



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:22 AM UTC

PDB ID : 3NMU / pdb_00003nmu
Title : Crystal Structure of substrate-bound halfmer box C/D RNP
Authors : Li, H.; Xue, S.; Wang, R.
Deposited on : 2010-06-22
Resolution : 2.73 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

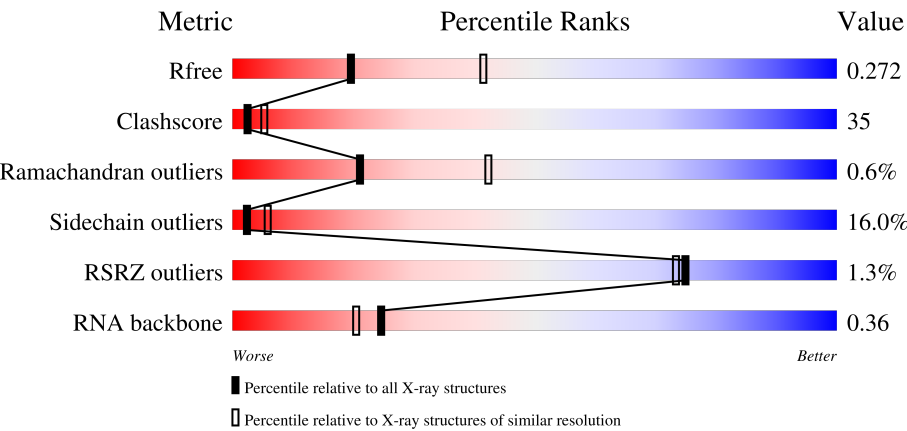
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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.



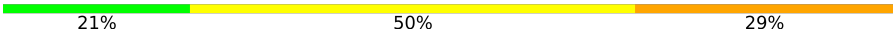
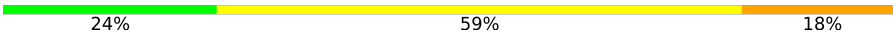
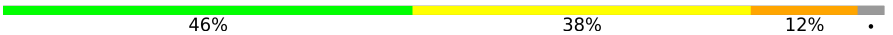
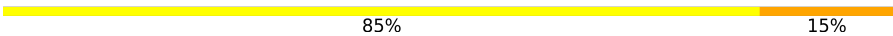
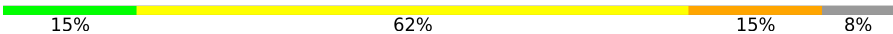
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)
RNA backbone	3983	1073 (2.94-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	379	45% 42% 9% ..
1	B	379	40% 46% 10% ..
2	C	129	7% 27% 52% 15% 6%
2	G	129	2% 40% 43% 11% 6%

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Mol	Chain	Length	Quality of chain
3	D	34	
3	E	34	
4	F	234	
4	J	234	
5	I	13	
5	K	13	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	SAM	J	228	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13531 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 NOP5/NOP56 related protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	366	Total	C	N	O	S	0	0	0
			2981	1903	518	553	7			
1	B	366	Total	C	N	O	S	0	0	0
			2981	1903	518	553	7			

- Molecule 2 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	121	Total	C	N	O	S	0	0	0
			926	591	153	179	3			
2	G	121	Total	C	N	O	S	0	0	0
			926	591	153	179	3			

- Molecule 3 is a RNA chain called RNA (34-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	34	Total	C	N	O	P	0	0	0
			732	326	136	236	34			
3	E	34	Total	C	N	O	P	0	0	0
			732	326	136	236	34			

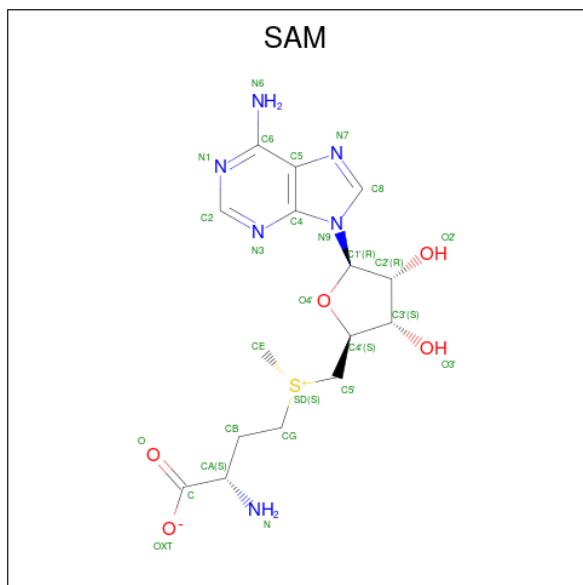
- Molecule 4 is a protein called Fibrillarin-like rRNA/tRNA 2'-O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	227	Total	C	N	O	S	0	0	0
			1822	1174	312	334	2			
4	J	227	Total	C	N	O	S	0	0	0
			1822	1174	312	334	2			

- Molecule 5 is a RNA chain called RNA (5'-R(*GP*AP*GP*CP*UP*UP*CP*AP*AP*CP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	13	Total	C	N	O	P	0	0	0
			275	124	51	88	12			
5	K	12	Total	C	N	O	P	0	0	0
			255	114	46	83	12			

- Molecule 6 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	F	1	Total	C	N	O	S	0	0
			26	15	6	4	1		
6	J	1	Total	C	N	O	S	0	0
			26	15	6	4	1		

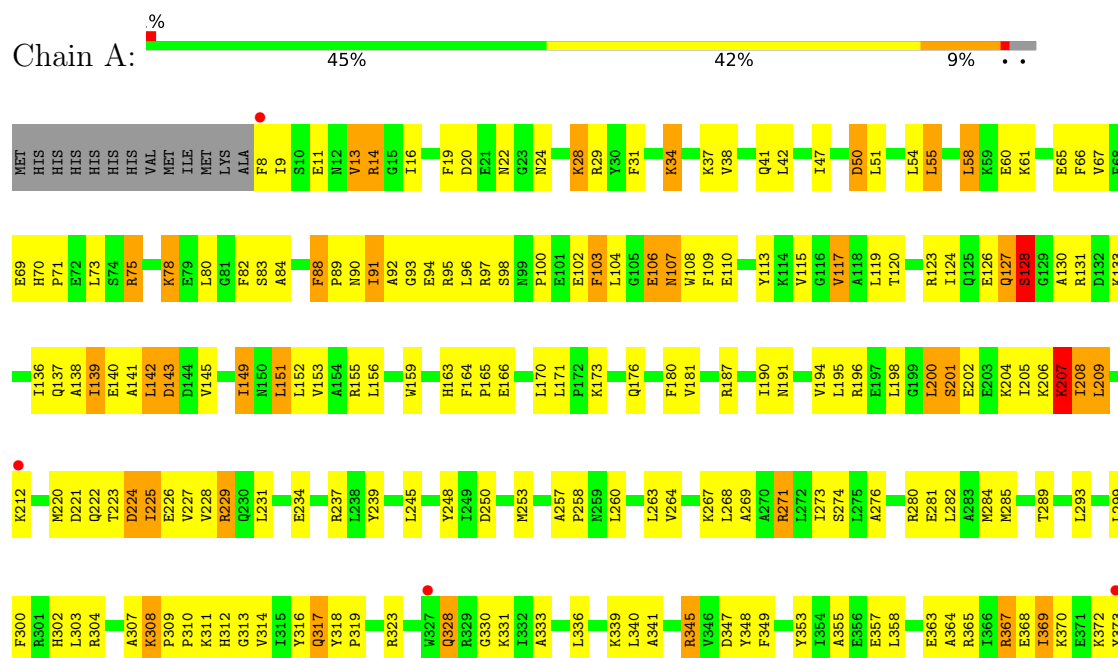
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	7	Total	O	0	0
			7	7		
7	B	5	Total	O	0	0
			5	5		
7	C	2	Total	O	0	0
			2	2		
7	F	8	Total	O	0	0
			8	8		
7	G	2	Total	O	0	0
			2	2		
7	J	3	Total	O	0	0
			3	3		

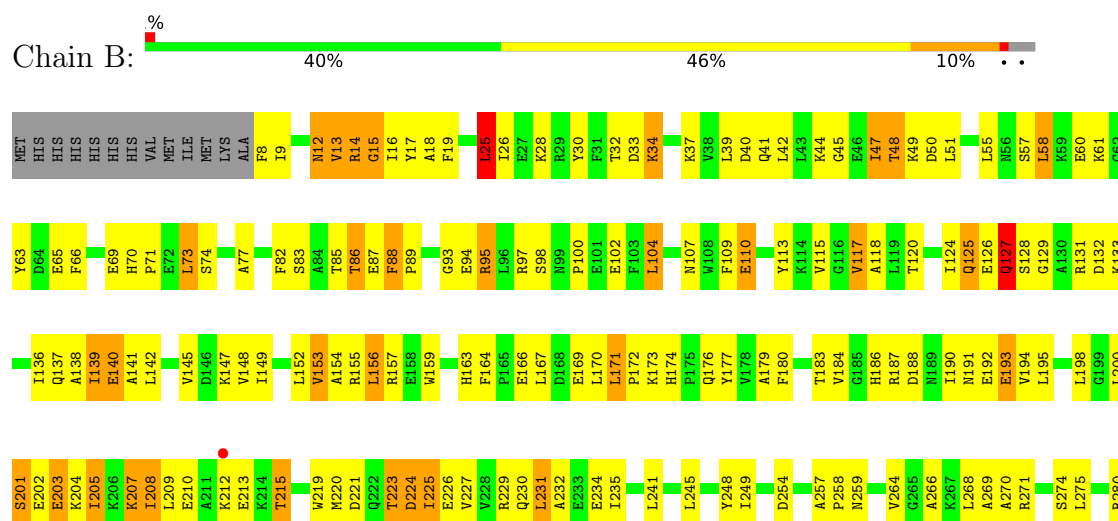
3 Residue-property plots

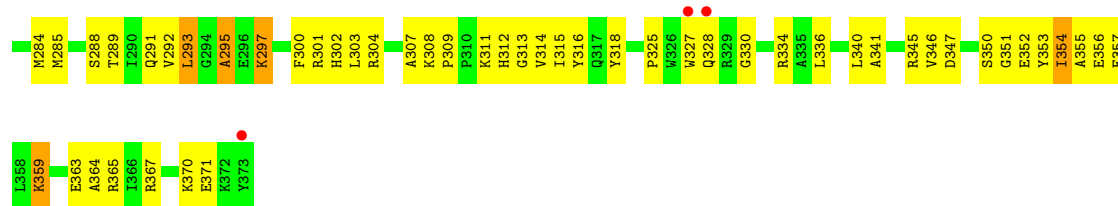
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: NOP5/NOP56 related protein

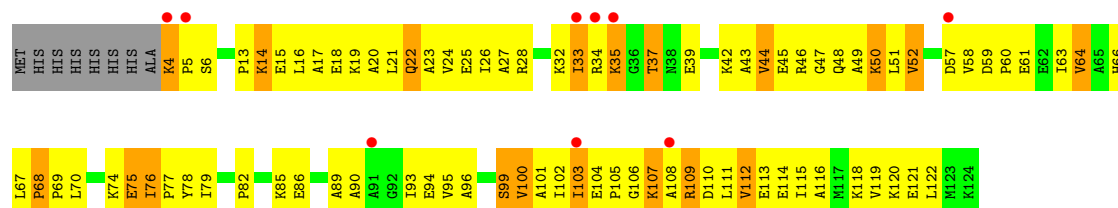


• Molecule 1: NOP5/NOP56 related protein





• Molecule 2: 50S ribosomal protein L7Ae



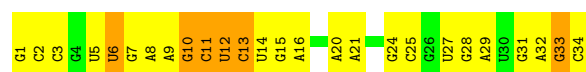
• Molecule 2: 50S ribosomal protein L7Ae



• Molecule 3: RNA (34-MER)

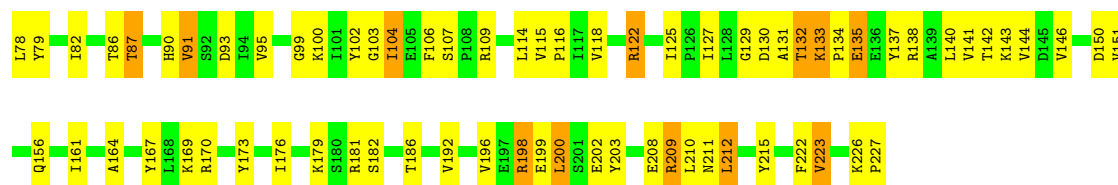


• Molecule 3: RNA (34-MER)

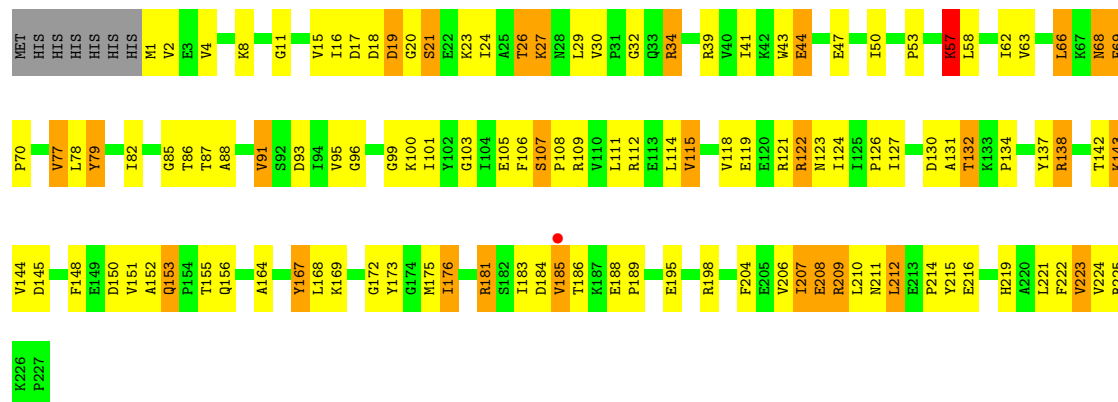


• Molecule 4: Fibrillar-like rRNA/tRNA 2'-O-methyltransferase

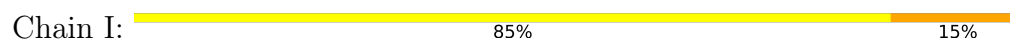




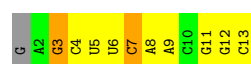
- Molecule 4: Fibrillarin-like rRNA/tRNA 2'-O-methyltransferase



- Molecule 5: RNA (5'-R(*GP*AP*GP*CP*UP*UP*CP*AP*AP*CP*GP*GP*C)-3')



- Molecule 5: RNA (5'-R(*GP*AP*GP*CP*UP*UP*CP*AP*AP*CP*GP*GP*C)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	293.51Å 94.05Å 96.81Å 90.00° 101.47° 90.00°	Depositor
Resolution (Å)	33.57 – 2.73 33.57 – 2.73	Depositor EDS
% Data completeness (in resolution range)	79.6 (33.57-2.73) 78.9 (33.57-2.73)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.73Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.222 , 0.284 0.208 , 0.272	Depositor DCC
R_{free} test set	2000 reflections (3.25%)	wwPDB-VP
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.828	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13531	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.66	0/3036	1.13	9/4085 (0.2%)
1	B	0.70	0/3036	1.12	17/4085 (0.4%)
2	C	0.57	0/938	1.08	7/1264 (0.6%)
2	G	0.55	0/938	1.01	2/1264 (0.2%)
3	D	0.29	0/819	0.51	0/1276
3	E	0.30	0/819	0.50	0/1276
4	F	0.71	0/1861	1.16	11/2515 (0.4%)
4	J	0.75	0/1861	1.23	14/2515 (0.6%)
5	I	0.27	0/307	0.41	0/477
5	K	0.25	0/284	0.45	0/440
All	All	0.63	0/13899	1.05	60/19197 (0.3%)

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	88	PHE	CA-C-N	-20.62	96.83	120.13
1	A	88	PHE	C-N-CA	-20.62	96.83	120.13
1	A	9	ILE	N-CA-C	8.54	120.41	107.77
2	C	76	ILE	CA-C-N	8.42	128.56	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	76	ILE	C-N-CA	8.42	128.56	120.31
1	B	171	LEU	CA-C-N	8.22	127.95	119.64
1	B	171	LEU	C-N-CA	8.22	127.95	119.64
4	F	35	VAL	N-CA-C	8.15	118.72	110.82
4	J	69	PHE	CA-C-N	8.07	128.26	119.87
4	J	69	PHE	C-N-CA	8.07	128.26	119.87
2	C	112	VAL	N-CA-C	7.93	117.99	110.53
1	A	207	LYS	N-CA-C	-7.80	97.67	109.60
4	J	19	ASP	N-CA-C	7.72	120.40	108.12
1	B	15	GLY	N-CA-C	7.72	121.69	110.80
2	C	4	LYS	CA-C-N	7.63	127.68	119.89
2	C	4	LYS	C-N-CA	7.63	127.68	119.89
4	F	151	VAL	N-CA-C	7.46	121.01	113.47
1	B	26	ILE	CB-CA-C	-7.40	99.16	111.29
2	G	12	VAL	CA-C-N	7.30	127.73	119.92
2	G	12	VAL	C-N-CA	7.30	127.73	119.92
1	B	9	ILE	N-CA-C	7.19	118.50	107.78
1	B	88	PHE	CA-C-N	-7.16	104.79	120.89
1	B	88	PHE	C-N-CA	-7.16	104.79	120.89
1	A	349	PHE	N-CA-C	6.92	119.85	111.40
1	B	142	LEU	N-CA-C	-6.77	105.02	113.28
1	B	34	LYS	N-CA-C	-6.67	101.36	109.57
4	F	107	SER	CA-C-N	6.58	126.02	118.85
4	F	107	SER	C-N-CA	6.58	126.02	118.85
4	J	153	GLN	N-CA-C	6.43	117.00	109.60
1	A	264	VAL	N-CA-C	6.16	118.92	112.83
4	F	69	PHE	CA-C-N	6.08	126.19	119.87
4	F	69	PHE	C-N-CA	6.08	126.19	119.87
4	F	133	LYS	CA-C-N	6.03	126.19	119.32
4	F	133	LYS	C-N-CA	6.03	126.19	119.32
4	J	77	VAL	N-CA-C	6.00	117.41	108.46
1	B	127	GLN	N-CA-C	5.99	123.55	110.80
4	J	127	ILE	N-CA-C	5.97	116.98	108.93
4	J	68	ASN	N-CA-C	5.88	118.31	108.96
4	F	167	TYR	N-CA-C	5.66	120.34	113.38
4	J	21	SER	N-CA-C	5.51	117.79	109.41
2	C	68	PRO	N-CA-C	5.50	117.41	110.70
1	B	132	ASP	N-CA-C	-5.45	105.50	111.82
4	J	57	LYS	N-CA-C	-5.43	103.25	111.34
1	A	308	LYS	CA-C-N	5.38	125.92	120.38
1	A	308	LYS	C-N-CA	5.38	125.92	120.38
4	J	115	VAL	CB-CA-C	-5.32	108.71	114.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	25	LEU	N-CA-C	5.32	116.77	110.97
1	A	103	PHE	N-CA-C	5.24	117.79	111.40
4	J	176	ILE	N-CA-C	5.23	116.23	107.18
4	J	206	VAL	CB-CA-C	-5.20	104.64	111.25
1	B	295	ALA	N-CA-C	-5.20	106.78	113.02
4	J	167	TYR	N-CA-C	5.15	120.42	113.72
1	B	118	ALA	N-CA-C	-5.12	105.70	111.28
1	B	285	MET	CA-C-N	5.11	125.39	119.92
1	B	285	MET	C-N-CA	5.11	125.39	119.92
4	F	222	PHE	CA-C-N	-5.10	116.46	123.14
4	F	222	PHE	C-N-CA	-5.10	116.46	123.14
4	J	19	ASP	CB-CA-C	-5.08	105.06	115.28
2	C	6	SER	N-CA-C	5.02	116.56	111.14
1	B	66	PHE	N-CA-C	5.02	117.15	109.07

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	SER	Peptide
1	B	213	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2981	0	3022	228	0
1	B	2981	0	3022	255	0
2	C	926	0	977	109	0
2	G	926	0	977	65	0
3	D	732	0	369	47	0
3	E	732	0	369	47	0
4	F	1822	0	1869	79	0
4	J	1822	0	1869	121	0
5	I	275	0	143	23	0
5	K	255	0	131	16	0
6	F	26	0	22	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	J	26	0	22	11	0
7	A	7	0	0	1	0
7	B	5	0	0	0	0
7	C	2	0	0	0	0
7	F	8	0	0	1	0
7	G	2	0	0	0	0
7	J	3	0	0	1	0
All	All	13531	0	12792	914	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 35.

All (914) 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:187:ARG:CG	1:A:212:LYS:HZ1	1.54	1.20
4:F:209:ARG:HG3	4:F:209:ARG:HH11	1.05	1.17
1:A:187:ARG:HB2	1:A:212:LYS:HE2	1.30	1.14
1:A:187:ARG:HB2	1:A:212:LYS:CE	1.82	1.08
1:A:187:ARG:HG3	1:A:212:LYS:HZ1	1.13	1.08
1:B:127:GLN:HE21	1:B:128:SER:HA	1.15	1.08
2:C:35:LYS:HA	2:C:100:VAL:HG22	1.35	1.05
1:A:328:GLN:HE22	1:A:370:LYS:HD3	1.17	1.02
1:B:271:ARG:HG2	1:B:314:VAL:HG11	1.39	1.02
2:C:112:VAL:HA	2:C:115:ILE:HG22	1.39	1.02
2:C:15:GLU:HG3	2:C:16:LEU:H	1.25	1.01
1:B:190:ILE:HD12	1:B:212:LYS:HE3	1.42	0.97
1:B:291:GLN:HE22	3:E:13:C:H41	1.02	0.96
2:C:45:GLU:HA	2:C:74:LYS:HE2	1.44	0.95
4:J:130:ASP:OD1	4:J:132:THR:HB	1.66	0.95
1:B:127:GLN:N	1:B:127:GLN:CD	2.25	0.95
1:B:127:GLN:HB2	1:B:129:GLY:N	1.81	0.94
1:B:187:ARG:HB2	1:B:212:LYS:HZ1	1.33	0.94
1:A:187:ARG:CB	1:A:212:LYS:HZ1	1.80	0.93
1:B:145:VAL:O	1:B:149:ILE:HG12	1.70	0.92
1:A:173:LYS:HD3	1:A:176:GLN:HG3	1.53	0.91
2:C:50:LYS:NZ	2:C:103:ILE:O	2.04	0.90
4:F:209:ARG:HG3	4:F:209:ARG:NH1	1.80	0.89
1:B:187:ARG:HB2	1:B:212:LYS:NZ	1.88	0.89
1:A:208:ILE:HG22	1:A:209:LEU:HD23	1.56	0.88
1:B:70:HIS:ND1	1:B:71:PRO:HD2	1.90	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:THR:HG22	1:B:50:ASP:H	1.40	0.87
1:B:190:ILE:CD1	1:B:212:LYS:HE3	2.05	0.87
1:A:187:ARG:HG3	1:A:212:LYS:NZ	1.90	0.87
4:F:95:VAL:HG13	4:F:99:GLY:HA3	1.57	0.87
1:B:88:PHE:HB3	1:B:89:PRO:HD3	1.56	0.86
4:J:95:VAL:CG1	4:J:99:GLY:HA3	2.06	0.86
4:F:132:THR:HG22	4:F:133:LYS:HG3	1.59	0.85
3:D:19:G:H5'	3:D:20:A:OP2	1.76	0.85
4:J:209:ARG:HG3	4:J:209:ARG:HH11	1.43	0.84
1:A:187:ARG:CG	1:A:212:LYS:NZ	2.41	0.83
1:A:328:GLN:HE22	1:A:370:LYS:CD	1.92	0.83
1:B:127:GLN:NE2	1:B:128:SER:HA	1.93	0.83
1:A:47:ILE:HG13	1:A:51:LEU:HD23	1.61	0.82
1:B:164:PHE:CZ	1:B:212:LYS:HE2	2.12	0.82
1:B:271:ARG:HG2	1:B:314:VAL:CG1	2.07	0.82
1:B:13:VAL:HG22	1:B:115:VAL:HG11	1.61	0.82
1:B:163:HIS:HE1	1:B:187:ARG:H	1.26	0.82
1:B:128:SER:HB3	4:J:112:ARG:HH12	1.44	0.82
1:A:164:PHE:CZ	1:A:212:LYS:HD3	2.15	0.81
2:C:109:ARG:HG3	2:C:109:ARG:HH11	1.45	0.81
1:B:271:ARG:CG	1:B:314:VAL:HG11	2.09	0.81
2:G:59:ASP:HA	2:G:60:PRO:C	2.04	0.81
4:J:95:VAL:HG13	4:J:99:GLY:HA3	1.61	0.81
1:B:156:LEU:HD11	1:B:232:ALA:HB2	1.62	0.81
2:C:15:GLU:HG3	2:C:16:LEU:N	1.93	0.81
4:J:216:GLU:HB3	4:J:219:HIS:CD2	2.15	0.81
3:E:10:G:H2'	3:E:11:C:H5'	1.61	0.81
2:C:47:GLY:HA3	5:K:4:C:O2'	1.81	0.81
1:B:18:ALA:O	1:B:25:LEU:O	1.97	0.81
1:B:125:GLN:HG2	1:B:131:ARG:NH2	1.96	0.81
1:B:127:GLN:N	1:B:127:GLN:NE2	2.29	0.81
2:C:18:GLU:HG3	2:C:19:LYS:N	1.96	0.80
1:B:193:GLU:CD	1:B:193:GLU:H	1.87	0.80
2:G:68:PRO:HB2	2:G:69:PRO:HD3	1.64	0.80
1:A:328:GLN:NE2	1:A:370:LYS:HD3	1.96	0.80
1:B:127:GLN:HB2	1:B:129:GLY:H	1.44	0.80
1:B:180:PHE:O	1:B:184:VAL:HG12	1.82	0.79
2:C:102:ILE:HG21	2:C:105:PRO:HB3	1.64	0.79
1:B:136:ILE:HG23	1:B:274:SER:OG	1.81	0.79
4:F:6:LYS:HD3	4:F:7:HIS:H	1.47	0.79
1:B:186:HIS:HD2	1:B:188:ASP:H	1.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:26:THR:HG22	4:J:27:LYS:H	1.49	0.78
4:F:209:ARG:HH11	4:F:209:ARG:CG	1.94	0.78
2:C:23:ALA:O	2:C:108:ALA:HB2	1.82	0.78
1:A:257:ALA:HB1	1:A:260:LEU:HB2	1.65	0.78
4:F:7:HIS:HB3	4:F:12:VAL:O	1.85	0.77
1:B:254:ASP:O	1:B:258:PRO:HG3	1.84	0.77
2:G:35:LYS:HA	2:G:100:VAL:HG22	1.67	0.77
1:B:152:LEU:HB3	1:B:235:ILE:HD11	1.68	0.76
1:A:133:LYS:HA	1:A:136:ILE:HD12	1.67	0.76
2:C:16:LEU:HD11	2:C:118:LYS:HG2	1.67	0.76
2:G:33:ILE:CD1	2:G:102:ILE:HA	2.16	0.76
1:B:201:SER:O	1:B:205:ILE:HG22	1.85	0.76
4:F:144:VAL:O	4:F:169:LYS:HG2	1.84	0.76
1:B:8:PHE:HZ	1:B:63:TYR:HD1	1.32	0.75
4:F:2:VAL:HG12	4:F:17:ASP:HA	1.68	0.75
1:B:328:GLN:HE22	1:B:370:LYS:HG3	1.51	0.75
4:J:57:LYS:HZ2	4:J:87:THR:HG22	1.52	0.75
1:A:88:PHE:CD1	1:A:88:PHE:C	2.63	0.75
1:A:163:HIS:NE2	1:A:187:ARG:HB3	2.02	0.75
3:D:4:G:C2	3:D:5:U:C4	2.75	0.75
1:B:152:LEU:HB3	1:B:235:ILE:CD1	2.16	0.75
1:B:45:GLY:HA2	1:B:73:LEU:HD22	1.69	0.74
1:B:291:GLN:NE2	3:E:13:C:H41	1.81	0.74
4:J:145:ASP:OD1	4:J:169:LYS:HE2	1.87	0.74
1:B:127:GLN:HG2	1:B:128:SER:C	2.12	0.73
4:J:209:ARG:HG3	4:J:209:ARG:NH1	1.99	0.73
1:A:78:LYS:HA	1:A:82:PHE:O	1.89	0.73
1:A:207:LYS:O	1:A:208:ILE:HB	1.87	0.73
1:B:139:ILE:HG12	1:B:249:ILE:HD13	1.70	0.73
2:C:105:PRO:O	2:C:109:ARG:HB3	1.88	0.73
1:A:187:ARG:CB	1:A:212:LYS:NZ	2.51	0.73
1:A:163:HIS:HD1	1:A:220:MET:HB2	1.53	0.72
1:A:91:ILE:HD12	1:A:91:ILE:H	1.54	0.72
1:A:190:ILE:HD12	1:A:212:LYS:HE3	1.70	0.72
1:A:341:ALA:O	1:A:345:ARG:HG3	1.90	0.72
1:B:13:VAL:HG22	1:B:115:VAL:CG1	2.18	0.72
1:A:331:LYS:HE3	1:A:373:TYR:CE2	2.24	0.72
1:A:88:PHE:C	1:A:88:PHE:HD1	1.98	0.72
2:C:68:PRO:HB2	2:C:69:PRO:HD3	1.72	0.71
1:B:191:ASN:OD1	1:B:194:VAL:HG22	1.90	0.71
4:J:173:TYR:CZ	4:J:225:ARG:HD2	2.26	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:LYS:HB2	1:A:34:LYS:NZ	2.05	0.71
1:A:113:TYR:O	1:A:117:VAL:HG12	1.91	0.71
1:B:163:HIS:CE1	1:B:187:ARG:H	2.07	0.71
2:C:44:VAL:HG12	2:C:45:GLU:N	2.05	0.70
1:B:127:GLN:NE2	1:B:127:GLN:H	1.87	0.70
4:F:115:VAL:O	4:F:118:VAL:HG22	1.90	0.70
1:B:100:PRO:HG3	4:J:142:THR:HG21	1.74	0.70
1:B:292:VAL:HG23	1:B:292:VAL:O	1.92	0.70
4:J:53:PRO:HB2	4:J:215:TYR:CE1	2.27	0.70
1:A:293:LEU:O	1:A:313:GLY:HA3	1.91	0.70
2:G:13:PRO:HG2	2:G:16:LEU:HB2	1.73	0.69
1:A:127:GLN:HB3	1:B:219:TRP:CD1	2.27	0.69
1:B:8:PHE:CZ	1:B:63:TYR:HD1	2.10	0.69
4:F:43:TRP:HB3	4:F:48:TYR:CE1	2.27	0.69
1:A:347:ASP:O	4:F:109:ARG:NH2	2.26	0.69
2:C:47:GLY:HA2	5:K:5:U:H4'	1.74	0.69
3:D:4:G:N2	5:I:10:C:N3	2.40	0.69
4:J:57:LYS:NZ	4:J:87:THR:HG22	2.06	0.69
1:A:196:ARG:HD3	1:A:205:ILE:HD12	1.75	0.69
1:B:17:TYR:HD2	1:B:25:LEU:HD21	1.57	0.69
2:C:19:LYS:HG2	2:C:111:LEU:HD21	1.75	0.69
3:E:16:A:C2	3:E:29:A:H1'	2.28	0.69
4:J:209:ARG:HH11	4:J:209:ARG:CG	2.06	0.69
1:B:126:GLU:C	1:B:127:GLN:CD	2.59	0.69
2:C:22:GLN:HA	2:C:25:GLU:HG2	1.75	0.68
1:A:234:GLU:HA	1:A:234:GLU:OE2	1.93	0.68
4:F:203:TYR:OH	4:F:226:LYS:HE2	1.92	0.68
1:B:14:ARG:HD2	1:B:30:TYR:CE2	2.29	0.68
2:C:47:GLY:HA2	5:K:5:U:C4'	2.24	0.68
1:A:187:ARG:HB2	1:A:212:LYS:NZ	2.08	0.67
2:C:51:LEU:CD1	2:C:77:PRO:HG2	2.24	0.67
4:F:57:LYS:HE2	4:F:150:ASP:OD2	1.94	0.67
2:G:58:VAL:HG11	2:G:64:VAL:HG22	1.76	0.67
2:G:63:ILE:HG12	2:G:63:ILE:O	1.94	0.67
1:A:170:LEU:O	1:A:204:LYS:HE3	1.95	0.67
2:C:70:LEU:O	2:C:74:LYS:HB3	1.94	0.67
4:F:43:TRP:HB3	4:F:48:TYR:HE1	1.58	0.67
1:A:28:LYS:O	1:A:28:LYS:HD3	1.93	0.67
1:B:356:GLU:HG3	4:J:153:GLN:OE1	1.93	0.67
4:J:68:ASN:HB2	4:J:208:GLU:OE1	1.95	0.67
2:G:33:ILE:HD12	2:G:102:ILE:HA	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:26:G:OP1	3:D:27:U:O2'	2.13	0.66
1:A:58:LEU:O	1:A:61:LYS:HB2	1.96	0.66
1:B:8:PHE:HZ	1:B:63:TYR:CD1	2.13	0.66
1:B:328:GLN:NE2	1:B:370:LYS:HG3	2.10	0.66
4:F:95:VAL:CG1	4:F:99:GLY:HA3	2.25	0.66
1:A:55:LEU:HA	1:A:58:LEU:HB2	1.78	0.66
1:A:187:ARG:CB	1:A:212:LYS:CE	2.69	0.66
1:A:208:ILE:HG22	1:A:209:LEU:N	2.11	0.66
1:A:109:PHE:CD2	4:F:100:LYS:HG2	2.31	0.66
1:A:353:TYR:CE2	1:A:355:ALA:HB3	2.31	0.65
1:A:331:LYS:HE3	1:A:373:TYR:CZ	2.31	0.65
1:B:125:GLN:HG2	1:B:131:ARG:CZ	2.25	0.65
1:B:167:LEU:HD22	1:B:180:PHE:CE1	2.31	0.65
2:C:27:ALA:HB1	2:C:105:PRO:HA	1.76	0.65
3:E:14:U:C2'	3:E:15:G:H5'	2.26	0.65
2:C:49:ALA:O	2:C:76:ILE:HD12	1.96	0.65
3:D:5:U:H2'	3:D:6:U:H5'	1.79	0.65
4:J:57:LYS:HZ1	6:J:228:SAM:HB2	1.61	0.65
2:C:14:LYS:CD	2:C:14:LYS:H	2.10	0.64
2:G:59:ASP:HA	2:G:61:GLU:N	2.12	0.64
3:D:27:U:H4'	3:D:28:G:OP2	1.96	0.64
1:B:127:GLN:CD	1:B:131:ARG:HH12	2.05	0.64
1:A:269:ALA:O	1:A:273:ILE:HG13	1.98	0.64
1:B:351:GLY:O	4:J:107:SER:OG	2.07	0.64
1:B:357:GLU:OE2	4:J:152:ALA:HB1	1.98	0.64
2:G:22:GLN:HA	2:G:25:GLU:HG3	1.78	0.64
4:J:62:ILE:HA	4:J:66:LEU:HD23	1.80	0.64
1:A:155:ARG:NH2	1:B:140:GLU:HB3	2.12	0.64
1:B:16:ILE:HD11	1:B:42:LEU:CD1	2.27	0.64
4:F:6:LYS:HD3	4:F:7:HIS:N	2.13	0.64
1:B:291:GLN:HE22	3:E:13:C:N4	1.87	0.64
1:A:163:HIS:CD2	1:A:187:ARG:HB3	2.32	0.64
1:A:258:PRO:HD2	1:A:347:ASP:OD1	1.97	0.64
4:J:119:GLU:O	4:J:122:ARG:HD3	1.98	0.64
1:B:164:PHE:CE2	1:B:212:LYS:HE2	2.33	0.63
2:C:18:GLU:HG3	2:C:19:LYS:H	1.61	0.63
2:C:109:ARG:HG3	2:C:109:ARG:NH1	2.13	0.63
1:B:120:THR:O	1:B:124:ILE:HG13	1.99	0.63
1:B:167:LEU:HD23	1:B:177:TYR:CE2	2.33	0.63
2:G:72:GLU:O	2:G:75:GLU:HG3	1.99	0.63
1:B:164:PHE:CE2	1:B:212:LYS:NZ	2.66	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:11:C:H42	5:I:3:G:H1	1.47	0.63
1:B:8:PHE:CZ	1:B:63:TYR:CD1	2.86	0.63
1:A:284:MET:HE3	2:G:70:LEU:HD12	1.80	0.62
3:D:19:G:C5'	3:D:20:A:OP2	2.47	0.62
5:I:9:A:O5'	5:I:9:A:H8	1.82	0.62
1:A:98:SER:C	1:A:100:PRO:HD3	2.23	0.62
1:A:293:LEU:O	1:A:314:VAL:HG23	1.99	0.62
4:F:4:VAL:HG22	4:F:15:VAL:HG12	1.80	0.62
1:A:94:GLU:O	1:A:98:SER:HB2	1.99	0.62
1:B:88:PHE:CD1	1:B:88:PHE:C	2.78	0.62
1:B:275:LEU:HB3	1:B:293:LEU:HD13	1.80	0.62
2:G:16:LEU:O	2:G:19:LYS:N	2.33	0.62
4:J:79:TYR:OH	4:J:87:THR:HG21	2.00	0.62
2:G:112:VAL:O	2:G:115:ILE:HG22	2.00	0.62
2:C:33:ILE:HG22	2:C:102:ILE:HG23	1.81	0.62
3:D:16:A:C6	3:D:29:A:C8	2.88	0.61
1:B:295:ALA:HB2	1:B:313:GLY:HA2	1.81	0.61
2:C:13:PRO:HD2	2:C:16:LEU:HD12	1.81	0.61
2:C:4:LYS:N	2:C:5:PRO:HD3	2.15	0.61
1:B:186:HIS:CD2	1:B:188:ASP:H	2.15	0.61
2:C:19:LYS:HG2	2:C:111:LEU:HD11	1.82	0.61
4:F:132:THR:C	4:F:134:PRO:HD3	2.25	0.61
1:B:187:ARG:CB	1:B:212:LYS:HZ1	2.09	0.61
3:D:20:A:C2	3:D:21:A:C4	2.89	0.61
5:I:9:A:H2'	5:I:10:C:H6	1.64	0.61
1:B:113:TYR:O	1:B:117:VAL:HG13	2.00	0.61
1:B:258:PRO:HD2	1:B:347:ASP:OD1	2.00	0.61
3:E:14:U:H2'	3:E:15:G:H5'	1.82	0.61
1:A:91:ILE:HD12	1:A:91:ILE:N	2.15	0.61
1:A:224:ASP:HB3	1:B:248:TYR:OH	2.00	0.61
1:B:12:ASN:OD1	1:B:17:TYR:CE1	2.54	0.60
2:C:15:GLU:O	2:C:18:GLU:HG2	2.01	0.60
2:C:105:PRO:HB2	2:C:109:ARG:N	2.15	0.60
4:F:198:ARG:HG3	4:F:199:GLU:N	2.17	0.60
4:J:207:ILE:CG1	4:J:207:ILE:O	2.46	0.60
1:A:16:ILE:HD11	1:A:42:LEU:HD11	1.83	0.60
1:A:180:PHE:HZ	1:A:190:ILE:HD11	1.67	0.60
1:B:297:LYS:HE3	1:B:297:LYS:HA	1.82	0.60
4:F:170:ARG:HD2	4:F:227:PRO:O	2.01	0.60
4:J:66:LEU:HD12	4:J:68:ASN:O	2.01	0.60
1:B:113:TYR:OH	4:J:118:VAL:O	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:PHE:CE2	1:B:212:LYS:CE	2.85	0.60
2:G:105:PRO:HB3	2:G:112:VAL:HG21	1.82	0.60
1:B:164:PHE:CD2	1:B:212:LYS:NZ	2.59	0.60
4:J:85:GLY:HA3	4:J:114:LEU:HD13	1.83	0.60
1:A:126:GLU:O	1:A:127:GLN:C	2.45	0.59
1:A:330:GLY:O	1:A:333:ALA:HB3	2.02	0.59
1:A:220:MET:SD	1:A:225:ILE:HD12	2.43	0.59
1:A:365:ARG:O	1:A:369:ILE:HG12	2.02	0.59
4:F:135:GLU:O	4:F:138:ARG:HB3	2.02	0.59
3:E:10:G:C6	3:E:11:C:C4	2.90	0.59
4:J:57:LYS:HD3	4:J:87:THR:HG21	1.84	0.59
4:J:184:ASP:CG	4:J:186:THR:HG22	2.28	0.59
4:J:195:GLU:HG2	4:J:198:ARG:NH1	2.17	0.59
2:C:43:ALA:HA	2:C:46:ARG:HG2	1.85	0.59
4:J:53:PRO:HB2	4:J:215:TYR:CD1	2.37	0.59
4:J:79:TYR:OH	4:J:87:THR:CG2	2.51	0.59
1:A:11:GLU:OE2	4:F:138:ARG:HD2	2.03	0.59
1:B:202:GLU:HA	1:B:205:ILE:CG2	2.33	0.59
3:D:4:G:N2	5:I:10:C:C2	2.71	0.59
1:A:120:THR:O	1:A:124:ILE:HG13	2.03	0.58
4:J:79:TYR:HD2	4:J:79:TYR:C	2.11	0.58
1:B:127:GLN:NE2	1:B:131:ARG:HH12	2.01	0.58
2:C:95:VAL:HG12	2:C:96:ALA:O	2.03	0.58
2:C:112:VAL:HA	2:C:115:ILE:CG2	2.26	0.58
3:E:2:C:C2'	3:E:3:C:H5'	2.34	0.58
4:J:210:LEU:HD23	4:J:210:LEU:C	2.29	0.58
3:D:4:G:C2	3:D:5:U:O4	2.56	0.58
3:D:4:G:N1	3:D:5:U:O4	2.36	0.58
3:E:1:G:H2'	3:E:2:C:C6	2.39	0.58
4:J:57:LYS:HG2	4:J:150:ASP:OD2	2.03	0.58
2:C:28:ARG:HD3	2:C:90:ALA:O	2.04	0.58
1:A:11:GLU:CD	4:F:138:ARG:HH21	2.11	0.58
1:A:119:LEU:HD23	4:F:140:LEU:HD11	1.85	0.58
1:B:8:PHE:CE2	1:B:65:GLU:HG2	2.38	0.58
1:B:107:ASN:HD21	1:B:110:GLU:HG2	1.69	0.58
3:E:7:G:H2'	3:E:8:A:H8	1.67	0.58
4:F:53:PRO:HG3	4:F:63:VAL:HG21	1.86	0.58
2:G:51:LEU:HD23	2:G:102:ILE:HG13	1.85	0.58
4:J:30:VAL:O	4:J:30:VAL:HG12	2.04	0.58
4:J:181:ARG:HA	4:J:184:ASP:O	2.03	0.58
1:A:149:ILE:O	1:A:153:VAL:HG23	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:LEU:CD2	1:A:208:ILE:H	2.16	0.58
3:E:16:A:C2	3:E:29:A:C1'	2.86	0.58
4:F:132:THR:O	4:F:134:PRO:HD3	2.02	0.58
1:B:359:LYS:O	1:B:363:GLU:HG3	2.03	0.58
1:B:128:SER:HB3	4:J:112:ARG:NH1	2.17	0.58
4:J:121:ARG:O	4:J:123:ASN:N	2.37	0.58
1:B:14:ARG:HD2	1:B:30:TYR:CZ	2.39	0.57
1:B:208:ILE:HG22	1:B:209:LEU:N	2.18	0.57
2:C:25:GLU:HA	2:C:28:ARG:HD3	1.85	0.57
4:F:130:ASP:OD1	4:F:132:THR:HB	2.03	0.57
1:A:312:HIS:CD2	1:A:316:TYR:HB2	2.39	0.57
1:A:58:LEU:HD23	1:A:66:PHE:HE2	1.69	0.57
1:A:194:VAL:O	1:A:198:LEU:HD13	2.04	0.57
1:A:364:ALA:HA	1:A:367:ARG:HD3	1.86	0.57
1:B:300:PHE:HB3	1:B:304:ARG:NH2	2.19	0.57
1:B:353:TYR:CE2	1:B:355:ALA:HB3	2.39	0.57
2:C:13:PRO:HB2	2:C:15:GLU:HG2	1.85	0.57
2:G:30:THR:OG1	2:G:106:GLY:HA3	2.04	0.57
4:J:26:THR:HG22	4:J:27:LYS:N	2.17	0.57
5:I:10:C:H2'	5:I:10:C:O2	2.04	0.57
1:A:248:TYR:OH	1:B:224:ASP:HB3	2.04	0.57
1:A:271:ARG:HG3	1:A:271:ARG:HH21	1.69	0.57
4:J:131:ALA:HA	4:J:137:TYR:OH	2.04	0.57
4:J:132:THR:C	4:J:134:PRO:HD3	2.29	0.57
4:J:195:GLU:HG2	4:J:198:ARG:HH11	1.70	0.57
2:C:99:SER:O	2:C:100:VAL:HG23	2.05	0.57
1:B:8:PHE:CZ	1:B:65:GLU:HG2	2.39	0.57
1:B:293:LEU:C	1:B:295:ALA:H	2.12	0.57
4:F:115:VAL:N	4:F:116:PRO:HD2	2.20	0.57
1:A:163:HIS:NE2	1:A:187:ARG:CG	2.68	0.56
1:B:126:GLU:C	1:B:127:GLN:OE1	2.48	0.56
1:B:230:GLN:HE21	1:B:230:GLN:HA	1.69	0.56
3:E:9:A:O5'	3:E:9:A:H8	1.88	0.56
2:G:67:LEU:HB2	2:G:68:PRO:HD3	1.88	0.56
1:A:20:ASP:OD1	1:A:24:ASN:HB2	2.05	0.56
1:B:39:LEU:C	1:B:41:GLN:N	2.62	0.56
1:B:179:ALA:O	1:B:183:THR:OG1	2.23	0.56
3:D:16:A:C2	3:D:29:A:H1'	2.40	0.56
2:G:59:ASP:CA	2:G:60:PRO:C	2.78	0.56
4:J:4:VAL:HB	4:J:43:TRP:CD1	2.40	0.56
6:J:228:SAM:CA	6:J:228:SAM:HE2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:220:MET:SD	1:B:225:ILE:HD13	2.45	0.56
2:C:51:LEU:HG	2:C:52:VAL:N	2.20	0.56
1:B:45:GLY:O	1:B:73:LEU:HD13	2.04	0.56
1:B:133:LYS:O	1:B:136:ILE:N	2.39	0.56
1:A:88:PHE:HD1	1:A:88:PHE:O	1.88	0.56
2:C:14:LYS:H	2:C:14:LYS:HE2	1.70	0.56
1:B:221:ASP:HB3	1:B:224:ASP:OD1	2.05	0.56
2:G:37:THR:O	2:G:41:THR:OG1	2.23	0.56
4:J:66:LEU:HB3	4:J:210:LEU:HD13	1.88	0.56
2:C:20:ALA:HB2	2:C:79:ILE:HD13	1.87	0.56
6:J:228:SAM:HE2	6:J:228:SAM:C	2.36	0.56
1:B:341:ALA:O	1:B:345:ARG:HG3	2.06	0.55
3:E:9:A:H2'	3:E:10:G:C8	2.41	0.55
3:E:9:A:H2	5:K:6:U:H3	1.53	0.55
1:B:88:PHE:C	1:B:88:PHE:HD1	2.13	0.55
1:A:163:HIS:NE2	1:A:187:ARG:CB	2.69	0.55
1:B:203:GLU:O	1:B:207:LYS:HB2	2.07	0.55
1:B:336:LEU:HD23	1:B:336:LEU:O	2.06	0.55
1:A:208:ILE:HG22	1:A:209:LEU:H	1.71	0.55
1:B:14:ARG:O	1:B:14:ARG:HG3	2.04	0.55
2:G:45:GLU:C	2:G:47:GLY:N	2.64	0.55
4:J:188:GLU:HG2	4:J:189:PRO:HD2	1.88	0.55
1:A:13:VAL:HG13	1:A:115:VAL:HG21	1.88	0.55
1:B:288:SER:HB2	2:C:42:LYS:CE	2.37	0.55
2:C:74:LYS:O	2:C:75:GLU:HB3	2.07	0.55
2:G:53:ILE:C	2:G:54:ILE:HD12	2.31	0.55
4:J:207:ILE:O	4:J:208:GLU:HB2	2.07	0.55
1:A:137:GLN:HG3	1:B:159:TRP:HA	1.87	0.55
1:A:142:LEU:C	1:A:142:LEU:HD13	2.31	0.55
1:A:163:HIS:ND1	1:A:220:MET:HB2	2.21	0.55
2:C:109:ARG:HD2	2:C:110:ASP:N	2.21	0.55
1:B:12:ASN:HB3	1:B:15:GLY:H	1.72	0.55
1:B:71:PRO:O	1:B:74:SER:HB2	2.07	0.54
4:J:173:TYR:CE2	4:J:225:ARG:HD2	2.42	0.54
1:B:12:ASN:OD1	1:B:17:TYR:HE1	1.90	0.54
3:E:12:U:C5'	3:E:13:C:OP1	2.55	0.54
4:F:211:ASN:OD1	4:F:212:LEU:N	2.40	0.54
4:J:79:TYR:C	4:J:79:TYR:CD2	2.83	0.54
2:G:8:VAL:HG23	2:G:8:VAL:O	2.07	0.54
4:J:138:ARG:HA	4:J:167:TYR:OH	2.07	0.54
1:A:51:LEU:O	1:A:54:LEU:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:MET:HB3	1:A:225:ILE:HD13	1.89	0.54
1:A:300:PHE:CE1	1:A:304:ARG:HD2	2.42	0.54
1:A:302:HIS:CD2	1:A:309:PRO:HG3	2.42	0.54
1:A:155:ARG:HD3	1:B:141:ALA:HB2	1.88	0.54
1:B:16:ILE:HD11	1:B:42:LEU:HD11	1.89	0.54
2:C:74:LYS:O	2:C:74:LYS:HG3	2.07	0.54
3:E:7:G:H2'	3:E:8:A:C8	2.43	0.54
4:F:43:TRP:CG	4:F:44:GLU:H	2.25	0.54
1:A:268:LEU:HD12	1:A:268:LEU:O	2.07	0.54
1:B:226:GLU:O	1:B:230:GLN:HG2	2.06	0.54
3:D:28:G:O6	2:G:36:GLY:HA3	2.08	0.54
1:A:88:PHE:HB3	1:A:89:PRO:HD3	1.88	0.54
1:A:281:GLU:O	1:A:285:MET:HG3	2.08	0.54
1:A:302:HIS:HD2	1:A:307:ALA:O	1.91	0.54
1:B:167:LEU:HD21	1:B:180:PHE:CD1	2.42	0.54
1:A:110:GLU:O	1:A:113:TYR:HB3	2.08	0.54
3:E:10:G:C2'	3:E:11:C:H5'	2.36	0.54
1:A:330:GLY:HA3	3:D:32:A:N1	2.22	0.54
1:B:127:GLN:HE21	1:B:128:SER:CA	2.03	0.54
1:B:152:LEU:CB	1:B:235:ILE:CD1	2.86	0.54
3:D:5:U:C2'	3:D:6:U:H5'	2.38	0.54
4:F:63:VAL:HG11	4:F:215:TYR:OH	2.08	0.54
1:A:165:PRO:HD2	1:A:166:GLU:OE1	2.08	0.53
4:J:145:ASP:OD1	4:J:169:LYS:CE	2.56	0.53
4:F:15:VAL:CG2	4:F:23:LYS:HB2	2.38	0.53
4:F:103:GLY:O	4:F:127:ILE:HB	2.08	0.53
4:F:104:ILE:O	4:F:104:ILE:HG22	2.07	0.53
4:J:212:LEU:HB2	4:J:219:HIS:O	2.07	0.53
1:A:163:HIS:NE2	1:A:187:ARG:HG2	2.23	0.53
1:B:12:ASN:HB3	1:B:14:ARG:H	1.72	0.53
1:B:241:LEU:O	1:B:241:LEU:HG	2.08	0.53
1:B:353:TYR:O	6:J:228:SAM:H8	2.08	0.53
1:A:16:ILE:HD13	1:A:51:LEU:HB2	1.91	0.53
1:B:94:GLU:OE1	4:J:143:LYS:NZ	2.41	0.53
5:K:3:G:H2'	5:K:4:C:C6	2.43	0.53
1:A:91:ILE:H	1:A:91:ILE:CD1	2.19	0.53
1:B:204:LYS:O	1:B:208:ILE:HD12	2.08	0.53
2:G:58:VAL:HG12	2:G:61:GLU:HA	1.89	0.53
4:J:57:LYS:HE2	6:J:228:SAM:CB	2.39	0.53
1:A:127:GLN:HG3	1:A:128:SER:H	1.73	0.53
1:A:271:ARG:HH21	1:A:271:ARG:CG	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:PHE:CE2	1:B:65:GLU:CG	2.92	0.53
2:C:37:THR:OG1	3:E:27:U:OP2	2.26	0.53
1:A:11:GLU:CD	4:F:138:ARG:NH2	2.66	0.53
3:D:27:U:O2	2:G:63:ILE:HG21	2.09	0.53
4:F:91:VAL:HG23	4:F:91:VAL:O	2.09	0.53
1:A:164:PHE:CE2	1:A:212:LYS:HD3	2.43	0.53
1:A:257:ALA:CB	1:A:260:LEU:HB2	2.39	0.53
2:C:21:LEU:O	2:C:24:VAL:HG22	2.09	0.53
2:G:122:LEU:CD2	2:G:122:LEU:H	2.22	0.53
2:C:14:LYS:H	2:C:14:LYS:CE	2.23	0.52
2:C:103:ILE:O	2:C:105:PRO:HD3	2.09	0.52
4:J:88:ALA:HA	4:J:91:VAL:HG13	1.91	0.52
1:A:19:PHE:CD1	1:A:92:ALA:HA	2.44	0.52
1:B:127:GLN:CB	1:B:129:GLY:N	2.65	0.52
4:F:79:TYR:HD2	4:F:79:TYR:C	2.17	0.52
4:J:210:LEU:HD23	4:J:210:LEU:O	2.09	0.52
4:F:57:LYS:CE	4:F:150:ASP:OD2	2.56	0.52
4:J:1:MET:CG	4:J:18:ASP:HA	2.39	0.52
1:A:119:LEU:O	1:A:123:ARG:HG3	2.09	0.52
1:A:119:LEU:HD11	1:A:123:ARG:NE	2.25	0.52
1:A:170:LEU:O	1:A:171:LEU:HD23	2.08	0.52
1:A:224:ASP:HA	1:B:248:TYR:CE2	2.44	0.52
1:B:8:PHE:HA	1:B:19:PHE:O	2.09	0.52
1:B:109:PHE:CE2	4:J:100:LYS:HB3	2.45	0.52
1:B:264:VAL:HB	1:B:268:LEU:HD23	1.89	0.52
1:A:263:LEU:HD23	1:A:340:LEU:HD23	1.91	0.52
1:B:139:ILE:HG13	1:B:270:ALA:HB3	1.92	0.52
2:C:14:LYS:CD	2:C:14:LYS:N	2.73	0.52
4:J:143:LYS:HD2	4:J:167:TYR:O	2.09	0.52
4:J:207:ILE:O	4:J:207:ILE:HG12	2.08	0.52
1:A:69:GLU:OE1	1:A:93:GLY:HA3	2.08	0.52
1:A:303:LEU:HD22	1:A:303:LEU:H	1.74	0.52
1:A:308:LYS:HB3	3:D:32:A:O2'	2.10	0.52
2:C:23:ALA:O	2:C:26:ILE:HG12	2.10	0.52
3:E:10:G:O6	3:E:11:C:C4	2.63	0.52
3:E:31:G:C2'	3:E:32:A:H5'	2.40	0.52
1:A:130:ALA:O	1:A:133:LYS:N	2.40	0.52
1:B:330:GLY:HA3	3:E:32:A:N1	2.24	0.52
2:C:105:PRO:HB2	2:C:109:ARG:H	1.74	0.52
3:D:5:U:H2'	3:D:6:U:C5'	2.39	0.52
1:B:293:LEU:O	1:B:314:VAL:HG23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:64:VAL:HG12	2:C:67:LEU:HD12	1.92	0.52
5:I:12:G:N1	5:I:13:C:N4	2.58	0.52
1:A:50:ASP:OD2	1:A:50:ASP:N	2.41	0.51
1:B:191:ASN:CG	1:B:194:VAL:HG22	2.34	0.51
1:B:275:LEU:CB	1:B:293:LEU:HD13	2.39	0.51
4:F:58:LEU:HD21	4:F:69:PHE:CE2	2.46	0.51
1:A:206:LYS:C	1:A:207:LYS:O	2.50	0.51
2:C:106:GLY:HA2	2:C:109:ARG:HH21	1.74	0.51
3:E:24:G:H2'	3:E:25:C:H5'	1.92	0.51
5:I:5:U:H2'	5:I:6:U:O4'	2.10	0.51
1:B:39:LEU:O	1:B:41:GLN:N	2.43	0.51
2:G:118:LYS:O	2:G:122:LEU:HD22	2.11	0.51
4:J:8:LYS:HG2	7:J:231:HOH:O	2.11	0.51
1:B:74:SER:OG	1:B:86:THR:HB	2.10	0.51
3:E:7:G:O2'	3:E:8:A:H5'	2.10	0.51
4:J:26:THR:CG2	4:J:93:ASP:HB3	2.40	0.51
4:J:29:LEU:HD13	4:J:96:GLY:HA2	1.92	0.51
1:A:34:LYS:HB2	1:A:34:LYS:HZ2	1.74	0.51
1:A:137:GLN:O	1:A:138:ALA:C	2.53	0.51
2:G:56:GLU:HG3	2:G:81:VAL:O	2.10	0.51
4:J:26:THR:HG21	4:J:93:ASP:CB	2.40	0.51
3:E:31:G:H2'	3:E:32:A:H5'	1.93	0.51
4:J:29:LEU:HB3	4:J:121:ARG:NH2	2.25	0.51
4:J:57:LYS:HE2	6:J:228:SAM:C	2.41	0.51
1:A:34:LYS:HB2	1:A:34:LYS:HZ3	1.74	0.51
1:B:230:GLN:HA	1:B:230:GLN:NE2	2.26	0.51
1:B:302:HIS:CD2	1:B:309:PRO:HG3	2.46	0.51
2:G:19:LYS:HG2	2:G:111:LEU:HD11	1.91	0.51
2:G:47:GLY:HA2	2:G:74:LYS:HE2	1.93	0.51
4:J:144:VAL:O	4:J:169:LYS:HG2	2.10	0.51
5:I:1:G:H3'	5:I:2:A:H8	1.76	0.51
1:A:271:ARG:O	1:A:274:SER:HB3	2.11	0.51
4:F:79:TYR:C	4:F:79:TYR:CD2	2.89	0.51
4:J:29:LEU:HB3	4:J:121:ARG:HH22	1.75	0.51
4:J:168:LEU:HD11	4:J:172:GLY:HA3	1.91	0.51
1:A:70:HIS:ND1	1:A:71:PRO:HD2	2.26	0.51
1:B:100:PRO:HG3	4:J:142:THR:CG2	2.41	0.51
2:C:18:GLU:O	2:C:21:LEU:HB3	2.10	0.51
4:J:175:MET:HA	4:J:222:PHE:O	2.11	0.51
2:C:15:GLU:O	2:C:18:GLU:CG	2.58	0.50
4:F:15:VAL:HG23	4:F:23:LYS:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:151:VAL:HG23	4:J:151:VAL:O	2.11	0.50
2:G:120:LYS:HG2	2:G:120:LYS:O	2.10	0.50
4:J:2:VAL:HG12	4:J:17:ASP:HA	1.91	0.50
1:B:33:ASP:HB3	1:B:37:LYS:NZ	2.26	0.50
1:B:202:GLU:HA	1:B:205:ILE:HG23	1.92	0.50
1:B:309:PRO:HD2	3:E:32:A:H1'	1.93	0.50
2:C:70:LEU:O	2:C:70:LEU:HG	2.12	0.50
2:G:10:PHE:CE2	2:G:123:MET:HG2	2.47	0.50
2:G:103:ILE:HG22	2:G:104:GLU:N	2.26	0.50
5:I:7:C:C6	5:I:7:C:H3'	2.46	0.50
1:A:37:LYS:O	1:A:41:GLN:HG3	2.11	0.50
1:A:221:ASP:HB3	1:A:224:ASP:OD2	2.11	0.50
1:A:237:ARG:HG2	1:A:237:ARG:HH21	1.76	0.50
1:B:167:LEU:CD2	1:B:180:PHE:CE1	2.94	0.50
1:B:221:ASP:C	1:B:223:THR:H	2.19	0.50
2:C:47:GLY:CA	5:K:4:C:O2'	2.56	0.50
3:D:4:G:H2'	3:D:5:U:C6	2.47	0.50
4:F:179:LYS:O	4:F:182:SER:HB3	2.11	0.50
2:G:119:VAL:HA	2:G:122:LEU:HD21	1.92	0.50
4:J:32:GLY:CA	4:J:34:ARG:HH21	2.24	0.50
1:A:69:GLU:HG2	1:A:90:ASN:ND2	2.27	0.50
1:B:95:ARG:HH12	1:B:102:GLU:CD	2.19	0.50
1:B:107:ASN:ND2	1:B:110:GLU:HG2	2.27	0.50
1:B:220:MET:HB3	1:B:225:ILE:HG12	1.93	0.50
3:E:16:A:C6	3:E:29:A:C8	3.00	0.50
4:J:105:GLU:CD	4:J:106:PHE:H	2.20	0.50
1:A:75:ARG:CZ	1:A:75:ARG:HB3	2.41	0.50
1:A:75:ARG:HB3	1:A:75:ARG:NH2	2.27	0.50
1:A:91:ILE:O	1:A:95:ARG:HG3	2.12	0.50
5:K:12:G:H2'	5:K:13:C:C6	2.47	0.50
1:A:319:PRO:HB2	7:A:375:HOH:O	2.11	0.50
4:F:56:SER:OG	4:F:87:THR:HB	2.12	0.50
3:D:10:G:N2	5:I:5:U:C2	2.80	0.50
1:A:145:VAL:HG12	1:A:145:VAL:O	2.11	0.49
1:B:191:ASN:OD1	1:B:193:GLU:HG2	2.12	0.49
1:B:245:LEU:O	1:B:249:ILE:HG13	2.11	0.49
1:B:308:LYS:O	3:E:33:G:H8	1.94	0.49
2:C:110:ASP:HA	2:C:113:GLU:OE1	2.12	0.49
5:I:7:C:H3'	5:I:7:C:H6	1.78	0.49
1:B:127:GLN:CD	1:B:131:ARG:HH22	2.20	0.49
3:E:8:A:N6	3:E:9:A:C2	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:181:ARG:HB2	4:J:185:VAL:HG22	1.94	0.49
1:A:66:PHE:O	1:A:84:ALA:HA	2.12	0.49
1:A:119:LEU:HD11	1:A:123:ARG:CZ	2.42	0.49
1:A:202:GLU:OE1	1:A:202:GLU:HA	2.11	0.49
2:C:22:GLN:HA	2:C:25:GLU:CG	2.42	0.49
2:G:4:LYS:O	2:G:4:LYS:HG2	2.11	0.49
1:A:143:ASP:OD1	1:A:143:ASP:C	2.55	0.49
1:A:159:TRP:CE2	1:A:228:VAL:HG22	2.46	0.49
1:B:301:ARG:NH1	3:E:33:G:C4	2.80	0.49
2:C:13:PRO:HB2	2:C:15:GLU:CG	2.42	0.49
2:C:16:LEU:CD2	2:C:115:ILE:HG13	2.42	0.49
4:J:108:PRO:HD2	4:J:109:ARG:H	1.76	0.49
1:B:157:ARG:HD3	1:B:177:TYR:CE1	2.47	0.49
1:B:302:HIS:NE2	1:B:309:PRO:HG3	2.28	0.49
2:C:17:ALA:HB1	2:C:82:PRO:HD3	1.94	0.49
1:A:127:GLN:HG3	1:A:128:SER:N	2.27	0.49
1:B:48:THR:HG22	1:B:50:ASP:N	2.18	0.49
1:B:170:LEU:HD12	1:B:208:ILE:HG13	1.94	0.49
1:B:356:GLU:CG	4:J:153:GLN:OE1	2.59	0.49
4:J:91:VAL:HG22	4:J:101:ILE:CD1	2.43	0.49
1:A:201:SER:OG	1:A:202:GLU:N	2.45	0.49
1:A:308:LYS:HE3	3:D:32:A:O3'	2.12	0.49
1:B:88:PHE:HB3	1:B:89:PRO:CD	2.35	0.49
4:J:57:LYS:NZ	4:J:87:THR:CG2	2.75	0.49
2:C:86:GLU:O	2:C:89:ALA:HB3	2.12	0.49
4:J:57:LYS:HE2	6:J:228:SAM:HB1	1.95	0.49
1:A:141:ALA:CA	1:B:155:ARG:HD3	2.43	0.49
1:A:309:PRO:HD2	3:D:32:A:H1'	1.93	0.49
1:B:266:ALA:O	1:B:269:ALA:HB3	2.11	0.49
2:C:119:VAL:O	2:C:120:LYS:C	2.54	0.49
4:J:26:THR:HG21	4:J:93:ASP:HB2	1.94	0.49
4:J:78:LEU:HB2	4:J:144:VAL:HG11	1.95	0.49
1:A:8:PHE:HA	1:A:19:PHE:O	2.12	0.49
1:A:70:HIS:HD2	4:F:138:ARG:NH1	2.11	0.49
1:B:156:LEU:HG	1:B:231:LEU:HD13	1.95	0.49
2:C:74:LYS:O	2:C:75:GLU:CB	2.59	0.49
2:G:33:ILE:CD1	2:G:101:ALA:O	2.61	0.48
1:A:196:ARG:NH1	1:A:202:GLU:OE2	2.46	0.48
2:C:51:LEU:HG	2:C:52:VAL:H	1.78	0.48
4:J:214:PRO:HD2	4:J:215:TYR:CD2	2.48	0.48
1:B:88:PHE:HE2	4:J:134:PRO:HB2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:4:LYS:O	2:C:4:LYS:HG3	2.12	0.48
5:I:12:G:O5'	5:I:12:G:H8	1.96	0.48
1:B:187:ARG:CB	1:B:212:LYS:NZ	2.70	0.48
2:C:19:LYS:CG	2:C:111:LEU:HD21	2.43	0.48
1:B:13:VAL:HG22	1:B:115:VAL:CB	2.43	0.48
1:B:153:VAL:HG11	1:B:174:HIS:ND1	2.28	0.48
1:B:259:ASN:HB2	1:B:347:ASP:OD2	2.13	0.48
2:G:33:ILE:HD12	2:G:101:ALA:O	2.12	0.48
2:G:114:GLU:HG3	2:G:115:ILE:N	2.27	0.48
4:J:82:ILE:HG21	4:J:103:GLY:HA3	1.95	0.48
1:A:237:ARG:HG2	1:A:237:ARG:NH2	2.27	0.48
1:B:145:VAL:O	1:B:145:VAL:HG12	2.14	0.48
1:B:170:LEU:O	1:B:204:LYS:HE3	2.13	0.48
2:C:24:VAL:HG23	2:C:25:GLU:N	2.28	0.48
3:D:27:U:H3'	3:D:28:G:H5'	1.95	0.48
3:E:31:G:H2'	3:E:32:A:C5'	2.42	0.48
4:J:32:GLY:HA2	4:J:34:ARG:NH2	2.29	0.48
1:B:17:TYR:CD2	1:B:25:LEU:HD21	2.44	0.48
1:B:207:LYS:HD3	1:B:210:GLU:OE2	2.14	0.48
1:A:95:ARG:NH1	1:A:102:GLU:OE2	2.43	0.48
1:A:170:LEU:HD21	1:A:208:ILE:H	1.79	0.48
1:B:302:HIS:CD2	1:B:307:ALA:O	2.66	0.48
2:C:13:PRO:CB	2:C:15:GLU:HG2	2.43	0.48
2:C:42:LYS:HB3	2:C:46:ARG:HD2	1.95	0.48
2:C:44:VAL:HG11	2:C:70:LEU:HG	1.95	0.48
2:G:4:LYS:N	2:G:5:PRO:HD3	2.29	0.48
1:A:308:LYS:O	3:D:33:G:H8	1.97	0.48
1:B:318:TYR:CG	1:B:336:LEU:HD11	2.49	0.48
4:J:11:GLY:O	4:J:26:THR:HG23	2.14	0.48
1:A:257:ALA:HA	1:A:347:ASP:CG	2.39	0.47
4:F:51:TRP:CD1	4:F:90:HIS:CD2	3.02	0.47
1:A:271:ARG:HB3	1:A:314:VAL:HG11	1.96	0.47
2:C:16:LEU:HD23	2:C:115:ILE:HG13	1.97	0.47
2:C:43:ALA:HB1	2:C:103:ILE:HD11	1.96	0.47
4:F:156:GLN:NE2	7:F:229:HOH:O	2.47	0.47
1:A:187:ARG:O	1:A:212:LYS:NZ	2.46	0.47
1:A:201:SER:OG	1:A:204:LYS:HB2	2.14	0.47
1:A:220:MET:SD	1:A:225:ILE:CD1	3.02	0.47
1:B:39:LEU:C	1:B:41:GLN:H	2.22	0.47
2:C:24:VAL:HG23	2:C:25:GLU:H	1.78	0.47
3:E:11:C:C2	5:K:3:G:N1	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:30:VAL:O	4:F:30:VAL:CG2	2.61	0.47
1:A:221:ASP:OD2	1:B:125:GLN:HG3	2.13	0.47
1:A:299:LEU:HD21	3:D:13:C:OP2	2.15	0.47
1:B:39:LEU:O	1:B:40:ASP:C	2.56	0.47
1:B:57:SER:O	1:B:61:LYS:HG3	2.13	0.47
1:B:292:VAL:O	1:B:292:VAL:CG2	2.61	0.47
3:D:7:G:C8	3:D:7:G:H3'	2.49	0.47
4:F:5:LYS:HB2	4:F:14:VAL:HG12	1.97	0.47
5:I:1:G:N3	5:I:1:G:H2'	2.29	0.47
5:I:7:C:C6	5:I:7:C:C3'	2.98	0.47
3:D:16:A:H2'	3:D:26:G:O6	2.14	0.47
1:A:109:PHE:CG	4:F:100:LYS:HG2	2.50	0.47
1:A:372:LYS:C	1:A:373:TYR:CD1	2.93	0.47
2:C:66:HIS:C	2:C:66:HIS:CD2	2.92	0.47
1:A:302:HIS:NE2	1:A:309:PRO:HG3	2.29	0.47
1:B:207:LYS:HD2	1:B:208:ILE:N	2.30	0.47
1:B:208:ILE:O	1:B:209:LEU:C	2.56	0.47
1:B:264:VAL:CG1	1:B:340:LEU:HD21	2.45	0.47
1:B:280:ARG:O	1:B:284:MET:HG2	2.15	0.47
3:D:2:C:H2'	3:D:3:C:O4'	2.14	0.47
3:D:20:A:O5'	3:D:20:A:C8	2.67	0.47
3:E:12:U:O5'	3:E:13:C:OP1	2.32	0.47
4:F:106:PHE:CD1	4:F:106:PHE:C	2.91	0.47
1:A:88:PHE:O	1:A:89:PRO:C	2.48	0.47
3:E:24:G:C2'	3:E:25:C:H5'	2.45	0.47
5:I:2:A:C2	5:I:3:G:H1'	2.50	0.47
1:A:187:ARG:C	1:A:212:LYS:NZ	2.73	0.47
1:B:93:GLY:HA3	1:B:97:ARG:NH1	2.29	0.47
2:C:118:LYS:NZ	2:C:122:LEU:HD21	2.30	0.47
3:D:2:C:N3	5:I:12:G:N2	2.59	0.47
4:J:15:VAL:CG2	4:J:23:LYS:HB2	2.45	0.47
1:A:126:GLU:O	1:A:127:GLN:O	2.33	0.47
1:B:12:ASN:CB	1:B:15:GLY:H	2.28	0.47
4:F:82:ILE:HG21	4:F:103:GLY:HA3	1.97	0.47
1:A:190:ILE:HD12	1:A:212:LYS:HG2	1.98	0.46
1:B:352:GLU:HG2	6:J:228:SAM:O3'	2.15	0.46
4:J:63:VAL:HG11	4:J:215:TYR:OH	2.16	0.46
2:C:102:ILE:CG2	2:C:105:PRO:HB3	2.41	0.46
2:C:105:PRO:HG2	2:C:109:ARG:HB2	1.97	0.46
2:C:109:ARG:O	2:C:113:GLU:OE1	2.33	0.46
3:E:27:U:H4'	3:E:28:G:OP2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:164:ALA:O	4:F:226:LYS:HE3	2.15	0.46
2:G:45:GLU:C	2:G:47:GLY:H	2.23	0.46
4:J:204:PHE:HB3	4:J:224:VAL:HB	1.98	0.46
5:K:3:G:H2'	5:K:4:C:H6	1.79	0.46
1:B:77:ALA:O	1:B:82:PHE:HB2	2.16	0.46
1:B:312:HIS:NE2	1:B:316:TYR:CD2	2.83	0.46
1:A:312:HIS:HD2	1:A:316:TYR:HB2	1.79	0.46
1:B:207:LYS:O	1:B:209:LEU:N	2.49	0.46
2:G:10:PHE:HE2	2:G:123:MET:HG2	1.79	0.46
2:G:16:LEU:HD23	2:G:16:LEU:HA	1.73	0.46
1:A:364:ALA:HA	1:A:367:ARG:HH21	1.80	0.46
1:B:171:LEU:HA	1:B:172:PRO:HD3	1.73	0.46
1:B:300:PHE:HB3	1:B:304:ARG:CZ	2.46	0.46
1:B:225:ILE:HD13	1:B:225:ILE:HA	1.66	0.46
3:E:2:C:H2'	3:E:3:C:H5'	1.98	0.46
5:K:12:G:H2'	5:K:13:C:C5	2.50	0.46
1:A:16:ILE:CD1	1:A:51:LEU:HB2	2.45	0.46
1:A:280:ARG:HB2	1:A:348:TYR:CE1	2.51	0.46
2:C:19:LYS:HB3	2:C:115:ILE:HD12	1.98	0.46
4:F:78:LEU:HD11	4:F:104:ILE:HD13	1.97	0.46
4:F:208:GLU:HB3	4:F:223:VAL:HG13	1.96	0.46
2:G:119:VAL:O	2:G:122:LEU:HD23	2.16	0.46
4:J:118:VAL:HG12	4:J:124:ILE:HB	1.97	0.46
1:A:94:GLU:O	1:A:98:SER:CB	2.64	0.45
1:A:131:ARG:NH2	1:B:224:ASP:OD1	2.49	0.45
1:A:308:LYS:HA	1:A:309:PRO:HD3	1.78	0.45
1:A:369:ILE:HG12	1:A:369:ILE:H	1.59	0.45
1:B:325:PRO:C	1:B:327:TRP:N	2.72	0.45
3:E:10:G:O6	3:E:11:C:N4	2.48	0.45
4:F:38:GLU:O	4:F:38:GLU:HG2	2.14	0.45
2:G:108:ALA:O	2:G:111:LEU:N	2.49	0.45
4:J:4:VAL:HG22	4:J:15:VAL:HG12	1.97	0.45
4:J:111:LEU:HD21	4:J:126:PRO:O	2.16	0.45
5:K:12:G:O5'	5:K:12:G:H8	1.98	0.45
1:B:180:PHE:CE2	1:B:184:VAL:HG11	2.51	0.45
4:J:32:GLY:HA2	4:J:34:ARG:HH21	1.80	0.45
1:A:310:PRO:HA	3:D:33:G:H3'	1.98	0.45
2:G:54:ILE:HD12	2:G:54:ILE:N	2.31	0.45
2:G:84:LYS:HG3	2:G:85:LYS:N	2.31	0.45
4:J:119:GLU:O	4:J:122:ARG:CD	2.64	0.45
5:I:4:C:O5'	5:I:4:C:H6	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:VAL:O	1:A:145:VAL:CG1	2.64	0.45
1:A:190:ILE:HG23	1:A:195:LEU:HD11	1.97	0.45
1:A:307:ALA:HB1	3:D:33:G:N7	2.32	0.45
2:C:78:TYR:CD2	2:C:78:TYR:N	2.85	0.45
4:J:155:THR:O	4:J:156:GLN:C	2.60	0.45
5:I:12:G:C2	5:I:13:C:N4	2.85	0.45
1:A:11:GLU:OE2	1:A:11:GLU:N	2.42	0.45
1:B:153:VAL:HG21	1:B:174:HIS:HB3	1.98	0.45
2:C:58:VAL:O	2:C:61:GLU:HA	2.17	0.45
2:G:51:LEU:HG	2:G:52:VAL:N	2.31	0.45
1:A:70:HIS:HD2	4:F:138:ARG:HH11	1.65	0.45
1:A:253:MET:HE1	1:A:273:ILE:HD11	1.98	0.45
1:B:8:PHE:O	1:B:18:ALA:HA	2.17	0.45
1:B:173:LYS:HB2	1:B:176:GLN:HG3	1.99	0.45
1:B:220:MET:SD	1:B:225:ILE:CD1	3.04	0.45
2:C:28:ARG:CD	2:C:90:ALA:O	2.65	0.45
4:F:106:PHE:HA	4:F:129:GLY:O	2.15	0.45
2:G:12:VAL:HA	2:G:13:PRO:HD2	1.79	0.45
1:A:209:LEU:HD23	1:A:209:LEU:N	2.31	0.45
1:B:69:GLU:OE2	1:B:88:PHE:O	2.34	0.45
1:B:297:LYS:HE3	1:B:297:LYS:CA	2.47	0.45
3:E:12:U:O2	3:E:12:U:H2'	2.17	0.45
2:G:16:LEU:O	2:G:17:ALA:C	2.58	0.45
2:C:23:ALA:HB2	2:C:111:LEU:HD22	1.99	0.45
3:E:7:G:N2	5:K:8:A:C6	2.84	0.45
2:G:115:ILE:O	2:G:119:VAL:HG23	2.15	0.45
1:A:67:VAL:HG13	1:A:67:VAL:O	2.17	0.45
1:A:364:ALA:HA	1:A:367:ARG:CD	2.48	0.44
1:B:167:LEU:CD2	1:B:180:PHE:CD1	3.00	0.44
2:C:59:ASP:OD2	2:C:60:PRO:HA	2.17	0.44
2:G:25:GLU:O	2:G:29:ASP:OD2	2.35	0.44
4:J:57:LYS:HZ1	6:J:228:SAM:CB	2.28	0.44
1:A:14:ARG:O	1:A:31:PHE:HD2	2.01	0.44
1:B:133:LYS:HA	1:B:136:ILE:HD12	2.00	0.44
1:B:153:VAL:HG12	1:B:154:ALA:N	2.32	0.44
1:B:293:LEU:H	1:B:313:GLY:HA3	1.81	0.44
2:C:32:LYS:HG3	2:C:33:ILE:N	2.31	0.44
4:F:86:THR:HG22	4:F:87:THR:N	2.32	0.44
4:F:49:ARG:NH2	4:F:93:ASP:OD2	2.51	0.44
1:A:171:LEU:HD21	1:A:200:LEU:HD21	2.00	0.44
1:B:300:PHE:HB3	1:B:304:ARG:HH22	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:359:LYS:HB3	1:B:359:LYS:HE2	1.77	0.44
3:E:5:U:C4	3:E:6:U:N3	2.85	0.44
3:E:11:C:N3	5:K:3:G:C6	2.85	0.44
1:B:124:ILE:HG22	1:B:125:GLN:O	2.17	0.44
3:E:20:A:C2	3:E:21:A:C4	3.05	0.44
1:A:220:MET:CB	1:A:225:ILE:HD13	2.48	0.44
1:B:70:HIS:CE1	1:B:71:PRO:HD2	2.52	0.44
1:B:195:LEU:HD22	1:B:200:LEU:CD1	2.47	0.44
1:B:268:LEU:O	1:B:268:LEU:HD12	2.16	0.44
2:C:39:GLU:HG2	3:E:15:G:N7	2.33	0.44
1:A:14:ARG:O	1:A:31:PHE:CD2	2.70	0.44
1:A:131:ARG:O	1:A:131:ARG:HG3	2.18	0.44
1:A:311:LYS:HG2	3:D:32:A:C4	2.53	0.44
1:B:127:GLN:CG	1:B:128:SER:C	2.89	0.44
2:C:105:PRO:HB2	2:C:109:ARG:HB3	1.98	0.44
4:J:43:TRP:CD1	4:J:44:GLU:OE2	2.70	0.44
4:J:66:LEU:CD1	4:J:68:ASN:O	2.66	0.44
1:A:151:LEU:HD23	1:A:151:LEU:HA	1.72	0.44
1:A:365:ARG:CZ	1:A:369:ILE:CD1	2.95	0.44
1:A:149:ILE:HD13	1:A:239:TYR:CD2	2.53	0.44
3:D:16:A:C2	3:D:29:A:C1'	3.00	0.43
3:E:31:G:O2'	3:E:32:A:H5'	2.18	0.43
5:I:11:G:O5'	5:I:11:G:H8	2.01	0.43
1:B:104:LEU:N	1:B:104:LEU:CD1	2.81	0.43
4:J:105:GLU:OE1	6:J:228:SAM:H1'	2.18	0.43
4:J:150:ASP:CG	6:J:228:SAM:HE3	2.43	0.43
1:B:137:GLN:O	1:B:138:ALA:C	2.59	0.43
1:B:186:HIS:CD2	1:B:187:ARG:N	2.86	0.43
1:B:325:PRO:C	1:B:327:TRP:H	2.25	0.43
2:C:19:LYS:O	2:C:20:ALA:C	2.60	0.43
2:C:116:ALA:HA	2:C:119:VAL:HG23	1.99	0.43
1:B:33:ASP:HB3	1:B:37:LYS:CE	2.48	0.43
1:B:65:GLU:HG2	1:B:65:GLU:O	2.18	0.43
1:B:195:LEU:HD23	1:B:195:LEU:HA	1.81	0.43
2:C:46:ARG:O	2:C:47:GLY:C	2.61	0.43
1:B:48:THR:CG2	1:B:49:LYS:N	2.80	0.43
1:B:139:ILE:HG13	1:B:270:ALA:CB	2.49	0.43
1:B:295:ALA:C	1:B:297:LYS:N	2.75	0.43
2:G:13:PRO:O	2:G:15:GLU:O	2.35	0.43
2:G:122:LEU:H	2:G:122:LEU:HD23	1.84	0.43
4:J:58:LEU:HD23	4:J:58:LEU:HA	1.69	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:LYS:HD3	1:A:28:LYS:C	2.43	0.43
1:B:293:LEU:C	1:B:295:ALA:N	2.77	0.43
2:C:14:LYS:N	2:C:14:LYS:HD3	2.33	0.43
1:A:108:TRP:CZ2	4:F:100:LYS:HE2	2.54	0.43
2:C:47:GLY:CA	5:K:5:U:H4'	2.45	0.43
4:F:43:TRP:CG	4:F:44:GLU:N	2.86	0.43
2:G:108:ALA:O	2:G:112:VAL:N	2.35	0.43
4:J:85:GLY:O	4:J:86:THR:C	2.59	0.43
1:B:208:ILE:O	1:B:212:LYS:N	2.45	0.43
4:F:30:VAL:O	4:F:30:VAL:HG23	2.18	0.43
4:F:39:ARG:HD3	4:F:41:ILE:HD13	2.01	0.43
1:A:358:LEU:HD23	1:A:358:LEU:HA	1.71	0.43
1:B:12:ASN:HB3	1:B:14:ARG:N	2.33	0.43
1:B:353:TYR:CZ	1:B:355:ALA:HB3	2.54	0.43
4:F:127:ILE:HD13	4:F:140:LEU:HB3	2.00	0.43
1:A:363:GLU:O	1:A:367:ARG:HD2	2.19	0.43
1:B:192:GLU:O	1:B:195:LEU:HB2	2.19	0.43
1:B:212:LYS:O	1:B:215:THR:HG22	2.19	0.43
2:C:22:GLN:O	2:C:26:ILE:HG23	2.19	0.43
2:G:32:LYS:HB2	2:G:103:ILE:HG22	2.01	0.43
2:G:85:LYS:HE2	2:G:94:GLU:O	2.19	0.43
4:J:79:TYR:CE1	4:J:88:ALA:HB2	2.54	0.43
5:I:12:G:C2	5:I:13:C:C4	3.06	0.43
1:A:365:ARG:O	1:A:368:GLU:HB2	2.18	0.42
1:B:234:GLU:OE2	1:B:234:GLU:HA	2.18	0.42
1:B:325:PRO:HB2	1:B:327:TRP:HB3	2.01	0.42
2:C:57:ASP:CG	2:C:57:ASP:O	2.62	0.42
3:D:11:C:H4'	3:D:12:U:OP1	2.18	0.42
3:D:21:A:O2'	3:D:22:A:H5'	2.19	0.42
4:F:196:VAL:HG12	4:F:200:LEU:HD22	2.01	0.42
4:J:1:MET:HG3	4:J:18:ASP:HA	2.00	0.42
4:J:184:ASP:OD1	4:J:186:THR:HG22	2.19	0.42
4:J:210:LEU:HD23	4:J:211:ASN:O	2.19	0.42
4:J:221:LEU:C	4:J:222:PHE:CD1	2.97	0.42
1:A:328:GLN:H	1:A:328:GLN:HG2	1.60	0.42
3:D:30:U:H2'	3:D:31:G:C8	2.55	0.42
2:G:31:GLY:HA3	2:G:104:GLU:O	2.19	0.42
1:A:280:ARG:O	1:A:284:MET:HG2	2.18	0.42
1:B:308:LYS:HA	1:B:309:PRO:HD3	1.76	0.42
3:D:1:G:H2'	3:D:2:C:C6	2.54	0.42
3:D:7:G:N2	5:I:8:A:N7	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:24:ILE:HG13	4:F:51:TRP:HB3	2.02	0.42
2:G:68:PRO:HB2	2:G:69:PRO:CD	2.42	0.42
2:G:79:ILE:HG12	2:G:80:TYR:H	1.82	0.42
1:B:94:GLU:O	1:B:98:SER:HB2	2.19	0.42
1:B:180:PHE:C	1:B:184:VAL:HG12	2.43	0.42
1:B:302:HIS:HD2	1:B:307:ALA:O	2.01	0.42
2:C:34:ARG:HD2	2:C:39:GLU:HB3	2.00	0.42
2:C:59:ASP:O	3:E:27:U:N3	2.46	0.42
5:K:9:A:H3'	5:K:9:A:C8	2.55	0.42
1:A:190:ILE:CG2	1:A:209:LEU:HD22	2.50	0.42
1:B:164:PHE:CZ	1:B:212:LYS:CE	2.95	0.42
1:B:207:LYS:HD2	1:B:208:ILE:H	1.85	0.42
4:F:192:VAL:O	4:F:196:VAL:HG23	2.20	0.42
1:A:237:ARG:HB3	1:B:234:GLU:OE1	2.19	0.42
1:A:271:ARG:CG	1:A:271:ARG:NH2	2.81	0.42
1:B:195:LEU:O	1:B:198:LEU:HB2	2.20	0.42
3:D:28:G:C6	2:G:36:GLY:HA3	2.55	0.42
1:A:139:ILE:CG2	1:A:140:GLU:N	2.80	0.42
1:A:142:LEU:HD13	1:A:142:LEU:O	2.20	0.42
1:A:170:LEU:CD2	1:A:208:ILE:N	2.83	0.42
1:A:190:ILE:O	1:A:191:ASN:HB3	2.20	0.42
1:A:60:GLU:O	1:A:61:LYS:HG2	2.19	0.42
1:B:156:LEU:HD11	1:B:232:ALA:CB	2.40	0.42
2:C:63:ILE:HD12	3:E:27:U:C2	2.55	0.42
2:C:74:LYS:O	2:C:74:LYS:CG	2.68	0.42
2:C:100:VAL:CG1	2:C:101:ALA:N	2.83	0.42
4:F:131:ALA:HA	4:F:137:TYR:OH	2.20	0.42
4:J:19:ASP:CG	4:J:20:GLY:H	2.12	0.42
4:J:39:ARG:HD3	4:J:50:ILE:HG13	2.02	0.42
5:K:7:C:O2	5:K:7:C:H2'	2.19	0.42
1:A:268:LEU:HD22	1:A:317:GLN:HB3	2.01	0.42
1:A:316:TYR:CD1	3:D:34:C:C4	3.08	0.42
4:F:102:TYR:CE2	4:F:125:ILE:HD12	2.55	0.42
2:G:119:VAL:HG12	2:G:123:MET:HE2	2.00	0.41
1:A:229:ARG:HE	1:A:229:ARG:HB3	1.33	0.41
1:A:227:VAL:HG22	1:A:227:VAL:O	2.19	0.41
1:A:260:LEU:HD23	1:A:260:LEU:HA	1.77	0.41
1:B:126:GLU:N	1:B:127:GLN:OE1	2.53	0.41
1:B:127:GLN:HG2	1:B:129:GLY:N	2.36	0.41
1:B:311:LYS:HB2	1:B:311:LYS:HE2	1.93	0.41
2:C:85:LYS:HE2	2:C:94:GLU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:66:HIS:O	2:G:69:PRO:HD2	2.21	0.41
4:J:208:GLU:HB3	4:J:223:VAL:HG13	2.01	0.41
5:I:11:G:H2'	5:I:12:G:O4'	2.20	0.41
1:A:29:ARG:HG3	1:A:54:LEU:HB2	2.02	0.41
1:A:318:TYR:O	1:A:319:PRO:C	2.61	0.41
1:A:365:ARG:CZ	1:A:369:ILE:HD13	2.51	0.41
1:B:264:VAL:HG11	1:B:340:LEU:HD21	2.02	0.41
1:B:300:PHE:N	1:B:300:PHE:CD1	2.88	0.41
4:F:114:LEU:O	4:F:118:VAL:HG13	2.19	0.41
1:A:311:LYS:O	1:A:312:HIS:HB3	2.20	0.41
4:F:146:VAL:HA	4:F:173:TYR:O	2.21	0.41
1:A:119:LEU:O	1:A:119:LEU:HD12	2.20	0.41
1:B:152:LEU:CB	1:B:235:ILE:HD12	2.50	0.41
1:B:293:LEU:O	1:B:313:GLY:HA3	2.20	0.41
3:D:7:G:H3'	3:D:7:G:H8	1.85	0.41
4:J:41:ILE:HD12	4:J:41:ILE:O	2.20	0.41
4:J:164:ALA:HA	4:J:168:LEU:HB3	2.02	0.41
1:A:268:LEU:CD1	1:A:314:VAL:HG12	2.50	0.41
1:A:316:TYR:CE1	3:D:34:C:N4	2.89	0.41
2:C:46:ARG:O	2:C:46:ARG:CG	2.69	0.41
2:C:51:LEU:HD13	2:C:77:PRO:HG2	2.01	0.41
1:A:163:HIS:CD2	1:A:163:HIS:C	2.99	0.41
1:A:299:LEU:O	1:A:302:HIS:HB3	2.21	0.41
3:D:2:C:O2'	3:D:3:C:H5'	2.21	0.41
4:F:58:LEU:HD21	4:F:69:PHE:HE2	1.85	0.41
1:A:106:GLU:HG3	1:A:107:ASN:ND2	2.36	0.41
1:A:225:ILE:HD12	1:A:225:ILE:HA	1.94	0.41
1:B:334:ARG:NH1	3:E:29:A:OP2	2.53	0.41
1:B:364:ALA:HA	1:B:367:ARG:CZ	2.51	0.41
4:J:57:LYS:HD2	4:J:87:THR:HB	2.01	0.41
4:J:121:ARG:C	4:J:123:ASN:H	2.29	0.41
1:A:66:PHE:HE1	1:A:82:PHE:HD2	1.69	0.41
1:A:97:ARG:HB3	4:F:142:THR:HA	2.03	0.41
1:A:276:ALA:CB	1:A:282:LEU:HB2	2.50	0.41
1:A:284:MET:HG2	1:A:284:MET:H	1.72	0.41
2:C:26:ILE:HD12	2:C:107:LYS:HB3	2.03	0.41
2:C:32:LYS:HD2	2:C:33:ILE:H	1.86	0.41
4:J:69:PHE:HA	4:J:70:PRO:HD3	1.81	0.41
1:A:245:LEU:HD23	1:A:245:LEU:HA	1.83	0.40
1:B:13:VAL:HG22	1:B:115:VAL:HB	2.03	0.40
1:B:47:ILE:HG22	1:B:48:THR:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:346:VAL:HG21	1:B:354:ILE:CD1	2.51	0.40
3:D:9:A:O5'	3:D:9:A:H8	2.04	0.40
4:F:43:TRP:CE3	4:F:43:TRP:HA	2.55	0.40
4:F:66:LEU:HD11	4:F:68:ASN:O	2.21	0.40
2:G:14:LYS:HG3	2:G:15:GLU:N	2.36	0.40
4:J:2:VAL:HG12	4:J:17:ASP:CA	2.50	0.40
1:A:319:PRO:O	1:A:323:ARG:HG2	2.22	0.40
1:B:8:PHE:O	1:B:19:PHE:N	2.52	0.40
1:B:58:LEU:HD12	1:B:58:LEU:HA	1.64	0.40
1:B:126:GLU:O	1:B:126:GLU:HG3	2.21	0.40
1:B:164:PHE:CE1	1:B:166:GLU:HB2	2.56	0.40
1:B:257:ALA:HA	1:B:347:ASP:CG	2.46	0.40
4:J:91:VAL:HG22	4:J:101:ILE:HD13	2.03	0.40
4:J:111:LEU:O	4:J:115:VAL:HG23	2.21	0.40
1:A:103:PHE:HB2	1:A:104:LEU:HD13	2.04	0.40
1:B:153:VAL:O	1:B:154:ALA:C	2.65	0.40
2:C:68:PRO:CB	2:C:69:PRO:HD3	2.47	0.40
4:J:79:TYR:CZ	4:J:148:PHE:CE2	3.10	0.40
1:A:113:TYR:HE2	4:F:122:ARG:HH21	1.69	0.40
1:A:152:LEU:HA	1:A:152:LEU:HD23	1.72	0.40
4:F:51:TRP:CH2	4:F:58:LEU:HD13	2.57	0.40
1:A:91:ILE:O	1:A:95:ARG:CG	2.69	0.40
1:A:156:LEU:HD11	1:A:181:VAL:HG11	2.03	0.40
1:A:173:LYS:O	1:A:176:GLN:HB2	2.21	0.40
1:B:127:GLN:CG	1:B:128:SER:HA	2.52	0.40
1:B:186:HIS:CD2	1:B:186:HIS:C	2.99	0.40
2:G:57:ASP:O	2:G:84:LYS:HE3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	364/379 (96%)	330 (91%)	30 (8%)	4 (1%)	11	27
1	B	364/379 (96%)	326 (90%)	37 (10%)	1 (0%)	36	59
2	C	119/129 (92%)	102 (86%)	16 (13%)	1 (1%)	16	35
2	G	119/129 (92%)	104 (87%)	14 (12%)	1 (1%)	16	35
4	F	225/234 (96%)	218 (97%)	7 (3%)	0	100	100
4	J	225/234 (96%)	206 (92%)	17 (8%)	2 (1%)	14	33
All	All	1416/1484 (95%)	1286 (91%)	121 (8%)	9 (1%)	21	42

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	J	122	ARG
1	A	208	ILE
1	B	208	ILE
4	J	208	GLU
1	A	128	SER
2	C	75	GLU
1	A	127	GLN
1	A	201	SER
2	G	16	LEU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	312/324 (96%)	264 (85%)	48 (15%)	2	6
1	B	312/324 (96%)	258 (83%)	54 (17%)	2	5
2	C	98/105 (93%)	79 (81%)	19 (19%)	1	3
2	G	98/105 (93%)	83 (85%)	15 (15%)	3	6
4	F	197/204 (97%)	164 (83%)	33 (17%)	2	5
4	J	197/204 (97%)	172 (87%)	25 (13%)	4	10
All	All	1214/1266 (96%)	1020 (84%)	194 (16%)	2	6

All (194) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	VAL
1	A	14	ARG
1	A	22	ASN
1	A	28	LYS
1	A	34	LYS
1	A	38	VAL
1	A	50	ASP
1	A	55	LEU
1	A	58	LEU
1	A	65	GLU
1	A	73	LEU
1	A	75	ARG
1	A	78	LYS
1	A	80	LEU
1	A	83	SER
1	A	91	ILE
1	A	96	LEU
1	A	106	GLU
1	A	107	ASN
1	A	117	VAL
1	A	128	SER
1	A	139	ILE
1	A	142	LEU
1	A	143	ASP
1	A	149	ILE
1	A	151	LEU
1	A	200	LEU
1	A	207	LYS
1	A	209	LEU
1	A	222	GLN
1	A	223	THR
1	A	224	ASP
1	A	225	ILE
1	A	226	GLU
1	A	229	ARG
1	A	231	LEU
1	A	250	ASP
1	A	267	LYS
1	A	271	ARG
1	A	289	THR
1	A	317	GLN
1	A	328	GLN

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Mol	Chain	Res	Type
1	A	336	LEU
1	A	339	LYS
1	A	345	ARG
1	A	357	GLU
1	A	367	ARG
1	A	369	ILE
1	B	12	ASN
1	B	13	VAL
1	B	14	ARG
1	B	25	LEU
1	B	28	LYS
1	B	32	THR
1	B	34	LYS
1	B	44	LYS
1	B	47	ILE
1	B	48	THR
1	B	51	LEU
1	B	55	LEU
1	B	58	LEU
1	B	60	GLU
1	B	73	LEU
1	B	83	SER
1	B	85	THR
1	B	86	THR
1	B	87	GLU
1	B	95	ARG
1	B	104	LEU
1	B	110	GLU
1	B	117	VAL
1	B	125	GLN
1	B	127	GLN
1	B	139	ILE
1	B	140	GLU
1	B	147	LYS
1	B	148	VAL
1	B	153	VAL
1	B	156	LEU
1	B	169	GLU
1	B	193	GLU
1	B	201	SER
1	B	203	GLU
1	B	205	ILE

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Mol	Chain	Res	Type
1	B	207	LYS
1	B	215	THR
1	B	223	THR
1	B	224	ASP
1	B	225	ILE
1	B	227	VAL
1	B	229	ARG
1	B	231	LEU
1	B	289	THR
1	B	293	LEU
1	B	297	LYS
1	B	303	LEU
1	B	315	ILE
1	B	350	SER
1	B	354	ILE
1	B	359	LYS
1	B	365	ARG
1	B	371	GLU
2	C	14	LYS
2	C	22	GLN
2	C	33	ILE
2	C	35	LYS
2	C	37	THR
2	C	44	VAL
2	C	48	GLN
2	C	50	LYS
2	C	52	VAL
2	C	64	VAL
2	C	93	ILE
2	C	99	SER
2	C	100	VAL
2	C	103	ILE
2	C	104	GLU
2	C	107	LYS
2	C	109	ARG
2	C	114	GLU
2	C	121	GLU
4	F	3	GLU
4	F	5	LYS
4	F	6	LYS
4	F	14	VAL
4	F	16	ILE

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Mol	Chain	Res	Type
4	F	21	SER
4	F	29	LEU
4	F	30	VAL
4	F	41	ILE
4	F	49	ARG
4	F	55	ARG
4	F	58	LEU
4	F	66	LEU
4	F	77	VAL
4	F	87	THR
4	F	91	VAL
4	F	104	ILE
4	F	122	ARG
4	F	132	THR
4	F	135	GLU
4	F	141	VAL
4	F	143	LYS
4	F	161	ILE
4	F	176	ILE
4	F	181	ARG
4	F	186	THR
4	F	198	ARG
4	F	200	LEU
4	F	202	GLU
4	F	209	ARG
4	F	210	LEU
4	F	212	LEU
4	F	223	VAL
2	G	21	LEU
2	G	26	ILE
2	G	29	ASP
2	G	30	THR
2	G	35	LYS
2	G	51	LEU
2	G	58	VAL
2	G	63	ILE
2	G	64	VAL
2	G	72	GLU
2	G	79	ILE
2	G	86	GLU
2	G	100	VAL
2	G	102	ILE

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Mol	Chain	Res	Type
2	G	122	LEU
4	J	16	ILE
4	J	21	SER
4	J	24	ILE
4	J	26	THR
4	J	27	LYS
4	J	34	ARG
4	J	44	GLU
4	J	47	GLU
4	J	57	LYS
4	J	66	LEU
4	J	77	VAL
4	J	79	TYR
4	J	91	VAL
4	J	107	SER
4	J	132	THR
4	J	138	ARG
4	J	143	LYS
4	J	176	ILE
4	J	181	ARG
4	J	183	ILE
4	J	185	VAL
4	J	207	ILE
4	J	209	ARG
4	J	212	LEU
4	J	223	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	ASN
1	A	125	GLN
1	A	137	GLN
1	A	150	ASN
1	A	222	GLN
1	A	302	HIS
1	A	312	HIS
1	A	328	GLN
1	B	107	ASN
1	B	127	GLN
1	B	163	HIS
1	B	174	HIS

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Mol	Chain	Res	Type
1	B	186	HIS
1	B	230	GLN
1	B	240	GLN
1	B	291	GLN
1	B	302	HIS
1	B	328	GLN
2	C	48	GLN
4	F	156	GLN
4	J	219	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	D	33/34 (97%)	11 (33%)	1 (3%)
3	E	33/34 (97%)	7 (21%)	1 (3%)
5	I	12/13 (92%)	2 (16%)	0
5	K	11/13 (84%)	3 (27%)	0
All	All	89/94 (94%)	23 (25%)	2 (2%)

All (23) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	D	11	C
3	D	12	U
3	D	13	C
3	D	18	C
3	D	19	G
3	D	20	A
3	D	21	A
3	D	27	U
3	D	28	G
3	D	33	G
3	D	34	C
3	E	6	U
3	E	10	G
3	E	11	C
3	E	12	U
3	E	13	C
3	E	33	G
3	E	34	C
5	I	7	C

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Mol	Chain	Res	Type
5	I	8	A
5	K	3	G
5	K	7	C
5	K	11	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	D	11	C
3	E	11	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	SAM	F	228	-	26,28,29	1.03	2 (7%)	32,40,42	2.24	11 (34%)
6	SAM	J	228	-	26,28,29	0.95	0	32,40,42	2.31	9 (28%)

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
6	SAM	F	228	-	-	7/14/31/33	0/3/3/3
6	SAM	J	228	-	-	5/14/31/33	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	228	SAM	C2-N1	2.33	1.38	1.33
6	F	228	SAM	C8-N7	2.31	1.36	1.31

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	228	SAM	N3-C2-N1	-7.05	117.92	128.58
6	F	228	SAM	N3-C2-N1	-5.54	120.19	128.58
6	F	228	SAM	C5-C4-N3	-5.08	119.72	126.72
6	J	228	SAM	N9-C8-N7	-4.92	106.95	113.94
6	J	228	SAM	C5-C4-N3	-4.25	120.86	126.72
6	J	228	SAM	C2-N3-C4	4.05	121.73	111.83
6	J	228	SAM	C5-N7-C8	3.92	109.62	103.45
6	F	228	SAM	C5-N7-C8	3.75	109.35	103.45
6	F	228	SAM	N9-C8-N7	-3.74	108.63	113.94
6	F	228	SAM	C2-N3-C4	3.68	120.82	111.83
6	F	228	SAM	N3-C4-N9	3.20	132.60	127.17
6	F	228	SAM	O4'-C4'-C5'	2.95	116.34	108.88
6	F	228	SAM	C2'-C3'-C4'	2.92	108.25	102.61
6	J	228	SAM	N3-C4-N9	2.84	132.00	127.17
6	F	228	SAM	C4-C5-N7	-2.80	107.38	110.58
6	J	228	SAM	C4-N9-C8	2.80	108.68	105.74
6	J	228	SAM	CG-SD-C5'	2.69	110.01	103.43
6	F	228	SAM	CE-SD-C5'	2.63	121.18	100.54
6	J	228	SAM	C4-C5-N7	-2.58	107.63	110.58
6	F	228	SAM	C6-C5-C4	2.37	120.41	117.18

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	F	228	SAM	C-CA-CB-CG
6	F	228	SAM	CB-CG-SD-CE
6	F	228	SAM	C4'-C5'-SD-CE
6	F	228	SAM	O4'-C4'-C5'-SD
6	F	228	SAM	C3'-C4'-C5'-SD

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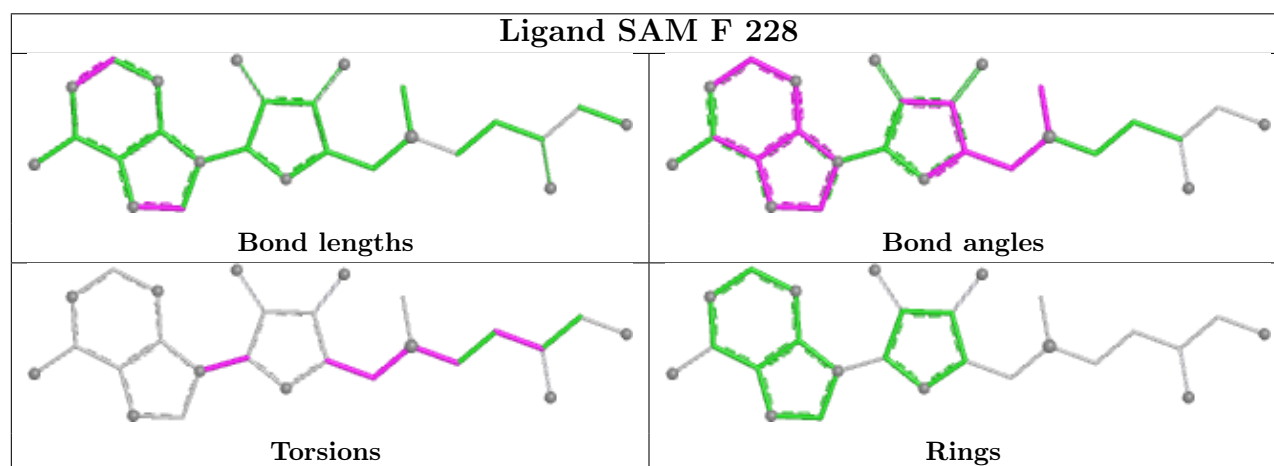
Mol	Chain	Res	Type	Atoms
6	J	228	SAM	C-CA-CB-CG
6	J	228	SAM	C2'-C1'-N9-C8
6	F	228	SAM	CB-CG-SD-C5'
6	J	228	SAM	CB-CG-SD-C5'
6	J	228	SAM	CB-CG-SD-CE
6	J	228	SAM	CA-CB-CG-SD
6	F	228	SAM	C2'-C1'-N9-C8

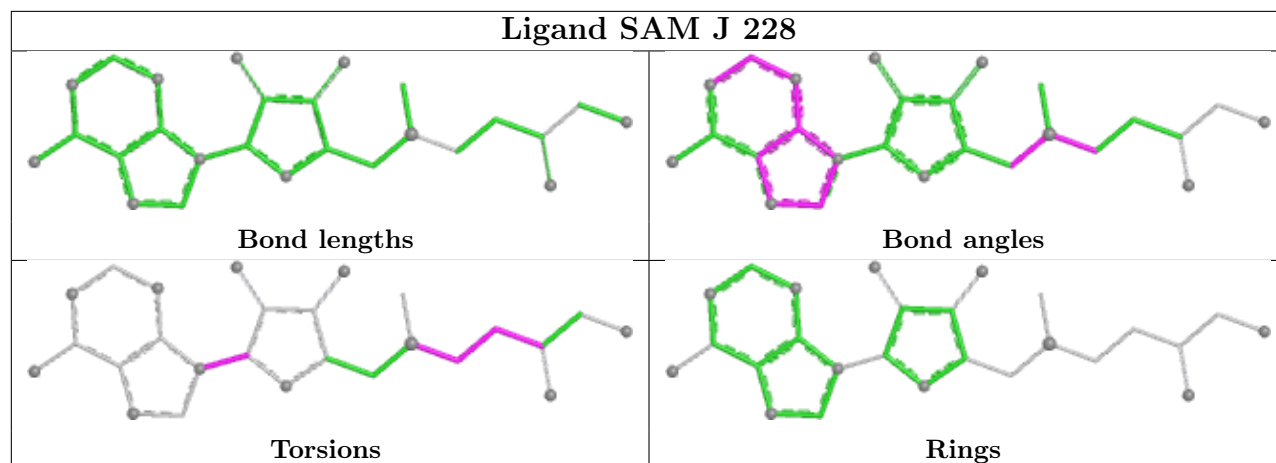
There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	J	228	SAM	11	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	366/379 (96%)	-0.02	4 (1%) 78 76	61, 83, 116, 157	0
1	B	366/379 (96%)	0.02	4 (1%) 78 76	52, 78, 113, 136	0
2	C	121/129 (93%)	0.77	9 (7%) 20 18	88, 132, 160, 167	0
2	G	121/129 (93%)	0.32	2 (1%) 69 66	83, 108, 132, 143	0
3	D	34/34 (100%)	0.10	0 100 100	93, 125, 214, 217	0
3	E	34/34 (100%)	0.33	0 100 100	103, 129, 212, 215	0
4	F	227/234 (97%)	-0.33	0 100 100	55, 69, 91, 112	0
4	J	227/234 (97%)	-0.14	1 (0%) 88 88	52, 70, 112, 140	0
5	I	13/13 (100%)	0.66	0 100 100	167, 192, 219, 221	0
5	K	12/13 (92%)	0.39	0 100 100	176, 191, 213, 214	0
All	All	1521/1578 (96%)	0.03	20 (1%) 75 73	52, 82, 148, 221	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	327	TRP	6.7
1	B	327	TRP	5.6
2	G	48	GLN	3.8
1	A	8	PHE	3.5
1	A	212	LYS	3.2
2	C	108	ALA	3.1
2	G	4	LYS	3.0
1	B	373	TYR	2.9
2	C	5	PRO	2.6
2	C	57	ASP	2.5
1	B	212	LYS	2.4
4	J	185	VAL	2.4
2	C	34	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
2	C	91	ALA	2.3
2	C	4	LYS	2.3
2	C	33	ILE	2.2
1	A	373	TYR	2.2
2	C	103	ILE	2.1
2	C	35	LYS	2.0
1	B	328	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

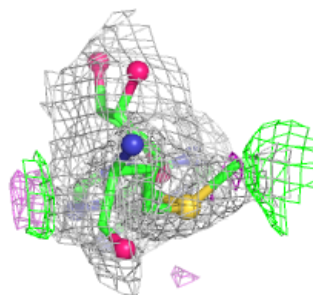
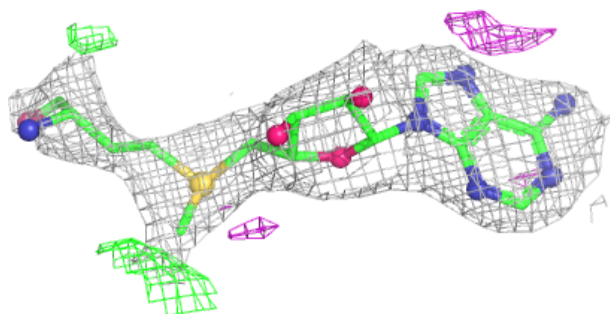
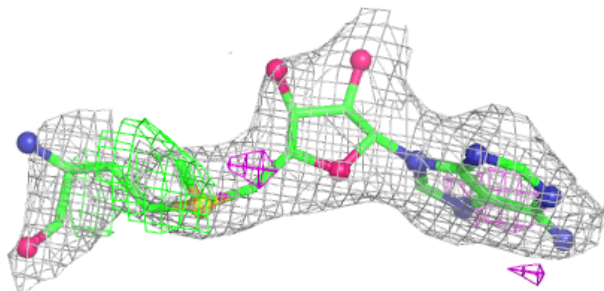
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	SAM	F	228	26/27	0.83	0.11	52,69,102,106	0
6	SAM	J	228	26/27	0.90	0.12	54,70,105,108	0

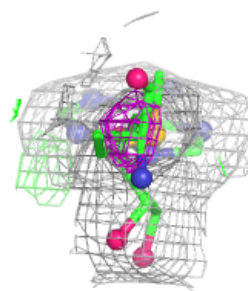
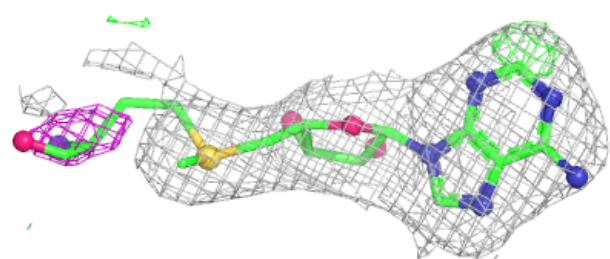
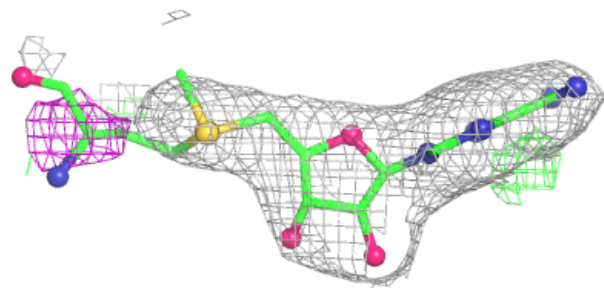
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around SAM F 228:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around SAM J 228:**

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.