRO	CA-CB-CG	5.93	115.76	104.50
5	L	1106	G	O3'-P-O5'	-5.90	95.15	104.00
34	a	66	LYS	N-CA-C	-5.90	104.76	111.07
23	v	617	PRO	N-CA-CB	5.89	109.44	103.25
17	c	229	ASP	N-CA-C	5.87	119.48	111.39
24	n	274	HIS	CA-CB-CG	-5.83	107.97	113.80
6	M	502	C	OP1-P-O3'	5.83	125.49	108.00
24	n	436	PRO	CA-CB-CG	5.79	115.51	104.50
12	Q	213	SER	N-CA-C	5.78	117.58	111.28
35	b	60	THR	CA-C-O	5.75	127.65	121.55
35	b	44	PRO	CB-CA-C	-5.74	106.17	111.40
1	A	668	ARG	N-CA-C	5.72	117.59	111.36
5	L	1107	C	P-O3'-C3'	5.70	128.75	120.20
16	Z	16	GLU	CA-C-N	5.68	128.35	120.29
16	Z	16	GLU	C-N-CA	5.68	128.35	120.29
5	L	1111	U	O4'-C1'-C2'	-5.65	101.95	107.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	b	158	ASN	CB-CA-C	-5.62	102.06	110.16
5	L	1108	A	N9-C1'-C2'	5.62	120.42	112.00
16	Z	105	GLN	CB-CG-CD	5.60	122.12	112.60
16	Z	91	GLY	CA-C-N	5.59	128.09	120.54
16	Z	91	GLY	C-N-CA	5.59	128.09	120.54
2	C	458	ILE	CA-C-N	-5.57	112.88	119.84
2	C	458	ILE	C-N-CA	-5.57	112.88	119.84
24	n	380	HIS	CA-CB-CG	-5.49	108.31	113.80
26	t	77	PRO	CA-CB-CG	5.47	114.89	104.50
35	b	15	TYR	O-C-N	5.46	129.45	123.22
16	Z	8	ASP	CA-CB-CG	-5.42	107.18	112.60
33	e	81	GLY	N-CA-C	5.41	119.50	112.25
33	g	81	GLY	N-CA-C	5.41	119.50	112.25
35	b	50	LEU	N-CA-C	-5.40	106.19	112.89
35	b	71	SER	N-CA-CB	-5.40	102.67	110.45
34	a	93	ARG	CA-CB-CG	-5.38	103.33	114.10
35	b	141	ARG	CD-NE-CZ	5.36	131.90	124.40
24	n	219	GLN	CA-CB-CG	-5.35	103.39	114.10
35	b	133	GLN	CA-CB-CG	-5.33	103.44	114.10
10	O	444	PRO	CA-N-CD	-5.30	104.58	112.00
34	a	41	MET	N-CA-C	5.30	117.47	111.11
11	P	172	TRP	N-CA-C	5.28	117.04	111.28
5	L	1113	U	O4'-C1'-C2'	-5.27	100.53	105.80
35	b	155	ASP	CA-C-N	5.27	130.04	122.40
35	b	155	ASP	C-N-CA	5.27	130.04	122.40
35	b	44	PRO	CA-C-O	-5.27	114.32	120.85
35	b	38	THR	CA-CB-OG1	5.26	117.49	109.60
23	v	641	PRO	N-CA-CB	5.25	108.77	103.25
16	Z	182	GLN	N-CA-C	5.25	117.08	111.36
24	n	295	SER	N-CA-CB	-5.22	102.79	110.26
12	Q	291	ILE	N-CA-C	5.21	120.14	108.88
35	b	100	ASN	CA-CB-CG	5.21	117.81	112.60
34	a	71	GLN	N-CA-C	5.20	117.58	109.52
35	b	134	VAL	CA-C-N	5.19	127.76	120.28
35	b	134	VAL	C-N-CA	5.19	127.76	120.28
24	n	258	THR	N-CA-CB	-5.17	102.52	110.01
16	Z	46	GLN	OE1-CD-NE2	-5.15	117.45	122.60
24	n	219	GLN	N-CA-CB	-5.14	102.53	110.25
16	Z	108	ARG	NE-CZ-NH2	5.13	123.81	119.20
10	O	443	ASN	CA-C-N	-5.12	113.44	119.84
10	O	443	ASN	C-N-CA	-5.12	113.44	119.84
16	Z	223	HIS	CB-CG-CD2	-5.12	124.55	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Z	236	ASN	CA-C-N	5.11	127.84	120.38
16	Z	236	ASN	C-N-CA	5.11	127.84	120.38
16	Z	84	ASN	OD1-CG-ND2	-5.11	117.49	122.60
35	b	56	ILE	CA-C-O	-5.08	115.17	120.76
24	n	250	PRO	N-CA-CB	5.06	107.70	103.25
34	a	68	GLN	N-CA-C	5.06	119.45	113.28
23	v	721	GLY	CA-C-N	5.06	124.67	119.05
23	v	721	GLY	C-N-CA	5.06	124.67	119.05
5	L	19	U	C2'-C3'-O3'	5.05	117.08	109.50
30	x	42	ASP	N-CA-C	5.05	117.20	110.53
30	j	42	ASP	N-CA-C	5.04	117.19	110.53
24	n	68	PRO	N-CA-C	5.04	120.64	114.35
11	P	106	LEU	CB-CA-C	-5.03	110.39	117.23
31	l	81	ALA	CA-C-N	5.02	126.12	119.84
31	l	81	ALA	C-N-CA	5.02	126.12	119.84
35	b	107	SER	N-CA-CB	-5.02	102.93	111.17
35	b	148	VAL	CA-C-N	5.01	124.67	119.56
35	b	148	VAL	C-N-CA	5.01	124.67	119.56
24	n	185	HIS	CA-CB-CG	-5.01	108.79	113.80
31	y	81	ALA	CA-C-N	5.00	126.09	119.84
31	y	81	ALA	C-N-CA	5.00	126.09	119.84

There are no chirality outliers.

All (41) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1346	PHE	Peptide
1	A	1375	LEU	Peptide
1	A	1377	SER	Peptide
1	A	257	ASN	Peptide
1	A	483	PRO	Mainchain
1	A	539	PRO	Peptide
1	A	773	SER	Peptide
2	C	170	LEU	Peptide
2	C	534	THR	Peptide
20	G	16	LEU	Peptide
10	O	123	PRO	Peptide
10	O	263	VAL	Peptide
10	O	278	ASP	Peptide
10	O	435	GLU	Peptide
10	O	436	SER	Peptide

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Mol	Chain	Res	Type	Group
10	O	437	GLU	Peptide
11	P	85	SER	Peptide
12	Q	103	GLU	Peptide
12	Q	291	ILE	Peptide
12	Q	45	HIS	Peptide
16	Z	211	GLY	Peptide
16	Z	219	SER	Peptide
16	Z	227	TYR	Sidechain
16	Z	232	GLU	Peptide
16	Z	241	ASN	Peptide
17	c	81	PRO	Peptide
33	e	81	GLY	Peptide,Mainchain
33	g	81	GLY	Peptide,Mainchain
30	j	41	ASP	Peptide
31	l	81	ALA	Peptide,Mainchain
24	n	290	ASP	Peptide
24	n	305	GLY	Peptide
24	n	67	GLY	Peptide,Mainchain
30	x	41	ASP	Peptide
31	y	81	ALA	Peptide,Mainchain

4.2 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	15775	0	15756	748	0
2	C	7019	0	7201	319	0
3	D	2465	0	1251	79	0
4	E	2192	0	1106	134	0
5	L	2673	0	1360	331	0
6	M	608	0	307	45	0
7	B	275	0	137	20	0
8	N	312	0	156	19	0
9	J	190	0	186	15	0
10	O	2646	0	2639	131	0
11	P	1583	0	1608	91	0
12	Q	1472	0	1485	183	0
13	R	2089	0	2053	121	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	S	560	0	545	68	0
15	T	1291	0	1312	56	0
16	Z	3651	0	3707	187	0
17	c	2971	0	2336	81	0
18	d	3590	0	2359	96	0
19	F	937	0	962	59	0
20	G	342	0	360	16	0
21	H	810	0	799	36	0
22	I	822	0	845	72	0
23	v	3580	0	1298	68	0
24	n	1890	0	1407	89	0
25	o	830	0	663	6	0
25	p	843	0	675	8	0
25	q	2345	0	1636	43	0
25	r	823	0	654	7	0
26	t	926	0	606	15	0
27	k	631	0	670	3	0
27	s	610	0	640	17	0
28	i	575	0	597	21	0
28	u	575	0	597	21	0
29	h	554	0	556	17	0
29	w	554	0	556	18	0
30	j	529	0	557	2	0
30	x	529	0	557	3	0
31	l	625	0	647	7	0
31	y	625	0	647	8	0
32	m	644	0	686	14	0
32	z	644	0	686	14	0
33	e	528	0	573	37	0
33	g	741	0	778	18	0
34	a	513	0	402	13	0
35	b	841	0	614	17	0
36	C	32	0	12	1	0
37	C	1	0	0	0	0
37	E	5	0	0	0	0
38	F	1	0	0	0	0
38	Q	2	0	0	0	0
38	R	1	0	0	0	0
38	T	3	0	0	0	0
All	All	75273	0	65184	2725	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 (2725) 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:426:PRO:HB3	16:Z:201:ARG:CG	1.38	1.50
1:A:1327:THR:CG2	5:L:35:U:H5'	1.41	1.48
1:A:1327:THR:HG22	5:L:35:U:C5'	1.47	1.44
5:L:15:C:H1'	5:L:16:U:C5	1.50	1.42
23:v:729:TYR:CZ	23:v:748:UNK:CB	2.03	1.42
16:Z:192:GLU:CA	16:Z:195:GLU:OE2	1.70	1.37
16:Z:170:HIS:CE1	16:Z:174:TRP:CZ3	2.20	1.30
12:Q:215:PRO:HB3	13:R:171:ASP:OD1	1.28	1.29
23:v:729:TYR:CE1	23:v:748:UNK:CB	2.14	1.29
24:n:59:ARG:O	24:n:62:THR:HG23	1.26	1.27
2:C:468:LEU:CD1	2:C:492:LEU:N	1.98	1.27
1:A:1904:ARG:HA	6:M:492:U:OP1	1.35	1.25
16:Z:192:GLU:HA	16:Z:195:GLU:OE2	1.08	1.25
25:q:422:GLY:O	25:q:442:SER:CB	1.85	1.24
2:C:126:MET:HE1	2:C:132:ARG:NH1	1.54	1.23
1:A:426:PRO:CB	16:Z:201:ARG:HG3	1.66	1.22
12:Q:212:ALA:O	13:R:237:ARG:NH2	1.71	1.22
1:A:2027:LEU:HD22	33:e:57:ARG:NH1	1.51	1.21
1:A:512:GLU:OE1	7:B:89:A:N1	1.73	1.21
16:Z:170:HIS:CE1	16:Z:174:TRP:HZ3	1.59	1.20
4:E:91:A:C2	18:d:99:ILE:HD11	1.77	1.19
2:C:462:SER:O	2:C:464:PRO:HD3	1.39	1.19
27:s:98:GLU:O	35:b:53:PRO:CB	1.92	1.17
5:L:14:C:C2'	5:L:15:C:H5'	1.75	1.17
5:L:1:A:H1'	23:v:504:UNK:N	1.56	1.17
24:n:251:ALA:HA	24:n:267:LEU:CB	1.75	1.16
16:Z:177:LEU:CD2	16:Z:194:LEU:HD21	1.76	1.15
5:L:5:A:C5'	22:I:114:THR:HG21	1.76	1.14
5:L:15:C:H41	22:I:209:ARG:CG	1.60	1.14
1:A:899:PRO:HD3	1:A:1006:ARG:HH22	1.03	1.14
5:L:1109:C:N4	34:a:109:LYS:H	1.48	1.11
2:C:468:LEU:HD12	2:C:491:GLY:CA	1.80	1.11
5:L:1111:U:C6	5:L:1111:U:H5''	1.86	1.11
1:A:928:ARG:NH2	5:L:32:G:C8	2.18	1.10
23:v:729:TYR:CE2	23:v:748:UNK:CB	2.33	1.10
5:L:5:A:H5'	22:I:114:THR:CG2	1.80	1.09
26:t:7:VAL:HG11	26:t:154:VAL:CB	1.82	1.09
16:Z:170:HIS:CE1	16:Z:174:TRP:CE3	2.41	1.08
1:A:2027:LEU:HD22	33:e:57:ARG:HH12	0.97	1.08
12:Q:49:SER:OG	12:Q:52:SER:CB	2.00	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Z:178:ARG:HG3	16:Z:198:PHE:CE2	1.87	1.08
15:T:126:ARG:HG3	24:n:72:TRP:CE2	1.88	1.07
2:C:126:MET:HE1	2:C:132:ARG:HH12	1.06	1.07
2:C:126:MET:CE	2:C:132:ARG:NH1	2.17	1.07
16:Z:178:ARG:CB	16:Z:198:PHE:HZ	1.68	1.07
4:E:21:U:OP2	24:n:54:SER:OG	1.73	1.06
16:Z:181:LEU:HG	16:Z:194:LEU:HD13	1.37	1.06
2:C:468:LEU:HD12	2:C:491:GLY:HA3	1.27	1.06
4:E:91:A:C2	18:d:99:ILE:CD1	2.40	1.05
1:A:2027:LEU:CD2	33:e:57:ARG:HH12	1.69	1.05
5:L:1102:C:H2'	5:L:1103:C:C6	1.91	1.05
16:Z:177:LEU:HD22	16:Z:194:LEU:HD21	1.35	1.04
14:S:134:GLY:O	14:S:135:ARG:HB2	1.54	1.04
1:A:899:PRO:HD3	1:A:1006:ARG:NH2	1.73	1.04
23:v:730:GLN:HA	23:v:733:ILE:HD11	1.37	1.04
5:L:20:G:H21	14:S:6:ARG:CB	1.70	1.04
5:L:1116:A:H2'	5:L:1117:G:H8	1.18	1.04
1:A:512:GLU:OE2	7:B:89:A:N6	1.90	1.03
15:T:120:CYS:HB2	15:T:122:CYS:HB3	1.37	1.03
25:o:51:VAL:HG21	25:p:20:ARG:CB	1.89	1.03
1:A:426:PRO:CB	16:Z:201:ARG:CG	2.29	1.03
4:E:29:U:H2'	4:E:30:G:H5'	1.41	1.03
5:L:14:C:H2'	5:L:15:C:C5'	1.89	1.03
27:s:99:ASP:CB	35:b:53:PRO:CB	2.35	1.03
1:A:431:ILE:HG23	16:Z:182:GLN:HG2	1.41	1.02
2:C:286:LEU:HD21	16:Z:183:THR:HG22	1.39	1.02
3:D:165:A:H4'	3:D:166:U:C5'	1.89	1.02
16:Z:174:TRP:CZ2	16:Z:197:LEU:HD11	1.93	1.02
1:A:512:GLU:CD	7:B:89:A:H61	1.67	1.02
16:Z:149:ARG:HH11	16:Z:193:SER:HB3	1.25	1.02
1:A:905:TYR:HE2	1:A:907:ASN:HB2	1.23	1.01
5:L:33:U:OP1	20:G:17:MET:HG3	1.60	1.01
16:Z:149:ARG:HH11	16:Z:193:SER:CB	1.73	1.01
23:v:718:SER:OG	23:v:725:THR:HG21	1.61	1.01
24:n:302:PHE:CG	24:n:306:SER:O	2.13	1.01
1:A:1904:ARG:CA	6:M:492:U:OP1	2.08	1.01
4:E:52:G:H21	14:S:5:HIS:CE1	1.77	1.00
5:L:110:A:C4'	5:L:111:C:H5'	1.92	1.00
5:L:110:A:H4'	5:L:111:C:C5'	1.89	1.00
16:Z:149:ARG:NH1	16:Z:193:SER:HB3	1.77	1.00
3:D:165:A:C4'	3:D:166:U:H5'	1.92	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2027:LEU:HD22	33:e:57:ARG:CZ	1.91	1.00
5:L:1116:A:H2'	5:L:1117:G:C8	1.95	1.00
24:n:55:GLU:OE2	24:n:58:ARG:NE	1.95	1.00
1:A:899:PRO:CD	1:A:1006:ARG:HH22	1.74	1.00
2:C:177:TYR:CE1	2:C:548:ARG:HG3	1.97	1.00
12:Q:226:LEU:CD1	12:Q:227:LEU:HD23	1.91	0.99
5:L:1114:G:O6	34:a:38:LYS:NZ	1.95	0.99
5:L:1097:G:N2	5:L:1119:C:O2	1.96	0.99
16:Z:181:LEU:HD21	16:Z:191:ARG:HG3	1.44	0.99
24:n:59:ARG:O	24:n:62:THR:CG2	2.10	0.99
11:P:174:ASN:HD21	11:P:177:GLY:CA	1.76	0.98
14:S:4:SER:O	14:S:6:ARG:HD3	1.63	0.98
16:Z:178:ARG:CG	16:Z:198:PHE:CZ	2.46	0.98
24:n:68:PRO:HD2	24:n:69:TRP:CE3	1.96	0.98
12:Q:215:PRO:CB	13:R:171:ASP:OD1	2.11	0.98
16:Z:170:HIS:HE1	16:Z:174:TRP:CZ3	1.70	0.98
2:C:126:MET:SD	2:C:132:ARG:NH1	2.37	0.97
5:L:15:C:C1'	5:L:16:U:C5	2.47	0.97
12:Q:226:LEU:HD21	12:Q:262:PHE:CD1	2.00	0.97
4:E:65:U:O2'	4:E:67:C:OP2	1.81	0.97
1:A:426:PRO:HB3	16:Z:201:ARG:HG2	1.45	0.97
11:P:174:ASN:HD21	11:P:177:GLY:HA2	1.27	0.97
5:L:33:U:OP1	20:G:17:MET:CG	2.13	0.96
2:C:468:LEU:HD11	2:C:492:LEU:N	1.78	0.96
5:L:15:C:N4	22:I:209:ARG:HB2	1.80	0.96
12:Q:212:ALA:HB1	13:R:237:ARG:HH12	1.30	0.96
12:Q:216:GLU:OE2	12:Q:240:LEU:HG	1.64	0.96
4:E:91:A:N1	18:d:99:ILE:HD11	1.80	0.96
5:L:1116:A:C2	5:L:1117:G:C4	2.54	0.95
19:F:4:ARG:HH12	19:F:5:LYS:HZ2	1.14	0.95
5:L:15:C:H1'	5:L:16:U:H5	1.28	0.95
1:A:899:PRO:CD	1:A:1006:ARG:NH2	2.28	0.95
12:Q:226:LEU:HD11	12:Q:227:LEU:HD23	1.49	0.95
12:Q:226:LEU:CG	12:Q:227:LEU:HD23	1.97	0.94
16:Z:199:GLU:O	16:Z:202:GLN:HG2	1.67	0.94
2:C:468:LEU:HD12	2:C:492:LEU:N	1.79	0.94
2:C:734:CYS:HG	2:C:755:TYR:HH	0.95	0.94
5:L:1111:U:H5''	5:L:1111:U:H6	1.25	0.94
5:L:1111:U:O4'	31:y:30:ARG:HD3	1.67	0.94
3:D:96:U:H3	7:B:99:G:H22	1.05	0.93
5:L:1102:C:H2'	5:L:1103:C:C5	2.03	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:110:A:C2	32:z:2:LYS:CE	2.51	0.93
16:Z:192:GLU:HA	16:Z:195:GLU:CD	1.91	0.93
6:M:498:C:O2'	21:H:2:SER:HA	1.67	0.93
1:A:902:PRO:HD2	1:A:905:TYR:HD1	1.34	0.93
3:D:165:A:C2	32:m:2:LYS:CE	2.51	0.93
5:L:14:C:H2'	5:L:15:C:H5'	0.93	0.93
5:L:1116:A:C6	5:L:1117:G:C6	2.57	0.93
5:L:15:C:H41	22:I:209:ARG:HG2	1.32	0.92
23:v:729:TYR:CD1	23:v:748:UNK:CB	2.52	0.92
1:A:1327:THR:HG22	5:L:35:U:H5''	1.50	0.92
18:d:199:MET:HB2	18:d:242:GLU:HG3	1.51	0.92
2:C:468:LEU:HD12	2:C:491:GLY:C	1.94	0.92
4:E:31:G:O6	12:Q:47:LYS:NZ	2.02	0.92
25:q:468:GLN:CB	25:q:481:CYS:SG	2.58	0.92
5:L:5:A:H5'	22:I:114:THR:CB	2.00	0.92
12:Q:49:SER:OG	12:Q:52:SER:HB2	1.68	0.92
12:Q:214:ILE:HD11	12:Q:218:LYS:CG	1.99	0.91
5:L:1099:G:C5	5:L:1100:A:C8	2.58	0.91
26:t:81:ASP:CB	26:t:85:THR:CB	2.49	0.91
1:A:2027:LEU:CD2	33:e:57:ARG:HH22	1.82	0.91
6:M:498:C:OP1	19:F:41:ILE:HD11	1.70	0.91
23:v:682:LYS:O	23:v:685:GLU:CG	2.18	0.91
1:A:140:ARG:O	1:A:144:ASN:HB2	1.71	0.90
4:E:63:G:HO2'	14:S:8:GLN:HG3	1.37	0.90
4:E:89:U:H5'	5:L:17:U:OP2	1.71	0.90
5:L:15:C:O2'	5:L:16:U:H5''	1.71	0.90
4:E:91:A:C6	18:d:99:ILE:HD11	2.06	0.90
5:L:20:G:H21	14:S:6:ARG:HB2	1.37	0.90
5:L:1101:C:N4	34:a:38:LYS:HZ3	1.68	0.90
17:c:229:ASP:HB2	22:I:151:LYS:HB3	1.52	0.90
1:A:312:TYR:O	1:A:319:ARG:NH2	2.05	0.90
23:v:726:ARG:NH2	23:v:760:UNK:CB	2.35	0.90
3:D:165:A:C2	32:m:2:LYS:HE2	2.08	0.89
5:L:15:C:O2'	5:L:16:U:C6	2.23	0.89
5:L:110:A:H4'	5:L:111:C:H5'	0.95	0.89
12:Q:255:SER:OG	12:Q:257:GLU:HG2	1.70	0.89
2:C:468:LEU:CD1	2:C:492:LEU:H	1.79	0.89
16:Z:178:ARG:HG3	16:Z:198:PHE:HE2	1.33	0.89
4:E:63:G:O2'	14:S:8:GLN:HG3	1.72	0.89
1:A:900:PHE:CD2	1:A:901:PRO:HD2	2.06	0.89
5:L:15:C:N4	22:I:209:ARG:CG	2.35	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:v:730:GLN:HA	23:v:733:ILE:CD1	2.02	0.89
1:A:1327:THR:HG22	5:L:35:U:H5'	0.90	0.89
5:L:5:A:H5'	22:I:114:THR:HG21	1.37	0.89
12:Q:242:VAL:O	13:R:161:ARG:NH2	2.05	0.89
5:L:110:A:C2	32:z:2:LYS:HE2	2.07	0.88
1:A:928:ARG:HG2	5:L:30:A:N3	1.89	0.88
4:E:88:U:H5''	5:L:17:U:H5	1.37	0.88
10:O:152:ASN:HD21	10:O:409:LYS:HB3	1.39	0.88
5:L:1099:G:C6	5:L:1100:A:N7	2.41	0.88
1:A:905:TYR:HB3	1:A:908:ASP:HB2	1.56	0.88
5:L:1:A:C1'	23:v:504:UNK:N	2.37	0.88
24:n:184:ASP:O	24:n:185:HIS:CG	2.27	0.88
1:A:2027:LEU:HD22	33:e:57:ARG:NH2	1.87	0.87
11:P:174:ASN:ND2	11:P:177:GLY:HA2	1.89	0.87
1:A:756:LEU:HD11	14:S:8:GLN:NE2	1.89	0.87
5:L:5:A:P	22:I:114:THR:HG21	2.14	0.87
5:L:1109:C:H41	34:a:109:LYS:H	1.21	0.87
12:Q:212:ALA:HB1	13:R:237:ARG:NH1	1.90	0.87
3:D:165:A:C2	32:m:2:LYS:HE3	2.10	0.86
2:C:206:LYS:HD3	2:C:208:ARG:HE	1.40	0.86
24:n:245:HIS:O	24:n:246:LEU:CB	2.24	0.86
1:A:737:ARG:HH11	1:A:737:ARG:HG2	1.37	0.86
1:A:972:MET:CE	6:M:505:A:C2	2.57	0.86
5:L:1099:G:N7	5:L:1100:A:C8	2.43	0.86
4:E:63:G:N2	14:S:6:ARG:HG2	1.90	0.85
4:E:50:G:N3	19:F:65:ASN:ND2	2.24	0.85
4:E:84:C:O2'	4:E:85:C:OP1	1.94	0.85
16:Z:192:GLU:C	16:Z:195:GLU:OE2	2.19	0.85
23:v:730:GLN:O	23:v:733:ILE:HD12	1.76	0.85
3:D:165:A:H4'	3:D:166:U:H5'	0.95	0.85
1:A:2027:LEU:O	33:e:71:ASN:CG	2.19	0.85
1:A:2030:PRO:HB3	33:e:57:ARG:HE	1.41	0.85
16:Z:178:ARG:CB	16:Z:198:PHE:CZ	2.58	0.85
2:C:468:LEU:CD1	2:C:491:GLY:C	2.47	0.85
5:L:1099:G:C5	5:L:1100:A:N7	2.44	0.85
10:O:223:HIS:ND1	10:O:245:ASP:OD2	2.10	0.84
16:Z:178:ARG:HA	16:Z:198:PHE:CZ	2.12	0.84
24:n:155:ILE:CG1	24:n:453:VAL:O	2.25	0.84
24:n:250:PRO:O	24:n:267:LEU:CB	2.25	0.84
5:L:15:C:N4	22:I:209:ARG:CB	2.39	0.84
12:Q:37:CYS:HB3	12:Q:64:CYS:SG	2.16	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Z:170:HIS:NE2	16:Z:174:TRP:CZ3	2.45	0.84
1:A:972:MET:HE1	6:M:505:A:C2	2.12	0.84
5:L:18:U:O2'	5:L:19:U:OP2	1.95	0.84
5:L:20:G:N2	14:S:6:ARG:CB	2.38	0.84
5:L:110:A:C2	32:z:2:LYS:HE3	2.10	0.84
4:E:31:G:O6	12:Q:47:LYS:CE	2.25	0.84
12:Q:226:LEU:HG	12:Q:227:LEU:HD23	1.59	0.84
16:Z:181:LEU:HG	16:Z:194:LEU:CD1	2.07	0.84
16:Z:192:GLU:OE1	16:Z:192:GLU:N	2.11	0.84
16:Z:152:ILE:HD13	16:Z:194:LEU:HA	1.60	0.84
28:i:86:ASN:HD21	29:h:32:LYS:HD3	1.43	0.83
1:A:1870:VAL:HB	5:L:46:C:H4'	1.59	0.83
16:Z:197:LEU:HD12	16:Z:197:LEU:O	1.77	0.83
1:A:1323:SER:O	1:A:1370:ARG:NH2	2.11	0.83
2:C:697:ARG:NH1	2:C:852:THR:OG1	2.12	0.83
25:q:51:VAL:HG13	25:r:20:ARG:CB	2.09	0.83
1:A:972:MET:CE	6:M:505:A:N1	2.42	0.83
1:A:1851:PHE:O	1:A:1881:THR:HA	1.77	0.83
1:A:426:PRO:HG2	16:Z:201:ARG:NE	1.94	0.83
8:N:113:U:C6	13:R:183:PHE:CE2	2.67	0.83
5:L:15:C:H1'	5:L:16:U:C6	2.13	0.83
5:L:18:U:OP1	22:I:199:LYS:NZ	2.11	0.83
23:v:724:VAL:O	23:v:727:GLU:CG	2.27	0.83
1:A:1642:LYS:HE3	19:F:7:ILE:HA	1.58	0.82
16:Z:178:ARG:HG3	16:Z:198:PHE:CZ	2.11	0.82
1:A:936:GLU:HG2	1:A:986:PRO:HB3	1.60	0.82
4:E:57:U:OP1	19:F:62:ARG:HA	1.79	0.82
24:n:405:SER:O	24:n:406:ARG:CB	2.26	0.82
15:T:27:GLU:OE2	15:T:31:ARG:NH1	2.12	0.82
2:C:286:LEU:HD23	16:Z:182:GLN:HB3	1.60	0.82
5:L:20:G:H21	14:S:6:ARG:HB3	1.45	0.82
16:Z:180:ILE:HG22	16:Z:186:LEU:HD21	1.61	0.82
26:t:114:LEU:O	26:t:117:VAL:HG12	1.78	0.82
5:L:15:C:N4	22:I:209:ARG:HG2	1.93	0.82
16:Z:152:ILE:CD1	16:Z:194:LEU:HA	2.09	0.82
3:D:43:G:O2'	3:D:45:A:H5'	1.78	0.82
5:L:1101:C:H41	34:a:38:LYS:HZ3	1.27	0.82
2:C:462:SER:O	2:C:464:PRO:CD	2.26	0.82
2:C:462:SER:C	2:C:464:PRO:HD3	2.05	0.82
12:Q:53:ASN:HD22	12:Q:54:ASN:H	1.26	0.82
19:F:4:ARG:HH12	19:F:5:LYS:NZ	1.77	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:PRO:CG	16:Z:201:ARG:NE	2.43	0.81
1:A:972:MET:HE1	6:M:505:A:H2	1.45	0.81
1:A:716:ARG:HD2	3:D:112:C:H1'	1.61	0.81
1:A:1485:ASP:O	1:A:1490:ARG:NH2	2.11	0.81
12:Q:209:ASN:ND2	12:Q:288:ILE:O	2.12	0.81
28:u:86:ASN:HD21	29:w:32:LYS:HD3	1.43	0.81
12:Q:49:SER:OG	12:Q:52:SER:N	2.13	0.81
15:T:31:ARG:HH11	15:T:31:ARG:HG3	1.44	0.81
16:Z:177:LEU:HD21	16:Z:194:LEU:HD21	1.61	0.81
1:A:1327:THR:CG2	5:L:35:U:C5'	2.26	0.81
4:E:88:U:H5''	5:L:17:U:C5	2.15	0.81
12:Q:207:LEU:HB2	12:Q:249:GLY:O	1.81	0.81
16:Z:178:ARG:CG	16:Z:198:PHE:CE2	2.61	0.81
23:v:724:VAL:HA	23:v:727:GLU:CG	2.11	0.81
27:s:19:LYS:NZ	35:b:34:LEU:CB	2.44	0.81
12:Q:209:ASN:ND2	12:Q:288:ILE:HG22	1.95	0.81
16:Z:168:LYS:NZ	16:Z:171:ASP:HB2	1.96	0.81
4:E:54:U:O4	17:c:165:LYS:HE2	1.81	0.81
1:A:728:ASN:ND2	4:E:72:C:O2'	2.14	0.80
4:E:63:G:O2'	14:S:8:GLN:CG	2.28	0.80
1:A:898:ILE:HA	1:A:1006:ARG:NH1	1.95	0.80
5:L:20:G:N2	14:S:6:ARG:HB3	1.96	0.80
6:M:498:C:C2'	6:M:499:U:H5'	2.11	0.80
29:h:74:ARG:NH2	33:g:64:HIS:O	2.14	0.80
4:E:29:U:C2'	4:E:30:G:H5'	2.11	0.80
25:q:178:LYS:HB3	25:q:468:GLN:CB	2.12	0.80
1:A:518:VAL:HG12	1:A:685:HIS:HB3	1.62	0.80
12:Q:56:ILE:HD12	13:R:105:ARG:NH2	1.97	0.80
12:Q:215:PRO:HG3	12:Q:217:TRP:CZ3	2.16	0.80
29:w:74:ARG:NH2	33:e:64:HIS:O	2.14	0.80
12:Q:256:SER:O	12:Q:259:GLY:N	2.14	0.80
13:R:161:ARG:O	13:R:165:SER:HB3	1.82	0.80
5:L:19:U:O2	11:P:176:ASN:HB2	1.82	0.80
10:O:433:THR:OG1	10:O:435:GLU:OE1	2.00	0.80
1:A:911:ILE:HG23	1:A:997:GLN:CG	2.12	0.80
5:L:1111:U:C6	5:L:1111:U:C5'	2.65	0.80
12:Q:222:THR:HA	12:Q:225:GLN:NE2	1.96	0.80
1:A:1696:SER:HA	1:A:1759:TYR:HE1	1.45	0.79
2:C:468:LEU:CD2	2:C:493:LEU:HD23	2.12	0.79
16:Z:178:ARG:CA	16:Z:198:PHE:HZ	1.94	0.79
5:L:1099:G:N3	5:L:1099:G:H5''	1.97	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Q:209:ASN:ND2	12:Q:209:ASN:O	2.15	0.79
5:L:17:U:H4'	5:L:18:U:OP2	1.83	0.79
25:q:369:PHE:O	25:q:370:PRO:CB	2.30	0.79
1:A:326:ASN:ND2	2:C:924:GLY:O	2.15	0.79
16:Z:180:ILE:O	16:Z:184:GLN:HB2	1.82	0.79
1:A:899:PRO:O	1:A:998:TYR:OH	2.01	0.79
5:L:18:U:H6	5:L:18:U:H5'	1.47	0.79
1:A:1044:GLY:HA3	1:A:1176:GLU:HG3	1.64	0.79
5:L:119:G:H5'	33:e:99:ASP:OD2	1.82	0.78
8:N:110:A:C2	13:R:46:ARG:NH1	2.47	0.78
3:D:174:G:H5'	33:g:99:ASP:OD2	1.82	0.78
5:L:1109:C:N4	34:a:109:LYS:N	2.30	0.78
12:Q:214:ILE:HD11	12:Q:218:LYS:HG2	1.62	0.78
1:A:928:ARG:NH2	5:L:32:G:H8	1.79	0.78
5:L:15:C:H41	22:I:209:ARG:CD	1.96	0.78
16:Z:174:TRP:CZ2	16:Z:197:LEU:CD1	2.67	0.78
12:Q:39:LEU:HD11	12:Q:111:ARG:HG3	1.65	0.78
13:R:25:GLN:HG3	21:H:24:GLY:HA3	1.65	0.78
13:R:96:GLU:OE2	13:R:187:LYS:NZ	2.17	0.78
27:s:102:LEU:C	35:b:13:GLN:HB3	2.07	0.78
1:A:796:ASN:ND2	1:A:861:GLN:OE1	2.17	0.78
1:A:905:TYR:HE2	1:A:907:ASN:CB	1.94	0.78
12:Q:217:TRP:CD1	13:R:187:LYS:HE2	2.18	0.78
5:L:5:A:H5'	22:I:114:THR:HB	1.66	0.78
16:Z:192:GLU:CB	16:Z:195:GLU:OE2	2.30	0.78
18:d:250:PHE:HD2	18:d:266:LEU:HD22	1.48	0.78
24:n:382:SER:OG	24:n:432:VAL:HG13	1.84	0.78
1:A:487:ASN:OD1	1:A:488:ARG:HG2	1.84	0.78
24:n:183:ASN:HA	24:n:208:PRO:CG	2.13	0.77
1:A:426:PRO:HB3	16:Z:201:ARG:HG3	0.79	0.77
1:A:905:TYR:CE2	1:A:907:ASN:HB2	2.14	0.77
5:L:1100:A:H61	5:L:1116:A:H61	1.30	0.77
15:T:31:ARG:NH1	15:T:31:ARG:HG3	1.99	0.77
1:A:1879:ILE:O	1:A:1891:LEU:HA	1.84	0.77
5:L:1102:C:H2'	5:L:1103:C:H6	1.42	0.77
4:E:31:G:O6	12:Q:47:LYS:HE2	1.85	0.77
4:E:90:U:OP2	18:d:104:ARG:NH2	2.17	0.77
12:Q:226:LEU:HD21	12:Q:262:PHE:CE1	2.18	0.77
12:Q:104:ALA:HB1	12:Q:110:LYS:HB3	1.66	0.77
1:A:431:ILE:CG2	16:Z:182:GLN:HG2	2.13	0.77
4:E:29:U:OP2	12:Q:51:ARG:NH2	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Q:56:ILE:CD1	13:R:105:ARG:NH2	2.47	0.77
1:A:1365:THR:O	1:A:1369:ASN:ND2	2.18	0.76
1:A:1906:SER:OG	6:M:493:A:OP1	2.02	0.76
2:C:501:ILE:HD13	2:C:567:ILE:HG23	1.65	0.76
5:L:1100:A:N1	5:L:1116:A:N1	2.33	0.76
6:M:498:C:H2'	6:M:499:U:H5'	1.67	0.76
1:A:900:PHE:CE2	1:A:901:PRO:HD2	2.20	0.76
2:C:365:GLU:HG3	2:C:366:ASN:H	1.49	0.76
1:A:227:GLU:OE2	1:A:231:ARG:NH1	2.18	0.76
1:A:484:PHE:CE1	3:D:81:A:N6	2.53	0.76
1:A:771:PRO:O	10:O:309:ARG:NH2	2.18	0.76
1:A:1650:ARG:NH2	6:M:495:A:C8	2.54	0.76
19:F:46:PRO:HG2	19:F:106:TYR:HE2	1.51	0.76
16:Z:178:ARG:CA	16:Z:198:PHE:CZ	2.69	0.76
1:A:900:PHE:CD2	1:A:901:PRO:CD	2.67	0.76
5:L:1109:C:H41	34:a:109:LYS:N	1.84	0.76
13:R:96:GLU:HG2	13:R:188:TYR:HE2	1.50	0.76
1:A:1403:SER:OG	1:A:1429:MET:SD	2.44	0.76
12:Q:209:ASN:HD22	12:Q:288:ILE:HG22	1.48	0.76
23:v:729:TYR:CD2	23:v:748:UNK:CB	2.69	0.76
18:d:103:ILE:HA	18:d:106:ILE:HD12	1.67	0.76
1:A:1889:LEU:HB2	1:A:1989:PHE:HB2	1.66	0.76
12:Q:212:ALA:C	13:R:237:ARG:NH2	2.43	0.76
12:Q:34:CYS:HB3	12:Q:36:ILE:H	1.51	0.76
19:F:12:PRO:HG2	19:F:15:TYR:HB2	1.65	0.75
1:A:791:ARG:NH2	11:P:173:LYS:HE2	2.00	0.75
5:L:99:U:O2'	24:n:324:ILE:O	2.03	0.75
24:n:253:VAL:CG2	24:n:297:LEU:O	2.34	0.75
12:Q:202:THR:HA	12:Q:252:ARG:HG3	1.68	0.75
1:A:1067:ASN:HD22	17:c:81:PRO:HB2	1.51	0.75
1:A:1405:ILE:HG22	1:A:1406:LEU:H	1.51	0.75
12:Q:70:ILE:HD13	12:Q:84:ILE:HD11	1.69	0.75
16:Z:178:ARG:CG	16:Z:198:PHE:HZ	1.92	0.75
24:n:253:VAL:HG21	24:n:297:LEU:O	1.87	0.75
1:A:1051:GLU:OE1	1:A:1204:ARG:NH2	2.20	0.75
1:A:2027:LEU:HD23	33:e:57:ARG:HH22	1.52	0.75
12:Q:34:CYS:SG	12:Q:61:CYS:N	2.60	0.75
12:Q:217:TRP:CZ3	13:R:171:ASP:OD1	2.40	0.75
12:Q:221:ASP:C	12:Q:225:GLN:HE21	1.93	0.75
1:A:185:GLN:HE21	1:A:263:PRO:HD3	1.52	0.75
1:A:756:LEU:HD11	14:S:8:GLN:HE22	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:91:A:C4	18:d:99:ILE:HD11	2.21	0.74
12:Q:215:PRO:HG3	12:Q:217:TRP:CH2	2.21	0.74
5:L:15:C:HO2'	5:L:16:U:H6	1.32	0.74
18:d:99:ILE:HA	18:d:102:TRP:HD1	1.51	0.74
2:C:234:LEU:HD21	2:C:439:ILE:HG23	1.67	0.74
1:A:1870:VAL:HG21	5:L:46:C:H5''	1.69	0.74
5:L:15:C:H42	22:I:209:ARG:HB2	1.53	0.74
5:L:1:A:H1'	23:v:504:UNK:H2	1.52	0.74
1:A:1860:VAL:HA	1:A:1873:LYS:O	1.88	0.74
2:C:831:ILE:HG13	2:C:832:ASP:H	1.51	0.74
1:A:1379:MET:HG2	7:B:94:U:H1'	1.68	0.74
5:L:1101:C:N4	34:a:38:LYS:NZ	2.36	0.74
16:Z:174:TRP:CH2	16:Z:197:LEU:HD11	2.22	0.74
16:Z:191:ARG:NH1	16:Z:192:GLU:OE2	2.21	0.74
24:n:165:THR:OG1	24:n:445:SER:CB	2.36	0.74
2:C:126:MET:CE	2:C:132:ARG:HH11	1.93	0.74
10:O:230:VAL:HG22	10:O:241:THR:HG22	1.70	0.74
23:v:669:TYR:HE2	23:v:686:ILE:HG13	1.53	0.74
2:C:236:LEU:HD21	2:C:435:LEU:HD11	1.70	0.73
23:v:726:ARG:HH22	23:v:760:UNK:CB	1.97	0.73
16:Z:186:LEU:HD12	16:Z:186:LEU:N	2.03	0.73
1:A:928:ARG:HG2	5:L:30:A:C2	2.24	0.73
2:C:133:ILE:HG22	2:C:209:MET:HB3	1.70	0.73
2:C:177:TYR:CE1	2:C:548:ARG:CG	2.69	0.73
4:E:64:U:O2'	4:E:65:U:OP1	2.06	0.73
10:O:382:HIS:CE1	10:O:442:TRP:H	2.06	0.73
14:S:134:GLY:O	14:S:135:ARG:CB	2.32	0.73
27:s:47:GLU:HG3	35:b:15:TYR:CB	2.18	0.73
2:C:468:LEU:HD21	2:C:493:LEU:HG	1.70	0.73
25:q:173:LYS:O	25:q:174:TRP:CB	2.36	0.73
1:A:426:PRO:HG2	16:Z:201:ARG:CZ	2.18	0.73
1:A:426:PRO:O	16:Z:202:GLN:HB3	1.88	0.73
1:A:737:ARG:HG2	1:A:737:ARG:NH1	2.00	0.73
1:A:512:GLU:OE1	7:B:89:A:C6	2.42	0.73
2:C:340:LYS:O	2:C:343:ASP:HB3	1.89	0.73
8:N:109:U:C6	8:N:109:U:OP2	2.42	0.73
5:L:18:U:O2	22:I:206:LYS:HD2	1.88	0.73
25:q:422:GLY:H	25:q:443:ASN:CG	1.96	0.73
2:C:385:PHE:HE1	2:C:425:LEU:HD11	1.54	0.72
17:c:204:LYS:HG2	17:c:205:LYS:H	1.54	0.72
2:C:468:LEU:CD2	2:C:493:LEU:CD2	2.67	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:i:86:ASN:HD21	29:h:32:LYS:CD	2.02	0.72
28:u:86:ASN:HD21	29:w:32:LYS:CD	2.02	0.72
1:A:238:ARG:NH2	1:A:1762:ASP:OD2	2.22	0.72
16:Z:167:LYS:NZ	16:Z:171:ASP:OD2	2.19	0.72
15:T:122:CYS:HB2	15:T:145:CYS:HB2	1.70	0.72
10:O:285:SER:OG	10:O:287:ASP:OD1	2.07	0.72
1:A:452:PHE:HZ	2:C:347:ARG:HG3	1.55	0.72
6:M:485:U:H5'	21:H:36:ARG:HE	1.55	0.72
4:E:66:C:C6	4:E:66:C:H5'	2.24	0.72
12:Q:259:GLY:O	12:Q:263:VAL:HG23	1.90	0.72
1:A:972:MET:HE2	6:M:505:A:C2	2.25	0.72
2:C:646:GLY:HA3	2:C:652:MET:HE3	1.72	0.72
16:Z:191:ARG:HE	16:Z:192:GLU:CD	1.98	0.72
18:d:198:GLN:OE1	18:d:200:GLN:NE2	2.23	0.72
1:A:1650:ARG:NH2	6:M:495:A:N7	2.38	0.72
1:A:2030:PRO:CB	33:e:57:ARG:HE	2.02	0.72
12:Q:125:ILE:C	12:Q:125:ILE:HD12	2.15	0.72
23:v:718:SER:OG	23:v:725:THR:CG2	2.38	0.71
1:A:1050:LEU:O	1:A:1169:TYR:HA	1.90	0.71
1:A:607:THR:OG1	8:N:101:U:H3'	1.90	0.71
1:A:713:ASN:ND2	3:D:83:C:H4'	2.04	0.71
1:A:1850:LEU:HD13	1:A:1930:PRO:HB3	1.71	0.71
3:D:174:G:OP1	3:D:174:G:H4'	1.90	0.71
5:L:119:G:OP1	5:L:119:G:H4'	1.90	0.71
16:Z:190:LEU:HD23	16:Z:190:LEU:C	2.15	0.71
1:A:681:LYS:O	1:A:684:LYS:HB3	1.89	0.71
1:A:1048:VAL:HG22	1:A:1250:VAL:HG22	1.71	0.71
16:Z:190:LEU:HD23	16:Z:191:ARG:N	2.06	0.71
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.73	0.71
1:A:1211:SER:O	1:A:1257:ASN:ND2	2.23	0.71
12:Q:226:LEU:C	12:Q:226:LEU:HD12	2.15	0.71
10:O:354:ASN:ND2	10:O:369:ASP:OD1	2.24	0.71
23:v:616:PRO:CG	23:v:617:PRO:N	2.53	0.71
24:n:312:SER:OG	24:n:314:ASP:OD1	2.07	0.71
2:C:655:LEU:O	2:C:658:ASP:N	2.24	0.71
6:M:495:A:O4'	6:M:495:A:OP2	2.08	0.71
4:E:63:G:O2'	14:S:8:GLN:CB	2.39	0.71
8:N:110:A:H2	13:R:46:ARG:CD	2.04	0.71
12:Q:118:VAL:HG23	12:Q:119:LYS:O	1.90	0.71
15:T:3:ARG:NH2	15:T:85:LYS:O	2.24	0.71
24:n:55:GLU:OE2	24:n:55:GLU:HA	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:905:TYR:HB3	1:A:908:ASP:CB	2.20	0.70
5:L:33:U:OP1	20:G:17:MET:CB	2.39	0.70
3:D:43:G:N3	3:D:43:G:H2'	2.06	0.70
5:L:25:A:H2'	5:L:27:A:OP2	1.92	0.70
24:n:55:GLU:OE2	24:n:58:ARG:CD	2.38	0.70
1:A:1362:LYS:NZ	9:J:13:GLY:O	2.24	0.70
1:A:1488:ILE:HG23	1:A:1489:PRO:HD3	1.72	0.70
12:Q:207:LEU:O	12:Q:248:CYS:HA	1.89	0.70
14:S:167:GLN:O	14:S:171:HIS:HB2	1.90	0.70
1:A:427:SER:HA	16:Z:202:GLN:HB2	1.73	0.70
3:D:173:U:H4'	3:D:174:G:OP1	1.91	0.70
5:L:19:U:C4	11:P:174:ASN:OD1	2.44	0.70
1:A:911:ILE:HG23	1:A:997:GLN:HG3	1.73	0.70
1:A:1431:HIS:CD2	1:A:1434:GLU:HA	2.26	0.70
5:L:15:C:H41	22:I:209:ARG:CB	2.01	0.70
4:E:84:C:O2'	14:S:4:SER:OG	2.09	0.70
12:Q:16:CYS:SG	13:R:105:ARG:NH2	2.64	0.70
12:Q:226:LEU:HD21	12:Q:262:PHE:HD1	1.57	0.70
12:Q:226:LEU:CD2	12:Q:262:PHE:CE1	2.75	0.70
1:A:972:MET:HE2	6:M:505:A:N1	2.06	0.70
5:L:69:G:H1	5:L:83:U:H3	1.40	0.70
5:L:1116:A:C6	5:L:1117:G:C5	2.79	0.70
8:N:110:A:H2	13:R:46:ARG:HH11	1.36	0.70
8:N:110:A:N3	13:R:46:ARG:NH1	2.37	0.70
1:A:140:ARG:HD2	1:A:566:GLU:OE2	1.92	0.70
12:Q:49:SER:OG	12:Q:52:SER:HB3	1.89	0.70
22:I:195:PHE:HE1	22:I:204:ASN:HD22	1.37	0.70
1:A:610:ARG:NH1	8:N:101:U:OP2	2.22	0.69
1:A:372:ARG:O	2:C:973:ARG:NH2	2.25	0.69
1:A:2029:ASP:OD1	33:e:90:PHE:HZ	1.75	0.69
31:y:30:ARG:O	31:y:47:VAL:HG23	1.92	0.69
10:O:317:HIS:NE2	10:O:362:ASP:OD1	2.20	0.69
15:T:120:CYS:CB	15:T:122:CYS:HB3	2.18	0.69
4:E:91:A:C5	18:d:99:ILE:HD11	2.27	0.69
10:O:111:ILE:HB	10:O:114:ARG:HH21	1.57	0.69
16:Z:170:HIS:CE1	16:Z:174:TRP:HE3	2.05	0.69
28:i:86:ASN:HD21	29:h:32:LYS:CE	2.06	0.69
15:T:126:ARG:HG3	24:n:72:TRP:CZ2	2.28	0.69
16:Z:194:LEU:HD22	16:Z:194:LEU:O	1.93	0.69
18:d:209:GLU:O	18:d:213:GLY:N	2.25	0.69
1:A:161:PHE:HE1	1:A:198:ALA:HA	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.57	0.69
2:C:320:PHE:HB2	2:C:429:PHE:HD2	1.57	0.69
12:Q:209:ASN:ND2	12:Q:288:ILE:CG2	2.56	0.69
23:v:504:UNK:O	23:v:508:UNK:N	2.26	0.69
4:E:63:G:O2'	14:S:8:GLN:HB2	1.93	0.69
5:L:1102:C:O2	5:L:1114:G:N2	2.24	0.69
5:L:1116:A:C2	5:L:1117:G:C5	2.80	0.69
12:Q:49:SER:OG	12:Q:52:SER:CA	2.40	0.69
12:Q:210:ILE:HG22	12:Q:211:ASP:O	1.93	0.69
18:d:176:GLU:OE1	18:d:181:ASN:ND2	2.21	0.69
1:A:1048:VAL:HA	1:A:1249:SER:O	1.92	0.68
2:C:132:ARG:NH2	31:l:13:GLU:O	2.25	0.68
23:v:602:MET:HA	23:v:605:PHE:HD2	1.57	0.68
1:A:751:ASP:OD1	1:A:752:ALA:N	2.26	0.68
1:A:1043:ARG:HG3	1:A:1044:GLY:H	1.58	0.68
5:L:1116:A:C4	5:L:1117:G:C8	2.81	0.68
16:Z:454:ASP:HB3	16:Z:457:HIS:HD2	1.58	0.68
23:v:601:VAL:O	23:v:604:SER:OG	2.09	0.68
24:n:68:PRO:HD2	24:n:69:TRP:HE3	1.53	0.68
29:h:74:ARG:NH1	33:g:65:CYS:SG	2.66	0.68
1:A:946:ASN:HB3	1:A:949:ASP:HB3	1.75	0.68
12:Q:53:ASN:HD22	12:Q:54:ASN:N	1.91	0.68
16:Z:170:HIS:HE1	16:Z:174:TRP:HZ3	1.14	0.68
1:A:1379:MET:HE1	1:A:1620:TYR:H	1.59	0.68
1:A:1618:ASN:N	1:A:1744:ASP:OD2	2.26	0.68
19:F:109:GLU:HG3	19:F:110:VAL:HG12	1.74	0.68
1:A:1627:LEU:HD11	1:A:1634:LEU:HG	1.74	0.68
5:L:18:U:C5	22:I:202:GLN:CG	2.76	0.68
5:L:19:U:N3	11:P:174:ASN:OD1	2.27	0.68
5:L:119:G:N7	32:z:20:LYS:HE2	2.08	0.68
5:L:120:G:C2	28:u:33:GLU:HG3	2.29	0.68
1:A:1710:GLU:HG2	1:A:1728:ILE:HG12	1.75	0.68
1:A:1859:ARG:NH2	1:A:1876:ASN:O	2.26	0.68
5:L:118:U:H4'	5:L:119:G:OP1	1.91	0.68
11:P:148:HIS:O	18:d:131:ARG:NE	2.25	0.68
21:H:34:ARG:HH12	21:H:36:ARG:HH11	1.41	0.68
29:w:74:ARG:NH1	33:e:65:CYS:SG	2.66	0.68
15:T:128:GLN:O	15:T:131:GLU:N	2.26	0.68
18:d:250:PHE:CD2	18:d:266:LEU:HD22	2.29	0.68
2:C:701:GLU:HB2	2:C:841:LEU:HD22	1.76	0.68
14:S:9:LEU:O	14:S:10:GLU:HB2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:u:86:ASN:HD21	29:w:32:LYS:CE	2.06	0.68
1:A:621:LEU:HD23	1:A:722:LEU:HD21	1.76	0.68
1:A:1755:LYS:HE3	1:A:1759:TYR:HE2	1.58	0.68
2:C:829:VAL:HG12	2:C:830:ASN:H	1.59	0.68
25:q:20:ARG:CB	25:r:53:ILE:HA	2.24	0.68
2:C:662:SER:O	2:C:665:LYS:NZ	2.24	0.67
3:D:174:G:N7	32:m:20:LYS:HE2	2.08	0.67
13:R:206:LEU:HD12	13:R:207:PRO:HD2	1.76	0.67
15:T:61:ARG:NH1	15:T:101:GLU:O	2.22	0.67
1:A:1049:LEU:HA	1:A:1170:MET:O	1.94	0.67
2:C:915:GLU:OE2	2:C:919:ARG:NE	2.21	0.67
10:O:275:THR:OG1	10:O:279:PRO:O	2.13	0.67
5:L:18:U:H5'	5:L:18:U:C6	2.29	0.67
5:L:20:G:C2	14:S:6:ARG:HB3	2.30	0.67
4:E:39:G:O6	13:R:127:ILE:O	2.13	0.67
5:L:1116:A:C4	5:L:1117:G:N7	2.63	0.67
19:F:69:GLU:OE1	19:F:83:ARG:NH2	2.27	0.67
22:I:196:ILE:HB	22:I:200:ASN:ND2	2.09	0.67
1:A:487:ASN:OD1	1:A:488:ARG:N	2.28	0.67
11:P:174:ASN:ND2	11:P:177:GLY:CA	2.52	0.67
25:o:51:VAL:HG11	25:p:20:ARG:CB	2.25	0.67
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.27	0.67
10:O:391:GLU:HG3	10:O:392:MET:H	1.60	0.67
18:d:119:ARG:NH1	18:d:143:GLU:OE2	2.27	0.67
25:q:306:ASP:CG	25:q:308:ARG:H	2.03	0.67
1:A:759:ARG:HH12	14:S:7:PRO:HB2	1.58	0.67
1:A:791:ARG:NH2	11:P:173:LYS:CE	2.58	0.67
1:A:992:ASP:OD2	1:A:1085:LYS:NZ	2.28	0.67
10:O:217:ILE:HG22	10:O:218:ARG:HG3	1.77	0.67
1:A:177:GLU:HB3	1:A:712:LEU:HD11	1.76	0.67
1:A:902:PRO:HD2	1:A:905:TYR:CD1	2.25	0.67
3:D:165:A:H2	32:m:2:LYS:HE2	1.58	0.67
5:L:18:U:C5	22:I:202:GLN:HG2	2.29	0.67
5:L:1102:C:O5'	5:L:1102:C:H6	1.76	0.67
12:Q:82:ILE:HD11	13:R:253:LEU:HD11	1.77	0.67
1:A:391:TYR:OH	2:C:912:ALA:O	2.10	0.67
1:A:705:GLN:HE21	1:A:709:ARG:HG3	1.60	0.67
1:A:1815:LEU:O	1:A:1818:ARG:N	2.28	0.67
3:D:78:A:O2'	3:D:79:C:O5'	2.12	0.67
5:L:119:G:C5'	33:e:99:ASP:HB2	2.24	0.67
16:Z:462:ILE:HG12	16:Z:474:THR:HB	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:v:709:TRP:HA	23:v:712:CYS:SG	2.34	0.67
3:D:175:G:C2	28:i:33:GLU:HG3	2.29	0.67
8:N:110:A:H2	13:R:46:ARG:HD2	1.58	0.67
10:O:362:ASP:OD2	10:O:379:LYS:NZ	2.27	0.66
1:A:213:TYR:CZ	1:A:217:TRP:CD1	2.83	0.66
25:q:348:TYR:CB	25:q:377:ILE:CB	2.74	0.66
1:A:512:GLU:CD	7:B:89:A:N6	2.46	0.66
1:A:2022:ALA:HB1	1:A:2055:MET:HE1	1.78	0.66
2:C:292:ILE:O	2:C:296:ASN:ND2	2.29	0.66
12:Q:125:ILE:HD12	12:Q:126:THR:N	2.11	0.66
25:q:20:ARG:CB	25:r:52:GLU:O	2.43	0.66
1:A:791:ARG:HH22	11:P:173:LYS:HD2	1.58	0.66
2:C:461:LYS:O	2:C:461:LYS:HD3	1.96	0.66
3:D:174:G:C5'	33:g:99:ASP:HB2	2.24	0.66
4:E:91:A:N3	18:d:99:ILE:HD11	2.10	0.66
1:A:2030:PRO:HA	33:e:57:ARG:HH21	1.60	0.66
6:M:500:A:N3	6:M:502:C:N4	2.43	0.66
2:C:101:GLN:HE21	3:D:75:A:H61	1.42	0.66
2:C:780:PRO:HA	2:C:783:ILE:HB	1.78	0.66
4:E:86:G:C2	18:d:57:TYR:CZ	2.83	0.66
16:Z:192:GLU:O	16:Z:195:GLU:OE2	2.13	0.66
23:v:729:TYR:CG	23:v:748:UNK:CB	2.79	0.66
1:A:803:GLY:O	11:P:166:PRO:HG2	1.96	0.66
1:A:854:ARG:NH2	5:L:25:A:H5''	2.11	0.66
1:A:911:ILE:HG23	1:A:997:GLN:HG2	1.75	0.66
1:A:1445:THR:OG1	1:A:1450:GLU:OE2	2.14	0.66
2:C:807:PRO:HG3	2:C:850:LEU:HD23	1.77	0.66
12:Q:214:ILE:CD1	12:Q:218:LYS:HG2	2.25	0.66
13:R:245:GLU:HA	13:R:248:ASN:HD22	1.59	0.66
16:Z:200:ILE:O	16:Z:204:ASP:N	2.27	0.66
1:A:914:LEU:HD13	1:A:1505:ASP:HB2	1.78	0.65
2:C:468:LEU:HD11	2:C:492:LEU:CA	2.26	0.65
16:Z:177:LEU:CD2	16:Z:194:LEU:CD2	2.65	0.65
32:z:82:LEU:HD12	32:z:85:ILE:HD11	1.77	0.65
1:A:416:GLU:HG2	1:A:418:ASP:H	1.60	0.65
1:A:1067:ASN:O	1:A:1071:ARG:HG2	1.96	0.65
2:C:922:THR:OG1	2:C:925:LEU:O	2.06	0.65
4:E:64:U:O2'	4:E:65:U:P	2.55	0.65
2:C:607:LEU:HD22	2:C:668:ILE:HD12	1.78	0.65
28:u:77:LEU:HD21	28:u:80:ILE:HD12	1.79	0.65
11:P:111:HIS:O	11:P:112:ILE:HG13	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:m:82:LEU:HD12	32:m:85:ILE:HD11	1.77	0.65
15:T:32:ASP:HA	15:T:35:LYS:HD3	1.77	0.65
17:c:163:GLN:HB3	17:c:167:ALA:HB3	1.79	0.65
24:n:60:ARG:O	24:n:62:THR:N	2.29	0.65
1:A:1372:LYS:HG2	1:A:1383:PHE:CD2	2.30	0.65
1:A:1882:LEU:HD22	1:A:1991:ILE:HD11	1.78	0.65
2:C:183:GLN:HE22	2:C:654:CYS:HA	1.60	0.65
16:Z:184:GLN:CA	16:Z:184:GLN:HE21	2.09	0.65
16:Z:184:GLN:HE21	16:Z:185:GLU:H	1.43	0.65
25:q:463:SER:O	25:q:464:ALA:HB3	1.96	0.65
1:A:1896:THR:HA	1:A:1899:TRP:HD1	1.62	0.65
11:P:197:ILE:HG23	17:c:90:MET:HE2	1.78	0.65
1:A:737:ARG:NH2	4:E:71:G:N7	2.45	0.65
2:C:830:ASN:HB2	2:C:834:MET:HG2	1.79	0.65
13:R:253:LEU:O	13:R:257:ASN:HB2	1.97	0.65
19:F:14:ASP:OD1	19:F:15:TYR:N	2.30	0.65
1:A:766:ILE:HG21	1:A:782:ILE:HG12	1.79	0.64
1:A:1195:PHE:HB3	1:A:1217:ARG:HE	1.61	0.64
2:C:218:HIS:HB3	2:C:221:PHE:HD2	1.62	0.64
24:n:163:GLU:CB	24:n:183:ASN:HB3	2.27	0.64
1:A:1051:GLU:OE2	1:A:1261:SER:N	2.24	0.64
2:C:761:ALA:HA	2:C:764:ASN:HB2	1.80	0.64
4:E:63:G:H22	14:S:6:ARG:HG2	1.60	0.64
10:O:206:VAL:HG21	10:O:241:THR:HG21	1.78	0.64
29:w:77:ASN:OD1	33:e:49:ARG:HD3	1.97	0.64
1:A:366:GLU:HG3	1:A:372:ARG:HH11	1.62	0.64
1:A:1063:PHE:HB2	17:c:83:GLN:HE21	1.62	0.64
1:A:2027:LEU:CD2	33:e:57:ARG:NH2	2.51	0.64
2:C:296:ASN:OD1	2:C:304:PHE:N	2.30	0.64
2:C:468:LEU:HD22	2:C:493:LEU:HD23	1.78	0.64
7:B:89:A:OP2	7:B:89:A:O4'	2.15	0.64
16:Z:188:SER:O	16:Z:192:GLU:HG2	1.96	0.64
23:v:724:VAL:C	23:v:727:GLU:CG	2.71	0.64
1:A:1309:ILE:HG12	1:A:1356:LEU:HD12	1.79	0.64
4:E:63:G:N2	14:S:6:ARG:CG	2.60	0.64
16:Z:299:LEU:HD21	16:Z:343:TYR:HE1	1.61	0.64
27:s:98:GLU:C	35:b:53:PRO:CB	2.70	0.64
1:A:907:ASN:ND2	1:A:1504:TYR:CE1	2.66	0.64
1:A:1842:GLU:OE1	1:A:1845:ASN:ND2	2.31	0.64
2:C:765:VAL:HG22	2:C:775:ILE:HG12	1.78	0.64
4:E:46:U:OP1	19:F:33:THR:OG1	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:5:A:C5'	22:I:114:THR:CB	2.73	0.64
5:L:5:A:OP1	22:I:114:THR:HG21	1.97	0.64
12:Q:87:ARG:NH2	12:Q:122:GLY:O	2.30	0.64
28:i:77:LEU:HD21	28:i:80:ILE:HD12	1.79	0.64
1:A:2028:SER:O	33:e:71:ASN:HB3	1.97	0.64
1:A:1087:ASN:ND2	1:A:1099:ASN:O	2.28	0.64
1:A:1991:ILE:HG21	1:A:2008:LEU:HD22	1.80	0.64
1:A:2029:ASP:OD1	33:e:90:PHE:CZ	2.51	0.64
4:E:86:G:N2	18:d:57:TYR:CE1	2.65	0.64
4:E:91:A:N1	18:d:99:ILE:CD1	2.53	0.64
5:L:70:A:H61	5:L:82:C:H42	1.44	0.64
13:R:15:GLU:OE1	15:T:44:LYS:NZ	2.30	0.64
14:S:8:GLN:HG2	14:S:10:GLU:O	1.96	0.64
17:c:12:VAL:HG22	17:c:13:TRP:H	1.62	0.64
26:t:81:ASP:CB	26:t:85:THR:OG1	2.46	0.64
1:A:1338:SER:O	1:A:1341:SER:OG	2.10	0.64
5:L:20:G:N3	14:S:6:ARG:HB3	2.13	0.64
5:L:5:A:C5'	22:I:114:THR:CG2	2.50	0.64
21:H:21:GLU:HG2	21:H:27:LYS:HB3	1.78	0.64
14:S:6:ARG:HG3	14:S:6:ARG:NH1	2.13	0.63
1:A:928:ARG:CZ	5:L:32:G:C8	2.81	0.63
1:A:1535:LYS:NZ	6:M:509:U:O2'	2.20	0.63
1:A:2030:PRO:HB3	33:e:57:ARG:NE	2.12	0.63
5:L:19:U:O4	11:P:174:ASN:OD1	2.17	0.63
16:Z:177:LEU:HD21	16:Z:194:LEU:CD2	2.25	0.63
23:v:722:PRO:O	23:v:725:THR:OG1	2.15	0.63
1:A:899:PRO:HD2	1:A:1006:ARG:NH2	2.12	0.63
3:D:83:C:O2'	3:D:84:A:O5'	2.15	0.63
16:Z:168:LYS:HZ3	16:Z:171:ASP:HB2	1.60	0.63
1:A:1458:TRP:HE1	1:A:1489:PRO:HD2	1.62	0.63
12:Q:226:LEU:HG	12:Q:227:LEU:CD2	2.29	0.63
15:T:121:ILE:HD11	15:T:129:LEU:HD21	1.80	0.63
18:d:122:MET:HE2	18:d:122:MET:HA	1.79	0.63
24:n:395:GLY:O	24:n:396:ARG:CB	2.47	0.63
29:h:77:ASN:OD1	33:g:49:ARG:HD3	1.97	0.63
1:A:645:ASP:OD1	1:A:646:ALA:N	2.32	0.63
1:A:905:TYR:HB3	1:A:908:ASP:CG	2.23	0.63
2:C:105:ILE:HD11	3:D:44:A:N7	2.12	0.63
4:E:50:G:C4	19:F:65:ASN:ND2	2.66	0.63
5:L:33:U:OP1	20:G:17:MET:HB2	1.99	0.63
1:A:488:ARG:C	1:A:489:THR:HG23	2.24	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:412:ALA:HA	2:C:415:TYR:CE2	2.34	0.63
16:Z:197:LEU:HD12	16:Z:197:LEU:C	2.24	0.63
23:v:611:THR:CB	23:v:623:LEU:HD13	2.29	0.63
1:A:581:LEU:O	1:A:585:ARG:HB2	1.99	0.63
1:A:1122:ASP:OD1	1:A:1161:TYR:OH	2.16	0.63
2:C:468:LEU:CD1	2:C:492:LEU:C	2.72	0.63
16:Z:178:ARG:HD3	16:Z:182:GLN:HE22	1.62	0.63
16:Z:178:ARG:HB2	16:Z:198:PHE:HZ	1.58	0.63
17:c:216:ASP:OD1	17:c:217:ILE:N	2.32	0.63
2:C:468:LEU:CD1	2:C:491:GLY:HA3	2.16	0.63
16:Z:195:GLU:HG2	16:Z:196:THR:N	2.13	0.63
1:A:407:VAL:O	2:C:272:ARG:NH2	2.32	0.63
12:Q:49:SER:HG	12:Q:52:SER:CB	2.12	0.63
18:d:227:ASP:O	18:d:231:ASN:HB2	1.99	0.63
24:n:380:HIS:CG	24:n:381:SER:N	2.66	0.63
1:A:1185:GLU:OE1	14:S:128:ARG:NH1	2.18	0.62
1:A:1696:SER:HA	1:A:1759:TYR:CE1	2.32	0.62
4:E:53:A:H5'	4:E:54:U:OP2	1.99	0.62
2:C:919:ARG:NH2	2:C:927:MET:SD	2.70	0.62
23:v:602:MET:HA	23:v:605:PHE:CD2	2.33	0.62
2:C:286:LEU:HD21	16:Z:183:THR:CG2	2.22	0.62
4:E:56:A:O2'	4:E:57:U:O5'	2.17	0.62
5:L:110:A:H2	32:z:2:LYS:HE2	1.58	0.62
15:T:107:ARG:HH21	15:T:147:HIS:CE1	2.17	0.62
13:R:157:GLU:OE2	13:R:161:ARG:NE	2.32	0.62
4:E:66:C:H3'	4:E:66:C:H6	1.63	0.62
1:A:364:TYR:OH	1:A:1205:LYS:NZ	2.31	0.62
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.82	0.62
1:A:1377:SER:HA	7:B:95:U:OP1	1.98	0.62
4:E:86:G:C2	18:d:57:TYR:CE1	2.87	0.62
5:L:19:U:N1	11:P:178:TYR:HD2	1.97	0.62
11:P:185:ARG:HD2	17:c:29:GLY:HA2	1.81	0.62
12:Q:108:MET:HA	12:Q:111:ARG:HB3	1.81	0.62
21:H:29:TYR:O	21:H:53:GLN:NE2	2.32	0.62
3:D:174:G:O5'	29:h:76:ASN:ND2	2.32	0.62
5:L:1099:G:C8	5:L:1100:A:C8	2.87	0.62
5:L:1120:G:H5''	5:L:1120:G:H8	1.65	0.62
13:R:170:ILE:HD13	13:R:173:ILE:HD11	1.81	0.62
1:A:209:ILE:HB	1:A:212:VAL:HB	1.81	0.62
1:A:701:CYS:SG	1:A:702:GLY:N	2.72	0.62
1:A:1411:ASP:H	9:J:6:ILE:HG22	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:31:G:H2'	3:D:32:G:H5'	1.81	0.62
12:Q:207:LEU:N	12:Q:249:GLY:O	2.31	0.62
1:A:467:GLU:O	2:C:387:TYR:OH	2.10	0.62
2:C:307:ILE:HA	2:C:324:ILE:HD11	1.82	0.62
4:E:57:U:OP1	19:F:62:ARG:HG2	1.99	0.62
13:R:161:ARG:O	13:R:165:SER:CB	2.47	0.62
15:T:126:ARG:HG3	24:n:72:TRP:NE1	2.14	0.62
5:L:119:G:O5'	29:w:76:ASN:ND2	2.32	0.62
5:L:1107:C:H6	5:L:1107:C:H5'	1.63	0.62
10:O:259:VAL:HG12	10:O:260:ILE:HG13	1.82	0.62
1:A:484:PHE:CE1	3:D:81:A:C6	2.88	0.61
2:C:727:THR:H	2:C:736:ASP:HB2	1.64	0.61
12:Q:61:CYS:O	12:Q:72:GLN:NE2	2.32	0.61
13:R:121:ARG:HD3	13:R:125:GLY:HA3	1.82	0.61
32:m:3:LEU:HD11	33:g:60:ALA:HB1	1.82	0.61
1:A:1563:LYS:O	1:A:1782:ASN:ND2	2.33	0.61
2:C:801:TRP:CD1	2:C:843:LYS:HD2	2.36	0.61
6:M:505:A:C3'	6:M:506:U:H4'	2.30	0.61
12:Q:215:PRO:HB2	12:Q:217:TRP:CE3	2.36	0.61
17:c:16:VAL:HG13	17:c:152:LEU:HD12	1.82	0.61
4:E:84:C:H4'	18:d:60:ARG:NH1	2.16	0.61
1:A:1811:ALA:O	1:A:1814:VAL:N	2.33	0.61
5:L:120:G:N7	29:w:32:LYS:HD2	2.15	0.61
13:R:23:PRO:O	13:R:37:TRP:NE1	2.28	0.61
13:R:254:ILE:O	13:R:258:THR:OG1	2.14	0.61
17:c:64:GLU:HG2	17:c:65:PHE:H	1.64	0.61
1:A:794:LYS:HB3	1:A:854:ARG:NH1	2.15	0.61
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.35	0.61
4:E:32:U:C4	12:Q:28:ILE:HD13	2.36	0.61
18:d:189:TYR:HB3	18:d:205:TRP:CD1	2.36	0.61
23:v:724:VAL:CA	23:v:727:GLU:CG	2.79	0.61
1:A:1856:ASN:ND2	1:A:1966:SER:O	2.34	0.61
5:L:19:U:C1'	11:P:178:TYR:CE2	2.83	0.61
5:L:1116:A:N1	5:L:1117:G:C6	2.68	0.61
22:I:196:ILE:HB	22:I:200:ASN:HD21	1.64	0.61
5:L:1098:C:O5'	5:L:1098:C:H6	1.83	0.61
13:R:255:ASN:O	13:R:259:ASN:ND2	2.34	0.61
16:Z:187:SER:OG	16:Z:190:LEU:HB3	2.00	0.61
16:Z:200:ILE:HA	16:Z:203:LYS:HB2	1.83	0.61
25:q:178:LYS:CB	25:q:468:GLN:CB	2.79	0.61
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	1.83	0.61
5:L:119:G:H5''	33:e:99:ASP:HB2	1.82	0.61
16:Z:168:LYS:HZ2	16:Z:171:ASP:HB2	1.65	0.61
3:D:174:G:H5''	33:g:99:ASP:HB2	1.82	0.61
3:D:175:G:N7	29:h:32:LYS:HD2	2.15	0.61
13:R:244:LEU:O	13:R:248:ASN:ND2	2.34	0.61
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.36	0.61
5:L:119:G:OP2	29:w:76:ASN:CB	2.49	0.61
22:I:180:LYS:O	22:I:183:MET:HB2	2.01	0.61
2:C:265:PHE:HD2	2:C:295:ILE:HD12	1.66	0.60
5:L:4:A:O3'	22:I:114:THR:CG2	2.49	0.60
14:S:6:ARG:CG	14:S:6:ARG:HH11	2.14	0.60
16:Z:170:HIS:NE2	16:Z:174:TRP:CE3	2.66	0.60
18:d:267:TYR:O	18:d:271:ILE:HD12	2.01	0.60
2:C:472:VAL:HB	2:C:575:ALA:O	2.00	0.60
11:P:34:ILE:HG23	11:P:35:ALA:H	1.67	0.60
16:Z:364:THR:O	16:Z:368:ASN:ND2	2.32	0.60
31:y:20:SER:OG	31:y:30:ARG:HD2	2.01	0.60
1:A:1270:LEU:HD12	1:A:1301:TYR:HE2	1.66	0.60
2:C:108:GLN:O	2:C:109:LEU:HD12	2.01	0.60
16:Z:181:LEU:CD2	16:Z:191:ARG:HG3	2.26	0.60
22:I:92:ARG:N	22:I:93:GLY:HA3	2.17	0.60
1:A:1488:ILE:CG2	1:A:1489:PRO:HD3	2.31	0.60
2:C:177:TYR:HE1	2:C:548:ARG:HG3	1.63	0.60
2:C:794:GLN:NE2	2:C:835:LYS:HD2	2.17	0.60
3:D:96:U:H3	7:B:99:G:N2	1.89	0.60
16:Z:184:GLN:HE21	16:Z:184:GLN:HA	1.66	0.60
24:n:357:ASP:CG	24:n:358:ASN:H	2.09	0.60
28:i:83:LYS:NZ	29:h:75:CYS:O	2.35	0.60
2:C:703:LEU:O	2:C:705:GLY:N	2.33	0.60
5:L:14:C:C2'	5:L:15:C:C5'	2.64	0.60
5:L:15:C:H41	22:I:209:ARG:HD3	1.67	0.60
11:P:134:VAL:HG22	12:Q:111:ARG:HD3	1.83	0.60
23:v:480:UNK:O	23:v:485:UNK:N	2.35	0.60
1:A:817:LYS:NZ	14:S:159:ASP:OD1	2.33	0.60
21:H:41:VAL:HG12	21:H:42:LYS:H	1.66	0.60
24:n:54:SER:O	24:n:58:ARG:HG2	2.01	0.60
28:i:86:ASN:ND2	29:h:32:LYS:HD3	2.13	0.60
2:C:468:LEU:HD13	2:C:492:LEU:H	1.61	0.60
4:E:88:U:H2'	5:L:17:U:H6	1.67	0.60
5:L:4:A:O3'	22:I:114:THR:HG22	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:212:GLU:OE1	14:S:38:LYS:NZ	2.29	0.60
10:O:373:LEU:HD21	10:O:402:VAL:HG21	1.84	0.60
12:Q:212:ALA:CB	13:R:237:ARG:NH1	2.64	0.60
28:u:83:LYS:NZ	29:w:75:CYS:O	2.35	0.60
1:A:662:GLN:HA	1:A:1622:GLY:O	2.02	0.60
1:A:744:THR:O	1:A:749:ARG:NH2	2.34	0.60
1:A:1377:SER:HB3	1:A:1379:MET:H	1.66	0.60
13:R:76:PHE:HB2	13:R:91:HIS:CD2	2.36	0.60
16:Z:148:LEU:HD12	16:Z:190:LEU:HD11	1.82	0.60
16:Z:455:ALA:HB2	16:Z:484:ILE:HG21	1.84	0.60
1:A:1852:VAL:HG22	1:A:1881:THR:HG22	1.84	0.60
10:O:229:THR:HG21	10:O:272:VAL:H	1.66	0.60
13:R:10:LYS:NZ	13:R:57:LEU:O	2.27	0.60
17:c:66:SER:OG	17:c:69:GLU:HG2	2.02	0.60
1:A:737:ARG:NH1	4:E:70:U:OP2	2.34	0.60
1:A:1275:MET:O	1:A:1276:GLU:HG2	2.01	0.60
2:C:468:LEU:HD21	2:C:493:LEU:CG	2.31	0.60
2:C:660:ARG:HH22	2:C:670:ILE:HD12	1.66	0.60
3:D:174:G:OP2	29:h:76:ASN:CB	2.49	0.60
4:E:50:G:O2'	19:F:65:ASN:ND2	2.34	0.60
15:T:123:ARG:HH11	15:T:153:CYS:HB3	1.66	0.60
20:G:11:SER:O	20:G:19:ASN:ND2	2.35	0.60
32:z:3:LEU:HD11	33:e:60:ALA:HB1	1.82	0.60
1:A:1637:LYS:NZ	19:F:3:GLU:OE1	2.32	0.59
5:L:19:U:C1'	11:P:178:TYR:HE2	2.15	0.59
5:L:75:A:O3'	12:Q:252:ARG:NH1	2.34	0.59
14:S:4:SER:C	14:S:6:ARG:HD3	2.26	0.59
15:T:156:THR:O	24:n:60:ARG:NH1	2.35	0.59
1:A:1125:LEU:O	1:A:1233:ARG:NH1	2.34	0.59
1:A:1195:PHE:HB3	1:A:1217:ARG:NE	2.17	0.59
2:C:307:ILE:HG12	2:C:346:THR:HA	1.83	0.59
10:O:156:ILE:HD13	10:O:197:LEU:HD22	1.83	0.59
19:F:49:MET:HE1	19:F:97:PHE:CE1	2.37	0.59
1:A:1326:THR:O	1:A:1327:THR:OG1	2.15	0.59
2:C:468:LEU:HD11	2:C:492:LEU:C	2.26	0.59
4:E:2:U:H2'	4:E:3:U:H6	1.68	0.59
4:E:89:U:C5	22:I:176:TYR:CD1	2.89	0.59
7:B:90:A:N1	9:J:6:ILE:HD11	2.17	0.59
10:O:392:MET:HG2	14:S:158:ASN:HD22	1.66	0.59
16:Z:152:ILE:HD11	16:Z:194:LEU:HA	1.84	0.59
1:A:161:PHE:CE1	1:A:198:ALA:HA	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:99:LYS:NZ	3:D:43:G:OP2	2.34	0.59
4:E:66:C:C6	4:E:66:C:C3'	2.85	0.59
4:E:89:U:C4	22:I:176:TYR:CE1	2.91	0.59
17:c:525:ARG:O	17:c:528:GLN:CG	2.51	0.59
1:A:168:LEU:HD23	1:A:622:MET:HE2	1.84	0.59
1:A:341:ALA:HA	1:A:355:LEU:HD23	1.85	0.59
1:A:1378:LYS:HB2	7:B:94:U:H4'	1.85	0.59
1:A:1904:ARG:N	6:M:492:U:OP1	2.35	0.59
2:C:161:ILE:HG22	2:C:163:ASP:H	1.67	0.59
12:Q:13:CYS:SG	12:Q:16:CYS:N	2.71	0.59
16:Z:317:ILE:HD13	16:Z:325:VAL:HG21	1.84	0.59
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.24	0.59
1:A:1512:ARG:NH2	1:A:1525:PHE:O	2.36	0.59
1:A:1870:VAL:CB	5:L:46:C:H4'	2.30	0.59
4:E:56:A:O2'	4:E:57:U:P	2.61	0.59
9:J:27:ASN:OD1	9:J:28:ASN:N	2.30	0.59
23:v:552:UNK:O	23:v:556:UNK:N	2.35	0.59
31:y:66:GLY:HA2	31:y:69:ILE:HD12	1.85	0.59
1:A:881:THR:O	1:A:884:SER:OG	2.20	0.59
2:C:683:ASN:HD22	2:C:713:GLU:HG2	1.68	0.59
3:D:78:A:O2'	3:D:79:C:P	2.61	0.59
11:P:85:SER:O	11:P:87:ASN:N	2.36	0.59
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.32	0.59
1:A:794:LYS:HB3	1:A:854:ARG:HH12	1.66	0.59
1:A:1862:VAL:HG13	1:A:1870:VAL:HG13	1.83	0.59
3:D:175:G:N1	28:i:33:GLU:O	2.36	0.59
5:L:1116:A:N1	5:L:1117:G:C5	2.71	0.59
16:Z:184:GLN:HA	16:Z:184:GLN:NE2	2.18	0.59
19:F:105:ASP:OD1	20:G:15:LYS:NZ	2.34	0.59
24:n:60:ARG:C	24:n:62:THR:H	2.11	0.59
1:A:191:VAL:HA	1:A:201:PHE:O	2.02	0.59
1:A:297:SER:HB3	3:D:32:G:OP1	2.02	0.59
2:C:706:LEU:HD21	2:C:834:MET:HE1	1.84	0.59
2:C:749:LYS:O	2:C:753:THR:OG1	2.14	0.59
10:O:277:VAL:HG13	11:P:63:ILE:HG22	1.83	0.59
12:Q:49:SER:HG	12:Q:52:SER:CA	2.15	0.59
19:F:75:TYR:HB3	19:F:79:ILE:HB	1.83	0.59
24:n:68:PRO:HD2	24:n:69:TRP:CZ3	2.36	0.59
24:n:251:ALA:CA	24:n:267:LEU:CB	2.67	0.59
1:A:1268:ARG:HE	1:A:1301:TYR:HD2	1.50	0.59
1:A:1327:THR:HG21	5:L:35:U:H5'	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:88:U:H2'	5:L:17:U:C6	2.37	0.59
13:R:253:LEU:O	13:R:257:ASN:CB	2.51	0.59
1:A:484:PHE:CZ	3:D:81:A:C5	2.91	0.58
1:A:905:TYR:HD2	1:A:908:ASP:N	2.01	0.58
1:A:1458:TRP:CZ2	1:A:1489:PRO:HB2	2.38	0.58
2:C:468:LEU:O	2:C:578:TYR:HA	2.04	0.58
25:q:194:THR:OG1	25:q:213:CYS:HB3	2.03	0.58
25:q:378:LYS:CG	25:q:423:THR:O	2.51	0.58
31:l:66:GLY:HA2	31:l:69:ILE:HD12	1.85	0.58
1:A:620:HIS:HB3	1:A:669:TYR:CE2	2.38	0.58
1:A:757:GLU:OE1	10:O:202:GLU:HG3	2.04	0.58
1:A:899:PRO:HD3	1:A:1006:ARG:CZ	2.34	0.58
1:A:2025:ILE:HD12	1:A:2058:LEU:HD11	1.84	0.58
3:D:167:A:N7	33:g:63:ARG:NE	2.51	0.58
11:P:34:ILE:HD11	18:d:155:LEU:HD13	1.85	0.58
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.86	0.58
1:A:532:ASN:ND2	3:D:84:A:OP2	2.35	0.58
1:A:912:LEU:HD21	1:A:916:LEU:HD11	1.85	0.58
1:A:791:ARG:NH2	11:P:173:LYS:HD2	2.18	0.58
5:L:21:G:N7	14:S:5:HIS:HB2	2.17	0.58
14:S:6:ARG:HG3	14:S:6:ARG:HH11	1.68	0.58
28:u:86:ASN:ND2	29:w:32:LYS:HD3	2.13	0.58
5:L:1102:C:C2'	5:L:1103:C:H6	2.15	0.58
23:v:687:LEU:HD23	23:v:713:ILE:HA	1.84	0.58
1:A:168:LEU:HD21	1:A:626:LEU:HD21	1.86	0.58
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.03	0.58
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.38	0.58
4:E:42:A:O2'	4:E:43:C:OP1	2.19	0.58
5:L:120:G:N1	28:u:33:GLU:O	2.36	0.58
11:P:101:PRO:O	11:P:103:ASN:N	2.36	0.58
13:R:121:ARG:HB3	13:R:125:GLY:H	1.69	0.58
18:d:329:UNK:CB	23:v:642:GLU:HG3	2.33	0.58
19:F:29:LYS:O	19:F:35:ASN:ND2	2.36	0.58
2:C:407:ASN:OD1	2:C:408:LEU:N	2.36	0.58
2:C:868:VAL:HG11	2:C:876:VAL:HG21	1.86	0.58
25:p:98:LEU:HD12	25:q:98:LEU:HD23	1.85	0.58
1:A:900:PHE:CD2	1:A:901:PRO:N	2.72	0.58
4:E:1:G:O2'	15:T:101:GLU:OE1	2.17	0.58
5:L:119:G:C5	32:z:20:LYS:HE2	2.39	0.58
11:P:35:ALA:HB3	18:d:158:LYS:HE2	1.86	0.58
12:Q:49:SER:HG	12:Q:52:SER:N	2.00	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:SER:O	1:A:384:LYS:N	2.37	0.58
1:A:1711:VAL:HG11	1:A:1789:ASN:HB3	1.86	0.58
2:C:775:ILE:HD12	2:C:817:GLN:HE21	1.69	0.58
4:E:85:C:OP1	4:E:85:C:O4'	2.21	0.58
5:L:5:A:H5''	22:I:114:THR:HG21	1.76	0.58
5:L:78:G:H5'	13:R:155:GLN:NE2	2.19	0.58
5:L:112:A:N7	33:e:63:ARG:NE	2.51	0.58
8:N:108:U:C4'	8:N:109:U:OP2	2.51	0.58
10:O:379:LYS:HA	11:P:47:ARG:HH21	1.68	0.58
15:T:31:ARG:HH11	15:T:31:ARG:CG	2.14	0.58
18:d:205:TRP:CH2	18:d:221:VAL:HG21	2.38	0.58
23:v:611:THR:CB	23:v:623:LEU:CD1	2.81	0.58
24:n:60:ARG:C	24:n:62:THR:N	2.59	0.58
10:O:392:MET:HG3	10:O:393:VAL:H	1.69	0.58
12:Q:54:ASN:ND2	13:R:70:LEU:HD12	2.19	0.58
27:s:47:GLU:HG3	35:b:15:TYR:CG	2.38	0.58
1:A:672:LYS:NZ	3:D:86:G:OP2	2.37	0.57
1:A:907:ASN:OD1	1:A:1504:TYR:CZ	2.57	0.57
19:F:23:LEU:C	21:H:18:GLN:HE22	2.12	0.57
1:A:133:GLU:HG3	1:A:560:THR:HA	1.85	0.57
1:A:1899:TRP:HE3	1:A:1905:LEU:HD22	1.68	0.57
4:E:89:U:C5'	5:L:17:U:OP2	2.50	0.57
11:P:112:ILE:HG12	12:Q:25:MET:HE3	1.86	0.57
16:Z:470:LEU:HD12	16:Z:471:GLY:H	1.69	0.57
24:n:357:ASP:CG	24:n:358:ASN:N	2.62	0.57
25:q:472:ALA:HB2	25:q:477:MET:CG	2.35	0.57
2:C:220:ASN:O	2:C:647:ASN:ND2	2.29	0.57
4:E:92:C:O2'	4:E:93:A:O4'	2.22	0.57
11:P:37:ASN:ND2	11:P:145:PRO:HD3	2.19	0.57
13:R:159:ARG:HD3	13:R:205:LEU:H	1.69	0.57
14:S:8:GLN:OE1	14:S:10:GLU:O	2.21	0.57
1:A:1281:ASN:ND2	1:A:1285:VAL:HG21	2.18	0.57
1:A:1441:PHE:HB3	16:Z:303:LEU:HD11	1.86	0.57
1:A:1449:ASN:HB3	16:Z:338:THR:HG21	1.86	0.57
3:D:174:G:C5	32:m:20:LYS:HE2	2.39	0.57
6:M:505:A:H3'	6:M:506:U:H4'	1.86	0.57
12:Q:49:SER:HG	12:Q:52:SER:HB2	1.69	0.57
24:n:302:PHE:CG	24:n:307:LYS:HA	2.39	0.57
1:A:1801:SER:O	1:A:1804:THR:OG1	2.19	0.57
1:A:2027:LEU:O	33:e:71:ASN:ND2	2.38	0.57
12:Q:219:ILE:O	12:Q:222:THR:OG1	2.16	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:G:29:ASP:O	20:G:32:THR:OG1	2.19	0.57
12:Q:105:LYS:HG3	17:c:215:GLU:HG3	1.87	0.57
12:Q:217:TRP:CD1	13:R:187:LYS:CE	2.88	0.57
1:A:217:TRP:O	1:A:220:THR:OG1	2.22	0.57
1:A:344:ASN:OD1	9:J:3:TYR:HD2	1.87	0.57
10:O:187:ASP:OD1	10:O:188:VAL:N	2.37	0.57
12:Q:217:TRP:HZ3	13:R:171:ASP:OD1	1.85	0.57
16:Z:192:GLU:HB3	16:Z:195:GLU:OE2	2.03	0.57
32:z:43:VAL:HG11	32:z:85:ILE:HD12	1.87	0.57
1:A:421:ALA:HB3	1:A:469:ILE:HD12	1.85	0.57
1:A:740:GLU:HG3	1:A:741:ILE:H	1.68	0.57
1:A:928:ARG:CG	5:L:30:A:N3	2.64	0.57
1:A:1376:ASN:O	1:A:1377:SER:OG	2.17	0.57
3:D:174:G:O6	32:m:20:LYS:HB3	2.05	0.57
12:Q:215:PRO:CB	12:Q:217:TRP:CE3	2.88	0.57
2:C:468:LEU:HD11	2:C:491:GLY:C	2.23	0.57
10:O:245:ASP:HB3	10:O:247:VAL:HG22	1.86	0.57
19:F:49:MET:HE1	19:F:97:PHE:HE1	1.70	0.57
24:n:253:VAL:HG21	24:n:298:ALA:HA	1.87	0.57
1:A:174:LYS:O	1:A:178:ASN:ND2	2.35	0.57
1:A:376:ARG:HD2	2:C:910:GLU:OE2	2.05	0.57
1:A:837:GLY:HA3	1:A:1317:ARG:HH22	1.70	0.57
5:L:5:A:P	22:I:114:THR:CG2	2.89	0.57
5:L:119:G:O6	32:z:20:LYS:HB3	2.05	0.57
21:H:72:GLU:HA	21:H:75:ILE:HG12	1.85	0.57
1:A:591:LEU:HB3	1:A:599:LEU:HD11	1.86	0.56
1:A:805:PRO:HG2	1:A:808:ILE:HD12	1.86	0.56
2:C:510:ARG:NH1	2:C:533:GLU:OE1	2.37	0.56
2:C:794:GLN:HB3	2:C:838:ILE:HG21	1.87	0.56
5:L:67:A:H2'	5:L:68:U:H6	1.70	0.56
6:M:498:C:OP1	19:F:41:ILE:CD1	2.47	0.56
11:P:174:ASN:HD21	11:P:177:GLY:C	2.12	0.56
12:Q:87:ARG:HH22	12:Q:122:GLY:C	2.13	0.56
16:Z:307:GLU:OE2	16:Z:311:LYS:HE3	2.04	0.56
19:F:36:LYS:HG3	19:F:38:HIS:H	1.70	0.56
1:A:716:ARG:HD2	3:D:112:C:C1'	2.34	0.56
1:A:1748:ILE:O	1:A:1751:TYR:N	2.39	0.56
2:C:447:GLU:O	2:C:451:ASN:ND2	2.38	0.56
2:C:811:GLU:HB3	2:C:812:PRO:HD2	1.86	0.56
2:C:952:PRO:HB2	2:C:955:LYS:HB2	1.87	0.56
5:L:55:G:H2'	5:L:56:U:H6	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:73:U:H2'	5:L:74:C:H6	1.70	0.56
11:P:105:LEU:HD21	12:Q:12:ILE:HB	1.87	0.56
12:Q:103:GLU:OE1	13:R:131:ARG:NH1	2.37	0.56
16:Z:118:LEU:HB3	16:Z:154:VAL:HG22	1.88	0.56
1:A:165:LEU:HD13	1:A:578:MET:HB3	1.86	0.56
1:A:420:PRO:HG2	1:A:423:PHE:HB2	1.87	0.56
1:A:817:LYS:HG2	10:O:399:GLU:OE2	2.05	0.56
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.41	0.56
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.40	0.56
1:A:1559:HIS:O	1:A:1612:PRO:HG2	2.05	0.56
1:A:1731:LYS:O	1:A:1769:SER:OG	2.19	0.56
2:C:755:TYR:HB2	2:C:757:TRP:HB2	1.87	0.56
4:E:39:G:N1	13:R:120:TYR:O	2.38	0.56
5:L:14:C:OP2	22:I:209:ARG:NH2	2.37	0.56
5:L:24:U:H5''	5:L:25:A:OP2	2.05	0.56
5:L:71:C:C2	5:L:72:C:C5	2.93	0.56
5:L:100:G:H2'	5:L:101:U:H6	1.71	0.56
10:O:118:LEU:HD21	11:P:48:GLN:HB3	1.87	0.56
10:O:121:GLN:NE2	11:P:49:SER:O	2.38	0.56
16:Z:174:TRP:HZ2	16:Z:197:LEU:CD1	2.16	0.56
17:c:63:THR:HG22	17:c:93:ARG:HH12	1.70	0.56
1:A:1454:SER:HA	1:A:1487:GLY:HA2	1.86	0.56
1:A:1880:PHE:HD1	1:A:1891:LEU:HD21	1.69	0.56
4:E:38:U:H4'	13:R:121:ARG:HH12	1.71	0.56
5:L:96:A:H2'	5:L:97:U:H6	1.71	0.56
12:Q:226:LEU:HD12	12:Q:226:LEU:O	2.05	0.56
13:R:63:ARG:HH21	15:T:143:HIS:CD2	2.22	0.56
21:H:79:ASN:HA	21:H:82:LEU:HD12	1.88	0.56
22:I:111:ASN:O	22:I:114:THR:OG1	2.21	0.56
1:A:318:LEU:HD13	1:A:501:LEU:HD23	1.88	0.56
1:A:1604:ARG:HA	1:A:1640:THR:HG21	1.86	0.56
2:C:265:PHE:CD2	2:C:295:ILE:HD12	2.40	0.56
5:L:72:C:C2	5:L:73:U:C5	2.94	0.56
5:L:101:U:H2'	5:L:102:U:H6	1.70	0.56
12:Q:119:LYS:C	12:Q:120:LEU:HD23	2.31	0.56
16:Z:470:LEU:HD12	16:Z:471:GLY:N	2.20	0.56
18:d:51:ARG:NE	18:d:75:GLU:OE2	2.37	0.56
20:G:16:LEU:O	20:G:18:LYS:N	2.38	0.56
2:C:163:ASP:OD2	2:C:548:ARG:NH1	2.38	0.56
4:E:1:G:H2'	4:E:2:U:C6	2.41	0.56
5:L:106:A:H2'	5:L:107:U:H6	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:1116:A:N3	5:L:1117:G:C8	2.74	0.56
12:Q:86:LEU:O	12:Q:89:HIS:N	2.38	0.56
18:d:199:MET:O	18:d:202:TRP:N	2.38	0.56
19:F:4:ARG:NH1	19:F:5:LYS:NZ	2.51	0.56
28:u:77:LEU:HD21	28:u:80:ILE:CD1	2.36	0.56
2:C:770:ASN:OD1	2:C:771:GLY:N	2.39	0.56
24:n:59:ARG:NH1	24:n:59:ARG:HG2	2.21	0.56
32:m:43:VAL:HG11	32:m:85:ILE:HD12	1.87	0.56
1:A:352:PHE:O	9:J:10:SER:OG	2.21	0.56
1:A:856:TRP:CD1	14:S:174:VAL:HG21	2.41	0.56
3:D:79:C:H3'	3:D:80:G:H5'	1.88	0.56
5:L:21:G:N7	14:S:5:HIS:CB	2.69	0.56
5:L:70:A:H2'	5:L:71:C:H6	1.71	0.56
24:n:200:ARG:CG	24:n:201:ASP:N	2.69	0.56
35:b:68:PRO:O	35:b:69:ASP:CB	2.54	0.56
1:A:381:SER:HB3	9:J:3:TYR:O	2.06	0.56
1:A:1014:LYS:NZ	1:A:1016:SER:OG	2.32	0.56
2:C:200:CYS:SG	2:C:210:ILE:HD12	2.46	0.56
2:C:758:ASP:HB3	2:C:761:ALA:HB3	1.87	0.56
5:L:72:C:H2'	5:L:73:U:H6	1.70	0.56
5:L:98:U:C2	5:L:99:U:C5	2.94	0.56
5:L:103:A:H2'	5:L:104:C:H6	1.71	0.56
12:Q:240:LEU:HD12	12:Q:241:ILE:N	2.20	0.56
1:A:905:TYR:CD2	1:A:908:ASP:N	2.73	0.56
17:c:210:ASP:OD1	17:c:211:ILE:N	2.39	0.56
2:C:806:GLY:H	2:C:810:GLU:HA	1.71	0.55
5:L:61:A:H2'	5:L:62:C:H6	1.71	0.55
5:L:73:U:C2	5:L:74:C:C5	2.94	0.55
10:O:326:ALA:HB2	10:O:356:LEU:HD11	1.88	0.55
16:Z:192:GLU:O	16:Z:195:GLU:HG2	2.05	0.55
2:C:110:LYS:HE2	2:C:552:PRO:HG2	1.88	0.55
2:C:360:ARG:CZ	2:C:362:LYS:HD3	2.36	0.55
2:C:863:GLU:OE2	2:C:934:HIS:ND1	2.40	0.55
4:E:74:U:H5	14:S:27:HIS:CG	2.24	0.55
5:L:83:U:C2	5:L:84:C:C5	2.94	0.55
5:L:1105:C:N4	34:a:97:LYS:NZ	2.54	0.55
14:S:167:GLN:O	14:S:171:HIS:CB	2.54	0.55
16:Z:178:ARG:HA	16:Z:198:PHE:CE1	2.41	0.55
17:c:35:LYS:O	17:c:38:SER:OG	2.18	0.55
25:q:294:HIS:CG	25:q:338:LEU:H	2.24	0.55
35:b:44:PRO:O	35:b:69:ASP:CB	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:905:TYR:CD2	1:A:907:ASN:N	2.73	0.55
1:A:1122:ASP:OD2	1:A:1163:ARG:NE	2.29	0.55
1:A:1172:PHE:HZ	1:A:1230:ILE:HD11	1.71	0.55
2:C:468:LEU:HD21	2:C:493:LEU:CD2	2.36	0.55
4:E:52:G:N2	14:S:5:HIS:CE1	2.62	0.55
5:L:62:C:C2	5:L:63:U:C5	2.94	0.55
5:L:82:C:C2	5:L:83:U:C5	2.93	0.55
5:L:97:U:H2'	5:L:98:U:H6	1.71	0.55
10:O:147:ILE:HD13	10:O:408:ASP:HA	1.88	0.55
10:O:210:ASP:OD2	14:S:38:LYS:NZ	2.40	0.55
1:A:194:HIS:CD2	11:P:122:LEU:HD22	2.42	0.55
1:A:1161:TYR:CD1	1:A:1170:MET:HG2	2.40	0.55
2:C:787:LEU:HD12	2:C:790:LYS:HD2	1.88	0.55
5:L:61:A:C4	5:L:62:C:C5	2.95	0.55
5:L:97:U:C2	5:L:98:U:C5	2.94	0.55
5:L:98:U:H2'	5:L:99:U:H6	1.71	0.55
5:L:1100:A:C2	5:L:1101:C:C2	2.95	0.55
1:A:614:ARG:NH2	7:B:98:A:O3'	2.39	0.55
2:C:613:ARG:NH1	2:C:614:GLU:OE2	2.39	0.55
5:L:82:C:H2'	5:L:83:U:H6	1.70	0.55
5:L:100:G:C4	5:L:101:U:C5	2.95	0.55
10:O:306:HIS:CD2	11:P:147:LEU:HD11	2.41	0.55
21:H:34:ARG:HH12	21:H:36:ARG:NH1	2.04	0.55
1:A:1279:VAL:O	1:A:1299:LYS:NZ	2.40	0.55
5:L:101:U:C2	5:L:102:U:C5	2.94	0.55
12:Q:53:ASN:ND2	12:Q:54:ASN:H	2.02	0.55
13:R:96:GLU:HG2	13:R:188:TYR:CE2	2.35	0.55
16:Z:170:HIS:NE2	16:Z:174:TRP:HZ3	1.90	0.55
16:Z:203:LYS:O	16:Z:204:ASP:CB	2.55	0.55
27:s:47:GLU:HG3	35:b:15:TYR:HB2	1.87	0.55
5:L:15:C:O2	5:L:16:U:H5	1.90	0.55
5:L:15:C:H2'	5:L:16:U:OP2	2.07	0.55
5:L:19:U:O4'	11:P:178:TYR:CE2	2.59	0.55
5:L:58:A:H2'	5:L:59:C:H6	1.71	0.55
5:L:67:A:C4	5:L:68:U:C5	2.95	0.55
5:L:67:A:H2	5:L:85:A:H61	1.51	0.55
11:P:174:ASN:HB2	11:P:185:ARG:HH12	1.70	0.55
28:i:77:LEU:HD21	28:i:80:ILE:CD1	2.36	0.55
27:s:19:LYS:HZ1	35:b:34:LEU:CB	2.19	0.55
2:C:223:ASP:CG	2:C:647:ASN:HD21	2.15	0.55
2:C:437:ASP:OD1	2:C:441:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:2:U:H2'	4:E:3:U:C6	2.41	0.55
5:L:71:C:H2'	5:L:72:C:H6	1.71	0.55
11:P:196:THR:HA	17:c:90:MET:HE1	1.87	0.55
12:Q:257:GLU:HG3	12:Q:258:LEU:N	2.21	0.55
21:H:51:LYS:HG2	21:H:89:TRP:CZ3	2.42	0.55
25:q:292:TYR:CB	25:q:335:SER:HA	2.37	0.55
2:C:326:GLU:O	2:C:329:SER:N	2.40	0.55
5:L:55:G:C4	5:L:56:U:C5	2.95	0.55
5:L:81:G:C4	5:L:82:C:C5	2.94	0.55
5:L:81:G:H2'	5:L:82:C:H6	1.71	0.55
12:Q:226:LEU:HD11	12:Q:227:LEU:CD2	2.29	0.55
15:T:13:PRO:HG2	15:T:77:LEU:HA	1.87	0.55
17:c:39:LEU:HD21	17:c:159:LEU:HD21	1.87	0.55
18:d:99:ILE:O	18:d:102:TRP:N	2.39	0.55
23:v:718:SER:HG	23:v:725:THR:HG21	1.68	0.55
1:A:1282:ASP:OD1	1:A:1283:GLU:N	2.34	0.55
2:C:869:HIS:HD2	2:C:925:LEU:HB3	1.71	0.55
5:L:70:A:C4	5:L:71:C:C5	2.95	0.55
12:Q:116:LYS:HD3	12:Q:118:VAL:CG1	2.37	0.55
17:c:227:ILE:HG12	22:I:152:ILE:HG22	1.89	0.55
24:n:55:GLU:OE2	24:n:58:ARG:HD2	2.05	0.55
1:A:411:ILE:HD11	2:C:898:PRO:HG3	1.89	0.54
1:A:928:ARG:NH1	5:L:30:A:O3'	2.40	0.54
1:A:1458:TRP:NE1	1:A:1489:PRO:HD2	2.22	0.54
4:E:38:U:O4	13:R:222:LEU:HA	2.06	0.54
5:L:1102:C:C2'	5:L:1103:C:C6	2.80	0.54
13:R:146:LEU:HD23	13:R:147:ASN:H	1.70	0.54
16:Z:184:GLN:HE21	16:Z:185:GLU:N	2.05	0.54
18:d:265:ALA:O	18:d:269:ILE:HD12	2.07	0.54
1:A:1046:SER:HA	1:A:1251:TYR:O	2.07	0.54
2:C:291:ILE:O	2:C:294:ASN:N	2.39	0.54
4:E:38:U:H4'	13:R:121:ARG:NH1	2.23	0.54
4:E:56:A:H2'	4:E:57:U:C6	2.42	0.54
4:E:63:G:HO2'	14:S:8:GLN:CG	2.10	0.54
10:O:125:TRP:HE1	10:O:437:GLU:HB3	1.72	0.54
12:Q:208:TYR:O	12:Q:209:ASN:HB3	2.07	0.54
16:Z:204:ASP:C	16:Z:205:TYR:CD2	2.86	0.54
1:A:570:GLN:O	1:A:574:GLN:HG2	2.07	0.54
1:A:1372:LYS:HG2	1:A:1383:PHE:HD2	1.72	0.54
2:C:140:GLY:O	2:C:146:LYS:NZ	2.40	0.54
2:C:183:GLN:NE2	2:C:654:CYS:HA	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:58:A:C4	5:L:59:C:C5	2.95	0.54
5:L:62:C:H2'	5:L:63:U:H6	1.71	0.54
5:L:96:A:C4	5:L:97:U:C5	2.95	0.54
17:c:95:ALA:O	17:c:98:CYS:N	2.40	0.54
1:A:1468:ALA:HA	1:A:1473:ARG:HG2	1.88	0.54
2:C:251:GLN:NE2	2:C:255:GLN:HE21	2.06	0.54
2:C:697:ARG:NH1	2:C:852:THR:HG1	2.05	0.54
16:Z:149:ARG:CZ	16:Z:193:SER:HB3	2.37	0.54
23:v:606:GLN:HA	23:v:609:GLU:CG	2.37	0.54
1:A:653:ILE:HD11	1:A:704:TRP:CE2	2.43	0.54
2:C:139:ILE:HD12	2:C:252:LEU:HD22	1.89	0.54
2:C:477:ASP:HB2	2:C:628:TYR:CE1	2.43	0.54
5:L:83:U:H2'	5:L:84:C:H6	1.71	0.54
5:L:99:U:C5'	24:n:326:VAL:HG21	2.38	0.54
23:v:682:LYS:O	23:v:686:ILE:HG12	2.08	0.54
1:A:413:ASN:ND2	1:A:419:THR:OG1	2.40	0.54
1:A:874:ILE:O	1:A:875:THR:OG1	2.19	0.54
1:A:908:ASP:OD1	1:A:994:TYR:OH	2.21	0.54
1:A:2012:LEU:HD23	1:A:2015:LEU:HD12	1.89	0.54
2:C:101:GLN:NE2	3:D:77:A:N6	2.55	0.54
6:M:503:A:H2'	6:M:504:C:O4'	2.06	0.54
11:P:176:ASN:O	17:c:162:THR:HB	2.07	0.54
27:k:31:ILE:HD11	27:k:49:ILE:HD12	1.90	0.54
1:A:606:THR:OG1	1:A:609:GLU:HG2	2.08	0.54
1:A:1883:ASN:HD21	1:A:1886:THR:HG23	1.73	0.54
2:C:501:ILE:HD11	2:C:567:ILE:HD12	1.89	0.54
4:E:66:C:H6	4:E:66:C:C3'	2.20	0.54
5:L:1114:G:H2'	5:L:1115:G:C8	2.43	0.54
12:Q:226:LEU:CD2	12:Q:262:PHE:HE1	2.20	0.54
16:Z:179:TYR:C	16:Z:179:TYR:CD1	2.86	0.54
18:d:185:VAL:HA	18:d:188:ILE:HD12	1.89	0.54
24:n:55:GLU:O	24:n:59:ARG:HB2	2.07	0.54
1:A:756:LEU:CD1	14:S:8:GLN:NE2	2.65	0.54
1:A:1041:VAL:HG13	1:A:1253:LYS:HG2	1.90	0.54
1:A:1305:SER:OG	1:A:1307:GLU:OE1	2.24	0.54
2:C:231:ALA:HB2	2:C:473:LEU:HD11	1.89	0.54
4:E:38:U:O2	13:R:196:LYS:NZ	2.40	0.54
10:O:379:LYS:HD3	11:P:47:ARG:NH2	2.23	0.54
1:A:168:LEU:O	1:A:171:ALA:N	2.41	0.54
1:A:756:LEU:CD1	14:S:8:GLN:HE22	2.19	0.54
1:A:854:ARG:HD2	1:A:1095:MET:HE3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:936:GLU:O	1:A:940:ILE:HD12	2.08	0.54
1:A:1813:TYR:OH	1:A:1817:GLU:OE2	2.17	0.54
1:A:1990:ASN:ND2	1:A:1993:ASP:O	2.40	0.54
2:C:314:ALA:HB1	2:C:321:THR:HG22	1.89	0.54
2:C:468:LEU:CD1	2:C:491:GLY:CA	2.72	0.54
3:D:174:G:H8	33:g:99:ASP:OD2	1.91	0.54
5:L:15:C:C2'	5:L:16:U:OP2	2.56	0.54
5:L:1114:G:H8	5:L:1114:G:O5'	1.91	0.54
14:S:7:PRO:O	14:S:8:GLN:HB2	2.08	0.54
21:H:46:GLU:OE2	21:H:50:TRP:NE1	2.40	0.54
27:s:98:GLU:O	35:b:53:PRO:CA	2.56	0.54
1:A:364:TYR:CD1	1:A:1209:LYS:HE2	2.43	0.54
1:A:1051:GLU:HB3	1:A:1167:ARG:HH21	1.73	0.54
5:L:103:A:C4	5:L:104:C:C5	2.95	0.54
5:L:106:A:C4	5:L:107:U:C5	2.95	0.54
10:O:155:PHE:CZ	10:O:415:ILE:HG12	2.42	0.54
10:O:348:GLU:CD	10:O:349:LYS:H	2.16	0.54
11:P:170:SER:O	11:P:185:ARG:NH2	2.41	0.54
24:n:318:ARG:HD3	24:n:327:PRO:CG	2.38	0.54
1:A:372:ARG:HH21	2:C:973:ARG:HG3	1.73	0.53
1:A:923:TYR:HD1	1:A:926:LYS:HD3	1.73	0.53
1:A:1144:PHE:CZ	1:A:1162:THR:HG21	2.43	0.53
1:A:2030:PRO:HD3	33:e:71:ASN:HB3	1.89	0.53
2:C:499:VAL:O	2:C:536:SER:HA	2.08	0.53
12:Q:82:ILE:HG23	12:Q:86:LEU:HD23	1.90	0.53
12:Q:215:PRO:CG	12:Q:217:TRP:CE3	2.91	0.53
13:R:72:PHE:CE2	13:R:94:PRO:HG3	2.43	0.53
16:Z:179:TYR:O	16:Z:179:TYR:HD1	1.91	0.53
22:I:102:LYS:NZ	22:I:106:GLU:OE2	2.36	0.53
25:q:467:LEU:CG	25:q:481:CYS:SG	2.96	0.53
1:A:810:LYS:NZ	10:O:397:GLU:HB3	2.23	0.53
1:A:902:PRO:HG2	1:A:904:THR:O	2.08	0.53
4:E:14:C:H4'	4:E:15:C:O5'	2.08	0.53
5:L:15:C:O2'	5:L:16:U:H6	1.77	0.53
24:n:72:TRP:O	24:n:73:SER:OG	2.16	0.53
26:t:7:VAL:CG1	26:t:154:VAL:CB	2.73	0.53
10:O:127:ALA:HB3	10:O:428:GLN:HE21	1.73	0.53
12:Q:24:ARG:HD2	15:T:116:ASN:HD22	1.73	0.53
12:Q:253:PHE:HB3	12:Q:258:LEU:HD12	1.90	0.53
14:S:7:PRO:HG2	14:S:9:LEU:HD23	1.89	0.53
16:Z:181:LEU:HD21	16:Z:191:ARG:CG	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:c:110:ASP:OD1	17:c:111:SER:N	2.42	0.53
23:v:726:ARG:HA	23:v:729:TYR:CD2	2.43	0.53
1:A:900:PHE:CD2	1:A:900:PHE:C	2.86	0.53
2:C:766:TRP:CG	2:C:792:LYS:HE3	2.43	0.53
17:c:223:PRO:O	17:c:224:MET:HG2	2.08	0.53
19:F:27:MET:HE3	19:F:31:LEU:HD21	1.90	0.53
1:A:602:THR:HG22	19:F:10:TYR:HD2	1.73	0.53
1:A:886:MET:SD	1:A:1120:VAL:HG22	2.49	0.53
1:A:1047:ALA:O	1:A:1250:VAL:HA	2.09	0.53
1:A:1443:TYR:OH	1:A:1545:ASP:OD2	2.15	0.53
2:C:77:LEU:HD11	10:O:135:ILE:HG12	1.90	0.53
2:C:137:GLY:N	2:C:232:SER:OG	2.40	0.53
2:C:766:TRP:CE3	2:C:792:LYS:HG3	2.44	0.53
4:E:55:G:N7	17:c:35:LYS:HG2	2.24	0.53
13:R:4:TRP:HZ3	13:R:5:ARG:CZ	2.21	0.53
19:F:99:THR:O	19:F:101:PRO:HD3	2.08	0.53
25:p:102:LEU:O	25:p:105:LEU:CG	2.57	0.53
1:A:342:LEU:HD13	1:A:392:ASN:HD22	1.74	0.53
1:A:426:PRO:CB	16:Z:201:ARG:HG2	2.18	0.53
1:A:899:PRO:CD	1:A:1006:ARG:CZ	2.86	0.53
1:A:1963:LEU:HD13	1:A:1965:PHE:HE2	1.73	0.53
10:O:218:ARG:HB3	10:O:256:ARG:HD3	1.91	0.53
22:I:182:GLN:O	22:I:186:ALA:HB2	2.07	0.53
25:q:292:TYR:CB	25:q:336:GLY:N	2.72	0.53
25:q:341:ASP:O	25:q:342:SER:CB	2.56	0.53
1:A:259:GLU:HG3	1:A:260:PRO:HD2	1.91	0.53
1:A:905:TYR:HD2	1:A:908:ASP:H	1.54	0.53
1:A:928:ARG:NE	5:L:32:G:C8	2.77	0.53
1:A:1063:PHE:HB2	17:c:83:GLN:NE2	2.23	0.53
1:A:1652:HIS:CE1	19:F:17:PRO:HB2	2.43	0.53
10:O:190:VAL:HG22	10:O:197:LEU:HD13	1.89	0.53
12:Q:56:ILE:HD12	13:R:105:ARG:HH22	1.72	0.53
25:q:298:ASN:O	25:q:299:THR:CB	2.57	0.53
1:A:835:LYS:HD2	14:S:173:HIS:CE1	2.44	0.53
2:C:240:ASP:OD1	2:C:269:LYS:HD3	2.08	0.53
2:C:794:GLN:NE2	2:C:835:LYS:HA	2.24	0.53
4:E:49:A:C2'	4:E:50:G:H5'	2.39	0.53
5:L:19:U:O4'	11:P:178:TYR:HE2	1.91	0.53
5:L:119:G:H8	33:e:99:ASP:OD2	1.91	0.53
5:L:1103:C:C6	5:L:1114:G:N2	2.76	0.53
13:R:73:CYS:HB2	13:R:89:TYR:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Z:168:LYS:NZ	16:Z:168:LYS:O	2.37	0.53
1:A:412:GLN:OE1	1:A:412:GLN:N	2.42	0.53
1:A:488:ARG:CZ	3:D:81:A:N6	2.72	0.53
1:A:1389:TYR:CE1	1:A:1401:SER:HB3	2.44	0.53
1:A:2007:ARG:HH12	1:A:2048:TRP:HB3	1.73	0.53
3:D:79:C:H3'	3:D:79:C:O2	2.08	0.53
5:L:1097:G:N1	5:L:1119:C:N3	2.50	0.53
11:P:147:LEU:HD12	11:P:147:LEU:O	2.08	0.53
24:n:55:GLU:O	24:n:58:ARG:HG3	2.09	0.53
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.23	0.53
1:A:1184:ASP:O	1:A:1188:ALA:HB2	2.09	0.53
2:C:671:SER:OG	2:C:672:ASP:N	2.42	0.53
27:s:31:ILE:HD11	27:s:49:ILE:HD12	1.90	0.53
1:A:728:ASN:HD22	4:E:72:C:HO2'	1.50	0.52
1:A:928:ARG:NH2	5:L:30:A:O2'	2.42	0.52
2:C:286:LEU:CD2	16:Z:182:GLN:HB3	2.34	0.52
2:C:539:VAL:HG13	2:C:564:ILE:HG23	1.91	0.52
5:L:25:A:H3'	5:L:26:G:H5''	1.91	0.52
8:N:110:A:C2	13:R:46:ARG:HD2	2.43	0.52
17:c:162:THR:HG23	22:I:196:ILE:HG21	1.90	0.52
23:v:560:UNK:HA	23:v:570:THR:HG21	1.89	0.52
24:n:444:CYS:O	24:n:444:CYS:SG	2.67	0.52
1:A:732:ARG:NH2	4:E:71:G:OP2	2.43	0.52
1:A:907:ASN:OD1	1:A:1504:TYR:CE2	2.62	0.52
3:D:78:A:H4'	3:D:79:C:OP1	2.09	0.52
25:p:124:ALA:O	25:p:127:LEU:CG	2.58	0.52
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.74	0.52
5:L:1116:A:N6	5:L:1117:G:C6	2.78	0.52
10:O:138:HIS:CE1	10:O:159:SER:HB2	2.43	0.52
12:Q:213:SER:HA	13:R:237:ARG:NH2	2.25	0.52
21:H:86:PHE:CE2	21:H:90:LYS:HE3	2.44	0.52
1:A:291:LYS:HE2	1:A:292:LYS:HD3	1.90	0.52
1:A:426:PRO:CG	16:Z:201:ARG:CZ	2.83	0.52
1:A:484:PHE:O	1:A:485:PRO:C	2.52	0.52
1:A:1145:MET:SD	1:A:1160:LEU:HD22	2.49	0.52
1:A:1406:LEU:HB2	16:Z:307:GLU:HG3	1.91	0.52
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.41	0.52
2:C:316:THR:OG1	36:C:1500:GTP:N7	2.42	0.52
2:C:883:ARG:HH22	2:C:913:GLY:H	1.58	0.52
5:L:1107:C:H5'	5:L:1107:C:C6	2.44	0.52
18:d:238:TRP:HD1	18:d:242:GLU:OE2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ASP:OD1	1:A:596:ASN:ND2	2.43	0.52
1:A:1067:ASN:ND2	17:c:81:PRO:HB2	2.22	0.52
1:A:1449:ASN:ND2	16:Z:339:PHE:O	2.42	0.52
1:A:1567:PHE:CE1	1:A:1827:GLN:HB2	2.44	0.52
1:A:1899:TRP:HH2	1:A:1909:ALA:HA	1.75	0.52
10:O:365:PHE:HZ	10:O:373:LEU:HD22	1.75	0.52
10:O:397:GLU:HG3	10:O:400:ARG:HH12	1.74	0.52
12:Q:25:MET:HB2	12:Q:45:HIS:O	2.09	0.52
12:Q:208:TYR:HB2	12:Q:290:ILE:HD12	1.92	0.52
12:Q:215:PRO:CG	12:Q:217:TRP:CZ3	2.91	0.52
13:R:138:TYR:HD1	13:R:183:PHE:HE1	1.58	0.52
15:T:150:CYS:SG	15:T:151:ARG:N	2.82	0.52
16:Z:179:TYR:C	16:Z:179:TYR:HD1	2.17	0.52
19:F:68:LYS:HA	19:F:84:LEU:HD23	1.91	0.52
2:C:656:LEU:HD13	2:C:670:ILE:HD13	1.91	0.52
10:O:112:VAL:O	10:O:115:TYR:N	2.43	0.52
10:O:446:LEU:N	10:O:446:LEU:CD1	2.73	0.52
13:R:124:MET:HE3	13:R:227:ASN:ND2	2.25	0.52
1:A:1539:LEU:O	1:A:1542:TYR:N	2.39	0.52
2:C:468:LEU:HD13	2:C:492:LEU:C	2.34	0.52
12:Q:116:LYS:HD3	12:Q:118:VAL:HG11	1.92	0.52
12:Q:207:LEU:HB3	12:Q:210:ILE:HD11	1.90	0.52
12:Q:214:ILE:HD11	12:Q:218:LYS:HG3	1.89	0.52
18:d:136:TRP:CZ3	18:d:159:TRP:HB2	2.45	0.52
19:F:84:LEU:O	19:F:96:ALA:HA	2.10	0.52
25:q:405:ASP:CB	26:t:30:ASN:CG	2.83	0.52
1:A:299:LYS:HA	1:A:493:MET:HG2	1.91	0.52
2:C:416:ASP:HB2	2:C:419:PRO:HD2	1.91	0.52
5:L:1105:C:H42	34:a:97:LYS:NZ	2.07	0.52
5:L:1116:A:C5	5:L:1117:G:C5	2.97	0.52
2:C:246:THR:HG23	2:C:248:VAL:HG12	1.91	0.52
12:Q:13:CYS:N	12:Q:71:CYS:SG	2.80	0.52
14:S:8:GLN:CG	14:S:10:GLU:O	2.56	0.52
15:T:131:GLU:OE2	15:T:135:LYS:NZ	2.43	0.52
16:Z:305:GLY:HA2	16:Z:342:PHE:CE1	2.44	0.52
16:Z:480:ARG:HD3	16:Z:483:ILE:HD12	1.92	0.52
28:i:27:VAL:HG22	28:i:92:SER:HB2	1.91	0.52
1:A:1902:GLN:HG2	1:A:1908:LEU:HD22	1.91	0.52
6:M:505:A:OP2	6:M:505:A:H4'	2.10	0.52
10:O:407:PHE:CE1	10:O:414:LEU:HD13	2.45	0.52
24:n:51:PHE:HE1	24:n:55:GLU:HG3	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:PRO:CG	16:Z:201:ARG:CG	2.87	0.51
1:A:932:SER:O	1:A:936:GLU:HG3	2.10	0.51
1:A:1661:ILE:HG13	1:A:1809:ASN:ND2	2.25	0.51
1:A:1711:VAL:HG12	1:A:1712:SER:H	1.76	0.51
2:C:315:SER:HB3	2:C:320:PHE:CE1	2.46	0.51
2:C:393:LYS:O	2:C:397:LYS:HB2	2.10	0.51
10:O:365:PHE:CZ	10:O:373:LEU:HD22	2.44	0.51
17:c:202:LYS:O	17:c:204:LYS:N	2.37	0.51
22:I:196:ILE:H	22:I:200:ASN:HD22	1.58	0.51
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.44	0.51
5:L:1102:C:O2'	5:L:1103:C:H5'	2.10	0.51
27:s:47:GLU:CB	35:b:15:TYR:CG	2.93	0.51
1:A:416:GLU:HG2	1:A:418:ASP:N	2.25	0.51
1:A:1275:MET:C	1:A:1277:GLU:H	2.18	0.51
1:A:1843:LEU:HD22	1:A:1851:PHE:HZ	1.76	0.51
2:C:103:HIS:CD2	2:C:104:THR:HG23	2.46	0.51
2:C:768:PHE:HB3	2:C:773:VAL:HG23	1.91	0.51
21:H:58:ILE:O	21:H:62:SER:HB3	2.09	0.51
1:A:134:MET:HE1	15:T:107:ARG:HH11	1.76	0.51
1:A:1283:GLU:HB3	16:Z:341:LYS:HB2	1.92	0.51
1:A:2030:PRO:HD3	33:e:71:ASN:CB	2.41	0.51
2:C:468:LEU:HD13	2:C:492:LEU:N	2.10	0.51
2:C:795:ILE:HG23	2:C:842:MET:HE3	1.93	0.51
12:Q:291:ILE:HG23	12:Q:292:PRO:HA	1.92	0.51
27:s:99:ASP:CA	35:b:53:PRO:CB	2.88	0.51
2:C:829:VAL:O	2:C:830:ASN:ND2	2.43	0.51
2:C:885:GLY:HA3	2:C:906:VAL:HG23	1.91	0.51
5:L:18:U:C6	22:I:202:GLN:HG3	2.45	0.51
10:O:239:ILE:HB	10:O:251:TRP:HB2	1.93	0.51
18:d:182:TRP:O	18:d:186:ARG:NH1	2.44	0.51
19:F:14:ASP:CG	19:F:15:TYR:H	2.19	0.51
24:n:59:ARG:HH11	24:n:59:ARG:CG	2.24	0.51
1:A:138:HIS:CD2	15:T:49:LEU:HD22	2.45	0.51
1:A:837:GLY:HA3	1:A:1317:ARG:NH2	2.26	0.51
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.44	0.51
2:C:289:ASN:O	2:C:293:ALA:CB	2.59	0.51
3:D:103:A:O2'	3:D:104:G:OP2	2.23	0.51
4:E:66:C:C6	4:E:66:C:H3'	2.43	0.51
10:O:221:TYR:O	10:O:251:TRP:HH2	1.93	0.51
17:c:237:ILE:HD11	18:d:114:CYS:SG	2.51	0.51
22:I:190:TYR:HE2	22:I:195:PHE:HZ	1.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:613:SER:O	19:F:2:SER:OG	2.28	0.51
1:A:867:ILE:HG21	1:A:1101:TYR:CD1	2.45	0.51
1:A:1144:PHE:CE2	1:A:1145:MET:HE2	2.46	0.51
2:C:341:ILE:HG13	2:C:342:ASP:N	2.26	0.51
5:L:18:U:C5	22:I:202:GLN:HG3	2.46	0.51
12:Q:209:ASN:HB3	12:Q:288:ILE:O	2.10	0.51
25:q:309:GLY:O	25:q:325:HIS:CG	2.63	0.51
10:O:238:LEU:HD21	11:P:74:ILE:HD13	1.92	0.51
19:F:67:LYS:HB2	19:F:85:THR:OG1	2.10	0.51
28:u:86:ASN:HD21	29:w:32:LYS:NZ	2.09	0.51
1:A:468:LEU:HD12	1:A:469:ILE:HG12	1.91	0.51
1:A:503:LYS:HA	1:A:506:PHE:CE2	2.46	0.51
1:A:984:VAL:HG12	1:A:985:ASP:H	1.76	0.51
1:A:1476:ALA:C	1:A:1478:GLU:H	2.19	0.51
1:A:1540:ASN:O	1:A:1543:ARG:HB3	2.11	0.51
1:A:1687:HIS:CG	1:A:1688:PRO:HD2	2.46	0.51
1:A:1773:VAL:HA	1:A:1788:GLY:HA2	1.92	0.51
6:M:502:C:O2'	6:M:503:A:O4'	2.28	0.51
11:P:202:MET:HA	17:c:79:GLU:OE1	2.11	0.51
12:Q:209:ASN:CG	12:Q:288:ILE:O	2.54	0.51
12:Q:256:SER:O	12:Q:259:GLY:CA	2.58	0.51
17:c:176:LEU:O	17:c:179:SER:OG	2.26	0.51
25:r:124:ALA:O	25:r:127:LEU:CG	2.59	0.51
28:u:27:VAL:HG22	28:u:92:SER:HB2	1.91	0.51
2:C:101:GLN:NE2	3:D:75:A:H61	2.07	0.51
2:C:437:ASP:O	2:C:440:THR:N	2.43	0.51
16:Z:355:ARG:O	16:Z:358:GLN:HB2	2.10	0.51
25:o:51:VAL:CG2	25:p:20:ARG:CB	2.77	0.51
1:A:649:LEU:O	1:A:652:GLY:N	2.45	0.50
1:A:1881:THR:OG1	1:A:1890:PHE:HB2	2.11	0.50
4:E:66:C:H4'	11:P:133:LYS:HD3	1.93	0.50
21:H:41:VAL:HG21	21:H:92:TRP:CZ3	2.46	0.50
24:n:200:ARG:CG	24:n:201:ASP:H	2.24	0.50
1:A:933:GLU:OE1	1:A:933:GLU:N	2.36	0.50
1:A:1041:VAL:CG1	1:A:1253:LYS:HG2	2.40	0.50
10:O:152:ASN:ND2	10:O:409:LYS:HB3	2.18	0.50
10:O:308:LYS:HA	11:P:148:HIS:CE1	2.46	0.50
13:R:154:ALA:O	13:R:158:SER:OG	2.26	0.50
17:c:230:THR:O	17:c:232:THR:N	2.36	0.50
24:n:252:ASP:C	24:n:253:VAL:HG23	2.37	0.50
1:A:488:ARG:CZ	3:D:81:A:H61	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1658:HIS:NE2	1:A:1700:ASP:OD2	2.40	0.50
2:C:602:VAL:HG12	2:C:908:VAL:HG21	1.93	0.50
2:C:918:LEU:HD23	2:C:928:CYS:HB2	1.94	0.50
2:C:968:MET:O	2:C:972:ARG:NH1	2.44	0.50
3:D:31:G:C2'	3:D:32:G:H5'	2.41	0.50
12:Q:109:MET:SD	17:c:218:VAL:HA	2.51	0.50
12:Q:205:PHE:CD2	12:Q:291:ILE:HD11	2.46	0.50
17:c:14:THR:HG23	17:c:17:GLU:H	1.76	0.50
18:d:225:ALA:O	18:d:228:THR:OG1	2.24	0.50
21:H:41:VAL:HG12	21:H:42:LYS:N	2.26	0.50
25:q:175:PRO:O	25:q:467:LEU:CG	2.59	0.50
1:A:687:ILE:HD11	1:A:706:PRO:HG2	1.93	0.50
1:A:905:TYR:HB3	1:A:908:ASP:OD2	2.10	0.50
1:A:1111:SER:HA	1:A:1514:PHE:HE2	1.76	0.50
1:A:1870:VAL:HG21	5:L:46:C:C5'	2.38	0.50
1:A:2009:THR:O	1:A:2013:ARG:HG3	2.11	0.50
5:L:1116:A:C5	5:L:1117:G:N7	2.79	0.50
12:Q:119:LYS:O	12:Q:120:LEU:HD23	2.11	0.50
12:Q:205:PHE:O	12:Q:250:GLY:HA2	2.11	0.50
18:d:45:GLU:OE2	18:d:48:ARG:NH1	2.44	0.50
18:d:222:TYR:HB3	18:d:250:PHE:CD1	2.47	0.50
1:A:255:ILE:CG2	1:A:640:ARG:HG2	2.41	0.50
1:A:1907:GLN:O	1:A:1911:TRP:HD1	1.94	0.50
4:E:86:G:N3	18:d:57:TYR:CZ	2.80	0.50
4:E:87:U:OP1	4:E:87:U:C4'	2.60	0.50
10:O:414:LEU:HB3	10:O:426:TRP:HB2	1.93	0.50
12:Q:220:THR:HG23	12:Q:240:LEU:HD23	1.94	0.50
16:Z:178:ARG:HG2	16:Z:198:PHE:CZ	2.40	0.50
24:n:263:PHE:HB2	24:n:275:TYR:HB2	1.94	0.50
1:A:329:TYR:CE1	2:C:919:ARG:HD2	2.46	0.50
1:A:839:HIS:ND1	1:A:839:HIS:O	2.45	0.50
2:C:362:LYS:HE2	2:C:365:GLU:HB3	1.93	0.50
2:C:675:THR:OG1	2:C:676:VAL:N	2.44	0.50
2:C:683:ASN:ND2	2:C:713:GLU:HG2	2.26	0.50
2:C:752:ARG:HD3	2:C:759:SER:HA	1.92	0.50
11:P:35:ALA:O	11:P:37:ASN:N	2.45	0.50
13:R:4:TRP:NE1	13:R:92:HIS:HB3	2.27	0.50
22:I:184:GLN:HA	22:I:187:LYS:NZ	2.26	0.50
25:o:100:SER:O	25:o:103:ASP:CG	2.55	0.50
1:A:1755:LYS:HE3	1:A:1759:TYR:CE2	2.42	0.50
2:C:738:ASP:HA	2:C:768:PHE:CZ	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:738:ASP:HA	2:C:768:PHE:HZ	1.77	0.50
3:D:103:A:O2'	3:D:104:G:P	2.69	0.50
16:Z:416:GLY:O	16:Z:420:ILE:HD12	2.12	0.50
21:H:55:SER:HB3	21:H:89:TRP:CZ3	2.46	0.50
22:I:187:LYS:HA	22:I:201:LYS:NZ	2.27	0.50
1:A:128:TYR:HA	15:T:112:ASN:HD21	1.76	0.50
1:A:460:PRO:HG3	2:C:376:PHE:CD1	2.47	0.50
1:A:1862:VAL:HA	1:A:1871:ALA:O	2.12	0.50
4:E:88:U:C6	5:L:17:U:C6	3.00	0.50
16:Z:395:GLU:OE2	16:Z:439:ARG:NH2	2.30	0.50
1:A:790:TRP:NE1	1:A:794:LYS:HE3	2.26	0.50
1:A:1348:GLU:HG2	1:A:1446:THR:HB	1.93	0.50
1:A:1364:GLU:OE1	1:A:1403:SER:OG	2.29	0.50
2:C:758:ASP:OD1	2:C:759:SER:N	2.45	0.50
3:D:174:G:OP2	29:h:76:ASN:HB2	2.12	0.50
5:L:19:U:H1'	11:P:178:TYR:CE2	2.46	0.50
10:O:277:VAL:HG11	11:P:58:PRO:HB2	1.94	0.50
11:P:43:PHE:CD1	11:P:147:LEU:HD13	2.47	0.50
13:R:9:ALA:HB2	13:R:60:GLY:O	2.11	0.50
15:T:151:ARG:CD	24:n:71:SER:HA	2.42	0.50
15:T:151:ARG:NH2	24:n:69:TRP:O	2.45	0.50
19:F:31:LEU:O	21:H:33:GLN:NE2	2.45	0.50
22:I:184:GLN:HA	22:I:187:LYS:HZ3	1.76	0.50
1:A:427:SER:HA	16:Z:202:GLN:CB	2.41	0.49
1:A:724:ARG:HH21	1:A:725:TYR:HE1	1.60	0.49
1:A:1849:LYS:HG2	1:A:1932:GLN:HB2	1.93	0.49
1:A:1915:GLU:O	1:A:1918:SER:OG	2.17	0.49
2:C:363:PRO:O	2:C:364:PHE:CD2	2.65	0.49
10:O:201:SER:OG	10:O:202:GLU:N	2.45	0.49
10:O:343:THR:HB	11:P:47:ARG:HD3	1.94	0.49
13:R:75:PHE:O	13:R:80:MET:N	2.46	0.49
15:T:151:ARG:HD2	24:n:71:SER:HA	1.94	0.49
17:c:81:PRO:O	17:c:83:GLN:HG3	2.12	0.49
28:i:86:ASN:HD21	29:h:32:LYS:NZ	2.09	0.49
1:A:143:ILE:HD12	1:A:573:ARG:NH2	2.27	0.49
1:A:514:TYR:HB3	1:A:518:VAL:HG21	1.93	0.49
1:A:1315:ARG:O	1:A:1319:ILE:HD12	2.12	0.49
1:A:1906:SER:OG	6:M:493:A:P	2.70	0.49
4:E:91:A:N3	18:d:99:ILE:CD1	2.74	0.49
6:M:492:U:H2'	6:M:493:A:C8	2.47	0.49
6:M:493:A:H2'	6:M:494:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:R:22:ILE:HG13	13:R:22:ILE:O	2.13	0.49
23:v:730:GLN:CA	23:v:733:ILE:CD1	2.86	0.49
24:n:225:SER:OG	24:n:226:PHE:N	2.45	0.49
1:A:288:GLU:OE1	1:A:288:GLU:N	2.45	0.49
1:A:310:ASN:OD1	1:A:313:ARG:NH2	2.43	0.49
1:A:590:TYR:OH	1:A:609:GLU:OE1	2.21	0.49
1:A:1458:TRP:HZ2	1:A:1489:PRO:HB2	1.74	0.49
4:E:58:C:OP1	19:F:63:LYS:NZ	2.45	0.49
5:L:1:A:H1'	23:v:504:UNK:H	1.68	0.49
9:J:23:SER:HA	16:Z:310:HIS:HD2	1.76	0.49
11:P:157:GLU:HG2	22:I:95:ILE:HA	1.94	0.49
12:Q:105:LYS:O	12:Q:109:MET:HB2	2.11	0.49
12:Q:209:ASN:HD21	12:Q:288:ILE:CG2	2.23	0.49
12:Q:215:PRO:HG3	12:Q:217:TRP:CE3	2.47	0.49
15:T:143:HIS:O	15:T:151:ARG:HG2	2.13	0.49
29:w:74:ARG:HD3	33:e:101:VAL:O	2.12	0.49
1:A:555:LYS:HA	15:T:113:GLU:OE1	2.12	0.49
1:A:1348:GLU:OE2	1:A:1447:TRP:N	2.45	0.49
2:C:468:LEU:CD1	2:C:492:LEU:CA	2.82	0.49
5:L:15:C:O2'	5:L:16:U:C5'	2.53	0.49
5:L:1120:G:H8	5:L:1120:G:C5'	2.26	0.49
12:Q:53:ASN:HD22	12:Q:53:ASN:N	2.10	0.49
16:Z:168:LYS:HZ3	16:Z:171:ASP:CB	2.25	0.49
1:A:512:GLU:OE1	7:B:89:A:N6	2.43	0.49
1:A:600:LYS:HB2	19:F:10:TYR:HB2	1.94	0.49
1:A:618:SER:OG	1:A:725:TYR:HB3	2.13	0.49
6:M:499:U:OP2	20:G:10:LYS:NZ	2.45	0.49
8:N:108:U:H4'	8:N:109:U:OP2	2.12	0.49
17:c:513:ILE:HA	17:c:516:LYS:CG	2.43	0.49
18:d:238:TRP:HD1	18:d:242:GLU:CD	2.20	0.49
19:F:85:THR:HA	19:F:95:ILE:O	2.12	0.49
24:n:324:ILE:O	24:n:325:ASN:CB	2.60	0.49
1:A:218:SER:O	1:A:221:TRP:HB3	2.12	0.49
1:A:1602:PRO:HD2	1:A:1605:ARG:HH21	1.78	0.49
5:L:1109:C:N4	34:a:108:THR:HA	2.28	0.49
15:T:133:ALA:O	15:T:137:GLY:N	2.45	0.49
23:v:606:GLN:HA	23:v:609:GLU:HG3	1.94	0.49
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.48	0.49
1:A:1993:ASP:CG	1:A:2038:HIS:HB3	2.38	0.49
2:C:607:LEU:HD23	2:C:670:ILE:HG12	1.95	0.49
5:L:19:U:N1	11:P:178:TYR:CD2	2.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:c:93:ARG:NH1	17:c:101:ARG:HH22	2.10	0.49
1:A:912:LEU:HD23	1:A:916:LEU:HD12	1.95	0.49
2:C:69:PRO:HB3	10:O:390:ARG:HG2	1.94	0.49
2:C:468:LEU:HA	2:C:491:GLY:HA3	1.94	0.49
10:O:344:ASN:HD22	11:P:45:PRO:HG3	1.78	0.49
12:Q:220:THR:HG23	12:Q:240:LEU:CD2	2.43	0.49
16:Z:150:LEU:O	16:Z:154:VAL:HG23	2.12	0.49
23:v:726:ARG:HA	23:v:729:TYR:CE2	2.48	0.49
29:h:74:ARG:HD3	33:g:101:VAL:O	2.12	0.49
2:C:89:PRO:HA	10:O:212:GLU:O	2.13	0.49
2:C:154:VAL:O	2:C:157:SER:N	2.46	0.49
2:C:461:LYS:CD	2:C:461:LYS:N	2.75	0.49
12:Q:109:MET:HE1	17:c:218:VAL:HG13	1.93	0.49
14:S:7:PRO:O	14:S:8:GLN:CB	2.61	0.49
16:Z:168:LYS:NZ	16:Z:171:ASP:CB	2.73	0.49
21:H:28:ASP:HB3	21:H:30:SER:H	1.78	0.49
21:H:32:TYR:HB2	21:H:50:TRP:HH2	1.78	0.49
1:A:344:ASN:OD1	9:J:3:TYR:CD2	2.66	0.49
1:A:1111:SER:HA	1:A:1514:PHE:CE2	2.48	0.49
1:A:1282:ASP:CG	1:A:1283:GLU:H	2.20	0.49
2:C:122:TYR:CE2	31:l:82:PRO:HD3	2.48	0.49
5:L:1:A:C4	23:v:504:UNK:N	2.75	0.49
17:c:46:ARG:O	17:c:50:LEU:HB2	2.11	0.49
18:d:40:LEU:HD21	18:d:44:ARG:HH21	1.78	0.49
18:d:65:MET:HE3	18:d:95:ASP:HB3	1.94	0.49
1:A:1677:GLN:HB3	1:A:1706:VAL:HB	1.94	0.48
1:A:1812:LEU:HB3	1:A:1816:ARG:HH12	1.78	0.48
2:C:194:ASN:O	2:C:214:ASP:HB3	2.13	0.48
13:R:64:GLY:O	13:R:68:GLY:N	2.45	0.48
16:Z:299:LEU:HD21	16:Z:343:TYR:CE1	2.47	0.48
16:Z:433:LEU:HD21	16:Z:472:LEU:HD12	1.94	0.48
24:n:368:LYS:O	24:n:406:ARG:CB	2.61	0.48
25:q:405:ASP:HB2	26:t:30:ASN:CG	2.38	0.48
27:s:19:LYS:HZ3	35:b:34:LEU:CB	2.25	0.48
1:A:1080:ASP:HB3	17:c:82:ASN:HD22	1.78	0.48
1:A:1695:ASN:O	1:A:1759:TYR:OH	2.13	0.48
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.28	0.48
2:C:271:ASP:OD1	2:C:272:ARG:N	2.46	0.48
12:Q:214:ILE:HD11	12:Q:218:LYS:CB	2.43	0.48
13:R:150:HIS:HB3	13:R:155:GLN:HG3	1.94	0.48
1:A:1094:ASP:CG	11:P:172:TRP:HE1	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1129:GLU:O	1:A:1132:THR:OG1	2.23	0.48
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.48	0.48
10:O:151:ASP:HB3	10:O:153:GLU:HG2	1.95	0.48
12:Q:209:ASN:HD21	12:Q:288:ILE:HG23	1.77	0.48
15:T:151:ARG:O	24:n:68:PRO:O	2.31	0.48
16:Z:413:CYS:O	16:Z:417:ARG:N	2.38	0.48
24:n:252:ASP:O	24:n:253:VAL:CG2	2.61	0.48
26:t:86:LEU:O	26:t:89:GLU:CG	2.61	0.48
1:A:898:ILE:HA	1:A:1006:ARG:HH12	1.77	0.48
1:A:925:SER:O	6:M:507:U:OP2	2.31	0.48
2:C:503:ASP:HB2	2:C:506:GLN:HG2	1.95	0.48
2:C:629:TYR:OH	2:C:658:ASP:OD2	2.18	0.48
4:E:42:A:H8	4:E:42:A:O5'	1.96	0.48
19:F:46:PRO:HG2	19:F:106:TYR:CE2	2.39	0.48
1:A:263:PRO:HG2	1:A:265:ASN:ND2	2.28	0.48
1:A:772:GLU:HG3	1:A:773:SER:H	1.78	0.48
1:A:984:VAL:HG12	1:A:985:ASP:N	2.28	0.48
1:A:1422:ILE:HD13	1:A:1425:PHE:CZ	2.47	0.48
5:L:119:G:OP2	29:w:76:ASN:HB2	2.12	0.48
10:O:327:CYS:SG	10:O:328:THR:N	2.87	0.48
11:P:101:PRO:C	11:P:103:ASN:H	2.20	0.48
16:Z:194:LEU:HD22	16:Z:194:LEU:C	2.38	0.48
16:Z:319:ASN:HA	16:Z:322:LYS:HD3	1.95	0.48
18:d:106:ILE:HG12	18:d:122:MET:HE3	1.96	0.48
1:A:269:ASP:OD1	1:A:270:SER:N	2.47	0.48
1:A:930:ASN:HB3	1:A:933:GLU:OE1	2.13	0.48
2:C:136:VAL:O	2:C:212:PHE:HA	2.14	0.48
2:C:700:GLU:HG2	2:C:701:GLU:O	2.14	0.48
12:Q:53:ASN:ND2	12:Q:53:ASN:N	2.60	0.48
14:S:40:ARG:HG2	14:S:41:LYS:H	1.78	0.48
19:F:49:MET:HB2	19:F:58:ILE:HB	1.96	0.48
23:v:712:CYS:O	23:v:713:ILE:C	2.57	0.48
24:n:59:ARG:HG2	24:n:59:ARG:HH11	1.79	0.48
1:A:518:VAL:HG11	1:A:689:TYR:CD2	2.48	0.48
1:A:849:LEU:HD12	1:A:973:GLU:HB3	1.96	0.48
1:A:1863:HIS:CD2	1:A:1873:LYS:HD2	2.49	0.48
2:C:282:MET:HE1	2:C:371:PRO:HD3	1.96	0.48
2:C:461:LYS:CD	2:C:461:LYS:H	2.27	0.48
2:C:471:HIS:HB2	2:C:592:PHE:CZ	2.49	0.48
2:C:737:ILE:HD12	2:C:747:LEU:HD11	1.95	0.48
10:O:160:ASN:HA	10:O:184:THR:OG1	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:194:HIS:NE2	10:O:237:ASP:OD1	2.44	0.48
11:P:220:ARG:O	11:P:224:GLU:HG2	2.14	0.48
18:d:200:GLN:OE1	18:d:200:GLN:N	2.38	0.48
1:A:484:PHE:CD1	1:A:484:PHE:C	2.91	0.48
1:A:705:GLN:HE21	1:A:709:ARG:CG	2.26	0.48
1:A:775:ARG:O	1:A:779:ALA:N	2.42	0.48
1:A:1156:HIS:HD2	1:A:1158:ILE:HB	1.79	0.48
1:A:2060:LEU:HD11	1:A:2083:ILE:HD11	1.95	0.48
3:D:43:G:N3	3:D:43:G:C2'	2.76	0.48
5:L:1116:A:N6	5:L:1117:G:O6	2.46	0.48
10:O:345:PHE:CD2	10:O:381:GLY:HA2	2.49	0.48
11:P:126:PHE:HA	12:Q:30:GLN:HB2	1.95	0.48
11:P:205:SER:OG	17:c:79:GLU:OE1	2.29	0.48
1:A:183:TRP:HE3	1:A:220:THR:HG21	1.79	0.48
1:A:333:LYS:O	1:A:336:PHE:N	2.47	0.48
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.96	0.48
1:A:905:TYR:HD2	1:A:907:ASN:N	2.11	0.48
1:A:926:LYS:HE3	1:A:929:LEU:HD23	1.95	0.48
1:A:1208:PRO:HB2	1:A:1417:GLN:O	2.14	0.48
1:A:1661:ILE:HG13	1:A:1809:ASN:HD21	1.79	0.48
2:C:760:LEU:C	2:C:764:ASN:HD22	2.22	0.48
10:O:250:LEU:HB2	10:O:260:ILE:HB	1.96	0.48
11:P:174:ASN:ND2	11:P:174:ASN:O	2.46	0.48
1:A:300:LYS:HA	1:A:492:LYS:HA	1.96	0.48
1:A:477:MET:HE2	2:C:278:LYS:HE3	1.95	0.48
4:E:28:U:H5''	15:T:118:SER:O	2.14	0.48
11:P:37:ASN:HD21	11:P:145:PRO:HD3	1.79	0.48
15:T:114:THR:OG1	15:T:118:SER:HA	2.14	0.48
16:Z:148:LEU:HD12	16:Z:190:LEU:HD21	1.96	0.48
16:Z:363:GLU:O	16:Z:367:GLN:HG2	2.13	0.48
18:d:105:TYR:HE2	18:d:121:LEU:HD13	1.79	0.48
25:q:214:ARG:HB3	25:q:217:ASP:CG	2.38	0.48
1:A:134:MET:HE2	15:T:107:ARG:HD2	1.95	0.47
1:A:480:TYR:CE2	2:C:275:LEU:HD23	2.49	0.47
1:A:484:PHE:CZ	3:D:81:A:C6	3.02	0.47
1:A:1368:GLN:NE2	1:A:1389:TYR:OH	2.47	0.47
1:A:1368:GLN:O	1:A:1372:LYS:HG3	2.14	0.47
1:A:1870:VAL:HB	5:L:46:C:C4'	2.36	0.47
10:O:418:GLU:OE1	10:O:424:LYS:NZ	2.30	0.47
17:c:226:GLY:O	22:I:151:LYS:NZ	2.28	0.47
1:A:376:ARG:CD	2:C:910:GLU:OE2	2.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1014:LYS:HG3	1:A:1016:SER:OG	2.15	0.47
1:A:2043:PHE:HB3	1:A:2047:GLN:HB2	1.96	0.47
1:A:2071:ILE:HA	1:A:2074:LEU:HD12	1.96	0.47
2:C:167:ASN:O	2:C:171:GLY:HA2	2.15	0.47
2:C:545:LEU:HD12	2:C:545:LEU:O	2.15	0.47
4:E:14:C:C4'	4:E:15:C:OP2	2.63	0.47
10:O:200:VAL:HG11	10:O:230:VAL:HG23	1.96	0.47
12:Q:291:ILE:HG23	12:Q:292:PRO:N	2.29	0.47
23:v:730:GLN:C	23:v:733:ILE:HD12	2.38	0.47
28:u:34:GLN:HE21	28:u:37:ILE:HD12	1.79	0.47
1:A:518:VAL:HG11	1:A:689:TYR:HD2	1.79	0.47
1:A:653:ILE:HD11	1:A:704:TRP:NE1	2.30	0.47
1:A:872:PRO:HD3	11:P:201:PHE:CE1	2.48	0.47
1:A:2018:ASN:HB3	1:A:2021:SER:OG	2.14	0.47
2:C:418:GLN:HB3	2:C:419:PRO:HD3	1.94	0.47
2:C:707:SER:H	2:C:824:SER:HB3	1.80	0.47
4:E:12:A:H2'	4:E:12:A:N3	2.29	0.47
5:L:15:C:C5	22:I:209:ARG:HG2	2.49	0.47
12:Q:75:MET:HE1	13:R:130:PHE:CE1	2.49	0.47
16:Z:378:THR:HA	16:Z:381:LEU:HD12	1.96	0.47
24:n:51:PHE:HE1	24:n:55:GLU:CG	2.27	0.47
25:q:395:GLN:CG	25:q:421:THR:O	2.63	0.47
1:A:183:TRP:CD1	1:A:184:GLU:HG3	2.49	0.47
1:A:470:LEU:O	1:A:473:THR:HG22	2.15	0.47
1:A:617:ASN:O	1:A:621:LEU:HB3	2.15	0.47
1:A:1180:GLU:HA	1:A:1183:THR:HG22	1.96	0.47
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.49	0.47
12:Q:77:ASP:OD1	12:Q:78:SER:N	2.47	0.47
12:Q:227:LEU:HD21	12:Q:262:PHE:HD1	1.78	0.47
17:c:33:TRP:O	17:c:36:VAL:N	2.47	0.47
21:H:68:PRO:O	21:H:70:LEU:N	2.48	0.47
33:e:49:ARG:HD2	33:e:49:ARG:HA	1.64	0.47
1:A:912:LEU:CD2	1:A:916:LEU:CD1	2.93	0.47
1:A:1064:THR:HG22	17:c:81:PRO:HD2	1.95	0.47
1:A:1650:ARG:CZ	6:M:495:A:N7	2.77	0.47
2:C:735:LEU:HG	2:C:736:ASP:O	2.15	0.47
4:E:49:A:H2'	4:E:50:G:H5'	1.96	0.47
5:L:119:G:N7	32:z:20:LYS:CE	2.77	0.47
13:R:146:LEU:HD23	13:R:147:ASN:N	2.30	0.47
17:c:13:TRP:CE2	17:c:51:ARG:HD2	2.49	0.47
24:n:60:ARG:O	24:n:63:ARG:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:n:380:HIS:CG	24:n:381:SER:H	2.33	0.47
1:A:165:LEU:O	1:A:622:MET:HE1	2.15	0.47
1:A:199:ILE:HD12	1:A:578:MET:HE1	1.96	0.47
1:A:320:ASP:HB3	1:A:483:PRO:HG2	1.96	0.47
1:A:1329:THR:HG21	1:A:1600:GLN:HA	1.94	0.47
1:A:1339:LEU:HD22	1:A:1440:ILE:HD12	1.97	0.47
1:A:1810:PRO:O	1:A:1814:VAL:HG23	2.15	0.47
2:C:251:GLN:HE21	2:C:255:GLN:HG2	1.79	0.47
2:C:362:LYS:O	2:C:364:PHE:N	2.47	0.47
5:L:71:C:H2'	5:L:72:C:C6	2.49	0.47
5:L:81:G:H2'	5:L:82:C:C6	2.50	0.47
10:O:229:THR:HG21	10:O:272:VAL:N	2.30	0.47
10:O:379:LYS:HD3	11:P:47:ARG:HH22	1.79	0.47
18:d:149:VAL:HA	18:d:152:VAL:HG22	1.95	0.47
21:H:35:PRO:HD2	21:H:92:TRP:HH2	1.79	0.47
23:v:645:ARG:NE	23:v:669:TYR:OH	2.48	0.47
2:C:139:ILE:O	2:C:237:ILE:HA	2.15	0.47
2:C:206:LYS:CD	2:C:208:ARG:HE	2.18	0.47
3:D:30:A:H2'	3:D:31:G:O4'	2.15	0.47
4:E:28:U:H1'	15:T:121:ILE:HD13	1.96	0.47
5:L:101:U:H2'	5:L:102:U:C6	2.50	0.47
5:L:1115:G:H2'	5:L:1116:A:C8	2.50	0.47
6:M:499:U:O2'	8:N:101:U:O2	2.32	0.47
12:Q:256:SER:O	12:Q:260:GLU:OE1	2.32	0.47
16:Z:436:LEU:HD21	16:Z:473:LEU:HD11	1.97	0.47
17:c:243:GLN:O	17:c:247:LYS:HG2	2.15	0.47
17:c:581:GLN:O	17:c:584:LEU:CG	2.63	0.47
18:d:145:SER:HA	22:I:112:LEU:HD11	1.97	0.47
24:n:292:HIS:NE2	24:n:310:SER:OG	2.43	0.47
31:y:30:ARG:C	31:y:47:VAL:HG23	2.40	0.47
1:A:1880:PHE:HA	1:A:1891:LEU:HD23	1.97	0.47
8:N:108:U:H1'	8:N:109:U:OP1	2.15	0.47
16:Z:203:LYS:HA	16:Z:203:LYS:HD3	1.67	0.47
18:d:105:TYR:CE2	18:d:121:LEU:HD13	2.49	0.47
19:F:38:HIS:CE1	19:F:67:LYS:HB3	2.50	0.47
25:q:472:ALA:CB	25:q:477:MET:CG	2.93	0.47
1:A:756:LEU:CG	14:S:8:GLN:HE22	2.26	0.47
4:E:15:C:OP2	4:E:15:C:H6	1.98	0.47
4:E:59:A:H3'	4:E:60:G:H5''	1.97	0.47
5:L:31:A:O2'	5:L:32:G:H5'	2.15	0.47
5:L:1115:G:H2'	5:L:1116:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:y:39:SER:O	31:y:41:ASN:N	2.48	0.47
1:A:266:LEU:HD23	1:A:268:LEU:H	1.79	0.47
1:A:376:ARG:HH11	2:C:910:GLU:CD	2.23	0.47
1:A:1051:GLU:HG2	1:A:1169:TYR:CD1	2.50	0.47
1:A:1690:LYS:HD2	1:A:1698:ALA:H	1.79	0.47
1:A:1870:VAL:CG2	5:L:46:C:H5''	2.40	0.47
2:C:746:LYS:O	2:C:750:ILE:HG12	2.15	0.47
10:O:343:THR:HB	11:P:47:ARG:HB2	1.96	0.47
17:c:148:GLU:HA	17:c:151:MET:HE3	1.97	0.47
1:A:488:ARG:NH1	3:D:81:A:H61	2.12	0.46
1:A:1275:MET:HE1	1:A:1299:LYS:HD2	1.95	0.46
2:C:360:ARG:HG2	2:C:362:LYS:HB2	1.97	0.46
2:C:365:GLU:CG	2:C:366:ASN:H	2.25	0.46
3:D:103:A:O4'	9:J:12:LYS:NZ	2.48	0.46
4:E:42:A:HO2'	4:E:43:C:P	2.38	0.46
5:L:61:A:H2'	5:L:62:C:C6	2.50	0.46
13:R:33:TRP:HD1	13:R:34:TYR:CD1	2.33	0.46
18:d:37:ILE:HG21	18:d:43:LEU:HB2	1.97	0.46
19:F:75:TYR:CE2	19:F:76:LEU:HG	2.50	0.46
25:q:463:SER:O	25:q:464:ALA:CB	2.62	0.46
28:i:34:GLN:HE21	28:i:37:ILE:HD12	1.78	0.46
1:A:288:GLU:HG2	1:A:288:GLU:O	2.15	0.46
1:A:304:ASP:OD1	1:A:305:LEU:N	2.43	0.46
1:A:401:PRO:O	1:A:402:TRP:HB3	2.14	0.46
1:A:589:THR:OG1	13:R:38:SER:HB3	2.15	0.46
2:C:292:ILE:HG12	2:C:311:ILE:HD13	1.97	0.46
2:C:468:LEU:HD12	2:C:492:LEU:H	1.59	0.46
4:E:1:G:H2'	4:E:2:U:H6	1.81	0.46
5:L:73:U:H2'	5:L:74:C:C6	2.49	0.46
5:L:80:G:H2'	5:L:81:G:H8	1.81	0.46
13:R:206:LEU:HD23	13:R:208:SER:O	2.14	0.46
13:R:245:GLU:HG3	13:R:249:MET:HE2	1.98	0.46
15:T:31:ARG:O	15:T:35:LYS:HG3	2.16	0.46
16:Z:382:ARG:HA	16:Z:422:PHE:CD2	2.50	0.46
17:c:68:GLU:OE1	17:c:68:GLU:N	2.46	0.46
18:d:200:GLN:HA	18:d:203:LEU:HB3	1.97	0.46
1:A:610:ARG:O	1:A:614:ARG:HG3	2.16	0.46
1:A:757:GLU:HG3	1:A:758:LEU:N	2.29	0.46
1:A:791:ARG:NH2	11:P:173:LYS:CD	2.78	0.46
1:A:971:MET:HE3	1:A:978:ILE:HG22	1.97	0.46
1:A:1626:GLN:NE2	1:A:1692:TYR:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2041:PRO:HG2	1:A:2043:PHE:HE2	1.80	0.46
2:C:353:TYR:HD1	2:C:371:PRO:HA	1.80	0.46
2:C:945:LEU:HD12	2:C:945:LEU:O	2.15	0.46
3:D:167:A:N7	33:g:63:ARG:CZ	2.78	0.46
3:D:179:U:OP1	33:g:79:LYS:HG2	2.15	0.46
5:L:25:A:C2'	5:L:27:A:OP2	2.63	0.46
5:L:98:U:H2'	5:L:99:U:C6	2.50	0.46
10:O:187:ASP:OD2	10:O:230:VAL:N	2.28	0.46
10:O:446:LEU:N	10:O:446:LEU:HD13	2.30	0.46
13:R:62:THR:HG21	13:R:89:TYR:O	2.15	0.46
16:Z:437:GLN:HG2	16:Z:473:LEU:HD23	1.97	0.46
1:A:756:LEU:HD21	14:S:8:GLN:HE22	1.79	0.46
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.97	0.46
1:A:1882:LEU:HD21	1:A:1965:PHE:CE1	2.50	0.46
2:C:567:ILE:HG22	2:C:571:TYR:HE2	1.81	0.46
4:E:64:U:HO2'	4:E:65:U:P	2.32	0.46
5:L:54:U:H2'	5:L:55:G:H8	1.81	0.46
5:L:112:A:N7	33:e:63:ARG:CZ	2.78	0.46
10:O:279:PRO:HG2	10:O:292:LEU:HB3	1.97	0.46
10:O:329:ASP:OD2	10:O:349:LYS:HG3	2.16	0.46
12:Q:217:TRP:CD1	12:Q:217:TRP:C	2.93	0.46
13:R:170:ILE:HG12	13:R:186:PHE:CE1	2.51	0.46
24:n:227:ASP:OD1	24:n:229:SER:OG	2.31	0.46
29:w:16:LYS:N	29:w:17:PRO:CD	2.79	0.46
1:A:177:GLU:CB	1:A:712:LEU:HD11	2.45	0.46
1:A:354:PRO:O	1:A:355:LEU:HB3	2.16	0.46
1:A:1011:ASN:HD21	1:A:1142:ASN:C	2.23	0.46
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	1.97	0.46
1:A:2063:TYR:CD1	1:A:2067:TYR:HD2	2.34	0.46
3:D:175:G:H4'	3:D:176:A:O4'	2.15	0.46
5:L:120:G:H4'	5:L:121:C:O4'	2.15	0.46
5:L:1099:G:N3	5:L:1099:G:C5'	2.73	0.46
14:S:5:HIS:O	14:S:6:ARG:HD2	2.15	0.46
14:S:159:ASP:OD1	14:S:160:MET:N	2.49	0.46
15:T:34:GLN:O	15:T:36:ASP:N	2.49	0.46
16:Z:152:ILE:HG23	16:Z:197:LEU:HB2	1.98	0.46
23:v:712:CYS:O	23:v:715:LYS:N	2.49	0.46
29:h:16:LYS:N	29:h:17:PRO:CD	2.79	0.46
1:A:133:GLU:OE2	1:A:561:THR:HG23	2.16	0.46
1:A:1327:THR:HG23	5:L:35:U:H5'	1.70	0.46
1:A:1773:VAL:HG22	1:A:1788:GLY:HA3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1805:ILE:HA	1:A:1808:ALA:HB3	1.97	0.46
5:L:58:A:H2'	5:L:59:C:C6	2.50	0.46
5:L:1100:A:C2	5:L:1101:C:N1	2.82	0.46
12:Q:98:ASN:O	12:Q:99:VAL:HG12	2.16	0.46
1:A:905:TYR:CE2	1:A:907:ASN:CB	2.86	0.46
1:A:1019:GLU:OE2	1:A:1027:LYS:NZ	2.31	0.46
2:C:144:SER:HA	2:C:240:ASP:OD1	2.14	0.46
2:C:306:PRO:HG2	2:C:349:TRP:CE3	2.51	0.46
2:C:544:LEU:HD23	2:C:562:VAL:HG12	1.97	0.46
3:D:174:G:N7	32:m:20:LYS:CE	2.77	0.46
10:O:317:HIS:CE1	10:O:319:LYS:HB2	2.51	0.46
10:O:317:HIS:HE1	10:O:319:LYS:HB2	1.81	0.46
15:T:61:ARG:HH22	15:T:101:GLU:HG2	1.81	0.46
17:c:75:ASP:O	17:c:79:GLU:HG2	2.16	0.46
18:d:140:LEU:HD21	18:d:155:LEU:HG	1.98	0.46
18:d:248:ASN:O	18:d:252:HIS:CB	2.64	0.46
22:I:205:GLU:O	22:I:208:SER:OG	2.21	0.46
28:i:86:ASN:ND2	29:h:32:LYS:NZ	2.64	0.46
1:A:617:ASN:O	1:A:621:LEU:CB	2.64	0.46
1:A:909:THR:O	1:A:913:VAL:HG23	2.14	0.46
1:A:1308:GLU:HG2	1:A:1311:LYS:HD2	1.98	0.46
1:A:1365:THR:HG22	1:A:1429:MET:HE3	1.97	0.46
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.51	0.46
2:C:268:ASN:HA	2:C:314:ALA:O	2.16	0.46
2:C:667:GLU:OE1	2:C:667:GLU:N	2.49	0.46
2:C:869:HIS:NE2	2:C:925:LEU:HD22	2.31	0.46
5:L:67:A:H2'	5:L:68:U:C6	2.50	0.46
10:O:427:LYS:HE2	10:O:430:GLU:OE2	2.16	0.46
16:Z:393:SER:OG	16:Z:430:GLU:OE1	2.19	0.46
16:Z:424:PHE:CE2	16:Z:448:MET:HE1	2.51	0.46
22:I:159:LYS:O	22:I:160:LEU:HB2	2.16	0.46
28:i:30:TRP:CE2	28:i:89:LEU:HD22	2.51	0.46
32:m:6:PHE:CZ	32:m:10:LEU:HD11	2.51	0.46
1:A:426:PRO:O	16:Z:202:GLN:CB	2.61	0.46
1:A:997:GLN:OE1	1:A:1511:ARG:NH2	2.49	0.46
1:A:1602:PRO:HD2	1:A:1605:ARG:NH2	2.31	0.46
2:C:464:PRO:O	2:C:465:GLU:HG2	2.16	0.46
5:L:15:C:C4	22:I:209:ARG:HG2	2.48	0.46
5:L:19:U:H1'	11:P:178:TYR:HE2	1.80	0.46
5:L:68:U:H2'	5:L:69:G:H8	1.81	0.46
5:L:79:A:H2'	5:L:80:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Z:205:TYR:C	16:Z:207:SER:H	2.23	0.46
17:c:64:GLU:HG2	17:c:65:PHE:N	2.29	0.46
18:d:214:ASN:O	18:d:218:THR:OG1	2.27	0.46
23:v:606:GLN:HA	23:v:609:GLU:HG2	1.98	0.46
27:k:20:LEU:O	27:k:31:ILE:HA	2.16	0.46
32:z:6:PHE:CZ	32:z:10:LEU:HD11	2.51	0.46
1:A:484:PHE:CZ	3:D:81:A:N7	2.84	0.46
1:A:1033:ASN:HD22	1:A:1288:LEU:HB3	1.81	0.46
2:C:101:GLN:NE2	3:D:77:A:H61	2.14	0.46
2:C:348:LEU:HD21	2:C:377:ILE:HD11	1.97	0.46
2:C:680:SER:OG	2:C:681:CYS:N	2.49	0.46
5:L:25:A:H2'	5:L:27:A:P	2.55	0.46
7:B:88:U:H2'	7:B:89:A:C4'	2.46	0.46
10:O:218:ARG:NH1	10:O:253:MET:O	2.49	0.46
10:O:348:GLU:CD	10:O:349:LYS:N	2.73	0.46
12:Q:222:THR:CA	12:Q:225:GLN:NE2	2.75	0.46
17:c:44:THR:HG22	17:c:45:ALA:N	2.30	0.46
31:l:39:SER:O	31:l:41:ASN:N	2.48	0.46
1:A:759:ARG:HH12	14:S:7:PRO:CB	2.26	0.45
1:A:772:GLU:HG3	1:A:773:SER:N	2.31	0.45
1:A:1434:GLU:HG2	1:A:1435:LYS:N	2.30	0.45
1:A:1716:LEU:HB2	1:A:1719:GLU:HG3	1.97	0.45
1:A:1964:PRO:HG3	1:A:2013:ARG:HG3	1.98	0.45
2:C:712:ALA:HA	2:C:817:GLN:O	2.16	0.45
5:L:69:G:H2'	5:L:70:A:H8	1.82	0.45
5:L:72:C:H2'	5:L:73:U:C6	2.50	0.45
5:L:78:G:H2'	5:L:79:A:H8	1.82	0.45
5:L:83:U:H2'	5:L:84:C:C6	2.50	0.45
5:L:106:A:H2'	5:L:107:U:C6	2.50	0.45
7:B:90:A:H61	9:J:6:ILE:HD11	1.81	0.45
10:O:265:HIS:NE2	10:O:283:SER:OG	2.43	0.45
12:Q:56:ILE:HD13	13:R:105:ARG:NH2	2.29	0.45
18:d:115:ILE:O	18:d:118:ALA:N	2.49	0.45
20:G:18:LYS:O	20:G:22:LYS:HG2	2.16	0.45
28:u:30:TRP:CE2	28:u:89:LEU:HD22	2.51	0.45
1:A:220:THR:O	1:A:224:MET:HG2	2.16	0.45
1:A:742:VAL:HG12	10:O:224:LEU:HD23	1.97	0.45
2:C:142:LEU:HB3	2:C:143:HIS:CD2	2.51	0.45
3:D:83:C:HO2'	3:D:84:A:P	2.38	0.45
3:D:167:A:N7	33:g:63:ARG:NH1	2.65	0.45
5:L:19:U:C6	11:P:178:TYR:HD2	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:62:C:H2'	5:L:63:U:C6	2.50	0.45
5:L:103:A:H2'	5:L:104:C:C6	2.50	0.45
5:L:119:G:C8	33:e:99:ASP:OD2	2.69	0.45
5:L:1103:C:N1	5:L:1114:G:N2	2.64	0.45
16:Z:152:ILE:HD13	16:Z:194:LEU:CA	2.40	0.45
18:d:169:TRP:O	18:d:172:PHE:N	2.49	0.45
19:F:99:THR:HG22	19:F:106:TYR:CE1	2.50	0.45
2:C:869:HIS:CD2	2:C:925:LEU:HD13	2.51	0.45
4:E:4:C:H2'	4:E:5:G:O4'	2.16	0.45
4:E:66:C:H5'	4:E:66:C:H6	1.79	0.45
5:L:112:A:N7	33:e:63:ARG:NH1	2.65	0.45
12:Q:53:ASN:ND2	12:Q:54:ASN:N	2.60	0.45
12:Q:245:LYS:HA	12:Q:245:LYS:HZ2	1.81	0.45
13:R:170:ILE:HG21	13:R:173:ILE:HG13	1.98	0.45
18:d:205:TRP:CE3	18:d:221:VAL:HG11	2.52	0.45
19:F:42:ARG:O	20:G:10:LYS:HE3	2.16	0.45
24:n:276:ASP:HB2	24:n:286:VAL:CG2	2.47	0.45
2:C:485:LEU:HA	2:C:563:LEU:HD23	1.98	0.45
2:C:760:LEU:O	2:C:764:ASN:ND2	2.49	0.45
5:L:100:G:H2'	5:L:101:U:C6	2.50	0.45
10:O:342:LEU:HB3	11:P:47:ARG:CD	2.47	0.45
12:Q:104:ALA:HB1	12:Q:110:LYS:CB	2.42	0.45
12:Q:206:PHE:HB3	12:Q:208:TYR:OH	2.17	0.45
16:Z:190:LEU:C	16:Z:190:LEU:CD2	2.86	0.45
19:F:38:HIS:CE1	19:F:67:LYS:HD3	2.52	0.45
19:F:51:CYS:O	19:F:55:ASN:HA	2.17	0.45
1:A:680:CYS:SG	1:A:711:TRP:NE1	2.89	0.45
1:A:1289:VAL:HG22	1:A:1296:ARG:HG2	1.97	0.45
1:A:1435:LYS:O	1:A:1436:LEU:HD12	2.16	0.45
1:A:1734:PHE:CD1	1:A:1773:VAL:HB	2.52	0.45
4:E:12:A:C2	4:E:13:A:O4'	2.70	0.45
10:O:252:ASP:HB2	10:O:259:VAL:CG2	2.47	0.45
10:O:372:VAL:HA	10:O:387:LEU:O	2.17	0.45
13:R:154:ALA:O	13:R:158:SER:CB	2.64	0.45
15:T:123:ARG:HD2	15:T:153:CYS:HB2	1.98	0.45
1:A:234:PHE:HE1	1:A:648:GLN:HG2	1.82	0.45
1:A:294:ASN:HB2	1:A:299:LYS:O	2.17	0.45
4:E:84:C:H3'	4:E:85:C:H5''	1.97	0.45
17:c:39:LEU:HD12	17:c:158:ARG:HH11	1.82	0.45
18:d:168:ALA:O	18:d:171:SER:OG	2.30	0.45
21:H:60:GLN:O	21:H:63:THR:OG1	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:r:62:LEU:O	25:r:63:THR:C	2.59	0.45
1:A:275:TYR:HB2	1:A:310:ASN:HD22	1.82	0.45
1:A:371:ASP:HB3	2:C:972:ARG:HD3	1.99	0.45
1:A:869:LYS:O	11:P:198:ASN:ND2	2.44	0.45
1:A:878:GLU:O	1:A:881:THR:OG1	2.26	0.45
1:A:911:ILE:CG2	1:A:997:GLN:CG	2.88	0.45
1:A:995:LEU:HD11	1:A:1078:ILE:HG23	1.99	0.45
1:A:1508:HIS:HD2	1:A:1529:ASN:HD22	1.64	0.45
2:C:131:GLU:OE2	2:C:445:PRO:HG3	2.17	0.45
2:C:135:ASN:O	2:C:233:ASP:N	2.47	0.45
3:D:107:C:O2'	14:S:34:HIS:HE1	1.99	0.45
5:L:56:U:H2'	5:L:57:A:H8	1.82	0.45
5:L:96:A:H2'	5:L:97:U:C6	2.50	0.45
10:O:214:ASN:O	10:O:215:GLN:NE2	2.50	0.45
24:n:274:HIS:HB2	24:n:287:GLN:HB2	1.97	0.45
1:A:299:LYS:HA	1:A:493:MET:CG	2.46	0.45
1:A:609:GLU:OE2	4:E:43:C:O2'	2.26	0.45
1:A:1051:GLU:HG2	1:A:1169:TYR:CE1	2.52	0.45
2:C:500:ARG:NH1	2:C:536:SER:OG	2.50	0.45
5:L:97:U:H2'	5:L:98:U:C6	2.50	0.45
10:O:304:LEU:HD13	10:O:334:TRP:CE3	2.52	0.45
13:R:9:ALA:HB2	13:R:60:GLY:C	2.42	0.45
13:R:145:ALA:HB2	13:R:204:LEU:HD12	1.99	0.45
14:S:5:HIS:C	14:S:6:ARG:CD	2.90	0.45
15:T:156:THR:HG23	15:T:157:ASP:H	1.81	0.45
16:Z:203:LYS:O	16:Z:204:ASP:HB2	2.17	0.45
17:c:15:ASN:O	17:c:19:GLN:HG2	2.16	0.45
18:d:222:TYR:HD1	18:d:250:PHE:HB2	1.82	0.45
28:u:30:TRP:CD2	28:u:89:LEU:HD22	2.52	0.45
28:u:86:ASN:ND2	29:w:32:LYS:NZ	2.64	0.45
1:A:203:ASN:O	1:A:204:GLU:HG3	2.16	0.45
1:A:847:LYS:HG2	5:L:24:U:C6	2.51	0.45
1:A:852:LEU:HD23	1:A:852:LEU:HA	1.68	0.45
1:A:1539:LEU:O	1:A:1541:ALA:N	2.50	0.45
1:A:1689:ARG:NH2	19:F:12:PRO:O	2.50	0.45
1:A:1880:PHE:CE1	1:A:1889:LEU:HD22	2.52	0.45
2:C:749:LYS:O	2:C:753:THR:CB	2.64	0.45
5:L:25:A:H3'	5:L:26:G:C5'	2.46	0.45
5:L:59:C:H2'	5:L:60:A:H8	1.82	0.45
5:L:99:U:H4'	24:n:326:VAL:CG2	2.47	0.45
5:L:99:U:H2'	5:L:100:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:271:GLN:HG2	10:O:314:THR:H	1.82	0.45
12:Q:103:GLU:OE2	13:R:131:ARG:NH2	2.46	0.45
16:Z:174:TRP:CZ2	16:Z:201:ARG:HB2	2.52	0.45
16:Z:204:ASP:O	16:Z:205:TYR:CD2	2.70	0.45
16:Z:301:SER:O	16:Z:302:SER:OG	2.31	0.45
25:q:194:THR:HG1	25:q:213:CYS:HB3	1.82	0.45
1:A:548:LEU:O	1:A:551:LEU:N	2.49	0.45
1:A:867:ILE:HD13	1:A:1101:TYR:CE1	2.51	0.45
1:A:1907:GLN:HG3	6:M:493:A:OP1	2.17	0.45
2:C:245:VAL:HG11	2:C:295:ILE:HG22	1.98	0.45
5:L:19:U:OP1	5:L:19:U:H4'	2.17	0.45
12:Q:107:ASP:O	12:Q:110:LYS:HG2	2.17	0.45
13:R:4:TRP:CZ2	13:R:92:HIS:CD2	3.05	0.45
13:R:70:LEU:HB3	13:R:102:LEU:CD2	2.47	0.45
14:S:10:GLU:HG2	14:S:11:ALA:N	2.32	0.45
16:Z:179:TYR:CD1	16:Z:179:TYR:O	2.70	0.45
16:Z:186:LEU:N	16:Z:186:LEU:CD1	2.73	0.45
16:Z:191:ARG:NE	16:Z:192:GLU:OE2	2.50	0.45
17:c:45:ALA:O	17:c:48:SER:N	2.50	0.45
23:v:673:GLU:CB	23:v:683:SER:HB3	2.47	0.45
24:n:397:TYR:HA	24:n:412:TRP:O	2.17	0.45
25:p:98:LEU:HD21	25:q:102:LEU:HD12	1.98	0.45
25:p:100:SER:O	25:p:103:ASP:CG	2.60	0.45
1:A:213:TYR:OH	1:A:217:TRP:NE1	2.50	0.44
1:A:354:PRO:C	1:A:356:TYR:H	2.26	0.44
1:A:1899:TRP:CE3	1:A:1905:LEU:HD22	2.52	0.44
2:C:116:THR:HG22	2:C:158:HIS:CD2	2.51	0.44
2:C:780:PRO:O	2:C:784:SER:N	2.25	0.44
5:L:70:A:H2'	5:L:71:C:C6	2.50	0.44
23:v:574:TYR:CZ	23:v:591:PHE:HB2	2.52	0.44
25:o:96:PHE:HD2	25:r:5:ILE:HG23	1.80	0.44
1:A:249:LEU:HD13	1:A:254:HIS:HB2	1.99	0.44
1:A:402:TRP:O	1:A:402:TRP:CG	2.69	0.44
1:A:1716:LEU:HD11	1:A:1753:ARG:HH21	1.81	0.44
2:C:126:MET:SD	2:C:132:ARG:HD2	2.57	0.44
2:C:154:VAL:HG11	2:C:177:TYR:CD2	2.52	0.44
5:L:105:A:H2'	5:L:106:A:H8	1.82	0.44
6:M:498:C:O2	21:H:2:SER:HB3	2.18	0.44
10:O:220:TYR:CE1	10:O:256:ARG:HG2	2.53	0.44
12:Q:5:ILE:HG22	12:Q:42:THR:HG23	1.99	0.44
13:R:97:GLU:O	13:R:100:GLY:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:T:44:LYS:O	15:T:48:GLN:HG2	2.18	0.44
21:H:41:VAL:CG1	21:H:42:LYS:H	2.29	0.44
25:q:14:VAL:HG12	25:q:52:GLU:HA	1.99	0.44
1:A:484:PHE:HE1	1:A:488:ARG:CD	2.31	0.44
1:A:759:ARG:NH2	1:A:783:LEU:HD23	2.33	0.44
1:A:791:ARG:HH22	11:P:173:LYS:CD	2.27	0.44
1:A:1617:ALA:N	1:A:1744:ASP:OD2	2.50	0.44
1:A:1799:GLN:O	1:A:1803:ARG:HG3	2.18	0.44
5:L:1098:C:H2'	5:L:1099:G:H5''	1.98	0.44
6:M:493:A:H2'	6:M:494:G:C8	2.52	0.44
8:N:100:G:OP2	8:N:100:G:N2	2.45	0.44
10:O:121:GLN:OE1	10:O:121:GLN:N	2.51	0.44
12:Q:26:THR:O	12:Q:44:TYR:HA	2.17	0.44
23:v:624:TRP:HE1	23:v:651:ALA:CB	2.30	0.44
28:u:45:GLY:HA3	28:u:53:VAL:HG12	2.00	0.44
1:A:1711:VAL:CG1	1:A:1789:ASN:HB3	2.47	0.44
2:C:67:GLU:O	2:C:71:GLY:N	2.51	0.44
5:L:5:A:C5'	22:I:114:THR:HB	2.42	0.44
5:L:5:A:H2'	5:L:6:U:C6	2.52	0.44
5:L:55:G:H2'	5:L:56:U:C6	2.50	0.44
5:L:57:A:H2'	5:L:58:A:H8	1.82	0.44
5:L:1116:A:C4	5:L:1117:G:C5	3.05	0.44
7:B:88:U:H2'	7:B:89:A:H4'	2.00	0.44
13:R:46:ARG:NH2	13:R:220:GLY:O	2.50	0.44
1:A:234:PHE:HD1	1:A:235:LYS:N	2.16	0.44
1:A:928:ARG:HH12	5:L:31:A:P	2.40	0.44
1:A:1647:GLN:O	1:A:1650:ARG:NH1	2.51	0.44
2:C:867:THR:O	2:C:926:GLY:HA2	2.17	0.44
4:E:51:A:C1'	4:E:52:G:P	3.06	0.44
4:E:67:C:OP1	4:E:67:C:H6	2.00	0.44
5:L:102:U:H2'	5:L:103:A:H8	1.82	0.44
6:M:485:U:C5'	21:H:36:ARG:HE	2.29	0.44
9:J:9:LYS:O	9:J:10:SER:OG	2.36	0.44
10:O:251:TRP:CZ3	10:O:258:PRO:HB3	2.53	0.44
10:O:392:MET:HG3	10:O:393:VAL:N	2.32	0.44
10:O:437:GLU:N	10:O:438:PRO:HD3	2.32	0.44
13:R:117:PHE:O	13:R:129:SER:HA	2.17	0.44
16:Z:191:ARG:NE	16:Z:192:GLU:OE1	2.45	0.44
16:Z:285:SER:O	16:Z:288:ASP:N	2.51	0.44
18:d:187:GLU:O	18:d:190:SER:HB3	2.18	0.44
23:v:433:UNK:O	23:v:437:UNK:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:v:729:TYR:O	23:v:733:ILE:HG13	2.17	0.44
1:A:1160:LEU:H	1:A:1171:LEU:HB3	1.83	0.44
1:A:1449:ASN:HB3	16:Z:338:THR:CG2	2.48	0.44
1:A:1893:ILE:O	1:A:1984:PRO:HA	2.17	0.44
1:A:2081:ASP:O	1:A:2085:GLY:N	2.51	0.44
2:C:233:ASP:OD1	2:C:487:ARG:NH1	2.43	0.44
4:E:67:C:OP1	4:E:67:C:C6	2.70	0.44
5:L:21:G:N7	14:S:5:HIS:HB3	2.33	0.44
5:L:74:C:H2'	5:L:75:A:H8	1.81	0.44
5:L:82:C:H2'	5:L:83:U:C6	2.50	0.44
5:L:1120:G:C5'	5:L:1120:G:C8	3.00	0.44
11:P:216:ARG:HA	11:P:219:ILE:HD12	1.99	0.44
17:c:217:ILE:HD13	18:d:83:ARG:CZ	2.48	0.44
19:F:63:LYS:HE2	20:G:6:LEU:HD22	2.00	0.44
1:A:1350:ILE:HG23	1:A:1356:LEU:HD22	2.00	0.44
4:E:48:C:H2'	4:E:49:A:O4'	2.17	0.44
6:M:494:G:H2'	6:M:495:A:OP2	2.18	0.44
6:M:507:U:H2'	6:M:508:U:O4'	2.18	0.44
12:Q:51:ARG:HG3	12:Q:51:ARG:O	2.18	0.44
12:Q:246:ALA:O	12:Q:247:LYS:HB2	2.18	0.44
13:R:46:ARG:HH22	13:R:222:LEU:HG	1.83	0.44
13:R:76:PHE:C	13:R:79:GLY:H	2.26	0.44
23:v:127:UNK:HA	23:v:150:UNK:CB	2.47	0.44
24:n:60:ARG:O	24:n:61:LYS:C	2.61	0.44
27:s:20:LEU:O	27:s:31:ILE:HA	2.16	0.44
1:A:484:PHE:CE2	3:D:81:A:C5	3.06	0.44
1:A:1209:LYS:HD2	1:A:1417:GLN:HG2	2.00	0.44
1:A:1458:TRP:CZ2	1:A:1491:ILE:HD13	2.53	0.44
2:C:75:GLU:HB2	10:O:133:ARG:HG3	2.00	0.44
2:C:362:LYS:HG3	2:C:363:PRO:HD2	1.98	0.44
2:C:378:LEU:HD23	2:C:378:LEU:HA	1.82	0.44
2:C:831:ILE:HG13	2:C:832:ASP:N	2.26	0.44
4:E:5:G:H2'	4:E:6:C:C6	2.52	0.44
5:L:66:A:H2'	5:L:67:A:H8	1.82	0.44
13:R:221:LEU:HD12	13:R:221:LEU:O	2.18	0.44
25:q:405:ASP:HB3	26:t:30:ASN:CG	2.43	0.44
32:m:17:ILE:HG12	32:m:95:ILE:HG23	2.00	0.44
1:A:640:ARG:HH11	1:A:640:ARG:CG	2.31	0.44
1:A:912:LEU:HD12	1:A:951:LEU:HD21	2.00	0.44
1:A:1080:ASP:HB3	17:c:82:ASN:ND2	2.32	0.44
1:A:1211:SER:OG	1:A:1268:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1280:SER:HB3	16:Z:394:TYR:CD2	2.53	0.44
1:A:1703:MET:N	1:A:1732:MET:O	2.50	0.44
2:C:202:ASP:OD1	2:C:206:LYS:O	2.36	0.44
10:O:204:LYS:HG2	10:O:225:SER:HA	2.00	0.44
10:O:446:LEU:HD13	10:O:446:LEU:H	1.83	0.44
12:Q:205:PHE:HB3	12:Q:291:ILE:O	2.17	0.44
12:Q:239:SER:O	12:Q:251:LEU:HD12	2.18	0.44
13:R:54:GLN:H	13:R:58:HIS:HD2	1.66	0.44
16:Z:191:ARG:HB3	16:Z:192:GLU:OE1	2.18	0.44
24:n:65:GLY:C	24:n:66:ASP:CG	2.86	0.44
25:q:102:LEU:O	25:q:105:LEU:CG	2.66	0.44
1:A:428:LEU:HD22	2:C:896:GLY:O	2.18	0.43
1:A:1214:ARG:HB2	1:A:1255:ASN:OD1	2.17	0.43
2:C:237:ILE:HD12	2:C:265:PHE:HE1	1.82	0.43
4:E:88:U:H1'	18:d:70:ARG:NH1	2.33	0.43
5:L:104:C:H2'	5:L:105:A:H8	1.82	0.43
10:O:208:CYS:SG	10:O:209:TRP:N	2.91	0.43
17:c:46:ARG:O	17:c:50:LEU:CB	2.65	0.43
17:c:160:LEU:HA	22:I:196:ILE:HG23	2.00	0.43
21:H:86:PHE:HE2	21:H:90:LYS:HE3	1.83	0.43
28:i:30:TRP:CD2	28:i:89:LEU:HD22	2.52	0.43
28:i:45:GLY:HA3	28:i:53:VAL:HG12	2.00	0.43
1:A:645:ASP:HB3	1:A:648:GLN:HB2	1.99	0.43
2:C:767:SER:OG	2:C:796:ILE:HD13	2.18	0.43
3:D:43:G:H4'	3:D:44:A:OP1	2.18	0.43
5:L:5:A:OP1	22:I:114:THR:CG2	2.64	0.43
5:L:60:A:H2'	5:L:61:A:H8	1.82	0.43
5:L:78:G:OP2	13:R:151:LEU:HD13	2.18	0.43
10:O:162:THR:HG22	10:O:183:MET:C	2.43	0.43
10:O:229:THR:OG1	10:O:270:ASN:O	2.34	0.43
10:O:351:GLY:HA2	10:O:352:ILE:HA	1.65	0.43
10:O:391:GLU:O	10:O:392:MET:HB2	2.18	0.43
18:d:219:ARG:NH1	18:d:254:GLU:OE1	2.51	0.43
19:F:83:ARG:HG3	19:F:97:PHE:O	2.17	0.43
26:t:81:ASP:C	26:t:82:ASP:CG	2.86	0.43
32:z:17:ILE:HG12	32:z:95:ILE:HG23	2.00	0.43
1:A:466:GLU:HG2	1:A:467:GLU:N	2.33	0.43
1:A:676:GLN:OE1	1:A:676:GLN:N	2.44	0.43
1:A:911:ILE:CG2	1:A:997:GLN:HG2	2.46	0.43
5:L:1:A:C1'	23:v:504:UNK:H2	2.20	0.43
12:Q:16:CYS:HB2	13:R:104:LEU:HD21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Z:168:LYS:HD2	16:Z:168:LYS:HA	1.75	0.43
17:c:204:LYS:CG	17:c:205:LYS:H	2.27	0.43
29:h:16:LYS:CG	29:h:17:PRO:HD3	2.49	0.43
27:s:47:GLU:HB3	35:b:15:TYR:CG	2.52	0.43
1:A:404:ASN:OD1	2:C:927:MET:HE1	2.19	0.43
1:A:404:ASN:CG	1:A:405:ASN:N	2.76	0.43
1:A:902:PRO:CG	1:A:904:THR:O	2.66	0.43
1:A:1045:GLN:HG2	1:A:1175:GLU:HG2	2.00	0.43
1:A:1714:PRO:HB2	1:A:1787:TYR:CZ	2.53	0.43
1:A:2013:ARG:NH2	1:A:2084:LEU:O	2.52	0.43
1:A:2013:ARG:CZ	1:A:2085:GLY:HA2	2.48	0.43
2:C:380:PRO:O	2:C:384:ILE:HG13	2.19	0.43
4:E:85:C:N4	17:c:166:LYS:HE2	2.34	0.43
5:L:120:G:C2	28:u:33:GLU:O	2.71	0.43
10:O:359:ASN:OD1	10:O:411:GLY:HA3	2.19	0.43
12:Q:37:CYS:SG	12:Q:39:LEU:HB2	2.57	0.43
12:Q:205:PHE:CD1	12:Q:205:PHE:N	2.85	0.43
12:Q:241:ILE:HG12	13:R:161:ARG:HD3	1.98	0.43
19:F:20:ALA:O	19:F:24:SER:OG	2.33	0.43
31:l:14:ALA:HA	31:l:78:LEU:HD21	2.01	0.43
1:A:342:LEU:HD22	1:A:392:ASN:ND2	2.32	0.43
1:A:426:PRO:HG3	16:Z:201:ARG:NE	2.32	0.43
1:A:768:GLU:OE2	10:O:310:SER:HB3	2.18	0.43
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	2.19	0.43
2:C:458:ILE:H	2:C:458:ILE:HG12	1.57	0.43
2:C:576:THR:HG22	2:C:592:PHE:HB2	2.01	0.43
4:E:86:G:C6	4:E:87:U:C4	3.06	0.43
5:L:1102:C:C2	5:L:1103:C:C5	3.06	0.43
5:L:1105:C:N4	34:a:97:LYS:HZ1	2.15	0.43
10:O:437:GLU:OE1	10:O:438:PRO:HA	2.17	0.43
12:Q:125:ILE:C	12:Q:125:ILE:CD1	2.86	0.43
13:R:207:PRO:O	13:R:212:TRP:NE1	2.50	0.43
17:c:230:THR:C	17:c:232:THR:H	2.24	0.43
25:q:225:LEU:O	25:q:226:LYS:CB	2.65	0.43
1:A:831:ARG:HA	1:A:831:ARG:HD2	1.75	0.43
1:A:936:GLU:O	1:A:939:LEU:N	2.52	0.43
1:A:1865:THR:HG21	1:A:1869:ASN:HD22	1.84	0.43
1:A:1932:GLN:HG2	1:A:1955:ALA:HB3	1.99	0.43
2:C:223:ASP:OD2	2:C:647:ASN:ND2	2.40	0.43
2:C:231:ALA:O	2:C:487:ARG:NH1	2.52	0.43
2:C:473:LEU:HD12	2:C:485:LEU:CD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:952:PRO:HG3	2:C:957:ALA:HA	2.00	0.43
5:L:15:C:C1'	5:L:16:U:C6	2.92	0.43
5:L:1120:G:H5''	5:L:1120:G:C8	2.51	0.43
13:R:105:ARG:HG2	13:R:109:LEU:HD11	2.01	0.43
24:n:205:HIS:CE1	24:n:231:LYS:HD2	2.53	0.43
24:n:291:HIS:CB	24:n:320:TRP:CH2	3.02	0.43
27:s:87:LEU:HG	27:s:92:ILE:HD11	2.00	0.43
2:C:133:ILE:HD12	2:C:560:GLN:HB3	2.00	0.43
2:C:232:SER:OG	2:C:234:LEU:O	2.30	0.43
2:C:290:HIS:O	2:C:294:ASN:HB2	2.19	0.43
2:C:326:GLU:O	2:C:329:SER:OG	2.33	0.43
2:C:353:TYR:CD1	2:C:371:PRO:HA	2.53	0.43
2:C:373:PHE:O	2:C:377:ILE:HB	2.18	0.43
2:C:864:VAL:HG12	2:C:866:ILE:HG13	2.00	0.43
4:E:75:A:C2'	4:E:76:A:H5'	2.49	0.43
11:P:115:VAL:HG21	12:Q:24:ARG:NH1	2.34	0.43
11:P:178:TYR:HD1	22:I:200:ASN:OD1	2.02	0.43
12:Q:203:LYS:HG3	12:Q:256:SER:OG	2.18	0.43
17:c:101:ARG:O	17:c:105:LEU:HB2	2.19	0.43
21:H:20:ALA:HB1	21:H:26:TYR:HB3	2.01	0.43
22:I:173:LYS:O	22:I:177:GLU:HG2	2.19	0.43
23:v:609:GLU:HG2	23:v:609:GLU:H	1.67	0.43
24:n:432:VAL:HA	24:n:443:ILE:O	2.19	0.43
1:A:426:PRO:HG2	16:Z:201:ARG:HE	1.80	0.43
1:A:1285:VAL:HG22	1:A:1301:TYR:HD1	1.83	0.43
1:A:1468:ALA:HA	1:A:1473:ARG:CG	2.48	0.43
1:A:1812:LEU:HB3	1:A:1816:ARG:NH1	2.34	0.43
1:A:1920:LEU:O	1:A:1923:SER:OG	2.32	0.43
1:A:1934:ILE:HG12	1:A:1957:ARG:HB2	2.00	0.43
2:C:251:GLN:HE21	2:C:255:GLN:HE21	1.67	0.43
4:E:56:A:HO2'	4:E:57:U:P	2.42	0.43
5:L:112:A:N7	33:e:63:ARG:HB3	2.34	0.43
5:L:1105:C:N4	34:a:97:LYS:HZ3	2.16	0.43
12:Q:251:LEU:HD12	12:Q:252:ARG:N	2.33	0.43
12:Q:290:ILE:HG22	12:Q:292:PRO:HD2	2.00	0.43
13:R:55:PRO:HB3	13:R:93:ILE:HD11	2.00	0.43
13:R:163:VAL:HG11	13:R:199:MET:HE2	2.01	0.43
15:T:120:CYS:C	15:T:122:CYS:N	2.76	0.43
16:Z:205:TYR:O	16:Z:207:SER:N	2.50	0.43
22:I:190:TYR:CE2	22:I:195:PHE:HZ	2.35	0.43
24:n:72:TRP:O	24:n:73:SER:CB	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:o:112:VAL:O	25:o:115:GLU:CG	2.66	0.43
31:y:14:ALA:HA	31:y:78:LEU:HD21	2.01	0.43
1:A:1094:ASP:OD2	11:P:172:TRP:NE1	2.49	0.43
1:A:1616:ARG:NH2	1:A:1744:ASP:OD1	2.44	0.43
4:E:89:U:H5	22:I:176:TYR:O	2.02	0.43
5:L:1100:A:H61	5:L:1116:A:N6	2.07	0.43
6:M:498:C:O2'	21:H:2:SER:CA	2.54	0.43
6:M:506:U:H2'	6:M:507:U:C6	2.54	0.43
10:O:181:HIS:CE1	10:O:207:LYS:HD2	2.53	0.43
12:Q:206:PHE:C	12:Q:207:LEU:HD12	2.44	0.43
13:R:92:HIS:HE1	13:R:98:ASP:OD2	2.01	0.43
16:Z:431:LEU:HB3	16:Z:435:GLU:HB3	2.01	0.43
18:d:53:GLU:O	18:d:57:TYR:HD1	2.02	0.43
24:n:291:HIS:CB	24:n:320:TRP:CZ2	3.02	0.43
25:q:123:ALA:O	25:q:127:LEU:CG	2.67	0.43
1:A:856:TRP:NE1	14:S:174:VAL:HG11	2.34	0.43
1:A:1521:ARG:HD3	6:M:507:U:H5''	2.01	0.43
2:C:176:ARG:NH1	2:C:179:ASP:OD2	2.52	0.43
2:C:387:TYR:HA	2:C:391:MET:HG2	2.00	0.43
3:D:175:G:C2	28:i:33:GLU:O	2.71	0.43
3:D:176:A:O2'	32:m:20:LYS:HE3	2.19	0.43
8:N:114:U:C4'	13:R:231:ASP:HB3	2.48	0.43
16:Z:178:ARG:HB2	16:Z:198:PHE:CZ	2.43	0.43
18:d:172:PHE:O	18:d:175:PHE:HB3	2.19	0.43
28:i:88:THR:HG22	28:i:89:LEU:HD12	2.01	0.43
1:A:676:GLN:HE21	1:A:714:PHE:HB2	1.83	0.42
1:A:918:ASP:OD2	1:A:1511:ARG:NH1	2.51	0.42
1:A:1678:ILE:HD13	1:A:1703:MET:HE1	2.01	0.42
2:C:77:LEU:HD12	2:C:77:LEU:O	2.19	0.42
2:C:348:LEU:O	2:C:372:THR:HB	2.19	0.42
5:L:18:U:H5''	22:I:199:LYS:HG3	2.00	0.42
5:L:44:U:O5'	5:L:44:U:H6	2.02	0.42
10:O:132:SER:OG	10:O:425:ILE:O	2.25	0.42
10:O:263:VAL:O	10:O:293:TRP:HH2	2.03	0.42
12:Q:203:LYS:O	12:Q:251:LEU:O	2.37	0.42
13:R:94:PRO:HB2	13:R:191:ASN:ND2	2.34	0.42
18:d:46:TYR:HD1	18:d:49:ARG:HH22	1.67	0.42
20:G:7:ASN:O	20:G:13:ASN:ND2	2.52	0.42
22:I:110:ARG:O	22:I:114:THR:HG23	2.19	0.42
24:n:290:ASP:O	24:n:320:TRP:HH2	2.02	0.42
26:t:136:VAL:O	26:t:139:GLN:CG	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:k:87:LEU:HG	27:k:92:ILE:HD11	2.00	0.42
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.19	0.42
1:A:1438:PRO:HB2	1:A:1443:TYR:HE2	1.84	0.42
1:A:1602:PRO:HG2	1:A:1605:ARG:HB3	2.01	0.42
2:C:81:LYS:O	2:C:82:ASN:ND2	2.52	0.42
5:L:19:U:C1'	11:P:178:TYR:CD2	3.03	0.42
11:P:143:VAL:HG11	18:d:124:ARG:HG3	2.01	0.42
12:Q:261:ARG:O	12:Q:264:SER:HB2	2.19	0.42
13:R:55:PRO:O	13:R:59:SER:OG	2.27	0.42
13:R:171:ASP:N	13:R:185:LYS:O	2.52	0.42
13:R:234:ALA:HA	13:R:237:ARG:HD3	2.01	0.42
19:F:36:LYS:O	19:F:37:SER:OG	2.36	0.42
28:i:88:THR:HG23	30:j:67:SER:CB	2.49	0.42
31:y:6:ILE:N	31:y:7:PRO:CD	2.82	0.42
1:A:404:ASN:OD1	1:A:405:ASN:N	2.51	0.42
1:A:791:ARG:CZ	11:P:173:LYS:HE2	2.50	0.42
1:A:1361:VAL:HG21	1:A:1407:ILE:HD11	2.01	0.42
2:C:89:PRO:C	2:C:91:VAL:H	2.27	0.42
2:C:463:THR:O	2:C:463:THR:OG1	2.32	0.42
2:C:602:VAL:HG13	2:C:860:PRO:HG2	2.01	0.42
2:C:829:VAL:HG12	2:C:830:ASN:N	2.31	0.42
4:E:34:A:N1	13:R:73:CYS:HA	2.34	0.42
4:E:88:U:O2'	5:L:17:U:OP2	2.14	0.42
6:M:483:U:O2	21:H:91:ARG:NH2	2.52	0.42
11:P:86:ASN:ND2	14:S:24:GLY:O	2.52	0.42
12:Q:213:SER:HA	13:R:237:ARG:CZ	2.49	0.42
13:R:72:PHE:HE1	13:R:90:LEU:HD12	1.84	0.42
15:T:156:THR:HG23	15:T:157:ASP:N	2.34	0.42
16:Z:184:GLN:NE2	16:Z:185:GLU:H	2.13	0.42
28:u:88:THR:HG22	28:u:89:LEU:HD12	2.01	0.42
1:A:134:MET:CE	15:T:107:ARG:HD2	2.49	0.42
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.54	0.42
5:L:1097:G:H2'	5:L:1098:C:C6	2.54	0.42
10:O:184:THR:O	10:O:201:SER:OG	2.21	0.42
12:Q:207:LEU:HB2	12:Q:249:GLY:C	2.42	0.42
18:d:99:ILE:O	18:d:100:PRO:C	2.62	0.42
18:d:135:LEU:HD23	18:d:135:LEU:HA	1.85	0.42
29:w:16:LYS:CG	29:w:17:PRO:HD3	2.49	0.42
1:A:235:LYS:HB3	1:A:648:GLN:NE2	2.35	0.42
1:A:903:LEU:C	1:A:903:LEU:CD2	2.92	0.42
1:A:1070:LEU:HA	1:A:1073:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:144:SER:HB2	2:C:238:VAL:HG12	2.02	0.42
3:D:174:G:C8	33:g:99:ASP:OD2	2.69	0.42
5:L:36:A:N6	6:M:500:A:H61	2.17	0.42
5:L:121:C:O2'	32:z:20:LYS:HE3	2.19	0.42
8:N:110:A:H2	13:R:46:ARG:HD3	1.79	0.42
12:Q:259:GLY:O	12:Q:263:VAL:CG2	2.66	0.42
13:R:159:ARG:O	13:R:163:VAL:HG23	2.19	0.42
16:Z:67:LYS:HE2	16:Z:67:LYS:HA	2.02	0.42
18:d:140:LEU:HD22	18:d:156:TYR:CE2	2.54	0.42
19:F:58:ILE:HD12	19:F:64:PHE:HZ	1.84	0.42
22:I:184:GLN:OE1	22:I:187:LYS:NZ	2.50	0.42
28:i:34:GLN:NE2	28:i:37:ILE:HD12	2.34	0.42
1:A:607:THR:HG23	1:A:610:ARG:NH1	2.33	0.42
1:A:1538:ASN:C	1:A:1539:LEU:HD12	2.45	0.42
2:C:772:ASN:HD21	2:C:803:VAL:HG22	1.84	0.42
4:E:42:A:C2	13:R:38:SER:O	2.72	0.42
10:O:418:GLU:OE2	10:O:424:LYS:HD2	2.19	0.42
11:P:87:ASN:HB3	11:P:90:SER:H	1.84	0.42
15:T:34:GLN:C	15:T:36:ASP:H	2.28	0.42
16:Z:143:LEU:HD21	16:Z:177:LEU:HG	2.01	0.42
17:c:44:THR:HG22	17:c:45:ALA:H	1.85	0.42
17:c:154:GLU:HG3	19:F:57:TYR:CD2	2.54	0.42
23:v:605:PHE:O	23:v:609:GLU:HG2	2.19	0.42
1:A:1219:ASP:OD2	1:A:1255:ASN:ND2	2.53	0.42
1:A:1663:PHE:CZ	1:A:1902:GLN:HG3	2.55	0.42
1:A:1756:PHE:CZ	1:A:1760:THR:HG21	2.55	0.42
1:A:1870:VAL:CG2	5:L:46:C:H4'	2.49	0.42
1:A:2048:TRP:O	1:A:2052:GLU:HG3	2.20	0.42
1:A:2070:ASN:OD1	1:A:2071:ILE:N	2.52	0.42
4:E:58:C:H1'	20:G:2:GLY:O	2.20	0.42
5:L:1096:C:H2'	5:L:1097:G:H8	1.85	0.42
8:N:113:U:O4'	13:R:183:PHE:HE2	2.02	0.42
15:T:151:ARG:HB2	24:n:63:ARG:NH1	2.35	0.42
18:d:122:MET:HG3	18:d:139:TYR:CD1	2.54	0.42
18:d:126:ILE:HD12	18:d:136:TRP:CH2	2.54	0.42
24:n:416:ARG:O	24:n:417:LEU:HB2	2.19	0.42
1:A:213:TYR:CZ	1:A:217:TRP:HD1	2.32	0.42
1:A:770:MET:HE1	11:P:165:ILE:HD11	2.01	0.42
1:A:1369:ASN:HB3	1:A:1378:LYS:NZ	2.35	0.42
1:A:1440:ILE:O	1:A:1443:TYR:N	2.44	0.42
1:A:1605:ARG:HD2	1:A:1823:LEU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1856:ASN:HD22	1:A:1969:MET:HG2	1.84	0.42
1:A:2013:ARG:NH1	1:A:2085:GLY:HA2	2.35	0.42
2:C:462:SER:C	2:C:464:PRO:CD	2.86	0.42
2:C:542:ILE:HA	2:C:563:LEU:O	2.20	0.42
4:E:21:U:OP2	24:n:54:SER:CB	2.66	0.42
4:E:67:C:OP2	18:d:59:LYS:HE3	2.19	0.42
5:L:33:U:H2'	5:L:34:G:O4'	2.20	0.42
7:B:90:A:N6	9:J:6:ILE:HD11	2.34	0.42
10:O:342:LEU:HB3	11:P:47:ARG:HD2	2.01	0.42
12:Q:291:ILE:HG23	12:Q:292:PRO:CA	2.50	0.42
13:R:150:HIS:CE1	13:R:205:LEU:HD11	2.55	0.42
18:d:140:LEU:HD13	18:d:156:TYR:CZ	2.54	0.42
26:t:109:SER:O	26:t:110:GLU:CB	2.67	0.42
28:u:34:GLN:NE2	28:u:37:ILE:HD12	2.34	0.42
1:A:1012:TRP:CD1	1:A:1012:TRP:H	2.36	0.42
1:A:1389:TYR:CZ	1:A:1401:SER:HB3	2.55	0.42
1:A:1708:GLU:HG3	1:A:1730:ASN:OD1	2.19	0.42
5:L:18:U:C6	22:I:202:GLN:CG	3.02	0.42
10:O:405:SER:HA	10:O:415:ILE:O	2.19	0.42
12:Q:125:ILE:CD1	12:Q:126:THR:N	2.82	0.42
12:Q:240:LEU:HD12	12:Q:241:ILE:H	1.85	0.42
15:T:147:HIS:HB2	15:T:148:CYS:SG	2.59	0.42
18:d:115:ILE:HG23	18:d:116:ASN:N	2.34	0.42
18:d:153:ARG:NH2	18:d:181:ASN:HD21	2.18	0.42
28:u:77:LEU:HD23	28:u:78:GLY:N	2.35	0.42
33:e:102:ILE:HG22	33:e:103:VAL:HG23	2.02	0.42
1:A:874:ILE:O	1:A:878:GLU:HB2	2.20	0.42
1:A:1028:TRP:HD1	1:A:1260:PHE:CZ	2.37	0.42
2:C:428:ILE:HG22	2:C:429:PHE:CD1	2.55	0.42
2:C:626:SER:HB2	2:C:634:ILE:HD13	2.01	0.42
2:C:757:TRP:HD1	2:C:762:SER:OG	2.03	0.42
3:D:167:A:N7	33:g:63:ARG:HB3	2.34	0.42
4:E:66:C:H1'	12:Q:108:MET:SD	2.60	0.42
10:O:187:ASP:HB3	10:O:200:VAL:CG1	2.49	0.42
10:O:442:TRP:CG	10:O:442:TRP:O	2.70	0.42
12:Q:205:PHE:CE1	12:Q:293:TRP:HD1	2.37	0.42
16:Z:190:LEU:HD23	16:Z:191:ARG:CA	2.50	0.42
16:Z:203:LYS:C	16:Z:204:ASP:CG	2.88	0.42
24:n:252:ASP:O	24:n:253:VAL:HG23	2.20	0.42
24:n:294:SER:CB	24:n:313:GLU:CG	2.98	0.42
1:A:179:MET:HE1	1:A:653:ILE:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:PHE:HD1	2:C:335:SER:OG	2.02	0.41
1:A:484:PHE:HE1	1:A:488:ARG:HD2	1.85	0.41
1:A:770:MET:CE	11:P:165:ILE:HD11	2.50	0.41
1:A:1419:ASP:OD1	1:A:1419:ASP:O	2.38	0.41
1:A:1424:HIS:CD2	9:J:6:ILE:HD13	2.55	0.41
2:C:316:THR:O	2:C:319:GLY:N	2.48	0.41
2:C:338:SER:O	2:C:341:ILE:HG12	2.19	0.41
2:C:492:LEU:HD22	2:C:557:HIS:ND1	2.35	0.41
4:E:15:C:OP2	4:E:15:C:C6	2.73	0.41
5:L:34:G:H2'	5:L:35:U:O4'	2.20	0.41
12:Q:38:THR:O	12:Q:39:LEU:HD12	2.20	0.41
14:S:170:LEU:HA	14:S:170:LEU:HD23	1.81	0.41
16:Z:432:GLY:C	16:Z:434:ASP:H	2.27	0.41
19:F:36:LYS:HE2	19:F:38:HIS:O	2.20	0.41
19:F:87:SER:HA	19:F:93:ASN:O	2.19	0.41
23:v:648:PHE:CD1	23:v:669:TYR:HB2	2.55	0.41
23:v:708:LEU:O	23:v:712:CYS:SG	2.70	0.41
25:q:59:GLN:O	25:q:60:ALA:HB3	2.20	0.41
28:i:77:LEU:HD23	28:i:78:GLY:N	2.35	0.41
31:l:6:ILE:N	31:l:7:PRO:CD	2.82	0.41
1:A:266:LEU:CD2	1:A:268:LEU:H	2.33	0.41
1:A:351:LYS:HE3	7:B:91:A:OP1	2.20	0.41
1:A:386:ALA:O	1:A:401:PRO:HG3	2.21	0.41
1:A:563:ASP:OD2	1:A:640:ARG:NH2	2.54	0.41
1:A:780:ARG:NH2	5:L:20:G:C4	2.89	0.41
1:A:891:GLU:OE2	11:P:219:ILE:HG12	2.21	0.41
1:A:900:PHE:C	1:A:900:PHE:HD2	2.28	0.41
1:A:2054:GLN:O	1:A:2058:LEU:HG	2.21	0.41
2:C:116:THR:OG1	2:C:120:ARG:HG3	2.20	0.41
3:D:64:C:H2'	3:D:65:U:C6	2.55	0.41
10:O:159:SER:OG	10:O:160:ASN:N	2.53	0.41
13:R:210:LYS:HG3	13:R:211:GLU:N	2.36	0.41
15:T:123:ARG:O	15:T:154:ALA:HB2	2.20	0.41
16:Z:203:LYS:O	16:Z:204:ASP:CG	2.63	0.41
17:c:224:MET:HG2	18:d:124:ARG:HH11	1.84	0.41
18:d:136:TRP:CE3	18:d:159:TRP:HB2	2.55	0.41
18:d:233:GLN:HG2	18:d:274:TRP:CZ2	2.55	0.41
24:n:375:LYS:HA	24:n:376:ILE:HA	1.66	0.41
28:u:88:THR:HG23	30:x:67:SER:CB	2.49	0.41
1:A:834:ILE:O	1:A:837:GLY:N	2.52	0.41
1:A:1339:LEU:CD2	1:A:1440:ILE:HD12	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:118:TYR:CD1	2:C:199:LEU:HG	2.55	0.41
2:C:139:ILE:HG22	2:C:215:ALA:HB3	2.02	0.41
2:C:153:LEU:HD13	2:C:212:PHE:CZ	2.55	0.41
2:C:203:LEU:HD13	2:C:325:LYS:NZ	2.34	0.41
2:C:325:LYS:HE2	2:C:441:ARG:NH1	2.35	0.41
4:E:42:A:O2'	4:E:43:C:P	2.78	0.41
5:L:15:C:N4	22:I:209:ARG:HD3	2.34	0.41
10:O:161:ASP:O	10:O:162:THR:OG1	2.26	0.41
10:O:250:LEU:HA	10:O:250:LEU:HD23	1.79	0.41
12:Q:263:VAL:O	12:Q:263:VAL:HG12	2.20	0.41
13:R:108:VAL:HG23	13:R:109:LEU:HG	2.03	0.41
17:c:230:THR:HG22	18:d:116:ASN:HB2	2.02	0.41
17:c:533:LEU:O	17:c:536:GLN:CG	2.68	0.41
25:r:112:VAL:O	25:r:115:GLU:CG	2.68	0.41
29:w:32:LYS:HG3	29:w:77:ASN:HA	2.03	0.41
1:A:364:TYR:HD1	1:A:1209:LYS:HE2	1.85	0.41
1:A:584:HIS:O	1:A:587:GLY:N	2.47	0.41
1:A:672:LYS:HB2	3:D:101:C:OP1	2.20	0.41
1:A:821:ASP:HA	14:S:160:MET:HG3	2.02	0.41
1:A:1667:GLN:O	1:A:1670:ASP:HB3	2.21	0.41
1:A:2027:LEU:HB3	33:e:71:ASN:HD21	1.84	0.41
2:C:199:LEU:HD13	2:C:207:SER:HB2	2.01	0.41
2:C:237:ILE:HB	2:C:265:PHE:CD1	2.55	0.41
2:C:362:LYS:CG	2:C:363:PRO:HD2	2.51	0.41
2:C:452:LYS:O	2:C:455:HIS:N	2.54	0.41
2:C:772:ASN:OD1	2:C:772:ASN:N	2.54	0.41
11:P:104:LEU:HG	11:P:108:ASN:CG	2.46	0.41
13:R:159:ARG:NE	13:R:205:LEU:HA	2.35	0.41
16:Z:178:ARG:CD	16:Z:182:GLN:HE22	2.32	0.41
16:Z:195:GLU:O	16:Z:198:PHE:HB2	2.20	0.41
1:A:526:LEU:HD23	1:A:526:LEU:HA	1.90	0.41
1:A:722:LEU:HD23	1:A:722:LEU:HA	1.83	0.41
1:A:859:ASN:ND2	14:S:170:LEU:HD12	2.34	0.41
1:A:899:PRO:HD2	1:A:1006:ARG:CZ	2.50	0.41
1:A:1069:LEU:HD23	1:A:1120:VAL:HG21	2.01	0.41
1:A:1624:LEU:HA	1:A:1624:LEU:HD23	1.90	0.41
1:A:1724:PHE:HD1	1:A:1791:PHE:HA	1.86	0.41
2:C:123:MET:HA	2:C:199:LEU:HD23	2.02	0.41
2:C:282:MET:HE2	2:C:370:TYR:CD1	2.55	0.41
2:C:735:LEU:HB3	2:C:750:ILE:HG21	2.03	0.41
2:C:964:ARG:NH1	2:C:968:MET:HE3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:28:U:C1'	15:T:121:ILE:HD13	2.51	0.41
4:E:75:A:O2'	4:E:76:A:H5'	2.20	0.41
10:O:389:THR:HG22	10:O:426:TRP:HZ2	1.86	0.41
11:P:194:ASN:OD1	11:P:195:ASN:N	2.52	0.41
13:R:153:PRO:HB3	13:R:177:GLU:OE1	2.20	0.41
13:R:164:PHE:CE1	13:R:199:MET:HG3	2.56	0.41
15:T:127:ALA:HA	24:n:59:ARG:HH21	1.86	0.41
16:Z:368:ASN:O	16:Z:373:ILE:HG12	2.21	0.41
17:c:146:ASP:O	17:c:149:LYS:HB2	2.21	0.41
18:d:123:ASN:O	18:d:127:SER:OG	2.37	0.41
18:d:407:UNK:C	18:d:409:UNK:H2	2.33	0.41
19:F:44:MET:HB2	20:G:7:ASN:HD21	1.86	0.41
19:F:76:LEU:HD13	20:G:30:LEU:HD12	2.02	0.41
21:H:3:ARG:H	21:H:3:ARG:HG2	1.50	0.41
25:q:298:ASN:CG	25:q:300:GLU:H	2.29	0.41
33:g:102:ILE:HG22	33:g:103:VAL:HG23	2.01	0.41
1:A:151:SER:HB3	1:A:154:TYR:CD2	2.56	0.41
1:A:168:LEU:HB3	1:A:622:MET:CE	2.51	0.41
1:A:630:LYS:NZ	1:A:634:ASP:OD2	2.31	0.41
1:A:1033:ASN:HD22	1:A:1288:LEU:CB	2.34	0.41
1:A:1054:LEU:HA	1:A:1054:LEU:HD23	1.80	0.41
1:A:2058:LEU:O	1:A:2061:THR:OG1	2.33	0.41
2:C:832:ASP:HA	2:C:835:LYS:HG2	2.02	0.41
5:L:1115:G:C6	5:L:1116:A:N6	2.89	0.41
12:Q:77:ASP:HB2	12:Q:87:ARG:HD2	2.02	0.41
15:T:4:ILE:HG22	15:T:5:LYS:N	2.36	0.41
16:Z:336:GLU:C	16:Z:338:THR:H	2.29	0.41
17:c:224:MET:HE3	17:c:225:PRO:HD2	2.03	0.41
21:H:74:GLN:O	21:H:78:LEU:HG	2.20	0.41
1:A:685:HIS:O	1:A:686:ILE:C	2.64	0.41
1:A:806:ALA:N	1:A:807:PRO:HD2	2.35	0.41
1:A:1130:ARG:NH2	1:A:1158:ILE:O	2.54	0.41
1:A:1447:TRP:O	1:A:1448:GLU:C	2.63	0.41
1:A:1451:PHE:O	1:A:1454:SER:OG	2.23	0.41
1:A:1891:LEU:HD12	1:A:1989:PHE:CE2	2.56	0.41
1:A:1893:ILE:HG21	1:A:1981:ALA:HB3	2.03	0.41
3:D:89:U:H2'	3:D:90:C:O4'	2.21	0.41
4:E:51:A:H1'	4:E:52:G:P	2.60	0.41
4:E:56:A:C2'	4:E:57:U:O5'	2.69	0.41
5:L:1:A:C1'	23:v:504:UNK:H	2.26	0.41
10:O:406:THR:O	10:O:414:LEU:HD12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:c:229:ASP:HB2	22:I:151:LYS:HE3	2.03	0.41
17:c:230:THR:OG1	17:c:231:SER:N	2.48	0.41
18:d:153:ARG:HH21	18:d:181:ASN:HD21	1.67	0.41
23:v:669:TYR:CE2	23:v:686:ILE:HG13	2.43	0.41
1:A:264:ILE:HG22	1:A:265:ASN:O	2.21	0.41
1:A:284:ARG:NE	3:D:33:U:O4	2.54	0.41
1:A:903:LEU:HD23	1:A:903:LEU:O	2.21	0.41
1:A:1021:PRO:O	1:A:1024:LEU:HB3	2.20	0.41
1:A:1033:ASN:ND2	1:A:1297:THR:OG1	2.46	0.41
1:A:1405:ILE:HD12	16:Z:303:LEU:H	1.84	0.41
1:A:1686:VAL:HG12	1:A:1687:HIS:O	2.20	0.41
1:A:1690:LYS:HD2	1:A:1698:ALA:N	2.35	0.41
5:L:19:U:H3	11:P:174:ASN:CG	2.29	0.41
19:F:11:TYR:HE1	21:H:12:LEU:HD11	1.86	0.41
24:n:155:ILE:CG1	24:n:156:ARG:N	2.84	0.41
25:q:262:PRO:CG	25:q:271:SER:HB2	2.50	0.41
26:t:31:ILE:O	26:t:32:LYS:CB	2.68	0.41
35:b:62:ASN:HB2	35:b:84:ASN:OD1	2.20	0.41
1:A:728:ASN:ND2	4:E:72:C:HO2'	2.12	0.41
1:A:809:LYS:O	1:A:813:GLU:HG2	2.21	0.41
1:A:912:LEU:CD2	1:A:916:LEU:HD12	2.51	0.41
1:A:1050:LEU:CD2	1:A:1248:VAL:HG22	2.50	0.41
1:A:1144:PHE:HD2	1:A:1145:MET:HG2	1.84	0.41
1:A:1328:PHE:CE1	1:A:1371:VAL:HG13	2.56	0.41
1:A:1442:ARG:NH2	16:Z:302:SER:O	2.54	0.41
2:C:70:TYR:CE2	10:O:134:VAL:HG21	2.56	0.41
2:C:240:ASP:OD2	2:C:269:LYS:NZ	2.54	0.41
2:C:348:LEU:HD12	2:C:372:THR:HG22	2.02	0.41
2:C:801:TRP:NE1	2:C:843:LYS:HD2	2.35	0.41
2:C:919:ARG:HH12	2:C:927:MET:HE1	1.86	0.41
2:C:927:MET:HG3	2:C:928:CYS:N	2.36	0.41
4:E:21:U:H2'	4:E:22:G:H8	1.85	0.41
10:O:157:THR:HG21	10:O:423:ILE:HD11	2.01	0.41
10:O:198:PHE:HE1	10:O:208:CYS:SG	2.44	0.41
10:O:257:ILE:O	10:O:259:VAL:N	2.54	0.41
10:O:340:SER:OG	10:O:341:LEU:N	2.54	0.41
12:Q:222:THR:HA	12:Q:225:GLN:HE21	1.76	0.41
12:Q:254:GLN:O	12:Q:255:SER:HB2	2.21	0.41
17:c:227:ILE:HG12	22:I:152:ILE:CG2	2.50	0.41
21:H:41:VAL:HG21	21:H:92:TRP:CH2	2.56	0.41
23:v:463:UNK:O	23:v:467:UNK:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:q:101:THR:O	25:q:105:LEU:CG	2.69	0.41
26:t:113:LEU:O	26:t:116:ILE:CG1	2.69	0.41
30:j:26:ALA:C	30:j:43:ALA:HB3	2.46	0.41
33:g:49:ARG:HA	33:g:49:ARG:HD2	1.64	0.41
1:A:452:PHE:CZ	2:C:347:ARG:HG3	2.44	0.41
1:A:571:LEU:HG	1:A:629:MET:HE1	2.02	0.41
1:A:693:LYS:O	1:A:694:ASN:HB2	2.20	0.41
1:A:740:GLU:HG3	1:A:741:ILE:N	2.34	0.41
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.21	0.41
1:A:1752:VAL:HG12	1:A:1787:TYR:HB3	2.03	0.41
1:A:1857:VAL:HG13	1:A:1894:ILE:HD12	2.03	0.41
1:A:1865:THR:OG1	1:A:1869:ASN:HB2	2.21	0.41
2:C:341:ILE:HG13	2:C:342:ASP:H	1.84	0.41
2:C:807:PRO:HB2	2:C:851:LEU:HD21	2.03	0.41
10:O:385:GLN:HE21	10:O:387:LEU:HD21	1.86	0.41
17:c:220:GLU:CD	18:d:82:ARG:HH21	2.29	0.41
18:d:119:ARG:O	18:d:122:MET:N	2.54	0.41
30:x:26:ALA:C	30:x:43:ALA:HB3	2.46	0.41
2:C:152:LEU:HD11	2:C:316:THR:HA	2.02	0.40
2:C:416:ASP:O	2:C:420:PHE:HB3	2.21	0.40
2:C:887:ARG:HD3	2:C:889:TYR:OH	2.22	0.40
4:E:74:U:O4	14:S:30:LEU:HG	2.22	0.40
10:O:228:ARG:NH2	10:O:268:PRO:HB3	2.36	0.40
11:P:177:GLY:O	22:I:196:ILE:HD12	2.22	0.40
12:Q:208:TYR:HB2	12:Q:290:ILE:HB	2.02	0.40
12:Q:212:ALA:C	13:R:237:ARG:CZ	2.94	0.40
12:Q:255:SER:CB	12:Q:257:GLU:HG2	2.50	0.40
13:R:246:SER:O	13:R:250:MET:HG3	2.22	0.40
16:Z:192:GLU:N	16:Z:192:GLU:CD	2.73	0.40
16:Z:391:LEU:HD23	16:Z:391:LEU:HA	1.91	0.40
16:Z:462:ILE:HA	16:Z:474:THR:HG21	2.03	0.40
19:F:56:GLU:HG3	19:F:90:ARG:HG3	2.03	0.40
22:I:182:GLN:O	22:I:186:ALA:CB	2.69	0.40
1:A:388:PRO:O	1:A:392:ASN:HB3	2.21	0.40
1:A:426:PRO:HG2	16:Z:201:ARG:NH1	2.36	0.40
1:A:951:LEU:HD22	1:A:955:LYS:NZ	2.36	0.40
1:A:1192:ASP:OD2	1:A:1197:ASN:ND2	2.53	0.40
1:A:1372:LYS:HG2	1:A:1383:PHE:CE2	2.57	0.40
1:A:2050:THR:O	1:A:2053:SER:OG	2.22	0.40
2:C:122:TYR:CZ	31:l:82:PRO:HD3	2.56	0.40
2:C:706:LEU:HA	2:C:824:SER:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:21:U:P	24:n:54:SER:HG	2.18	0.40
4:E:63:G:HO2'	14:S:8:GLN:CB	2.33	0.40
5:L:19:U:C2	11:P:178:TYR:CD2	3.10	0.40
5:L:81:G:C6	5:L:82:C:N4	2.90	0.40
5:L:1102:C:H2'	5:L:1103:C:H5	1.70	0.40
7:B:90:A:C6	9:J:6:ILE:HD11	2.55	0.40
10:O:342:LEU:O	11:P:46:LYS:N	2.54	0.40
10:O:370:ASN:OD1	10:O:370:ASN:N	2.46	0.40
15:T:34:GLN:HE21	15:T:34:GLN:HB2	1.66	0.40
17:c:509:LEU:O	17:c:513:ILE:N	2.48	0.40
21:H:69:SER:O	21:H:70:LEU:HB2	2.21	0.40
23:v:520:UNK:O	23:v:524:UNK:N	2.54	0.40
26:t:89:GLU:CG	26:t:90:GLU:N	2.84	0.40
33:e:49:ARG:HA	33:e:102:ILE:HD11	2.03	0.40
1:A:143:ILE:HD12	1:A:573:ARG:HH21	1.86	0.40
1:A:460:PRO:HG3	2:C:376:PHE:CE1	2.55	0.40
1:A:654:HIS:CE1	1:A:658:ASN:HD21	2.39	0.40
1:A:709:ARG:NH2	3:D:82:A:O3'	2.50	0.40
1:A:780:ARG:HH22	14:S:9:LEU:HD22	1.85	0.40
1:A:1527:TRP:CD1	1:A:1527:TRP:H	2.37	0.40
8:N:108:U:C1'	8:N:109:U:P	3.09	0.40
12:Q:214:ILE:HD11	12:Q:218:LYS:HB3	2.03	0.40
16:Z:180:ILE:HG22	16:Z:186:LEU:CD2	2.43	0.40
16:Z:204:ASP:C	16:Z:205:TYR:CG	2.98	0.40
17:c:16:VAL:O	17:c:20:ILE:HD12	2.21	0.40
17:c:229:ASP:CB	22:I:151:LYS:HB3	2.35	0.40
18:d:175:PHE:HA	18:d:178:ARG:NH2	2.36	0.40
18:d:205:TRP:CZ3	18:d:221:VAL:HG21	2.56	0.40
18:d:232:LEU:HB2	18:d:238:TRP:HZ3	1.86	0.40
23:v:670:SER:CB	23:v:687:LEU:HD11	2.51	0.40
33:g:49:ARG:HA	33:g:102:ILE:HD11	2.03	0.40
30:x:37:ASN:OD1	30:x:65:GLY:N	2.55	0.40
1:A:176:LEU:O	1:A:179:MET:HG3	2.22	0.40
1:A:331:PHE:HD1	1:A:331:PHE:HA	1.73	0.40
1:A:1034:ASN:CG	1:A:1291:GLU:HG3	2.46	0.40
1:A:1859:ARG:O	1:A:1874:ALA:HA	2.21	0.40
2:C:544:LEU:HG	2:C:553:VAL:HG21	2.04	0.40
3:D:104:G:O2'	3:D:105:A:H5'	2.20	0.40
6:M:505:A:O3'	6:M:506:U:H4'	2.22	0.40
10:O:403:LEU:HD23	10:O:403:LEU:HA	1.86	0.40
12:Q:65:ALA:O	12:Q:69:ASN:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Q:106:ASN:HB2	12:Q:109:MET:CG	2.51	0.40
12:Q:124:GLN:OE1	12:Q:124:GLN:HA	2.20	0.40
16:Z:424:PHE:O	16:Z:428:VAL:HG23	2.21	0.40
17:c:228:TYR:HE1	18:d:123:ASN:ND2	2.20	0.40
18:d:160:CYS:HB3	18:d:169:TRP:CH2	2.56	0.40
23:v:680:ILE:O	23:v:683:SER:OG	2.22	0.40
24:n:396:ARG:CB	24:n:427:LYS:CG	3.00	0.40
1:A:131:LYS:HA	1:A:131:LYS:HD2	1.95	0.40
1:A:603:LYS:HG2	1:A:604:THR:O	2.22	0.40
1:A:695:LEU:HD12	1:A:695:LEU:O	2.21	0.40
1:A:1431:HIS:CG	1:A:1434:GLU:HA	2.56	0.40
1:A:1843:LEU:HD23	1:A:1849:LYS:NZ	2.36	0.40
2:C:461:LYS:HD3	2:C:461:LYS:C	2.44	0.40
2:C:869:HIS:CD2	2:C:925:LEU:HD22	2.56	0.40
2:C:933:TRP:O	2:C:935:LYS:HG3	2.22	0.40
10:O:279:PRO:HG3	10:O:301:MET:SD	2.62	0.40
12:Q:215:PRO:HG3	12:Q:217:TRP:CZ2	2.56	0.40
17:c:68:GLU:OE2	23:v:817:UNK:O	2.40	0.40
18:d:274:TRP:HA	18:d:275:PRO:HD3	1.91	0.40
25:q:183:LEU:CG	25:q:237:PRO:O	2.69	0.40

There are no symmetry-related clashes.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1902/2413 (79%)	1744 (92%)	149 (8%)	9 (0%)	24	54
2	C	872/1008 (86%)	796 (91%)	72 (8%)	4 (0%)	24	54
9	J	25/135 (18%)	20 (80%)	5 (20%)	0	100	100
10	O	335/451 (74%)	299 (89%)	31 (9%)	5 (2%)	8	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	P	193/379 (51%)	174 (90%)	17 (9%)	2 (1%)	12	40
12	Q	177/364 (49%)	154 (87%)	21 (12%)	2 (1%)	11	38
13	R	259/339 (76%)	241 (93%)	18 (7%)	0	100	100
14	S	63/175 (36%)	55 (87%)	5 (8%)	3 (5%)	2	11
15	T	155/157 (99%)	137 (88%)	16 (10%)	2 (1%)	9	33
16	Z	443/577 (77%)	390 (88%)	44 (10%)	9 (2%)	6	25
17	c	312/587 (53%)	291 (93%)	17 (5%)	4 (1%)	9	33
18	d	238/332 (72%)	221 (93%)	17 (7%)	0	100	100
19	F	-	104 (92%)	8 (7%)	1 (1%)	14	42
20	G	-	37 (95%)	1 (3%)	1 (3%)	4	21
21	H	-	78 (84%)	14 (15%)	1 (1%)	11	38
22	I	98/170 (58%)	95 (97%)	3 (3%)	0	100	100
23	v	121/859 (14%)	110 (91%)	7 (6%)	4 (3%)	3	17
24	n	279/455 (61%)	242 (87%)	29 (10%)	8 (3%)	3	19
25	o	120/503 (24%)	115 (96%)	4 (3%)	1 (1%)	16	44
25	p	122/503 (24%)	116 (95%)	6 (5%)	0	100	100
25	q	355/503 (71%)	327 (92%)	16 (4%)	12 (3%)	3	17
25	r	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	4	21
26	t	150/175 (86%)	134 (89%)	13 (9%)	3 (2%)	6	25
27	k	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
27	s	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
28	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
28	u	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
29	h	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	30
29	w	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	30
30	j	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
30	x	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
31	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	33
31	y	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	33
32	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
32	z	78/146 (53%)	74 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	e	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	7	29
33	g	92/110 (84%)	85 (92%)	6 (6%)	1 (1%)	11	38
34	a	77/111 (69%)	75 (97%)	2 (3%)	0	100	100
35	b	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	7	29
All	All	7810/12557 (62%)	7124 (91%)	604 (8%)	82 (1%)	15	40

All (82) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	483	PRO
2	C	364	PHE
2	C	463	THR
16	Z	206	LYS
20	G	17	MET
23	v	616	PRO
24	n	246	LEU
24	n	428	PRO
25	q	53	ILE
25	q	77	ILE
25	q	172	PRO
25	q	174	TRP
25	q	239	PRO
25	q	246	PRO
25	q	362	PRO
25	q	442	SER
25	r	64	GLU
26	t	77	PRO
35	b	68	PRO
1	A	1405	ILE
12	Q	99	VAL
12	Q	255	SER
14	S	8	GLN
14	S	9	LEU
16	Z	67	LYS
16	Z	69	ASN
16	Z	234	GLU
16	Z	235	ALA
17	c	230	THR
21	H	27	LYS
23	v	601	VAL
23	v	618	GLU

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Mol	Chain	Res	Type
24	n	61	LYS
24	n	291	HIS
24	n	406	ARG
25	q	196	PRO
26	t	110	GLU
1	A	484	PHE
2	C	829	VAL
16	Z	204	ASP
23	v	634	HIS
25	o	17	PRO
25	r	20	ARG
26	t	80	ASN
1	A	1628	ASP
10	O	444	PRO
11	P	86	ASN
11	P	112	ILE
14	S	10	GLU
17	c	231	SER
24	n	267	LEU
31	l	82	PRO
33	g	82	LYS
31	y	82	PRO
33	e	82	LYS
10	O	278	ASP
10	O	391	GLU
10	O	435	GLU
15	T	35	LYS
15	T	104	CYS
16	Z	146	ASN
16	Z	229	VAL
24	n	416	ARG
25	q	60	ALA
17	c	218	VAL
19	F	110	VAL
16	Z	214	ILE
25	q	36	GLY
29	h	15	PRO
29	w	15	PRO
35	b	52	LYS
1	A	407	VAL
1	A	562	ILE
10	O	277	VAL

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Mol	Chain	Res	Type
25	q	175	PRO
1	A	264	ILE
1	A	377	VAL
1	A	741	ILE
17	c	16	VAL
24	n	387	ILE
2	C	363	PRO
25	r	36	GLY

4.3.2 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	1736/2182 (80%)	1722 (99%)	14 (1%)	73	77
2	C	794/910 (87%)	788 (99%)	6 (1%)	73	77
9	J	21/121 (17%)	21 (100%)	0	100	100
10	O	295/397 (74%)	292 (99%)	3 (1%)	68	75
11	P	173/328 (53%)	173 (100%)	0	100	100
12	Q	171/332 (52%)	156 (91%)	15 (9%)	9	31
13	R	224/296 (76%)	223 (100%)	1 (0%)	84	83
14	S	56/151 (37%)	53 (95%)	3 (5%)	20	47
15	T	141/141 (100%)	138 (98%)	3 (2%)	47	64
16	Z	417/538 (78%)	382 (92%)	35 (8%)	10	34
17	c	212/316 (67%)	204 (96%)	8 (4%)	29	54
18	d	219/249 (88%)	216 (99%)	3 (1%)	59	70
19	F	-	104 (99%)	1 (1%)	68	75
20	G	-	39 (100%)	0	100	100
21	H	-	87 (99%)	1 (1%)	65	74
22	I	92/150 (61%)	92 (100%)	0	100	100
23	v	58/152 (38%)	47 (81%)	11 (19%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	n	124/413 (30%)	103 (83%)	21 (17%)	2	9
25	o	60/451 (13%)	54 (90%)	6 (10%)	7	26
25	p	62/451 (14%)	54 (87%)	8 (13%)	4	16
25	q	124/451 (28%)	106 (86%)	18 (14%)	3	13
25	r	60/451 (13%)	55 (92%)	5 (8%)	10	35
26	t	40/165 (24%)	27 (68%)	13 (32%)	0	0
27	k	70/176 (40%)	69 (99%)	1 (1%)	59	70
27	s	67/176 (38%)	66 (98%)	1 (2%)	57	69
28	i	65/83 (78%)	60 (92%)	5 (8%)	12	37
28	u	65/83 (78%)	60 (92%)	5 (8%)	12	37
29	h	61/77 (79%)	60 (98%)	1 (2%)	55	68
29	w	61/77 (79%)	60 (98%)	1 (2%)	55	68
30	j	58/66 (88%)	56 (97%)	2 (3%)	32	57
30	x	58/66 (88%)	56 (97%)	2 (3%)	32	57
31	l	69/89 (78%)	68 (99%)	1 (1%)	59	70
31	y	69/89 (78%)	68 (99%)	1 (1%)	59	70
32	m	77/129 (60%)	74 (96%)	3 (4%)	28	53
32	z	77/129 (60%)	74 (96%)	3 (4%)	28	53
33	e	59/103 (57%)	54 (92%)	5 (8%)	10	33
33	g	79/103 (77%)	73 (92%)	6 (8%)	12	38
34	a	26/100 (26%)	26 (100%)	0	100	100
35	b	47/219 (22%)	44 (94%)	3 (6%)	16	42
All	All	6319/10410 (61%)	6104 (97%)	215 (3%)	33	57

All (215) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	140	ARG
1	A	376	ARG
1	A	461	LEU
1	A	488	ARG
1	A	489	THR
1	A	495	ARG
1	A	588	LEU

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Mol	Chain	Res	Type
1	A	612	LYS
1	A	640	ARG
1	A	737	ARG
1	A	903	LEU
1	A	908	ASP
1	A	928	ARG
1	A	1661	ILE
2	C	176	ARG
2	C	206	LYS
2	C	458	ILE
2	C	461	LYS
2	C	465	GLU
2	C	468	LEU
10	O	443	ASN
10	O	445	ASN
10	O	446	LEU
12	Q	53	ASN
12	Q	55	ILE
12	Q	56	ILE
12	Q	119	LYS
12	Q	120	LEU
12	Q	125	ILE
12	Q	126	THR
12	Q	213	SER
12	Q	217	TRP
12	Q	220	THR
12	Q	222	THR
12	Q	226	LEU
12	Q	227	LEU
12	Q	245	LYS
12	Q	248	CYS
13	R	10	LYS
14	S	4	SER
14	S	6	ARG
14	S	9	LEU
15	T	31	ARG
15	T	34	GLN
15	T	120	CYS
16	Z	12	LYS
16	Z	16	GLU
16	Z	34	MET
16	Z	47	VAL

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Mol	Chain	Res	Type
16	Z	67	LYS
16	Z	94	LEU
16	Z	105	GLN
16	Z	132	GLU
16	Z	134	VAL
16	Z	138	ILE
16	Z	145	LYS
16	Z	149	ARG
16	Z	151	VAL
16	Z	162	LEU
16	Z	168	LYS
16	Z	174	TRP
16	Z	177	LEU
16	Z	179	TYR
16	Z	181	LEU
16	Z	183	THR
16	Z	184	GLN
16	Z	185	GLU
16	Z	186	LEU
16	Z	190	LEU
16	Z	192	GLU
16	Z	193	SER
16	Z	194	LEU
16	Z	195	GLU
16	Z	197	LEU
16	Z	199	GLU
16	Z	203	LYS
16	Z	216	ASP
16	Z	229	VAL
16	Z	245	CYS
16	Z	420	ILE
17	c	20	ILE
17	c	504	PRO
17	c	505	PRO
17	c	506	THR
17	c	517	VAL
17	c	523	LEU
17	c	532	PRO
17	c	550	PRO
18	d	155	LEU
18	d	269	ILE
18	d	271	ILE

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Mol	Chain	Res	Type
19	F	62	ARG
21	H	3	ARG
23	v	616	PRO
23	v	617	PRO
23	v	641	PRO
23	v	681	SER
23	v	706	LEU
23	v	712	CYS
23	v	722	PRO
23	v	723	SER
23	v	725	THR
23	v	726	ARG
23	v	733	ILE
24	n	51	PHE
24	n	55	GLU
24	n	57	LYS
24	n	58	ARG
24	n	59	ARG
24	n	62	THR
24	n	66	ASP
24	n	159	PRO
24	n	162	PRO
24	n	208	PRO
24	n	257	PRO
24	n	258	THR
24	n	260	PRO
24	n	295	SER
24	n	306	SER
24	n	327	PRO
24	n	340	PRO
24	n	373	PRO
24	n	424	PRO
24	n	428	PRO
24	n	436	PRO
25	o	17	PRO
25	o	26	SER
25	o	44	PRO
25	o	63	THR
25	o	109	LEU
25	o	134	SER
25	p	17	PRO
25	p	44	PRO

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Mol	Chain	Res	Type
25	p	63	THR
25	p	80	LEU
25	p	85	GLN
25	p	93	LEU
25	p	98	LEU
25	p	109	LEU
25	q	14	VAL
25	q	17	PRO
25	q	44	PRO
25	q	55	PRO
25	q	56	SER
25	q	61	SER
25	q	102	LEU
25	q	126	LEU
25	q	172	PRO
25	q	175	PRO
25	q	196	PRO
25	q	215	CYS
25	q	235	THR
25	q	239	PRO
25	q	262	PRO
25	q	271	SER
25	q	350	PRO
25	q	412	PRO
25	r	17	PRO
25	r	44	PRO
25	r	63	THR
25	r	93	LEU
25	r	109	LEU
26	t	5	SER
26	t	7	VAL
26	t	13	PRO
26	t	77	PRO
26	t	96	PRO
26	t	100	THR
26	t	105	PRO
26	t	108	SER
26	t	111	VAL
26	t	133	PRO
26	t	136	VAL
26	t	150	THR
26	t	152	THR

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Mol	Chain	Res	Type
27	k	47	GLU
28	i	16	CYS
28	i	18	PHE
28	i	25	THR
28	i	79	LYS
28	i	81	LEU
29	h	79	LEU
30	j	18	ASN
30	j	71	LEU
31	l	10	LEU
32	m	20	LYS
32	m	30	GLN
32	m	77	ASP
33	g	24	PHE
33	g	48	LEU
33	g	49	ARG
33	g	77	THR
33	g	99	ASP
33	g	100	SER
27	s	47	GLU
28	u	16	CYS
28	u	18	PHE
28	u	25	THR
28	u	79	LYS
28	u	81	LEU
29	w	79	LEU
30	x	18	ASN
30	x	71	LEU
31	y	10	LEU
32	z	20	LYS
32	z	30	GLN
32	z	77	ASP
33	e	48	LEU
33	e	49	ARG
33	e	77	THR
33	e	99	ASP
33	e	100	SER
35	b	4	THR
35	b	44	PRO
35	b	71	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (133) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	181	HIS
1	A	265	ASN
1	A	389	HIS
1	A	392	ASN
1	A	405	ASN
1	A	429	ASN
1	A	542	HIS
1	A	654	HIS
1	A	658	ASN
1	A	659	HIS
1	A	705	GLN
1	A	733	GLN
1	A	739	ASN
1	A	784	GLN
1	A	848	ASN
1	A	868	GLN
1	A	948	HIS
1	A	1011	ASN
1	A	1156	HIS
1	A	1368	GLN
1	A	1376	ASN
1	A	1449	ASN
1	A	1470	GLN
1	A	1508	HIS
1	A	1532	HIS
1	A	1559	HIS
1	A	1635	HIS
1	A	1652	HIS
1	A	1667	GLN
1	A	1737	GLN
1	A	1863	HIS
1	A	1947	HIS
1	A	2018	ASN
2	C	82	ASN
2	C	101	GLN
2	C	143	HIS
2	C	158	HIS
2	C	183	GLN
2	C	211	ASN
2	C	251	GLN
2	C	255	GLN
2	C	289	ASN

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Mol	Chain	Res	Type
2	C	309	ASN
2	C	423	HIS
2	C	444	GLN
2	C	560	GLN
2	C	683	ASN
2	C	764	ASN
2	C	817	GLN
2	C	830	ASN
2	C	869	HIS
2	C	960	ASN
9	J	19	HIS
10	O	126	HIS
10	O	138	HIS
10	O	215	GLN
10	O	344	ASN
10	O	382	HIS
10	O	428	GLN
11	P	110	HIS
11	P	111	HIS
11	P	148	HIS
11	P	174	ASN
12	Q	53	ASN
12	Q	81	HIS
12	Q	89	HIS
12	Q	209	ASN
12	Q	225	GLN
12	Q	244	HIS
13	R	25	GLN
13	R	58	HIS
13	R	91	HIS
13	R	92	HIS
13	R	150	HIS
13	R	155	GLN
13	R	191	ASN
13	R	201	ASN
13	R	227	ASN
13	R	248	ASN
14	S	5	HIS
14	S	8	GLN
14	S	27	HIS
14	S	34	HIS
14	S	158	ASN

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Mol	Chain	Res	Type
14	S	173	HIS
15	T	34	GLN
15	T	54	GLN
15	T	56	HIS
15	T	57	HIS
15	T	112	ASN
15	T	116	ASN
15	T	143	HIS
16	Z	54	ASN
16	Z	170	HIS
16	Z	184	GLN
16	Z	236	ASN
16	Z	247	ASN
16	Z	310	HIS
16	Z	354	HIS
16	Z	457	HIS
17	c	82	ASN
18	d	79	HIS
19	F	65	ASN
20	G	7	ASN
21	H	18	GLN
21	H	53	GLN
22	I	162	ASN
22	I	200	ASN
25	q	85	GLN
27	k	8	HIS
27	k	91	GLN
28	i	34	GLN
28	i	86	ASN
29	h	25	HIS
29	h	52	GLN
29	h	54	ASN
30	j	66	ASN
31	l	41	ASN
32	m	30	GLN
32	m	86	ASN
27	s	91	GLN
28	u	34	GLN
28	u	86	ASN
29	w	25	HIS
29	w	52	GLN
29	w	54	ASN

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Mol	Chain	Res	Type
30	x	66	ASN
31	y	17	HIS
31	y	41	ASN
32	z	86	ASN
33	e	71	ASN
35	b	62	ASN

4.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	D	114/214 (53%)	30 (26%)	3 (2%)
4	E	102/112 (91%)	34 (33%)	7 (6%)
5	L	120/1175 (10%)	25 (20%)	5 (4%)
6	M	28/29 (96%)	7 (25%)	0
7	B	12/13 (92%)	5 (41%)	0
8	N	14/15 (93%)	7 (50%)	1 (7%)
All	All	390/1558 (25%)	108 (27%)	16 (4%)

All (108) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	D	29	G
3	D	31	G
3	D	32	G
3	D	33	U
3	D	42	A
3	D	44	A
3	D	74	U
3	D	75	A
3	D	76	U
3	D	77	A
3	D	79	C
3	D	80	G
3	D	81	A
3	D	82	A
3	D	84	A
3	D	90	C
3	D	92	U
3	D	94	C
3	D	101	C
3	D	104	G

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Mol	Chain	Res	Type
3	D	127	U
3	D	164	C
3	D	165	A
3	D	166	U
3	D	170	U
3	D	171	U
3	D	172	U
3	D	173	U
3	D	174	G
3	D	175	G
4	E	12	A
4	E	13	A
4	E	14	C
4	E	15	C
4	E	16	C
4	E	30	G
4	E	33	C
4	E	36	U
4	E	37	U
4	E	39	G
4	E	43	C
4	E	50	G
4	E	51	A
4	E	52	G
4	E	54	U
4	E	57	U
4	E	60	G
4	E	62	A
4	E	65	U
4	E	66	C
4	E	67	C
4	E	68	C
4	E	73	A
4	E	74	U
4	E	75	A
4	E	80	U
4	E	81	G
4	E	85	C
4	E	86	G
4	E	87	U
4	E	88	U
4	E	90	U

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Mol	Chain	Res	Type
4	E	91	A
4	E	92	C
5	L	16	U
5	L	17	U
5	L	18	U
5	L	19	U
5	L	20	G
5	L	25	A
5	L	26	G
5	L	30	A
5	L	31	A
5	L	32	G
5	L	85	A
5	L	111	C
5	L	115	U
5	L	116	U
5	L	117	U
5	L	118	U
5	L	119	G
5	L	120	G
5	L	1099	G
5	L	1107	C
5	L	1108	A
5	L	1111	U
5	L	1112	G
5	L	1114	G
5	L	1120	G
6	M	495	A
6	M	499	U
6	M	501	A
6	M	503	A
6	M	504	C
6	M	505	A
6	M	506	U
7	B	88	U
7	B	89	A
7	B	90	A
7	B	93	U
7	B	94	U
8	N	101	U
8	N	102	A
8	N	108	U

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Mol	Chain	Res	Type
8	N	109	U
8	N	110	A
8	N	112	U
8	N	113	U

All (16) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	D	78	A
3	D	83	C
3	D	172	U
4	E	14	C
4	E	42	A
4	E	51	A
4	E	56	A
4	E	64	U
4	E	66	C
4	E	74	U
5	L	17	U
5	L	19	U
5	L	117	U
5	L	1107	C
5	L	1111	U
8	N	108	U

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 13 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	GTP	C	1500	37	33,34,34	0.94	1 (3%)	50,54,54	1.63	10 (20%)

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
36	GTP	C	1500	37	-	5/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	C	1500	GTP	C5-N7	-2.31	1.34	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	C	1500	GTP	C5-C4-N3	-4.94	120.52	128.39
36	C	1500	GTP	C2-N3-C4	4.47	120.00	112.30
36	C	1500	GTP	N9-C4-N3	3.24	132.43	125.95
36	C	1500	GTP	C2-N1-C6	-3.13	119.44	125.11
36	C	1500	GTP	N9-C8-N7	-2.93	107.98	113.40
36	C	1500	GTP	O6-C6-C5	-2.60	119.66	126.53
36	C	1500	GTP	C5-C6-N1	2.56	119.77	113.25
36	C	1500	GTP	C8-N7-C5	2.41	108.56	104.26
36	C	1500	GTP	C2'-C1'-N9	-2.30	106.86	113.25
36	C	1500	GTP	C3'-C2'-C1'	2.27	105.75	101.46

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	C	1500	GTP	C5'-O5'-PA-O3A
36	C	1500	GTP	C5'-O5'-PA-O1A
36	C	1500	GTP	C5'-O5'-PA-O2A
36	C	1500	GTP	C3'-C4'-C5'-O5'

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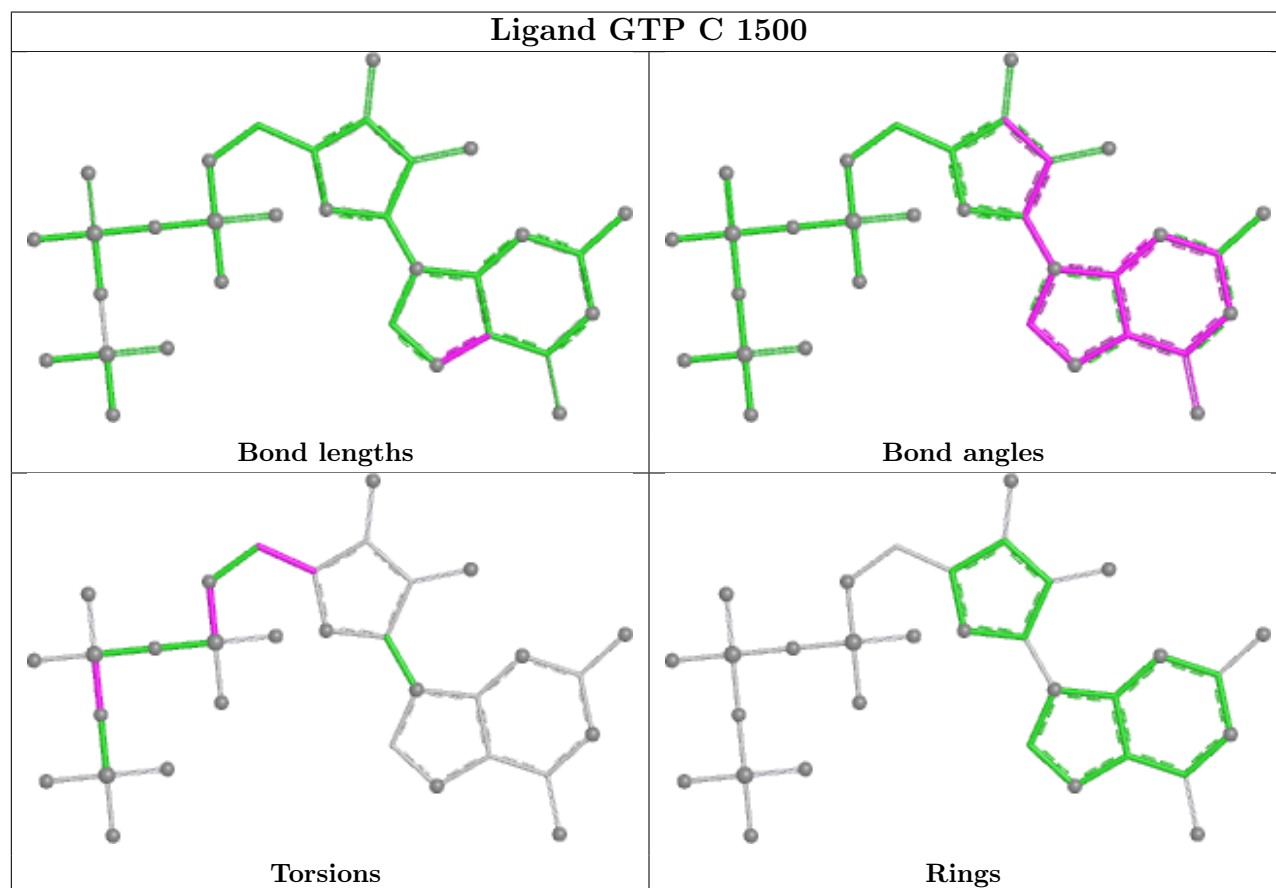
Mol	Chain	Res	Type	Atoms
36	C	1500	GTP	PG-O3B-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	C	1500	GTP	1	0

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



4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
23	v	33
18	d	21
17	c	6

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	d	275:PRO	C	295:UNK	N	28.30
1	v	103:UNK	C	106:UNK	N	18.26
1	d	377:UNK	C	379:UNK	N	14.04
1	c	382:UNK	C	384:UNK	N	13.70
1	c	469:UNK	C	482:GLU	N	13.69
1	c	401:UNK	C	411:UNK	N	13.25
1	v	152:UNK	C	155:UNK	N	12.35
1	v	561:UNK	C	569:LYS	N	12.18
1	v	385:UNK	C	387:UNK	N	11.77
1	v	317:UNK	C	319:UNK	N	11.69
1	v	417:UNK	C	419:UNK	N	11.55
1	v	218:UNK	C	220:UNK	N	11.50
1	v	88:UNK	C	90:UNK	N	11.25
1	v	734:GLN	C	740:UNK	N	11.22
1	c	438:UNK	C	444:UNK	N	11.17
1	d	333:UNK	C	340:UNK	N	10.93
1	d	391:UNK	C	393:UNK	N	10.62
1	v	169:UNK	C	171:UNK	N	10.40
1	v	120:UNK	C	124:UNK	N	10.28
1	v	366:UNK	C	368:UNK	N	9.81
1	d	480:UNK	C	485:UNK	N	9.47
1	v	137:UNK	C	139:UNK	N	9.44
1	v	234:UNK	C	236:UNK	N	9.39
1	v	756:UNK	C	758:UNK	N	9.21
1	v	183:UNK	C	186:UNK	N	9.18
1	c	365:UNK	C	370:UNK	N	9.12
1	v	502:UNK	C	504:UNK	N	9.08
1	c	420:UNK	C	422:UNK	N	8.94

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	794:UNK	C	796:UNK	N	8.38
1	v	401:UNK	C	403:UNK	N	8.16
1	v	72:UNK	C	74:UNK	N	7.96
1	d	444:UNK	C	450:UNK	N	7.94
1	d	576:UNK	C	580:UNK	N	7.92
1	d	465:UNK	C	467:UNK	N	7.84
1	d	622:UNK	C	625:UNK	N	7.43
1	d	425:UNK	C	427:UNK	N	7.02
1	v	202:UNK	C	204:UNK	N	6.96
1	v	543:UNK	C	545:UNK	N	6.90
1	v	335:UNK	C	337:UNK	N	6.84
1	d	531:UNK	C	533:UNK	N	6.37
1	v	775:UNK	C	777:UNK	N	6.27
1	v	460:UNK	C	462:UNK	N	6.25
1	v	299:UNK	C	301:UNK	N	6.24
1	d	500:UNK	C	502:UNK	N	6.20
1	v	283:UNK	C	285:UNK	N	6.08
1	v	437:UNK	C	439:UNK	N	5.53
1	v	252:UNK	C	254:UNK	N	5.40
1	v	525:UNK	C	527:UNK	N	5.31
1	v	267:UNK	C	269:UNK	N	5.21
1	d	598:UNK	C	600:UNK	N	4.93
1	d	517:UNK	C	519:UNK	N	4.58
1	d	375:UNK	C	377:UNK	N	3.95
1	d	355:UNK	C	357:UNK	N	3.91
1	d	554:UNK	C	559:UNK	N	3.83
1	d	533:UNK	C	535:UNK	N	3.64
1	d	410:UNK	C	412:UNK	N	3.29
1	v	485:UNK	C	487:UNK	N	3.25
1	d	407:UNK	C	409:UNK	N	3.18
1	d	536:UNK	C	538:UNK	N	3.17
1	v	353:UNK	C	355:UNK	N	3.16

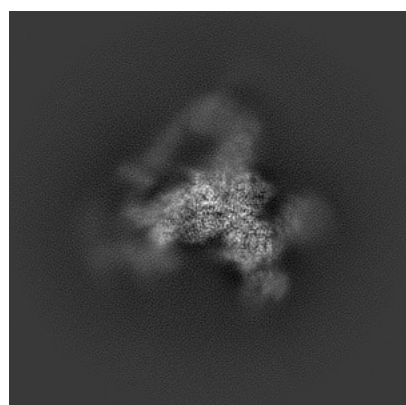
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9525. These allow visual inspection of the internal detail of the map and identification of artifacts.

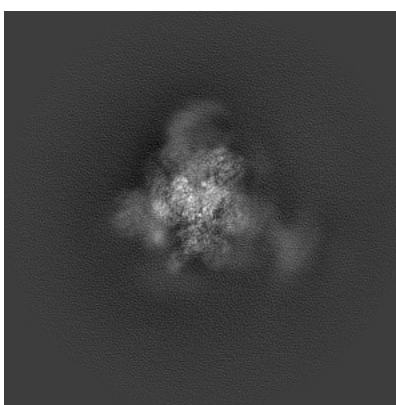
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

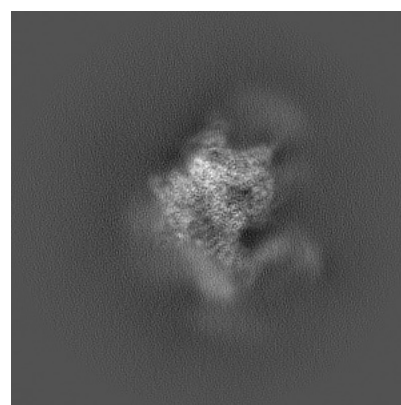
5.1.1 Primary map



X



Y

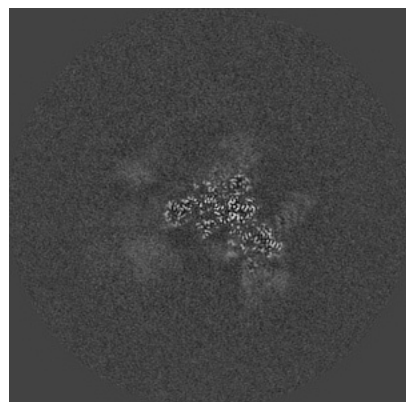


Z

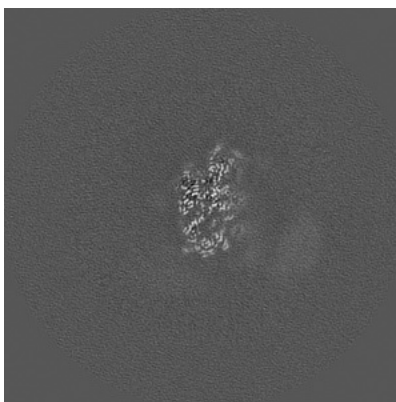
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

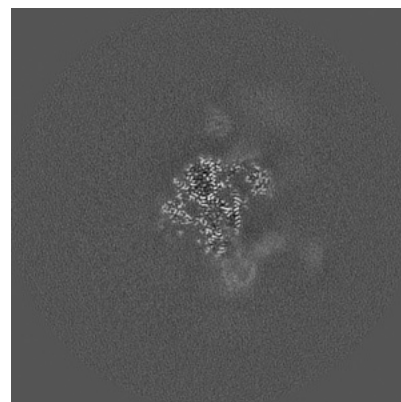
5.2.1 Primary map



X Index: 200



Y Index: 200

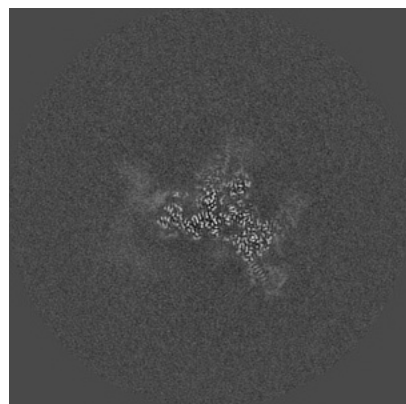


Z Index: 200

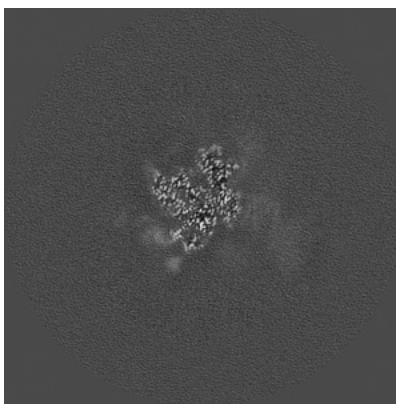
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

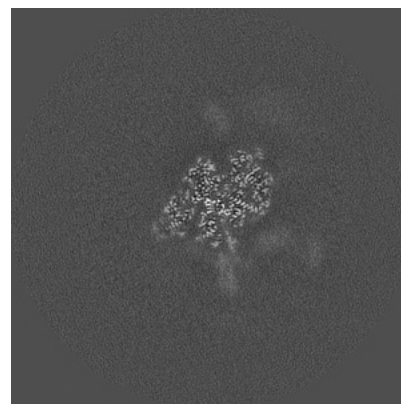
5.3.1 Primary map



X Index: 211



Y Index: 230

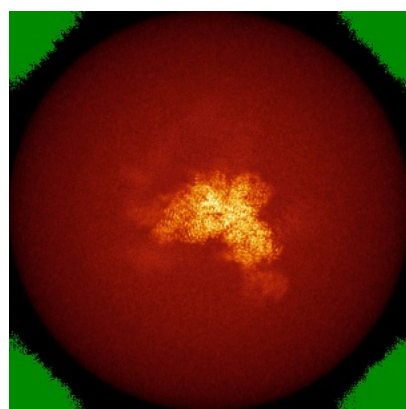


Z Index: 207

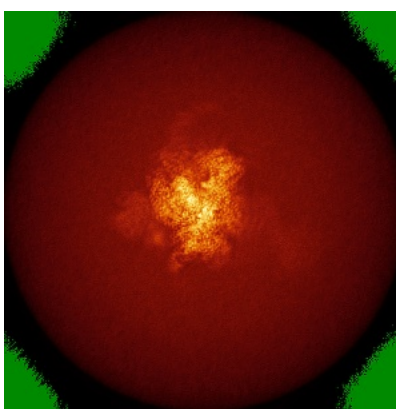
The images above show the largest variance slices of the map in three orthogonal directions.

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

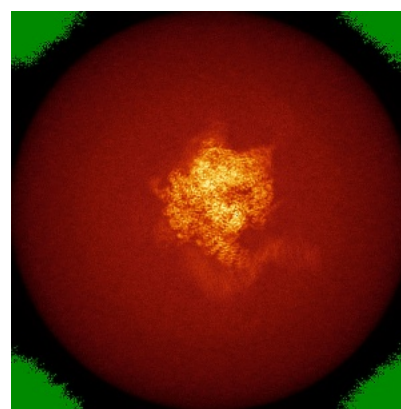
5.4.1 Primary map



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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0413. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

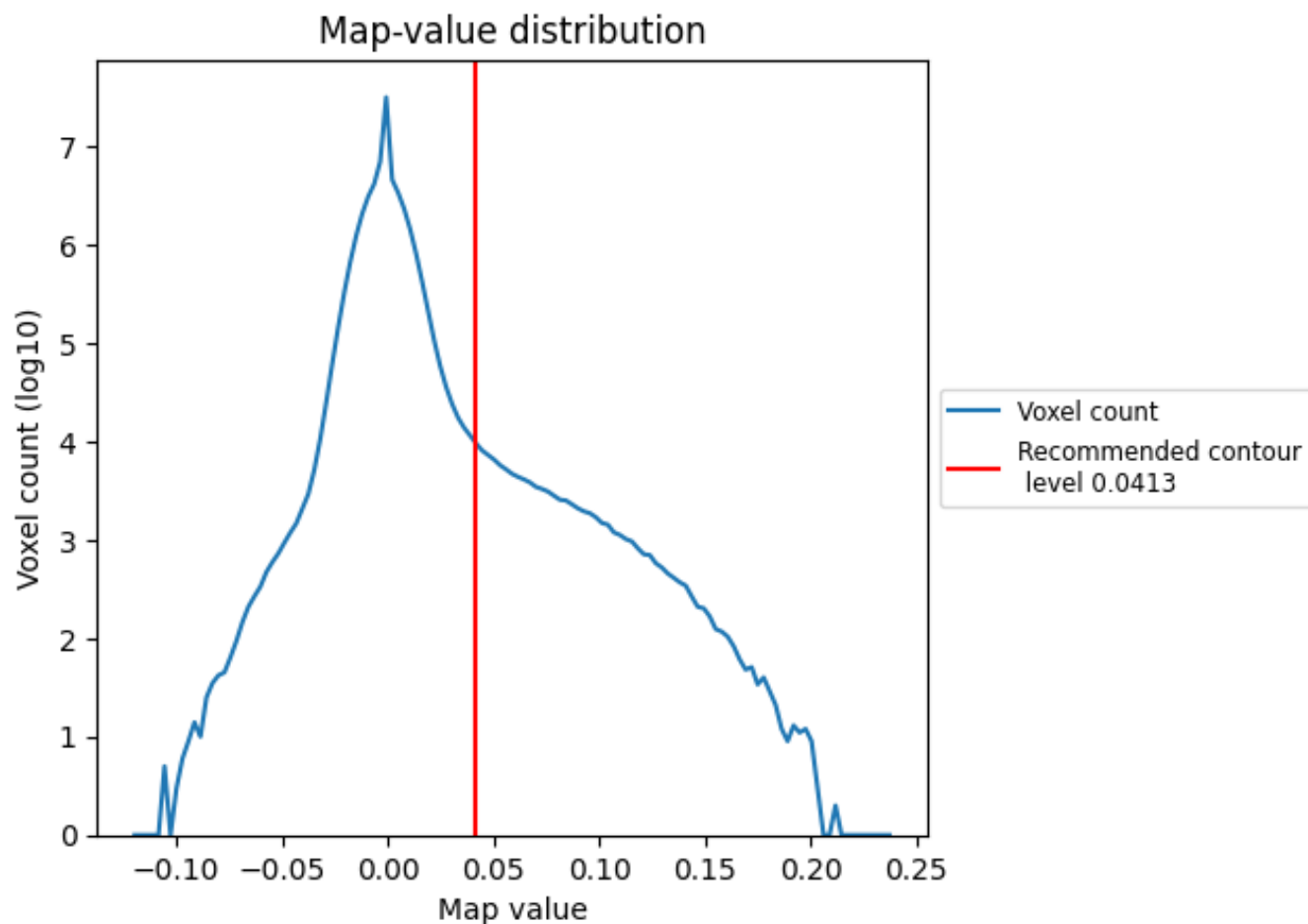
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

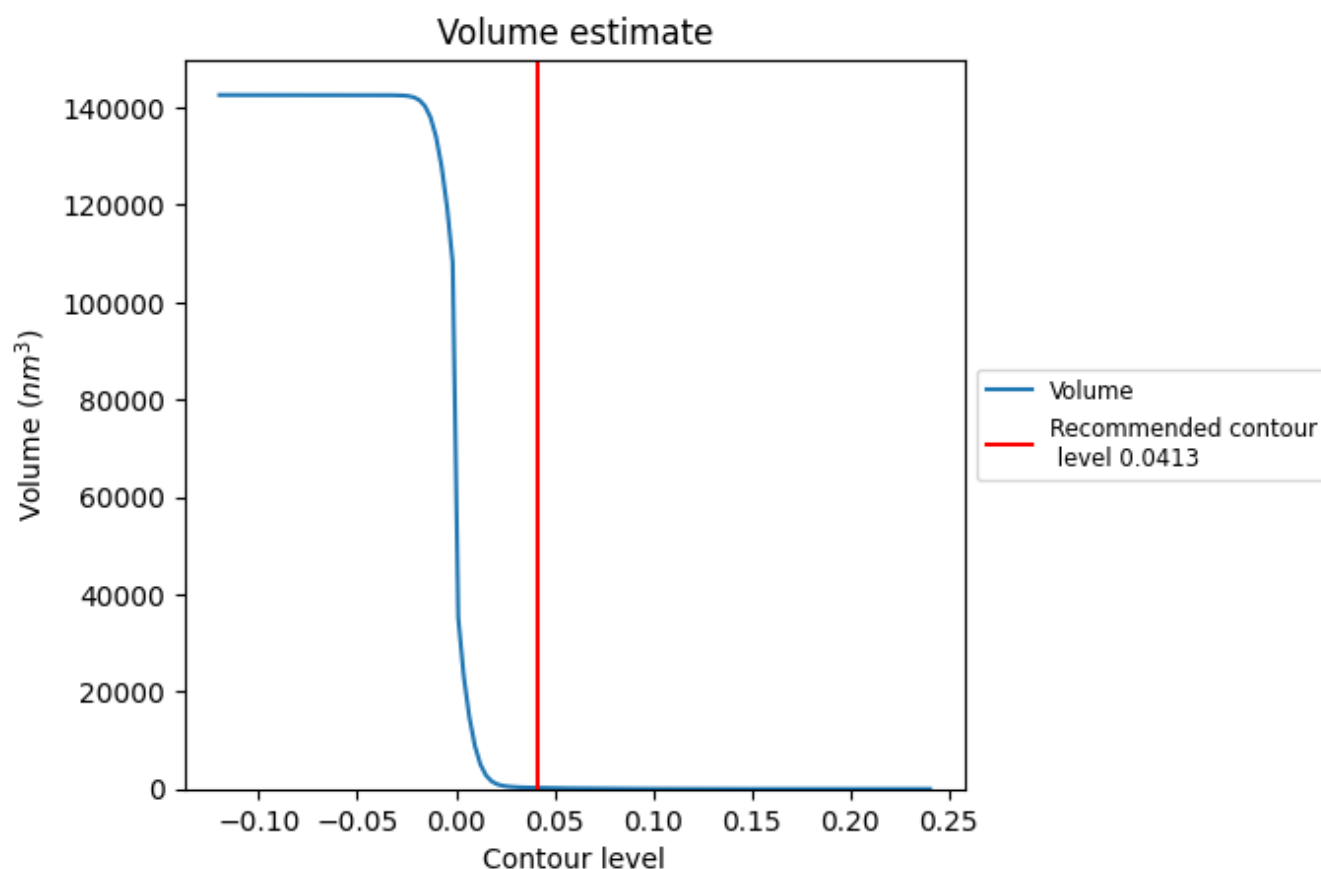
This section contains the results of statistical analysis of the map.

6.1 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.

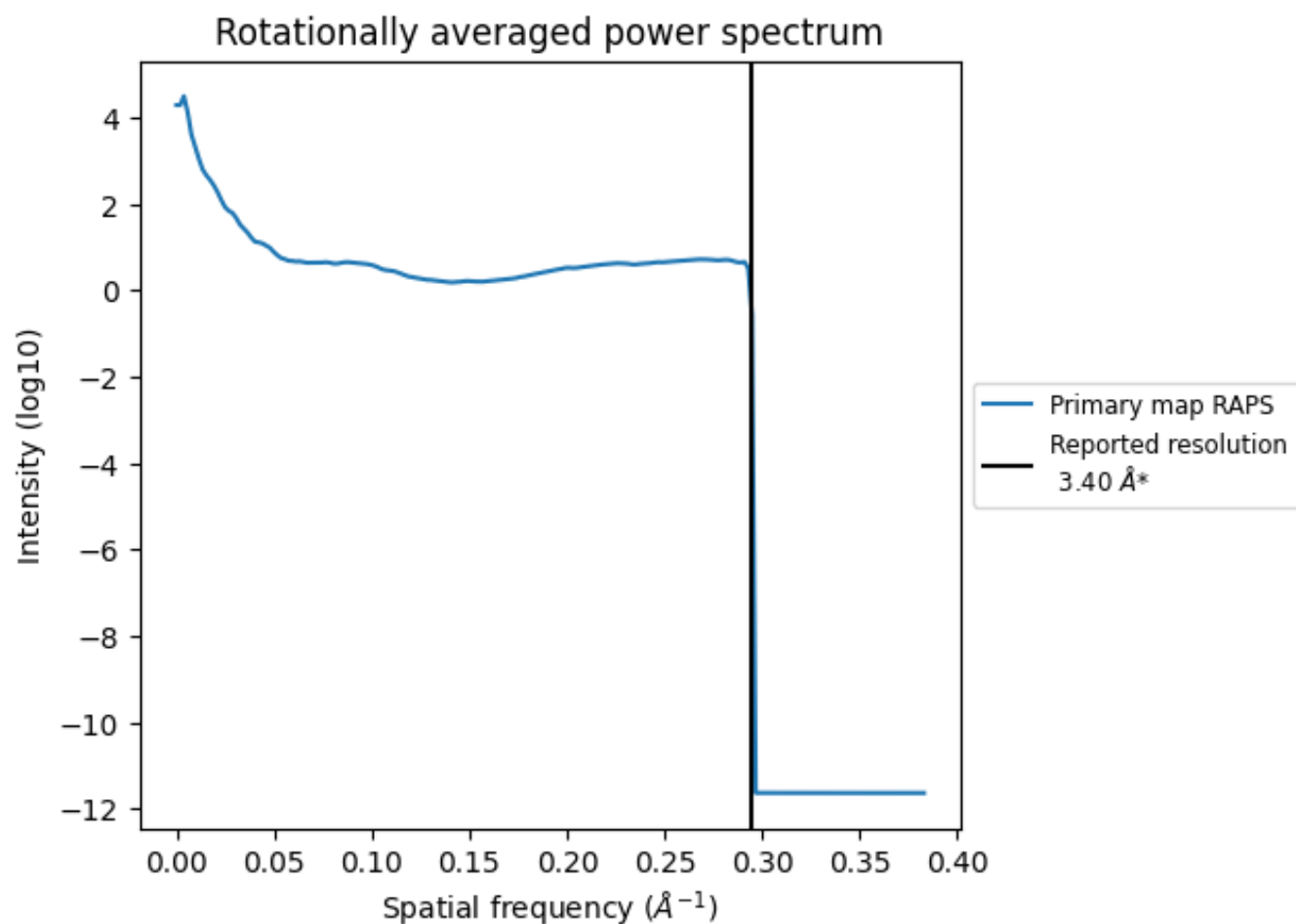
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 230 nm³; this corresponds to an approximate mass of 208 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

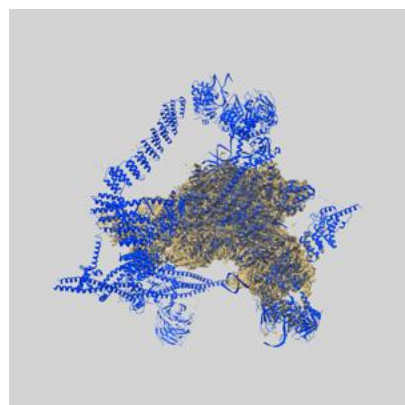
7 Fourier-Shell correlation ⓘ

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

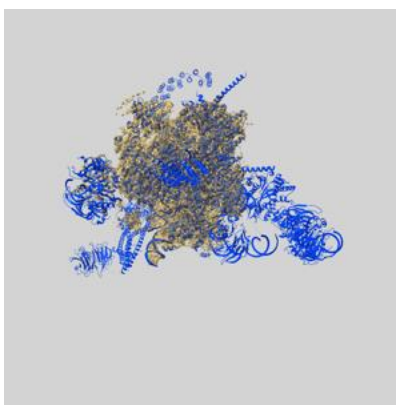
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9525 and PDB model 5GMK. Per-residue inclusion information can be found in section ?? on page ??.

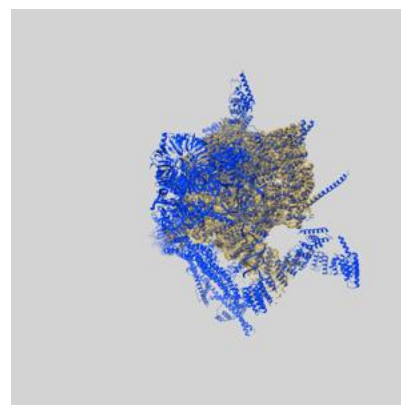
8.1 Map-model overlay [i](#)



X



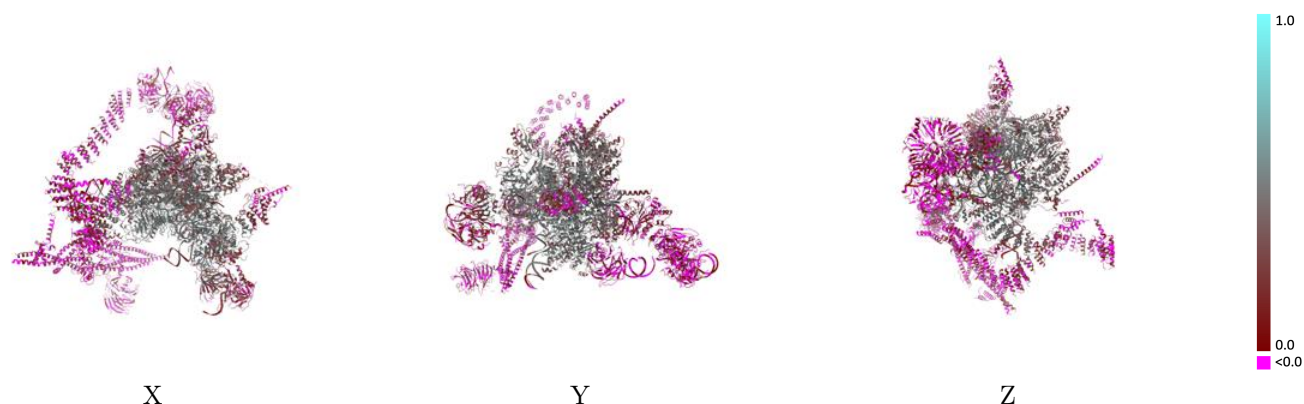
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0413 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.

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

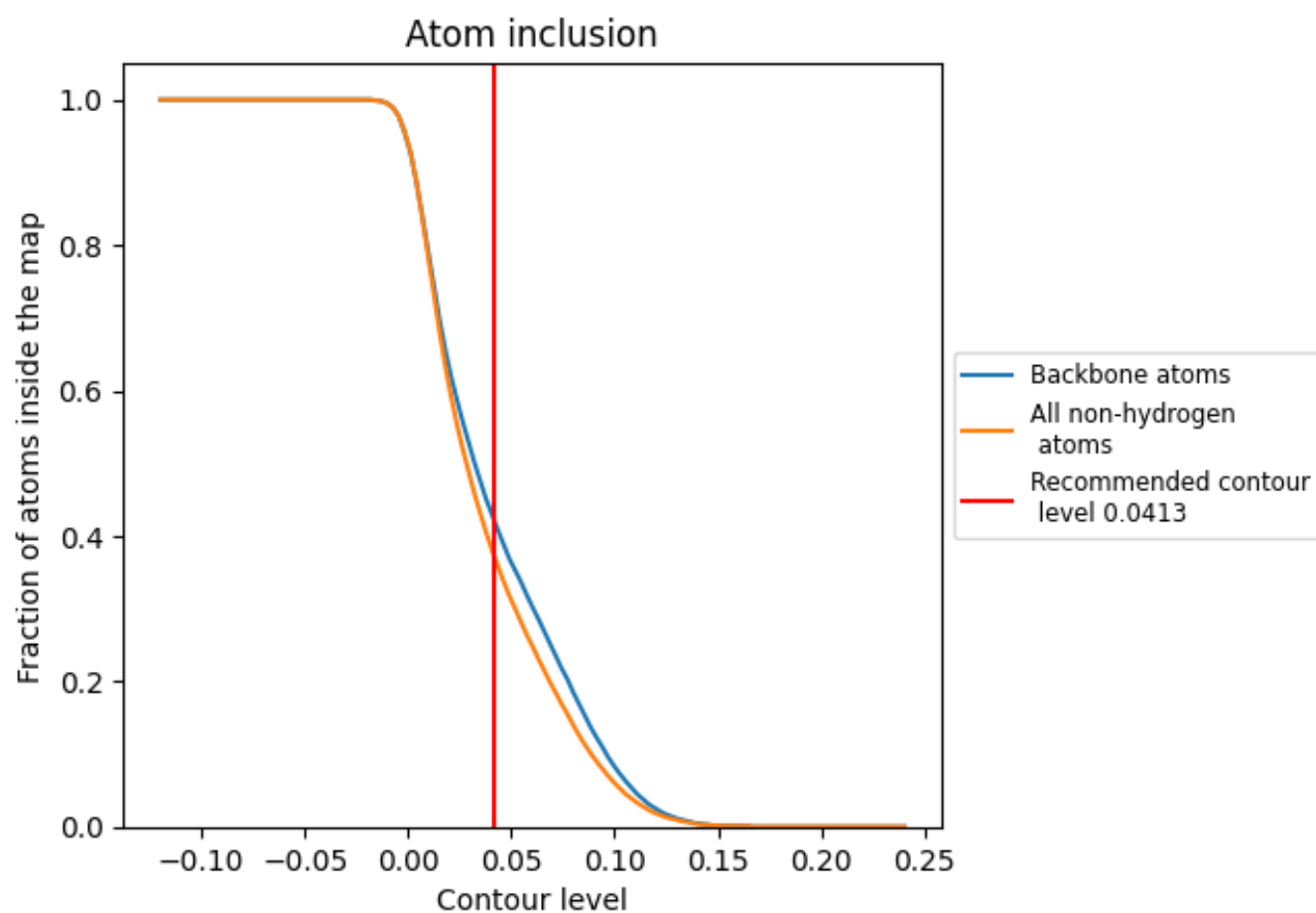


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

8.4 Atom inclusion [i](#)



At the recommended contour level, 42% of all backbone atoms, 38% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0413) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3750	 0.2790
A	 0.5810	 0.4060
B	 0.5600	 0.4420
C	 0.6550	 0.4330
D	 0.6350	 0.3920
E	 0.7210	 0.4230
F	 0.1440	 0.3760
G	 0.1400	 0.3200
H	 0.0990	 0.3320
I	 0.4220	 0.3730
J	 0.5450	 0.4740
L	 0.1590	 0.1240
M	 0.1170	 0.1810
N	 0.6030	 0.4150
O	 0.7510	 0.4890
P	 0.5040	 0.3740
Q	 0.5390	 0.4270
R	 0.6400	 0.4260
S	 0.4460	 0.4390
T	 0.6920	 0.4540
Z	 0.2320	 0.2360
a	 0.0000	 0.0020
b	 0.0000	 0.0090
c	 0.3240	 0.2250
d	 0.3840	 0.2600
e	 0.0000	 -0.0120
g	 0.0110	 0.1290
h	 0.0070	 0.0820
i	 0.0140	 0.1390
j	 0.0690	 0.2270
k	 0.0810	 0.2660
l	 0.2740	 0.3460
m	 0.0250	 0.1360
n	 0.0570	 0.0280
o	 0.0000	 -0.0230



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Chain	Atom inclusion	Q-score
p	 0.0000	 0.0070
q	 0.0000	 -0.0060
r	 0.0000	 0.0490
s	 0.0000	 0.0380
t	 0.0000	 -0.0000
u	 0.0000	 -0.0020
v	 0.0400	 0.0590
w	 0.0000	 0.0260
x	 0.0000	 0.0060
y	 0.0000	 0.0170
z	 0.0000	 0.0090