



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:08 am GMT

PDB ID : 3PU4
Title : Crystal Structure of a vesicular stomatitis virus nucleocapsid-polyU complex
Authors : Luo, M.; Green, T.J.; Rowse, M.
Deposited on : 2010-12-03
Resolution : 3.00 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

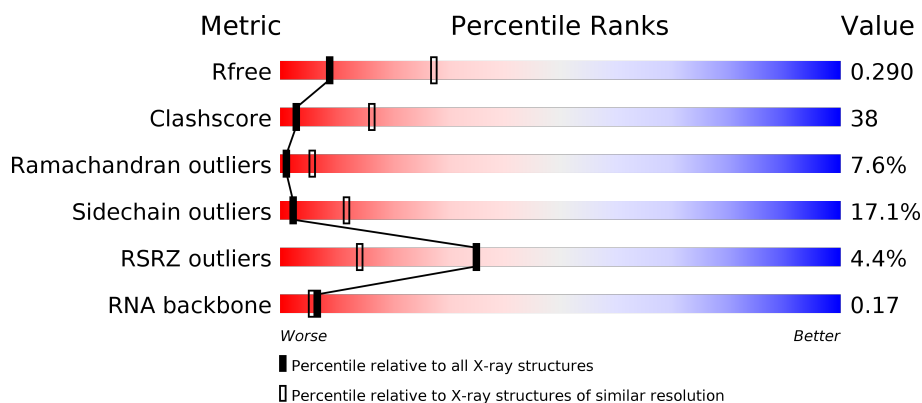
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)
RNA backbone	2435	1007 (3.34-2.66)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	421	<div> <div>4%</div> <div>48% 38% 12%</div> </div>
1	B	421	<div> <div>2%</div> <div>47% 38% 11%</div> </div>
1	C	421	<div> <div>3%</div> <div>48% 37% 11%</div> </div>
1	D	421	<div> <div>5%</div> <div>48% 37% 12%</div> </div>

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Mol	Chain	Length	Quality of chain
1	E	421	<div><div></div><div>4%</div><div>46%</div><div>39%</div><div>12%</div><div></div></div>
2	R	45	<div><div></div><div>42%</div><div>7%</div><div>24%</div><div>33%</div><div>36%</div><div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17437 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.

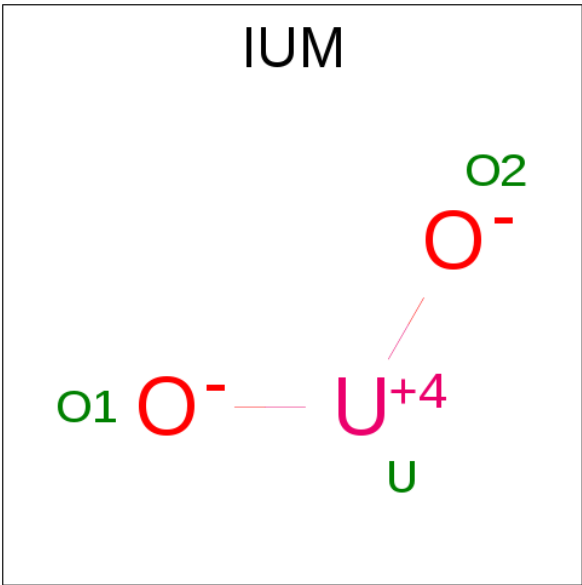
- Molecule 1 is a protein called Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3327	2118	558	633	18			
1	B	415	Total	C	N	O	S	0	0	0
			3290	2097	552	623	18			
1	C	413	Total	C	N	O	S	0	0	0
			3275	2089	550	618	18			
1	D	416	Total	C	N	O	S	0	0	0
			3298	2103	553	624	18			
1	E	421	Total	C	N	O	S	0	0	0
			3327	2118	558	633	18			

- Molecule 2 is a RNA chain called RNA (45-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	45	Total	C	N	O	P	0	0	0
			900	405	90	360	45			

- Molecule 3 is URANYL (VI) ION (three-letter code: IUM) (formula: O₂U).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0
3	B	1	Total U 1 1	0	0
3	B	1	Total U 1 1	0	0
3	B	1	Total U 1 1	0	0
3	C	1	Total U 1 1	0	0
3	C	1	Total U 1 1	0	0
3	C	1	Total U 1 1	0	0
3	D	1	Total U 1 1	0	0
3	D	1	Total U 1 1	0	0
3	E	1	Total U 1 1	0	0
3	E	1	Total U 1 1	0	0

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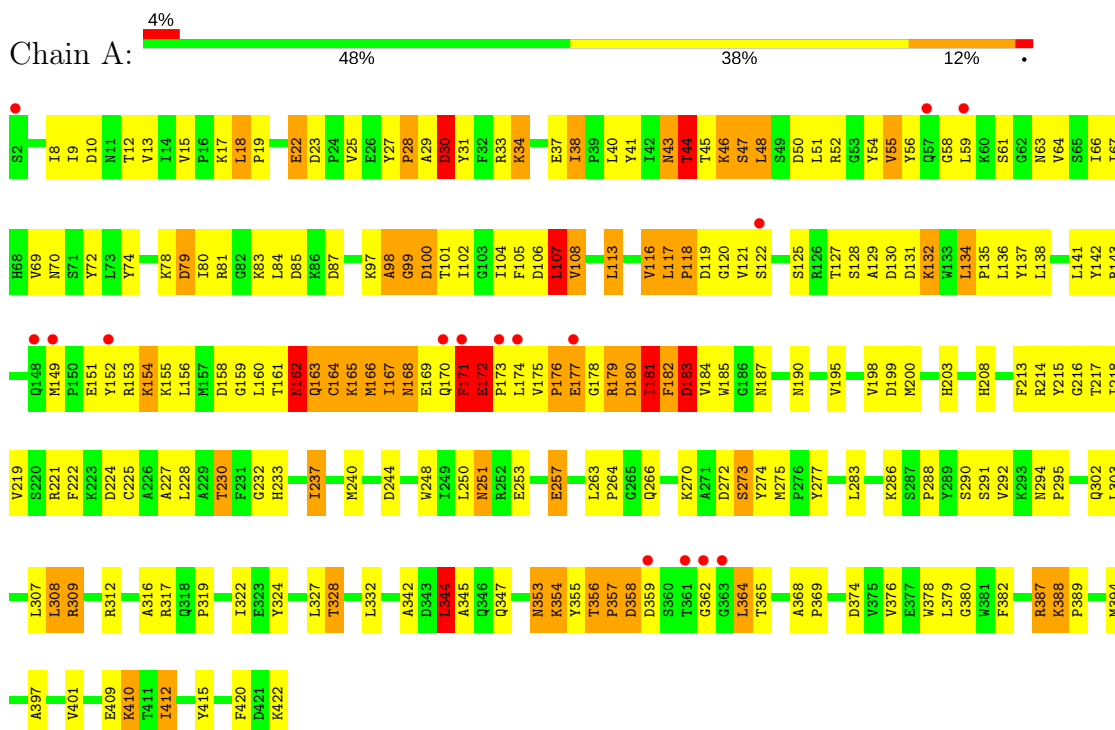
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	1	Total 1	U 1	0	0
3	R	1	Total 1	U 1	0	0
3	R	1	Total 1	U 1	0	0
3	R	1	Total 1	U 1	0	0
3	R	1	Total 1	U 1	0	0
3	R	1	Total 1	U 1	0	0

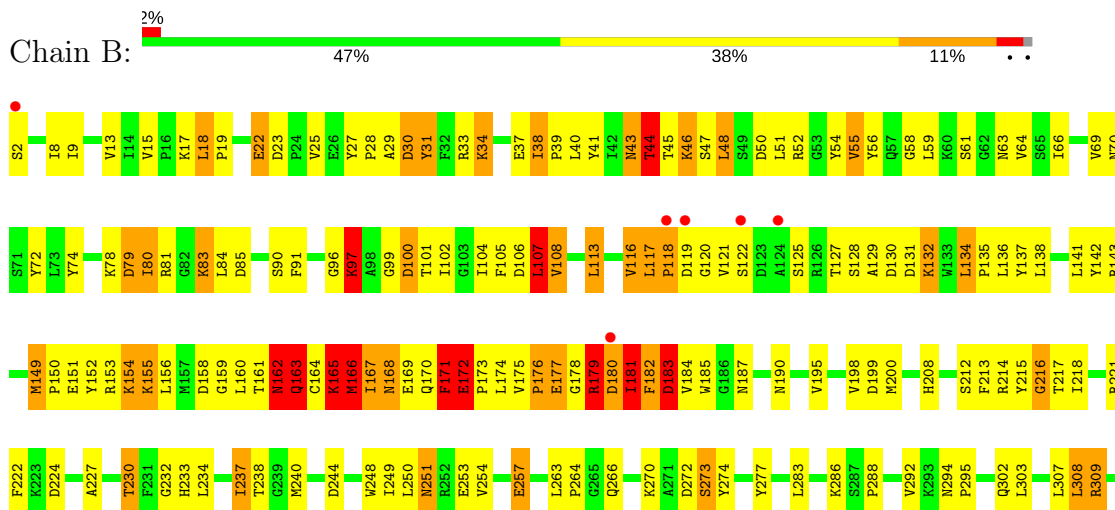
3 Residue-property plots

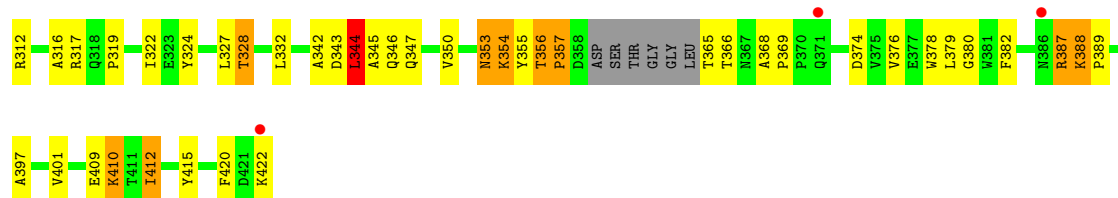
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Nucleoprotein

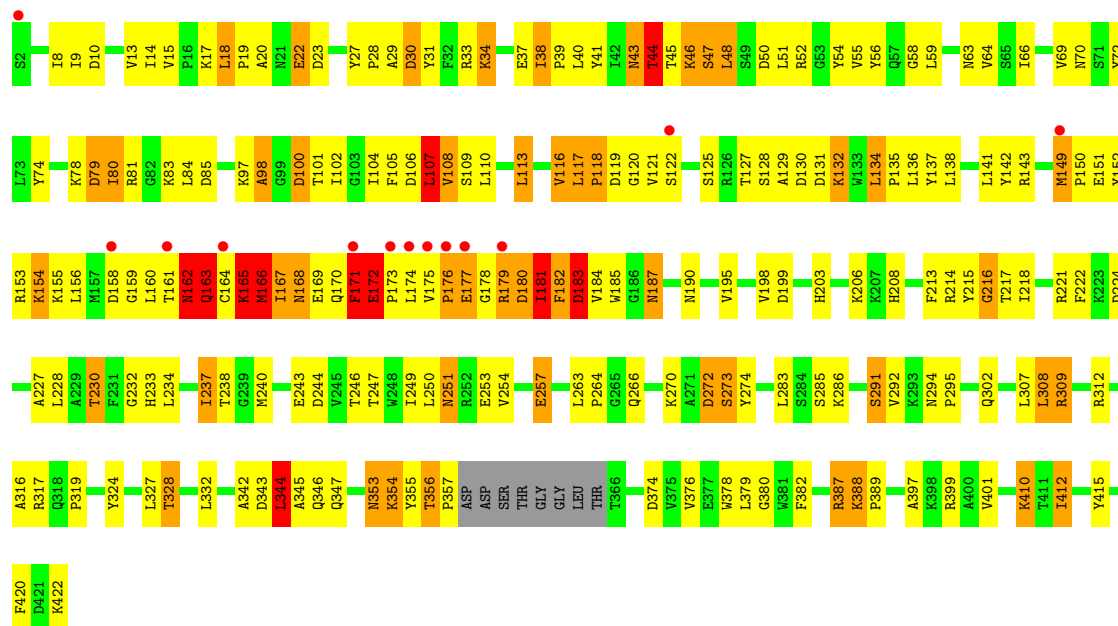


• Molecule 1: Nucleoprotein

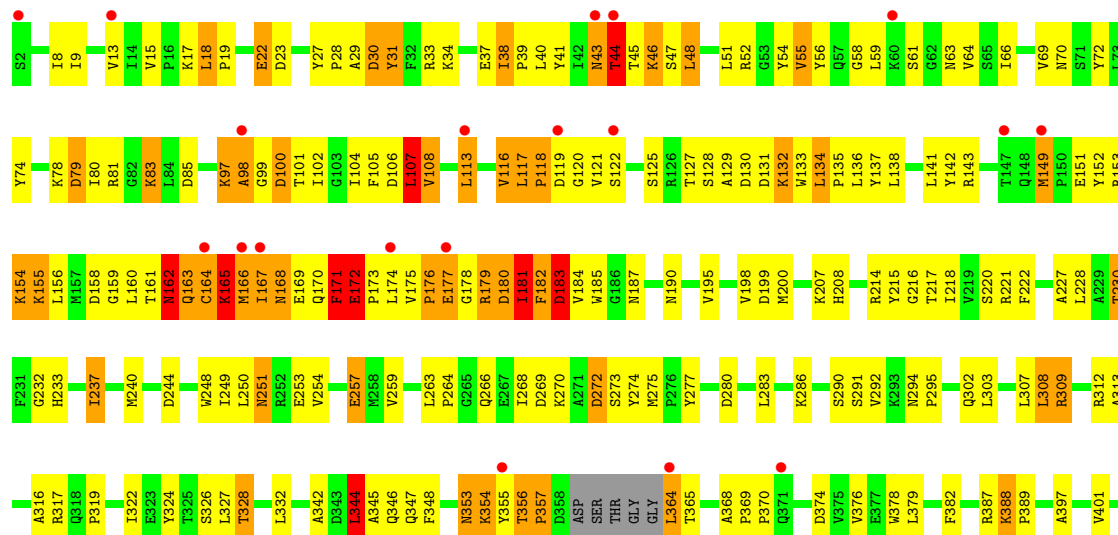




• Molecule 1: Nucleoprotein

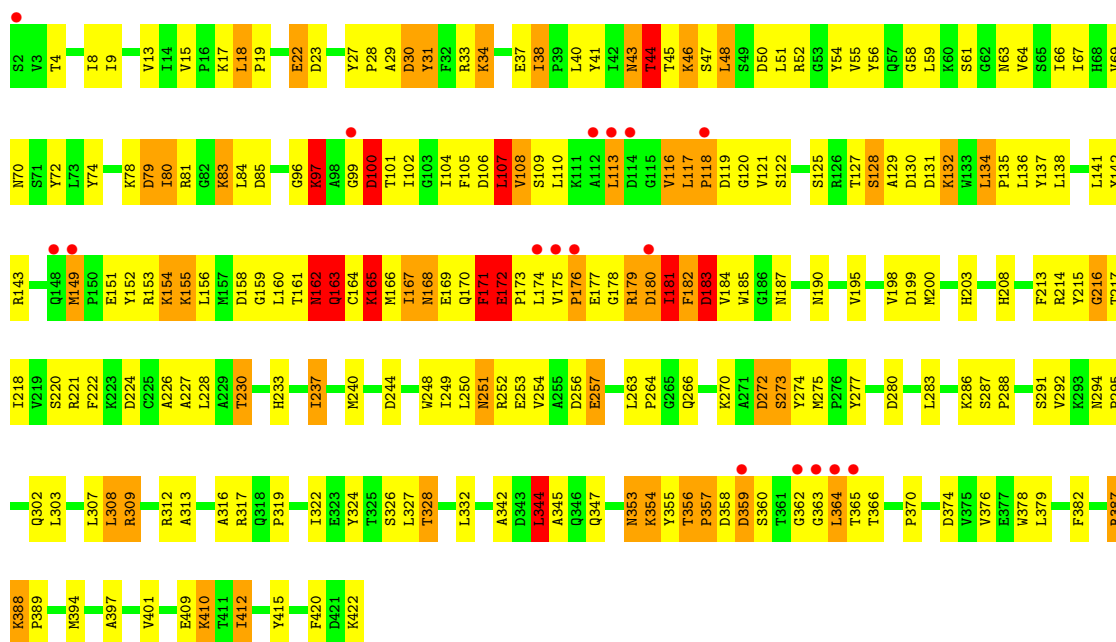


• Molecule 1: Nucleoprotein

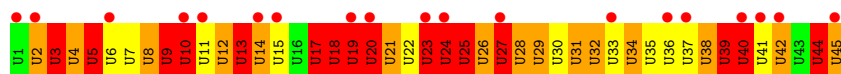




● Molecule 1: Nucleoprotein



● Molecule 2: RNA (45-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	165.48Å 235.06Å 75.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.77 – 3.00 40.88 – 2.85	Depositor EDS
% Data completeness (in resolution range)	83.0 (34.77-3.00) 74.2 (40.88-2.85)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6_289)	Depositor
R, R_{free}	0.251 , 0.288 0.246 , 0.290	Depositor DCC
R_{free} test set	1846 reflections (3.69%)	DCC
Wilson B-factor (Å ²)	73.9	Xtriage
Anisotropy	0.545	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	17437	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% 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: IUM

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	0.56	2/3403 (0.1%)	0.67	0/4607
1	B	0.54	1/3365 (0.0%)	0.67	1/4554 (0.0%)
1	C	0.55	0/3350	0.67	1/4533 (0.0%)
1	D	0.54	0/3373	0.67	0/4565
1	E	0.52	0/3403	0.65	0/4607
2	R	0.75	0/989	1.71	30/1526 (2.0%)
All	All	0.56	3/17883 (0.0%)	0.77	32/24392 (0.1%)

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	3
1	B	0	4
1	C	0	3
1	D	0	3
1	E	0	4
All	All	0	17

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	225	CYS	CB-SG	-5.97	1.72	1.81
1	B	179	ARG	C-N	5.42	1.46	1.34
1	A	30	ASP	CB-CG	5.20	1.62	1.51

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	13	U	O4'-C1'-N1	12.47	118.17	108.20
2	R	9	U	O4'-C1'-N1	11.70	117.56	108.20
2	R	27	U	O4'-C1'-N1	11.37	117.30	108.20
2	R	39	U	O4'-C1'-N1	-11.05	99.36	108.20
2	R	18	U	O4'-C1'-N1	9.81	116.05	108.20
1	B	166	MET	CB-CA-C	9.53	129.46	110.40
2	R	8	U	O4'-C1'-N1	8.78	115.22	108.20
2	R	17	U	O4'-C1'-N1	8.71	115.17	108.20
2	R	20	U	O4'-C1'-N1	8.23	114.79	108.20
2	R	44	U	O4'-C1'-N1	7.99	114.59	108.20
2	R	25	U	P-O3'-C3'	7.72	128.97	119.70
2	R	10	U	P-O3'-C3'	7.56	128.77	119.70
2	R	24	U	P-O3'-C3'	7.25	128.40	119.70
2	R	21	U	O4'-C1'-N1	-7.08	102.53	108.20
2	R	34	U	O4'-C1'-N1	7.07	113.86	108.20
2	R	19	U	P-O3'-C3'	6.94	128.03	119.70
1	C	166	MET	CB-CA-C	6.69	123.78	110.40
2	R	4	U	O4'-C1'-N1	6.67	113.54	108.20
2	R	39	U	N1-C1'-C2'	6.66	122.66	114.00
2	R	5	U	P-O3'-C3'	6.50	127.50	119.70
2	R	26	U	P-O3'-C3'	-6.42	112.00	119.70
2	R	39	U	P-O3'-C3'	6.27	127.22	119.70
2	R	39	U	C5-C6-N1	6.27	125.83	122.70
2	R	3	U	O4'-C1'-N1	-6.24	103.21	108.20
2	R	26	U	N1-C1'-C2'	-5.89	105.52	112.00
2	R	3	U	P-O3'-C3'	5.84	126.71	119.70
2	R	24	U	O4'-C1'-N1	-5.82	103.54	108.20
2	R	18	U	P-O3'-C3'	5.82	126.68	119.70
2	R	23	U	P-O3'-C3'	5.79	126.65	119.70
2	R	28	U	N1-C1'-C2'	5.64	121.34	114.00
2	R	40	U	O4'-C1'-N1	-5.49	103.81	108.20
2	R	14	U	O4'-C1'-N1	5.21	112.37	108.20

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	LEU	Peptide
1	A	98	ALA	Peptide
1	A	99	GLY	Peptide
1	B	107	LEU	Peptide
1	B	163	GLN	Peptide
1	B	165	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	B	97	LYS	Peptide
1	C	107	LEU	Peptide
1	C	163	GLN	Peptide
1	C	165	LYS	Peptide
1	D	107	LEU	Peptide
1	D	167	ILE	Peptide
1	D	97	LYS	Peptide
1	E	107	LEU	Peptide
1	E	128	SER	Peptide
1	E	165	LYS	Peptide
1	E	97	LYS	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	3327	0	3287	269	0
1	B	3290	0	3253	260	0
1	C	3275	0	3242	279	0
1	D	3298	0	3264	266	0
1	E	3327	0	3287	247	0
2	R	900	0	451	85	0
3	A	4	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	2	0	0	0	0
3	E	3	0	0	0	0
3	R	5	0	0	0	0
All	All	17437	0	16784	1310	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 38.

All (1310) 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:B:165:LYS:HB3	1:B:166:MET:SD	1.48	1.53
1:C:165:LYS:HB3	1:C:166:MET:SD	1.47	1.51
1:B:167:ILE:HD13	1:B:168:ASN:N	1.30	1.37
1:A:165:LYS:HB3	1:A:166:MET:SD	1.67	1.33
1:B:165:LYS:CB	1:B:166:MET:SD	2.28	1.22
1:C:165:LYS:CB	1:C:166:MET:SD	2.27	1.21
1:E:160:LEU:O	1:E:163:GLN:HB2	1.41	1.20
1:C:160:LEU:O	1:C:163:GLN:HB2	1.39	1.20
1:E:163:GLN:HA	1:E:163:GLN:OE1	1.43	1.19
1:A:87:ASP:OD2	1:A:97:LYS:HG3	1.38	1.17
1:C:163:GLN:HA	1:C:163:GLN:OE1	1.43	1.17
1:B:160:LEU:O	1:B:163:GLN:HB2	1.42	1.15
1:B:163:GLN:HA	1:B:163:GLN:OE1	1.43	1.10
1:E:117:LEU:HB3	1:E:118:PRO:CD	1.88	1.03
1:B:117:LEU:HB3	1:B:118:PRO:CD	1.89	1.01
1:D:117:LEU:HB3	1:D:118:PRO:CD	1.90	1.01
1:A:364:LEU:HB2	1:A:368:ALA:HB2	1.36	1.01
1:C:117:LEU:HB3	1:C:118:PRO:CD	1.89	1.01
1:A:117:LEU:HB3	1:A:118:PRO:CD	1.90	1.00
1:A:165:LYS:CB	1:A:166:MET:SD	2.49	0.99
1:D:165:LYS:C	1:D:166:MET:SD	2.41	0.99
1:E:117:LEU:HB3	1:E:118:PRO:HD2	1.45	0.99
1:B:167:ILE:CD1	1:B:168:ASN:N	2.25	0.98
1:C:137:TYR:HD1	1:C:163:GLN:HE21	1.12	0.97
1:C:48:LEU:HD22	1:C:48:LEU:H	1.30	0.96
1:A:117:LEU:HB3	1:A:118:PRO:HD2	1.49	0.95
1:C:184:VAL:HB	1:D:166:MET:HE1	1.47	0.95
1:A:48:LEU:H	1:A:48:LEU:HD22	1.32	0.94
1:E:37:GLU:HB2	1:E:108:VAL:HG11	1.49	0.94
1:E:137:TYR:HD1	1:E:163:GLN:HE21	1.07	0.94
1:C:117:LEU:HB3	1:C:118:PRO:HD2	1.48	0.94
1:D:117:LEU:HB3	1:D:118:PRO:HD2	1.49	0.93
1:E:167:ILE:HD13	1:E:168:ASN:H	1.33	0.93
1:E:302:GLN:HB3	1:E:412:ILE:CD1	1.99	0.93
1:B:48:LEU:HD22	1:B:48:LEU:H	1.34	0.92
1:B:117:LEU:HB3	1:B:118:PRO:HD2	1.50	0.92
1:D:48:LEU:H	1:D:48:LEU:HD22	1.36	0.91
1:C:160:LEU:HA	1:C:163:GLN:HG2	1.54	0.90
1:E:149:MET:HG3	2:R:42:U:O4'	1.71	0.90
1:B:302:GLN:HB3	1:B:412:ILE:CD1	2.02	0.90
1:C:180:ASP:H	1:C:183:ASP:CG	1.76	0.89
1:D:177:GLU:HA	1:D:181:ILE:HD13	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:302:GLN:HB3	1:D:412:ILE:CD1	2.03	0.89
2:R:10:U:H2'	2:R:11:U:C6	2.08	0.89
1:A:37:GLU:HB2	1:A:108:VAL:HG11	1.55	0.88
1:C:302:GLN:HB3	1:C:412:ILE:CD1	2.03	0.88
1:E:48:LEU:HD22	1:E:48:LEU:H	1.37	0.88
1:A:167:ILE:HD13	1:A:168:ASN:H	1.37	0.88
1:C:376:VAL:HG13	1:D:354:LYS:HB2	1.55	0.88
1:E:160:LEU:HA	1:E:163:GLN:HG2	1.55	0.87
1:B:137:TYR:HD1	1:B:163:GLN:HE21	1.16	0.87
1:D:167:ILE:O	1:D:167:ILE:HG22	1.73	0.87
1:D:97:LYS:O	1:D:100:ASP:HB2	1.74	0.86
1:A:177:GLU:HA	1:A:181:ILE:HD13	1.57	0.86
1:E:365:THR:HG23	1:E:366:THR:N	1.91	0.86
1:D:74:TYR:CE1	1:D:78:LYS:HD3	2.10	0.86
1:B:37:GLU:HB2	1:B:108:VAL:HG11	1.56	0.86
1:B:160:LEU:HA	1:B:163:GLN:HG2	1.58	0.86
2:R:25:U:H2'	2:R:26:U:C6	2.11	0.85
1:D:37:GLU:HB2	1:D:108:VAL:HG11	1.57	0.85
1:E:160:LEU:O	1:E:163:GLN:CB	2.24	0.85
1:A:97:LYS:HG2	1:A:98:ALA:H	1.40	0.85
1:C:354:LYS:HE3	1:C:356:THR:HA	1.58	0.85
1:A:302:GLN:HB3	1:A:412:ILE:CD1	2.06	0.85
1:C:177:GLU:HA	1:C:181:ILE:HD13	1.58	0.85
1:D:137:TYR:HD1	1:D:163:GLN:HE21	1.22	0.85
1:A:167:ILE:H	1:A:167:ILE:CD1	1.89	0.84
1:B:97:LYS:O	1:B:100:ASP:HB2	1.76	0.84
1:E:160:LEU:C	1:E:163:GLN:HB2	1.98	0.84
1:A:137:TYR:HD1	1:A:163:GLN:HE21	1.22	0.84
1:E:180:ASP:H	1:E:183:ASP:CG	1.80	0.84
1:B:18:LEU:HD12	1:C:232:GLY:HA2	1.59	0.84
1:D:165:LYS:CA	1:D:166:MET:SD	2.66	0.84
1:C:182:PHE:HD2	1:C:183:ASP:N	1.74	0.83
1:C:37:GLU:HB2	1:C:108:VAL:HG11	1.58	0.83
1:D:354:LYS:HE3	1:D:356:THR:HA	1.60	0.83
1:A:182:PHE:HD2	1:A:183:ASP:N	1.75	0.83
1:A:214:ARG:HA	1:A:217:THR:HG22	1.59	0.83
1:E:74:TYR:CE1	1:E:78:LYS:HD3	2.13	0.83
1:A:97:LYS:CG	1:A:98:ALA:H	1.90	0.83
1:B:167:ILE:HD13	1:B:168:ASN:H	1.04	0.83
1:A:74:TYR:CE1	1:A:78:LYS:HD3	2.14	0.83
1:E:364:LEU:HD12	1:E:364:LEU:H	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:328:THR:HG21	1:D:415:TYR:OH	1.79	0.82
1:D:182:PHE:HD2	1:D:183:ASP:N	1.77	0.82
1:B:153:ARG:NH2	1:B:176:PRO:HA	1.94	0.82
1:B:354:LYS:HE3	1:B:356:THR:HA	1.60	0.82
1:E:182:PHE:HD2	1:E:183:ASP:N	1.76	0.82
1:C:214:ARG:HA	1:C:217:THR:HG22	1.62	0.82
1:B:182:PHE:HD2	1:B:183:ASP:N	1.77	0.81
1:C:160:LEU:O	1:C:163:GLN:CB	2.25	0.81
1:E:215:TYR:CD1	2:R:45:U:H5''	2.15	0.81
1:A:97:LYS:HG2	1:A:98:ALA:N	1.96	0.81
1:A:180:ASP:H	1:A:183:ASP:CG	1.84	0.81
1:A:199:ASP:OD1	1:A:217:THR:HG23	1.80	0.81
1:D:133:TRP:HB3	1:D:167:ILE:CD1	2.10	0.81
1:D:166:MET:N	1:D:166:MET:SD	2.54	0.81
1:B:214:ARG:HA	1:B:217:THR:HG22	1.63	0.81
1:D:180:ASP:H	1:D:183:ASP:CG	1.85	0.81
1:C:181:ILE:HD12	1:C:181:ILE:N	1.96	0.80
1:E:354:LYS:HE3	1:E:356:THR:HA	1.61	0.80
1:A:364:LEU:HB2	1:A:368:ALA:CB	2.12	0.80
1:B:342:ALA:HB1	1:B:344:LEU:HD23	1.63	0.80
1:A:354:LYS:HE3	1:A:356:THR:HA	1.62	0.80
1:A:87:ASP:OD2	1:A:97:LYS:CG	2.25	0.80
1:B:167:ILE:HD13	1:B:167:ILE:C	2.01	0.80
1:C:199:ASP:OD1	1:C:217:THR:HG23	1.82	0.80
1:E:214:ARG:HA	1:E:217:THR:HG22	1.63	0.80
1:E:199:ASP:OD1	1:E:217:THR:HG23	1.81	0.80
1:A:167:ILE:HD13	1:A:167:ILE:H	1.44	0.79
1:B:74:TYR:CE1	1:B:78:LYS:HD3	2.17	0.79
1:C:160:LEU:C	1:C:163:GLN:HB2	2.02	0.79
1:C:167:ILE:HD13	1:C:168:ASN:H	1.47	0.79
1:C:66:ILE:HG13	1:C:70:ASN:HD21	1.47	0.79
1:B:199:ASP:OD1	1:B:217:THR:HG23	1.82	0.79
1:A:181:ILE:HD12	1:A:181:ILE:N	1.98	0.79
1:B:160:LEU:O	1:B:163:GLN:CB	2.29	0.79
1:D:141:LEU:HD13	1:D:182:PHE:HD1	1.48	0.79
1:B:152:TYR:OH	1:B:176:PRO:HB3	1.83	0.78
1:D:214:ARG:HA	1:D:217:THR:HG22	1.66	0.78
1:C:74:TYR:CE1	1:C:78:LYS:HD3	2.17	0.78
1:A:167:ILE:HD13	1:A:168:ASN:N	1.97	0.78
1:A:54:TYR:HE1	1:A:118:PRO:HB2	1.49	0.78
1:C:308:LEU:O	1:C:309:ARG:HB2	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:TRP:CD1	1:D:167:ILE:HD13	2.19	0.78
1:E:167:ILE:HD13	1:E:168:ASN:N	1.97	0.78
1:A:84:LEU:HD12	1:A:97:LYS:H	1.47	0.77
1:D:364:LEU:HB2	1:D:368:ALA:HB2	1.66	0.77
1:D:66:ILE:HG13	1:D:70:ASN:HD21	1.49	0.77
1:B:106:ASP:O	1:B:107:LEU:HG	1.85	0.77
1:C:48:LEU:CD2	1:C:48:LEU:H	1.97	0.77
1:B:141:LEU:HD13	1:B:182:PHE:HD1	1.50	0.76
1:C:342:ALA:HB1	1:C:344:LEU:HD23	1.67	0.76
1:D:302:GLN:HB3	1:D:412:ILE:HD11	1.67	0.76
1:A:342:ALA:HB1	1:A:344:LEU:HD23	1.67	0.76
1:B:328:THR:HG21	1:B:415:TYR:OH	1.85	0.76
1:C:48:LEU:N	1:C:48:LEU:HD22	1.99	0.76
1:A:181:ILE:H	1:A:181:ILE:HD12	1.50	0.76
1:B:28:PRO:HD2	1:B:266:GLN:HE21	1.50	0.76
1:C:54:TYR:HE1	1:C:118:PRO:HB2	1.51	0.76
1:D:199:ASP:OD1	1:D:217:THR:HG23	1.84	0.76
1:E:66:ILE:HG13	1:E:70:ASN:HD21	1.49	0.76
1:A:66:ILE:HG13	1:A:70:ASN:HD21	1.49	0.76
1:B:178:GLY:O	1:B:179:ARG:HB2	1.84	0.76
1:D:141:LEU:HD22	1:D:182:PHE:CE1	2.21	0.76
1:A:28:PRO:HD2	1:A:266:GLN:HE21	1.51	0.75
1:B:54:TYR:HE1	1:B:118:PRO:HB2	1.51	0.75
1:B:160:LEU:C	1:B:163:GLN:HB2	2.05	0.75
1:C:181:ILE:HD12	1:C:181:ILE:H	1.51	0.75
1:E:28:PRO:HD2	1:E:266:GLN:HE21	1.51	0.75
1:A:364:LEU:HD12	1:A:364:LEU:H	1.51	0.75
1:B:81:ARG:HB3	1:B:208:HIS:HE2	1.51	0.75
2:R:17:U:H2'	2:R:18:U:H5''	1.67	0.75
2:R:19:U:HO2'	2:R:20:U:H6	1.33	0.75
1:A:48:LEU:HD22	1:A:48:LEU:N	2.01	0.75
1:E:181:ILE:H	1:E:181:ILE:HD12	1.52	0.75
1:D:286:LYS:HD2	2:R:2:U:H5''	1.67	0.75
1:D:106:ASP:O	1:D:107:LEU:HG	1.87	0.75
1:A:48:LEU:H	1:A:48:LEU:CD2	1.98	0.75
1:A:308:LEU:O	1:A:309:ARG:HB2	1.86	0.75
1:D:81:ARG:HB3	1:D:208:HIS:HE2	1.50	0.75
1:E:181:ILE:N	1:E:181:ILE:HD12	2.02	0.75
1:E:175:VAL:O	1:E:176:PRO:O	2.04	0.74
1:E:54:TYR:HE1	1:E:118:PRO:HB2	1.50	0.74
1:B:180:ASP:H	1:B:183:ASP:CG	1.91	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:ARG:HB3	1:C:208:HIS:HE2	1.51	0.74
1:D:181:ILE:H	1:D:181:ILE:HD12	1.51	0.74
1:D:28:PRO:HD2	1:D:266:GLN:HE21	1.53	0.74
1:B:380:GLY:HA2	1:C:354:LYS:NZ	2.03	0.74
1:B:107:LEU:HD23	1:B:274:TYR:OH	1.88	0.74
1:D:54:TYR:HE1	1:D:118:PRO:HB2	1.53	0.74
1:E:117:LEU:CB	1:E:118:PRO:HD2	2.17	0.73
1:E:160:LEU:HA	1:E:163:GLN:CG	2.17	0.73
1:C:117:LEU:CB	1:C:118:PRO:HD2	2.19	0.73
1:A:167:ILE:N	1:A:167:ILE:CD1	2.49	0.73
1:B:181:ILE:HD12	1:B:181:ILE:N	2.03	0.73
1:B:141:LEU:HD22	1:B:182:PHE:CE1	2.23	0.73
1:D:342:ALA:HB1	1:D:344:LEU:HD23	1.70	0.73
1:B:48:LEU:CD2	1:B:48:LEU:H	2.01	0.73
1:C:141:LEU:HD13	1:C:182:PHE:HD1	1.52	0.73
1:D:181:ILE:HD12	1:D:181:ILE:N	2.02	0.73
1:E:177:GLU:HG2	1:E:183:ASP:OD1	1.88	0.73
1:E:302:GLN:HB3	1:E:412:ILE:HD11	1.68	0.73
1:D:141:LEU:HD22	1:D:182:PHE:HE1	1.54	0.73
1:E:28:PRO:HD2	1:E:266:GLN:NE2	2.04	0.73
1:E:81:ARG:HB3	1:E:208:HIS:HE2	1.52	0.73
1:A:117:LEU:CB	1:A:118:PRO:HD2	2.19	0.73
1:B:66:ILE:HG13	1:B:70:ASN:HD21	1.53	0.73
1:E:69:VAL:HG23	1:E:138:LEU:HD13	1.70	0.73
1:E:237:ILE:HD13	1:E:237:ILE:O	1.88	0.72
1:A:81:ARG:HB3	1:A:208:HIS:HE2	1.53	0.72
1:A:143:ARG:HD2	1:A:216:GLY:HA2	1.71	0.72
1:E:160:LEU:CA	1:E:163:GLN:HB2	2.19	0.72
1:E:342:ALA:HB1	1:E:344:LEU:HD23	1.71	0.72
1:B:224:ASP:CG	2:R:21:U:H4'	2.10	0.72
1:D:48:LEU:H	1:D:48:LEU:CD2	2.02	0.72
1:E:141:LEU:HD13	1:E:182:PHE:HD1	1.52	0.72
1:A:354:LYS:HB2	1:E:376:VAL:HG13	1.71	0.72
1:D:117:LEU:CB	1:D:118:PRO:HD2	2.20	0.72
1:B:181:ILE:H	1:B:181:ILE:HD12	1.53	0.72
1:C:167:ILE:HD13	1:C:168:ASN:N	2.03	0.72
1:A:143:ARG:HH12	2:R:36:U:H5'	1.53	0.72
1:B:79:ASP:O	1:B:79:ASP:OD2	2.08	0.72
1:E:160:LEU:HA	1:E:163:GLN:HB2	1.72	0.72
1:B:308:LEU:O	1:B:309:ARG:HB2	1.87	0.72
1:C:107:LEU:HD23	1:C:274:TYR:OH	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:163:GLN:CA	1:E:163:GLN:OE1	2.30	0.72
1:A:106:ASP:O	1:A:107:LEU:HG	1.90	0.72
1:B:163:GLN:OE1	1:B:163:GLN:CA	2.30	0.72
1:B:365:THR:HG23	1:B:366:THR:N	2.05	0.72
1:C:162:ASN:O	1:C:164:CYS:N	2.22	0.71
1:D:308:LEU:O	1:D:309:ARG:HB2	1.90	0.71
1:B:162:ASN:O	1:B:164:CYS:N	2.22	0.71
1:E:29:ALA:O	1:E:31:TYR:N	2.22	0.71
1:E:137:TYR:HD1	1:E:163:GLN:NE2	1.87	0.71
1:B:28:PRO:HD2	1:B:266:GLN:NE2	2.05	0.71
1:C:141:LEU:HD22	1:C:182:PHE:CE1	2.26	0.71
1:A:143:ARG:HE	1:A:155:LYS:NZ	1.89	0.71
1:C:143:ARG:HD2	1:C:216:GLY:HA2	1.71	0.71
1:B:376:VAL:HG13	1:C:354:LYS:HB2	1.73	0.71
1:D:160:LEU:O	1:D:163:GLN:HB2	1.91	0.71
1:B:117:LEU:CB	1:B:118:PRO:HD2	2.20	0.71
1:B:302:GLN:HB3	1:B:412:ILE:HD11	1.71	0.71
1:D:48:LEU:HD22	1:D:48:LEU:N	2.06	0.71
1:E:97:LYS:O	1:E:100:ASP:HB2	1.91	0.71
1:E:117:LEU:CB	1:E:118:PRO:CD	2.69	0.71
1:A:141:LEU:HD22	1:A:182:PHE:CE1	2.25	0.71
1:B:141:LEU:HD22	1:B:182:PHE:HE1	1.56	0.71
1:A:163:GLN:O	1:A:165:LYS:N	2.23	0.70
1:A:376:VAL:HG13	1:B:354:LYS:HB2	1.72	0.70
1:B:18:LEU:CD1	1:C:232:GLY:HA2	2.21	0.70
1:B:143:ARG:HD2	1:B:216:GLY:HA2	1.72	0.70
1:C:160:LEU:HA	1:C:163:GLN:CG	2.22	0.70
1:E:141:LEU:HD22	1:E:182:PHE:CE1	2.25	0.70
1:C:117:LEU:CB	1:C:118:PRO:CD	2.69	0.70
1:C:165:LYS:HB2	1:C:166:MET:SD	2.31	0.70
1:E:308:LEU:O	1:E:309:ARG:HB2	1.90	0.70
1:E:328:THR:HG21	1:E:415:TYR:OH	1.91	0.70
1:D:69:VAL:HG23	1:D:138:LEU:HD13	1.74	0.70
1:E:143:ARG:HD2	1:E:216:GLY:HA2	1.72	0.70
1:A:141:LEU:HD13	1:A:182:PHE:HD1	1.54	0.70
1:E:107:LEU:HD23	1:E:274:TYR:OH	1.92	0.70
1:A:160:LEU:O	1:A:163:GLN:HB2	1.92	0.70
1:C:28:PRO:HD2	1:C:266:GLN:HE21	1.56	0.70
1:D:107:LEU:HD23	1:D:274:TYR:OH	1.90	0.70
1:E:152:TYR:OH	1:E:176:PRO:HB3	1.91	0.70
2:R:36:U:H2'	2:R:37:U:O4'	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:LEU:N	1:B:48:LEU:HD22	2.07	0.69
1:C:28:PRO:HD2	1:C:266:GLN:NE2	2.07	0.69
1:B:117:LEU:CB	1:B:118:PRO:CD	2.69	0.69
1:B:179:ARG:O	1:C:161:THR:HG22	1.92	0.69
1:A:214:ARG:HA	1:A:217:THR:CG2	2.22	0.69
1:A:69:VAL:HG23	1:A:138:LEU:HD13	1.74	0.69
1:E:48:LEU:HD22	1:E:48:LEU:N	2.05	0.69
1:E:153:ARG:NH2	1:E:176:PRO:HA	2.07	0.69
1:E:48:LEU:CD2	1:E:48:LEU:H	2.04	0.69
1:A:141:LEU:HD22	1:A:182:PHE:HE1	1.58	0.69
1:A:328:THR:HG21	1:A:415:TYR:OH	1.92	0.69
1:E:106:ASP:O	1:E:107:LEU:HG	1.91	0.69
1:C:163:GLN:CA	1:C:163:GLN:OE1	2.30	0.69
1:D:28:PRO:HD2	1:D:266:GLN:NE2	2.07	0.69
1:A:54:TYR:CE1	1:A:118:PRO:HB2	2.27	0.69
1:D:257:GLU:HG2	1:D:294:ASN:HA	1.72	0.69
1:B:214:ARG:HA	1:B:217:THR:CG2	2.22	0.69
1:B:356:THR:N	1:B:357:PRO:HD2	2.07	0.69
1:D:141:LEU:HD13	1:D:182:PHE:CD1	2.28	0.68
1:D:51:LEU:O	1:D:55:VAL:HG22	1.93	0.68
1:B:167:ILE:CD1	1:B:168:ASN:H	1.94	0.68
1:A:161:THR:HB	1:E:179:ARG:HB2	1.75	0.68
1:B:69:VAL:HG23	1:B:138:LEU:HD13	1.74	0.68
1:C:328:THR:HG21	1:C:415:TYR:OH	1.94	0.68
1:C:141:LEU:HD22	1:C:182:PHE:HE1	1.58	0.68
1:D:29:ALA:O	1:D:31:TYR:N	2.22	0.68
1:E:141:LEU:HD22	1:E:182:PHE:HE1	1.57	0.68
1:A:28:PRO:HD2	1:A:266:GLN:NE2	2.08	0.68
1:A:290:SER:HB2	2:R:30:U:H5'	1.73	0.68
1:A:29:ALA:O	1:A:31:TYR:N	2.26	0.68
1:B:29:ALA:O	1:B:31:TYR:N	2.23	0.68
1:D:133:TRP:HB3	1:D:167:ILE:HD12	1.76	0.68
1:E:358:ASP:CG	1:E:359:ASP:H	1.97	0.68
1:B:177:GLU:CD	1:B:178:GLY:H	1.97	0.67
1:E:214:ARG:HA	1:E:217:THR:CG2	2.24	0.67
1:A:87:ASP:CG	1:A:97:LYS:HG3	2.14	0.67
1:E:365:THR:HG23	1:E:366:THR:H	1.57	0.67
1:B:58:GLY:HA3	1:B:64:VAL:HB	1.76	0.67
1:C:29:ALA:O	1:C:31:TYR:N	2.24	0.67
1:C:54:TYR:CE1	1:C:118:PRO:HB2	2.29	0.67
1:C:172:GLU:HB3	1:C:173:PRO:HD3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:69:VAL:HG23	1:C:138:LEU:HD13	1.76	0.67
1:C:214:ARG:HA	1:C:217:THR:CG2	2.24	0.67
1:C:58:GLY:HA3	1:C:64:VAL:HB	1.77	0.67
1:D:165:LYS:HA	1:D:166:MET:SD	2.33	0.67
1:B:141:LEU:HD13	1:B:182:PHE:CD1	2.30	0.67
1:C:79:ASP:OD2	1:C:79:ASP:O	2.13	0.67
1:E:54:TYR:CE1	1:E:118:PRO:HB2	2.29	0.67
1:B:237:ILE:O	1:B:237:ILE:HD13	1.95	0.67
1:B:160:LEU:HA	1:B:163:GLN:CG	2.25	0.67
1:B:54:TYR:CE1	1:B:118:PRO:HB2	2.29	0.66
2:R:39:U:H5"	2:R:39:U:H6	1.61	0.66
1:B:70:ASN:H	1:B:70:ASN:HD22	1.43	0.66
1:C:97:LYS:O	1:C:100:ASP:HB2	1.96	0.66
1:D:356:THR:N	1:D:357:PRO:HD2	2.10	0.66
1:E:58:GLY:HA3	1:E:64:VAL:HB	1.77	0.66
1:B:130:ASP:CG	1:B:131:ASP:N	2.49	0.66
1:B:179:ARG:HB3	1:C:161:THR:HB	1.77	0.66
1:B:165:LYS:HB2	1:B:166:MET:SD	2.31	0.66
1:B:129:ALA:HA	1:B:132:LYS:CE	2.26	0.66
1:B:22:GLU:OE2	1:B:22:GLU:HA	1.94	0.66
1:C:141:LEU:HD13	1:C:182:PHE:CD1	2.30	0.66
1:C:257:GLU:HG2	1:C:294:ASN:HA	1.77	0.66
1:A:356:THR:N	1:A:357:PRO:HD2	2.11	0.66
1:B:130:ASP:CG	1:B:131:ASP:H	1.97	0.66
1:C:70:ASN:H	1:C:70:ASN:HD22	1.44	0.66
1:E:257:GLU:HG2	1:E:294:ASN:HA	1.78	0.66
1:D:143:ARG:HH21	2:R:8:U:H5"	1.59	0.66
1:D:117:LEU:CB	1:D:118:PRO:CD	2.70	0.65
1:E:162:ASN:O	1:E:164:CYS:N	2.28	0.65
1:A:98:ALA:O	1:A:100:ASP:N	2.30	0.65
1:B:106:ASP:C	1:B:107:LEU:HG	2.14	0.65
1:B:380:GLY:HA2	1:C:354:LYS:HZ3	1.59	0.65
1:C:302:GLN:HB3	1:C:412:ILE:HD11	1.77	0.65
1:A:117:LEU:CB	1:A:118:PRO:CD	2.69	0.65
1:D:54:TYR:CE1	1:D:118:PRO:HB2	2.31	0.65
1:D:58:GLY:HA3	1:D:64:VAL:HB	1.79	0.65
1:D:133:TRP:CG	1:D:167:ILE:HD13	2.30	0.65
1:D:177:GLU:CD	1:D:178:GLY:H	2.00	0.65
1:D:143:ARG:HD2	1:D:216:GLY:HA2	1.77	0.65
1:D:253:GLU:H	1:D:253:GLU:CD	1.99	0.65
1:D:70:ASN:HD22	1:D:70:ASN:H	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:130:ASP:CG	1:E:131:ASP:H	1.99	0.65
1:A:58:GLY:HA3	1:A:64:VAL:HB	1.78	0.65
1:E:177:GLU:HA	1:E:181:ILE:HD13	1.79	0.65
1:A:107:LEU:HD23	1:A:274:TYR:OH	1.97	0.65
1:D:214:ARG:HA	1:D:217:THR:CG2	2.26	0.65
1:A:177:GLU:CD	1:A:178:GLY:H	2.00	0.65
1:D:74:TYR:O	1:D:78:LYS:HG3	1.96	0.65
1:E:104:ILE:O	1:E:107:LEU:HD12	1.97	0.65
1:A:84:LEU:HD12	1:A:97:LYS:N	2.12	0.65
1:B:152:TYR:CE1	1:B:177:GLU:HB2	2.32	0.65
1:C:163:GLN:O	1:C:165:LYS:N	2.30	0.65
1:C:97:LYS:O	1:C:98:ALA:C	2.35	0.65
1:A:141:LEU:HD13	1:A:182:PHE:CD1	2.32	0.64
1:B:163:GLN:O	1:B:165:LYS:N	2.30	0.64
1:E:163:GLN:O	1:E:165:LYS:N	2.30	0.64
1:B:136:LEU:O	1:B:136:LEU:HD23	1.97	0.64
1:E:141:LEU:HD13	1:E:182:PHE:CD1	2.31	0.64
1:A:151:GLU:O	1:A:154:LYS:HB2	1.97	0.64
1:E:70:ASN:H	1:E:70:ASN:HD22	1.44	0.64
1:B:257:GLU:HG2	1:B:294:ASN:HA	1.80	0.64
1:C:160:LEU:CA	1:C:163:GLN:HB2	2.27	0.64
1:C:177:GLU:CD	1:C:178:GLY:H	2.00	0.64
1:D:131:ASP:O	1:D:135:PRO:HD2	1.98	0.64
1:E:130:ASP:CG	1:E:131:ASP:N	2.51	0.64
1:A:129:ALA:HA	1:A:132:LYS:CE	2.28	0.64
1:B:151:GLU:O	1:B:154:LYS:HB2	1.98	0.64
1:B:51:LEU:O	1:B:55:VAL:HG22	1.98	0.64
1:D:167:ILE:CG2	1:D:167:ILE:O	2.45	0.64
1:A:23:ASP:HB2	1:A:286:LYS:HD3	1.80	0.64
1:C:356:THR:N	1:C:357:PRO:HD2	2.12	0.63
1:D:129:ALA:HA	1:D:132:LYS:CE	2.28	0.63
1:D:133:TRP:HB3	1:D:167:ILE:HD13	1.79	0.63
1:D:364:LEU:CB	1:D:368:ALA:HB2	2.28	0.63
1:A:74:TYR:O	1:A:78:LYS:HG3	1.98	0.63
1:C:106:ASP:O	1:C:107:LEU:HG	1.98	0.63
1:D:30:ASP:HA	1:D:33:ARG:HE	1.62	0.63
1:E:151:GLU:O	1:E:154:LYS:HB2	1.98	0.63
1:A:302:GLN:HB3	1:A:412:ILE:HD11	1.79	0.63
1:E:354:LYS:CE	1:E:356:THR:HA	2.28	0.63
1:D:136:LEU:O	1:D:136:LEU:HD23	1.99	0.63
1:E:74:TYR:O	1:E:78:LYS:HG3	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:GLU:O	1:C:154:LYS:HB2	1.98	0.63
1:D:237:ILE:O	1:D:237:ILE:HD13	1.99	0.63
1:A:131:ASP:O	1:A:135:PRO:HD2	1.98	0.63
1:E:23:ASP:HB2	1:E:286:LYS:HD3	1.81	0.63
1:A:181:ILE:H	1:A:181:ILE:CD1	2.12	0.63
1:A:130:ASP:CG	1:A:131:ASP:H	2.01	0.62
1:A:22:GLU:HA	1:A:22:GLU:OE2	1.98	0.62
1:D:22:GLU:HA	1:D:22:GLU:OE2	1.98	0.62
1:A:143:ARG:HG2	1:A:155:LYS:HE3	1.79	0.62
1:D:163:GLN:OE1	1:D:163:GLN:HA	1.99	0.62
1:C:137:TYR:HD1	1:C:163:GLN:NE2	1.91	0.62
1:C:28:PRO:O	1:C:31:TYR:HB3	1.99	0.62
1:D:28:PRO:O	1:D:31:TYR:HB3	1.98	0.62
1:E:28:PRO:O	1:E:31:TYR:HB3	1.98	0.62
1:D:151:GLU:O	1:D:154:LYS:HB2	1.99	0.62
1:D:143:ARG:NH2	2:R:9:U:OP2	2.31	0.62
1:A:136:LEU:HD23	1:A:136:LEU:O	1.99	0.62
1:A:163:GLN:C	1:A:165:LYS:H	2.02	0.62
1:A:176:PRO:O	1:A:177:GLU:HB2	2.00	0.62
1:A:257:GLU:HG2	1:A:294:ASN:HA	1.82	0.62
1:E:160:LEU:HA	1:E:163:GLN:CB	2.29	0.62
1:E:356:THR:N	1:E:357:PRO:HD2	2.14	0.62
2:R:18:U:H4'	2:R:18:U:OP1	1.98	0.62
1:B:179:ARG:O	1:C:161:THR:CG2	2.47	0.62
1:E:224:ASP:CG	2:R:39:U:H4'	2.20	0.62
1:B:59:LEU:HB3	1:B:172:GLU:HG2	1.80	0.62
1:D:130:ASP:CG	1:D:131:ASP:N	2.53	0.62
1:A:70:ASN:H	1:A:70:ASN:HD22	1.45	0.62
1:C:130:ASP:CG	1:C:131:ASP:H	2.01	0.62
1:C:181:ILE:CD1	1:C:181:ILE:H	2.12	0.62
1:E:106:ASP:C	1:E:107:LEU:HG	2.20	0.62
2:R:19:U:O2'	2:R:20:U:H6	1.82	0.62
1:C:81:ARG:CB	1:C:208:HIS:HE2	2.13	0.61
2:R:6:U:H6	2:R:6:U:O5'	1.83	0.61
1:A:51:LEU:O	1:A:55:VAL:HG22	1.99	0.61
1:B:177:GLU:HA	1:B:181:ILE:HD13	1.81	0.61
1:E:79:ASP:O	1:E:79:ASP:OD2	2.18	0.61
1:E:81:ARG:CB	1:E:208:HIS:HE2	2.13	0.61
1:A:172:GLU:HB3	1:A:173:PRO:HD3	1.82	0.61
1:B:160:LEU:CA	1:B:163:GLN:HB2	2.29	0.61
1:B:81:ARG:CB	1:B:208:HIS:HE2	2.12	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:169:GLU:C	1:D:170:GLN:HG2	2.21	0.61
1:D:172:GLU:HB3	1:D:173:PRO:HD3	1.82	0.61
1:D:182:PHE:CD2	1:D:183:ASP:N	2.66	0.61
1:D:401:VAL:HG21	1:D:420:PHE:HB2	1.82	0.61
1:E:104:ILE:HD13	1:E:198:VAL:HG22	1.82	0.61
1:B:30:ASP:HA	1:B:33:ARG:HE	1.64	0.61
1:E:353:ASN:N	1:E:353:ASN:OD1	2.33	0.61
1:A:106:ASP:C	1:A:107:LEU:HG	2.19	0.61
1:D:164:CYS:O	1:D:166:MET:N	2.33	0.61
1:E:129:ALA:HA	1:E:132:LYS:CE	2.30	0.61
1:D:104:ILE:O	1:D:107:LEU:HD12	2.00	0.61
1:D:38:ILE:O	1:D:38:ILE:HG13	1.99	0.61
1:E:136:LEU:O	1:E:136:LEU:HD23	2.00	0.61
1:B:28:PRO:O	1:B:31:TYR:HB3	2.01	0.61
1:C:129:ALA:HA	1:C:132:LYS:CE	2.30	0.61
1:C:23:ASP:HB2	1:C:286:LYS:HD3	1.82	0.61
1:D:130:ASP:CG	1:D:131:ASP:H	2.03	0.61
1:C:176:PRO:O	1:C:177:GLU:HB2	2.00	0.61
1:B:160:LEU:HA	1:B:163:GLN:HB2	1.81	0.61
1:C:302:GLN:HG2	1:C:316:ALA:CB	2.31	0.61
1:D:354:LYS:CE	1:D:356:THR:HA	2.30	0.61
1:A:219:VAL:HG12	2:R:35:U:O4	2.01	0.60
1:A:237:ILE:HD13	1:A:237:ILE:O	2.01	0.60
1:C:160:LEU:HA	1:C:163:GLN:HB2	1.81	0.60
1:C:182:PHE:CD2	1:C:183:ASP:N	2.65	0.60
1:E:178:GLY:O	1:E:179:ARG:HB2	2.01	0.60
1:B:253:GLU:H	1:B:253:GLU:CD	2.03	0.60
1:E:182:PHE:CD2	1:E:183:ASP:N	2.66	0.60
1:A:130:ASP:CG	1:A:131:ASP:N	2.54	0.60
1:B:38:ILE:O	1:B:38:ILE:HG13	2.01	0.60
1:C:401:VAL:HG21	1:C:420:PHE:HB2	1.83	0.60
1:C:51:LEU:O	1:C:55:VAL:HG22	2.01	0.60
1:A:354:LYS:CE	1:A:356:THR:HA	2.31	0.60
1:A:79:ASP:OD2	1:A:79:ASP:O	2.19	0.60
1:D:176:PRO:O	1:D:177:GLU:HB2	2.00	0.60
1:B:365:THR:HG22	1:B:368:ALA:CB	2.32	0.60
1:C:22:GLU:OE2	1:C:22:GLU:HA	2.01	0.60
1:E:131:ASP:O	1:E:135:PRO:HD2	2.02	0.60
1:E:253:GLU:CD	1:E:253:GLU:H	2.02	0.60
1:E:283:LEU:N	1:E:283:LEU:HD23	2.16	0.60
1:A:28:PRO:O	1:A:31:TYR:HB3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:22:GLU:HA	1:E:22:GLU:OE2	2.01	0.60
1:A:232:GLY:HA2	1:E:18:LEU:HD12	1.84	0.60
1:A:283:LEU:N	1:A:283:LEU:HD23	2.17	0.60
1:C:136:LEU:O	1:C:136:LEU:HD23	2.01	0.60
1:E:164:CYS:O	1:E:165:LYS:C	2.40	0.60
1:E:172:GLU:HB3	1:E:173:PRO:HD3	1.83	0.60
1:D:59:LEU:HB3	1:D:172:GLU:HG2	1.82	0.60
1:E:59:LEU:HB3	1:E:172:GLU:HG2	1.82	0.60
1:A:81:ARG:CB	1:A:208:HIS:HE2	2.15	0.59
1:B:72:TYR:CZ	1:B:134:LEU:HD12	2.37	0.59
1:A:163:GLN:OE1	1:A:163:GLN:HA	2.03	0.59
1:B:172:GLU:HB3	1:B:173:PRO:HD3	1.85	0.59
1:E:30:ASP:HA	1:E:33:ARG:HE	1.67	0.59
1:E:401:VAL:HG21	1:E:420:PHE:HB2	1.83	0.59
1:C:59:LEU:HB3	1:C:172:GLU:HG2	1.83	0.59
1:C:72:TYR:CZ	1:C:134:LEU:HD12	2.37	0.59
1:A:312:ARG:HG2	2:R:32:U:C2	2.37	0.59
1:B:74:TYR:O	1:B:78:LYS:HG3	2.01	0.59
1:C:237:ILE:O	1:C:237:ILE:HD13	2.02	0.59
2:R:9:U:O3'	2:R:10:U:H6	1.85	0.59
1:B:104:ILE:O	1:B:107:LEU:HD12	2.03	0.59
1:C:354:LYS:CE	1:C:356:THR:HA	2.29	0.59
1:E:151:GLU:HA	1:E:154:LYS:NZ	2.17	0.59
1:A:59:LEU:HB3	1:A:172:GLU:HG2	1.83	0.59
1:E:181:ILE:H	1:E:181:ILE:CD1	2.14	0.59
1:A:116:VAL:C	1:A:117:LEU:HD12	2.23	0.59
1:C:130:ASP:CG	1:C:131:ASP:N	2.53	0.59
1:C:74:TYR:O	1:C:78:LYS:HG3	2.02	0.59
1:D:23:ASP:HB2	1:D:286:LYS:HD3	1.83	0.59
1:A:182:PHE:CD2	1:A:183:ASP:N	2.65	0.59
1:A:253:GLU:CD	1:A:253:GLU:H	2.03	0.59
1:B:117:LEU:HB3	1:B:118:PRO:HD3	1.83	0.59
1:B:178:GLY:O	1:B:179:ARG:CB	2.50	0.59
1:C:131:ASP:O	1:C:132:LYS:C	2.41	0.59
1:D:106:ASP:C	1:D:107:LEU:HG	2.21	0.59
1:D:81:ARG:CB	1:D:208:HIS:HE2	2.15	0.59
1:B:169:GLU:C	1:B:170:GLN:HG2	2.23	0.59
1:B:365:THR:HG23	1:B:366:THR:H	1.68	0.59
1:C:131:ASP:O	1:C:135:PRO:HD2	2.02	0.59
1:C:180:ASP:CG	1:D:164:CYS:SG	2.81	0.59
1:E:72:TYR:CZ	1:E:134:LEU:HD12	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:ILE:HD13	1:B:198:VAL:HG22	1.85	0.58
1:C:181:ILE:N	1:C:183:ASP:OD2	2.35	0.58
1:C:43:ASN:O	1:C:44:THR:C	2.42	0.58
1:D:79:ASP:OD2	1:D:79:ASP:O	2.21	0.58
1:A:380:GLY:HA2	1:B:354:LYS:NZ	2.18	0.58
1:D:181:ILE:CD1	1:D:181:ILE:H	2.14	0.58
1:A:131:ASP:O	1:A:132:LYS:C	2.42	0.58
1:C:105:PHE:C	1:C:107:LEU:H	2.07	0.58
1:C:246:THR:HG22	1:D:348:PHE:CG	2.38	0.58
2:R:39:U:H2'	2:R:40:U:O4'	2.03	0.58
1:A:152:TYR:HE1	1:A:176:PRO:O	1.87	0.58
1:B:181:ILE:H	1:B:181:ILE:CD1	2.16	0.58
1:B:401:VAL:HG21	1:B:420:PHE:HB2	1.85	0.58
1:A:214:ARG:HH21	1:A:218:ILE:HG13	1.68	0.58
1:A:302:GLN:HG2	1:A:316:ALA:CB	2.33	0.58
1:B:18:LEU:HD12	1:C:232:GLY:CA	2.31	0.58
1:E:131:ASP:O	1:E:132:LYS:C	2.41	0.58
1:B:131:ASP:O	1:B:135:PRO:HD2	2.03	0.58
1:D:152:TYR:CE2	1:D:153:ARG:HG2	2.39	0.58
1:B:131:ASP:O	1:B:132:LYS:C	2.42	0.58
1:E:38:ILE:O	1:E:108:VAL:HB	2.04	0.58
1:C:181:ILE:CD1	1:C:181:ILE:N	2.66	0.57
1:A:169:GLU:C	1:A:170:GLN:HG2	2.25	0.57
1:A:152:TYR:CE2	1:A:153:ARG:HG2	2.40	0.57
1:B:365:THR:HG22	1:B:368:ALA:HB3	1.85	0.57
1:A:224:ASP:CG	2:R:30:U:H4'	2.24	0.57
1:B:355:TYR:C	1:B:357:PRO:HD2	2.25	0.57
1:C:43:ASN:O	1:C:44:THR:O	2.23	0.57
1:D:286:LYS:NZ	2:R:2:U:OP1	2.35	0.57
1:D:286:LYS:NZ	2:R:2:U:P	2.77	0.57
1:A:104:ILE:O	1:A:107:LEU:HD12	2.04	0.57
1:D:81:ARG:O	1:D:102:ILE:O	2.23	0.57
1:A:104:ILE:HD13	1:A:198:VAL:HG22	1.87	0.57
1:A:178:GLY:O	1:A:179:ARG:HB2	2.05	0.57
1:C:104:ILE:HD13	1:C:198:VAL:HG22	1.87	0.57
1:A:179:ARG:O	1:A:180:ASP:HB2	2.04	0.57
1:D:104:ILE:HD13	1:D:198:VAL:HG22	1.87	0.57
1:E:397:ALA:O	1:E:401:VAL:HG22	2.05	0.57
1:A:97:LYS:CG	1:A:98:ALA:N	2.53	0.57
1:A:30:ASP:HA	1:A:33:ARG:HE	1.70	0.56
1:A:38:ILE:O	1:A:108:VAL:HB	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:ILE:O	1:C:108:VAL:HB	2.05	0.56
1:D:129:ALA:HA	1:D:132:LYS:NZ	2.20	0.56
1:E:169:GLU:C	1:E:170:GLN:HG2	2.25	0.56
1:A:151:GLU:HA	1:A:154:LYS:NZ	2.19	0.56
1:A:72:TYR:CZ	1:A:134:LEU:HD12	2.40	0.56
1:C:214:ARG:CA	1:C:217:THR:HG22	2.33	0.56
1:D:218:ILE:HD12	2:R:10:U:OP2	2.05	0.56
1:D:214:ARG:HH21	1:D:218:ILE:HG13	1.70	0.56
1:A:66:ILE:HG13	1:A:70:ASN:ND2	2.19	0.56
1:B:152:TYR:CE2	1:B:153:ARG:HG2	2.40	0.56
1:E:152:TYR:CE1	1:E:153:ARG:NH1	2.73	0.56
1:C:149:MET:HG3	2:R:15:U:O4'	2.05	0.56
1:A:66:ILE:HD12	1:A:69:VAL:CG1	2.35	0.56
1:B:43:ASN:O	1:B:44:THR:C	2.44	0.56
1:B:151:GLU:HA	1:B:154:LYS:NZ	2.20	0.56
1:C:152:TYR:HE1	1:C:176:PRO:O	1.87	0.56
1:C:283:LEU:N	1:C:283:LEU:HD23	2.20	0.56
1:C:380:GLY:HA2	1:D:354:LYS:NZ	2.21	0.56
1:D:38:ILE:O	1:D:108:VAL:HB	2.05	0.56
1:A:317:ARG:O	1:A:319:PRO:HD3	2.06	0.56
1:D:151:GLU:HA	1:D:154:LYS:NZ	2.20	0.56
1:A:43:ASN:O	1:A:44:THR:C	2.44	0.56
1:D:214:ARG:CA	1:D:217:THR:HG22	2.35	0.56
1:A:344:LEU:HD13	1:E:250:LEU:HB3	1.87	0.56
1:E:355:TYR:C	1:E:357:PRO:HD2	2.26	0.56
1:E:66:ILE:HG13	1:E:70:ASN:ND2	2.19	0.56
1:B:152:TYR:CE1	1:B:153:ARG:NH1	2.74	0.56
1:C:302:GLN:HB3	1:C:412:ILE:HD13	1.88	0.56
1:C:66:ILE:HD12	1:C:69:VAL:CG1	2.36	0.56
1:D:152:TYR:HE1	1:D:176:PRO:O	1.88	0.56
1:A:43:ASN:O	1:A:44:THR:O	2.24	0.56
1:C:179:ARG:O	1:C:180:ASP:HB2	2.05	0.56
1:A:143:ARG:HE	1:A:155:LYS:HZ2	1.52	0.56
1:D:55:VAL:HG23	1:D:56:TYR:H	1.70	0.56
1:A:345:ALA:O	1:A:347:GLN:HG2	2.06	0.55
1:C:104:ILE:O	1:C:107:LEU:HD12	2.06	0.55
1:C:106:ASP:C	1:C:107:LEU:HG	2.25	0.55
1:D:72:TYR:CZ	1:D:134:LEU:HD12	2.42	0.55
1:E:143:ARG:HH22	2:R:44:U:H3'	1.70	0.55
1:C:151:GLU:HA	1:C:154:LYS:NZ	2.21	0.55
1:D:116:VAL:C	1:D:117:LEU:HD12	2.27	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:66:ILE:HD12	1:E:69:VAL:CG1	2.35	0.55
1:A:364:LEU:CB	1:A:368:ALA:HB2	2.24	0.55
1:C:169:GLU:C	1:C:170:GLN:HG2	2.26	0.55
1:C:15:VAL:O	1:C:17:LYS:HG2	2.06	0.55
1:C:66:ILE:HG13	1:C:70:ASN:ND2	2.19	0.55
1:C:180:ASP:HB3	1:C:181:ILE:HD12	1.89	0.55
1:C:324:TYR:O	1:C:328:THR:CG2	2.55	0.55
1:C:355:TYR:C	1:C:357:PRO:HD2	2.27	0.55
1:D:178:GLY:O	1:D:179:ARG:HB2	2.07	0.55
1:E:105:PHE:C	1:E:107:LEU:H	2.09	0.55
1:E:43:ASN:O	1:E:44:THR:C	2.45	0.55
1:A:312:ARG:HG2	2:R:32:U:O2	2.06	0.55
1:B:23:ASP:HB2	1:B:286:LYS:HD3	1.87	0.55
1:C:116:VAL:C	1:C:117:LEU:HD12	2.27	0.55
1:C:30:ASP:HA	1:C:33:ARG:HE	1.70	0.55
1:C:353:ASN:N	1:C:353:ASN:OD1	2.38	0.55
1:C:253:GLU:H	1:C:253:GLU:CD	2.08	0.55
1:D:131:ASP:O	1:D:132:LYS:C	2.45	0.55
1:D:353:ASN:OD1	1:D:353:ASN:N	2.38	0.55
1:A:214:ARG:CA	1:A:217:THR:HG22	2.33	0.55
1:B:379:LEU:CD1	1:C:346:GLN:HB2	2.37	0.55
1:B:38:ILE:O	1:B:108:VAL:HB	2.07	0.55
1:C:151:GLU:OE1	2:R:17:U:OP1	2.24	0.55
1:D:182:PHE:HD2	1:D:183:ASP:H	1.54	0.55
1:E:51:LEU:O	1:E:55:VAL:HG22	2.06	0.55
1:B:214:ARG:CA	1:B:217:THR:HG22	2.34	0.55
1:D:169:GLU:O	1:D:170:GLN:HG2	2.07	0.55
1:C:162:ASN:O	1:C:163:GLN:C	2.44	0.55
1:D:364:LEU:O	1:D:368:ALA:HB3	2.07	0.55
1:E:81:ARG:O	1:E:102:ILE:O	2.24	0.55
1:E:214:ARG:HH21	1:E:218:ILE:HG13	1.71	0.55
1:A:15:VAL:O	1:A:17:LYS:HG2	2.07	0.54
1:A:401:VAL:HG21	1:A:420:PHE:HB2	1.88	0.54
1:B:283:LEU:HD23	1:B:283:LEU:N	2.20	0.54
1:B:354:LYS:CE	1:B:356:THR:HA	2.32	0.54
1:A:355:TYR:C	1:A:357:PRO:HD2	2.28	0.54
1:D:179:ARG:HA	1:D:183:ASP:CG	2.27	0.54
1:E:38:ILE:O	1:E:38:ILE:HG13	2.05	0.54
1:B:129:ALA:HA	1:B:132:LYS:NZ	2.21	0.54
1:C:214:ARG:HH21	1:C:218:ILE:HG13	1.71	0.54
1:D:117:LEU:HB3	1:D:118:PRO:HD3	1.86	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:214:ARG:O	1:D:217:THR:HG22	2.06	0.54
1:E:41:TYR:HB2	1:E:190:ASN:HD21	1.71	0.54
2:R:31:U:H6	2:R:31:U:H3'	1.72	0.54
1:A:353:ASN:N	1:A:353:ASN:OD1	2.39	0.54
1:A:45:THR:H	1:A:46:LYS:NZ	2.06	0.54
1:D:155:LYS:O	1:D:159:GLY:N	2.38	0.54
1:D:374:ASP:O	1:D:378:TRP:HD1	1.90	0.54
1:A:128:SER:HA	1:A:130:ASP:HB2	1.89	0.54
1:A:302:GLN:HB3	1:A:412:ILE:HD13	1.89	0.54
1:B:43:ASN:O	1:B:44:THR:O	2.26	0.54
1:C:152:TYR:CE2	1:C:153:ARG:HG2	2.42	0.54
1:B:162:ASN:O	1:B:163:GLN:C	2.46	0.54
1:C:160:LEU:HA	1:C:163:GLN:CB	2.38	0.54
1:C:221:ARG:O	1:C:222:PHE:HB2	2.08	0.54
1:D:165:LYS:HB3	1:D:166:MET:SD	2.47	0.54
1:E:227:ALA:HA	1:E:230:THR:HG23	1.90	0.54
2:R:28:U:H2'	2:R:29:U:O4'	2.08	0.54
1:A:27:TYR:HB3	1:A:266:GLN:NE2	2.22	0.54
1:B:137:TYR:HD1	1:B:163:GLN:NE2	1.95	0.54
1:C:180:ASP:N	1:C:183:ASP:CG	2.55	0.54
1:C:397:ALA:O	1:C:401:VAL:HG22	2.07	0.54
1:D:181:ILE:CD1	1:D:181:ILE:N	2.71	0.54
1:E:152:TYR:CE2	1:E:153:ARG:HG2	2.43	0.54
2:R:39:U:C6	2:R:39:U:H5''	2.41	0.54
1:A:41:TYR:HB2	1:A:190:ASN:HD21	1.73	0.54
1:B:136:LEU:HD23	1:B:136:LEU:C	2.28	0.54
1:C:38:ILE:O	1:C:38:ILE:HG13	2.06	0.54
1:B:214:ARG:HH21	1:B:218:ILE:HG13	1.73	0.54
1:C:155:LYS:O	1:C:159:GLY:N	2.39	0.54
1:C:214:ARG:O	1:C:217:THR:HG22	2.07	0.54
1:D:355:TYR:C	1:D:357:PRO:HD2	2.28	0.54
1:E:162:ASN:O	1:E:163:GLN:C	2.45	0.54
1:A:38:ILE:O	1:A:38:ILE:HG13	2.07	0.53
1:C:143:ARG:NH2	2:R:17:U:H5''	2.23	0.53
1:C:178:GLY:O	1:C:179:ARG:HB2	2.08	0.53
1:B:128:SER:HA	1:B:130:ASP:HB2	1.91	0.53
1:B:214:ARG:O	1:B:217:THR:HG22	2.08	0.53
1:C:66:ILE:O	1:C:70:ASN:ND2	2.41	0.53
1:D:152:TYR:CE1	1:D:153:ARG:NH1	2.76	0.53
1:D:302:GLN:HG2	1:D:316:ALA:CB	2.37	0.53
1:E:182:PHE:HD2	1:E:183:ASP:H	1.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:GLU:CB	1:C:173:PRO:HD3	2.38	0.53
1:B:221:ARG:O	1:B:222:PHE:HB2	2.06	0.53
1:D:105:PHE:C	1:D:107:LEU:H	2.12	0.53
1:A:165:LYS:C	1:A:166:MET:SD	2.87	0.53
1:B:182:PHE:HD2	1:B:183:ASP:H	1.54	0.53
1:C:379:LEU:CD1	1:D:346:GLN:HB2	2.38	0.53
1:C:143:ARG:HH22	2:R:17:U:H3'	1.74	0.53
1:B:342:ALA:CB	1:B:344:LEU:HD23	2.38	0.53
1:B:353:ASN:OD1	1:B:353:ASN:N	2.41	0.53
1:B:422:LYS:HE3	1:C:399:ARG:HB3	1.91	0.53
1:D:74:TYR:CD1	1:D:78:LYS:HD3	2.44	0.53
1:E:116:VAL:C	1:E:117:LEU:HD12	2.29	0.53
1:E:365:THR:CG2	1:E:366:THR:N	2.61	0.53
1:B:41:TYR:HB2	1:B:190:ASN:HD21	1.74	0.53
1:D:397:ALA:O	1:D:401:VAL:HG22	2.09	0.53
1:E:43:ASN:O	1:E:44:THR:O	2.27	0.53
1:C:291:SER:HB3	2:R:13:U:OP2	2.08	0.53
1:B:55:VAL:HG23	1:B:56:TYR:H	1.73	0.53
1:B:66:ILE:HG13	1:B:70:ASN:ND2	2.22	0.53
1:E:136:LEU:C	1:E:136:LEU:HD23	2.29	0.53
1:A:291:SER:HB3	2:R:31:U:OP2	2.09	0.53
1:A:129:ALA:HA	1:A:132:LYS:NZ	2.24	0.53
1:A:152:TYR:CE1	1:A:153:ARG:NH1	2.76	0.53
1:A:374:ASP:O	1:A:378:TRP:HD1	1.91	0.53
1:B:116:VAL:C	1:B:117:LEU:HD12	2.30	0.53
1:A:248:TRP:O	1:A:250:LEU:HG	2.09	0.53
1:B:155:LYS:O	1:B:159:GLY:N	2.38	0.53
1:C:151:GLU:OE1	1:C:155:LYS:HE2	2.09	0.53
1:D:15:VAL:O	1:D:17:LYS:HG2	2.09	0.53
1:E:15:VAL:O	1:E:17:LYS:HG2	2.08	0.53
2:R:8:U:C3'	2:R:9:U:H5''	2.38	0.53
1:A:155:LYS:O	1:A:159:GLY:N	2.39	0.52
1:B:302:GLN:HG2	1:B:316:ALA:CB	2.38	0.52
1:A:181:ILE:N	1:A:183:ASP:OD2	2.43	0.52
1:B:227:ALA:HA	1:B:230:THR:HG23	1.91	0.52
1:C:152:TYR:CE1	1:C:153:ARG:NH1	2.77	0.52
1:C:342:ALA:CB	1:C:344:LEU:HD23	2.37	0.52
1:A:81:ARG:O	1:A:102:ILE:O	2.26	0.52
1:A:105:PHE:C	1:A:107:LEU:H	2.12	0.52
1:D:257:GLU:CG	1:D:294:ASN:HA	2.40	0.52
1:D:79:ASP:OD2	1:D:81:ARG:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:177:GLU:CD	1:E:178:GLY:H	2.12	0.52
1:C:143:ARG:CD	1:C:216:GLY:HA2	2.37	0.52
1:E:151:GLU:HA	1:E:154:LYS:HZ2	1.73	0.52
1:C:182:PHE:HD2	1:C:183:ASP:H	1.53	0.52
1:D:133:TRP:CB	1:D:167:ILE:HD13	2.39	0.52
1:D:66:ILE:HG13	1:D:70:ASN:ND2	2.21	0.52
1:B:169:GLU:O	1:B:170:GLN:HG2	2.10	0.52
1:B:182:PHE:CD2	1:B:183:ASP:N	2.66	0.52
1:C:81:ARG:O	1:C:102:ILE:O	2.28	0.52
1:D:133:TRP:CG	1:D:167:ILE:HG21	2.44	0.52
1:E:214:ARG:O	1:E:217:THR:HG22	2.09	0.52
1:A:84:LEU:CD1	1:A:97:LYS:N	2.73	0.52
1:B:105:PHE:C	1:B:107:LEU:H	2.13	0.52
1:D:136:LEU:C	1:D:136:LEU:HD23	2.30	0.52
1:D:227:ALA:HA	1:D:230:THR:HG23	1.92	0.52
1:E:365:THR:HG23	1:E:366:THR:O	2.10	0.52
1:A:160:LEU:HA	1:A:163:GLN:HB2	1.92	0.52
1:A:84:LEU:HD12	1:A:97:LYS:O	2.10	0.52
1:B:15:VAL:O	1:B:17:LYS:HG2	2.09	0.52
1:B:160:LEU:HA	1:B:163:GLN:CB	2.40	0.52
1:E:155:LYS:O	1:E:159:GLY:N	2.39	0.52
1:C:179:ARG:HA	1:C:183:ASP:CG	2.29	0.52
1:E:214:ARG:CA	1:E:217:THR:HG22	2.35	0.52
1:E:345:ALA:O	1:E:347:GLN:HG2	2.10	0.52
1:B:81:ARG:O	1:B:102:ILE:O	2.27	0.51
1:B:200:MET:HB2	1:B:277:TYR:CE2	2.46	0.51
1:D:388:LYS:HE2	1:D:389:PRO:HD2	1.92	0.51
1:A:167:ILE:H	1:A:167:ILE:HD12	1.74	0.51
1:B:44:THR:HG22	1:B:46:LYS:NZ	2.25	0.51
1:D:149:MET:HG3	2:R:6:U:C1'	2.41	0.51
1:D:31:TYR:CD1	1:D:31:TYR:C	2.84	0.51
1:E:388:LYS:HE2	1:E:389:PRO:HD2	1.92	0.51
1:A:397:ALA:O	1:A:401:VAL:HG22	2.11	0.51
1:B:66:ILE:HD13	1:B:185:TRP:CD1	2.46	0.51
1:D:179:ARG:O	1:D:180:ASP:HB2	2.10	0.51
1:D:41:TYR:HB2	1:D:190:ASN:HD21	1.75	0.51
1:E:167:ILE:CD1	1:E:168:ASN:N	2.72	0.51
1:A:179:ARG:HA	1:A:183:ASP:CG	2.31	0.51
1:B:374:ASP:O	1:B:378:TRP:HD1	1.94	0.51
1:E:221:ARG:O	1:E:222:PHE:HB2	2.08	0.51
2:R:21:U:O4	2:R:22:U:O4	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:ASP:O	1:B:121:VAL:N	2.44	0.51
1:C:153:ARG:NH2	1:C:176:PRO:HA	2.25	0.51
1:E:302:GLN:HG2	1:E:316:ALA:CB	2.40	0.51
1:A:117:LEU:HB3	1:A:118:PRO:HD3	1.85	0.51
1:A:137:TYR:HB2	1:A:163:GLN:HE22	1.75	0.51
1:A:153:ARG:NH2	1:A:176:PRO:HA	2.25	0.51
1:B:248:TRP:O	1:B:250:LEU:HG	2.11	0.51
1:C:136:LEU:C	1:C:136:LEU:HD23	2.31	0.51
1:E:169:GLU:O	1:E:170:GLN:HG2	2.10	0.51
1:A:169:GLU:O	1:A:170:GLN:HG2	2.11	0.51
1:A:200:MET:HB2	1:A:277:TYR:CE2	2.46	0.51
1:C:180:ASP:N	1:C:183:ASP:OD2	2.31	0.51
1:C:46:LYS:N	1:C:46:LYS:HD2	2.25	0.51
1:A:22:GLU:O	1:A:23:ASP:C	2.49	0.51
1:B:45:THR:C	1:B:46:LYS:HE3	2.31	0.51
1:C:240:MET:HE3	1:C:244:ASP:HB3	1.92	0.51
1:D:356:THR:O	1:D:357:PRO:C	2.49	0.51
1:E:128:SER:HA	1:E:130:ASP:HB2	1.92	0.51
1:E:74:TYR:CD1	1:E:78:LYS:HD3	2.44	0.51
1:A:227:ALA:HA	1:A:230:THR:HG23	1.93	0.51
1:D:128:SER:HA	1:D:130:ASP:HB2	1.92	0.51
1:A:143:ARG:CD	1:A:216:GLY:HA2	2.40	0.50
1:B:31:TYR:C	1:B:31:TYR:CD1	2.82	0.50
1:B:397:ALA:O	1:B:401:VAL:HG22	2.11	0.50
1:D:286:LYS:HZ2	2:R:2:U:P	2.33	0.50
1:E:119:ASP:O	1:E:121:VAL:N	2.44	0.50
1:E:374:ASP:O	1:E:378:TRP:HD1	1.94	0.50
2:R:21:U:H5''	2:R:21:U:H6	1.76	0.50
1:A:136:LEU:HD23	1:A:136:LEU:C	2.31	0.50
1:A:380:GLY:HA2	1:B:354:LYS:HZ3	1.75	0.50
1:C:27:TYR:HB3	1:C:266:GLN:NE2	2.26	0.50
1:E:302:GLN:HB3	1:E:412:ILE:HD13	1.88	0.50
1:D:290:SER:HB2	2:R:3:U:H5'	1.93	0.50
1:C:169:GLU:O	1:C:170:GLN:HG2	2.12	0.50
1:E:143:ARG:CD	1:E:216:GLY:HA2	2.40	0.50
1:A:182:PHE:CD2	1:A:182:PHE:C	2.85	0.50
1:B:66:ILE:HD12	1:B:69:VAL:CG1	2.42	0.50
1:D:240:MET:HE3	1:D:244:ASP:HB3	1.93	0.50
1:C:380:GLY:HA2	1:D:354:LYS:HZ3	1.76	0.50
1:D:143:ARG:NH2	2:R:8:U:C5'	2.75	0.50
1:B:22:GLU:O	1:B:23:ASP:C	2.49	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:LEU:HD12	1:B:232:GLY:HA2	1.93	0.50
1:B:27:TYR:HB3	1:B:266:GLN:NE2	2.26	0.50
1:C:117:LEU:HB3	1:C:118:PRO:HD3	1.84	0.50
1:D:171:PHE:O	1:D:172:GLU:OE2	2.29	0.50
1:D:66:ILE:HD13	1:D:185:TRP:CD1	2.46	0.50
1:E:248:TRP:O	1:E:250:LEU:HG	2.12	0.50
1:D:345:ALA:O	1:D:347:GLN:HG2	2.12	0.50
1:E:129:ALA:HA	1:E:132:LYS:NZ	2.27	0.50
1:E:172:GLU:CB	1:E:173:PRO:HD3	2.42	0.50
1:A:180:ASP:HB3	1:A:181:ILE:HD12	1.94	0.50
1:A:182:PHE:HD2	1:A:183:ASP:H	1.56	0.50
1:B:45:THR:H	1:B:46:LYS:NZ	2.09	0.50
1:E:275:MET:SD	1:E:275:MET:C	2.90	0.50
1:A:273:SER:OG	1:A:274:TYR:N	2.43	0.50
1:D:43:ASN:O	1:D:44:THR:C	2.51	0.50
1:C:41:TYR:HB2	1:C:190:ASN:HD21	1.76	0.49
1:C:143:ARG:HB2	1:C:216:GLY:HA2	1.94	0.49
1:D:137:TYR:HB2	1:D:163:GLN:HE22	1.77	0.49
1:C:247:THR:HA	1:D:348:PHE:HB2	1.95	0.49
1:E:45:THR:C	1:E:46:LYS:HE3	2.32	0.49
1:A:172:GLU:CB	1:A:173:PRO:HD3	2.43	0.49
1:B:388:LYS:HE2	1:B:389:PRO:HD2	1.93	0.49
1:B:52:ARG:HD3	1:B:127:THR:O	2.12	0.49
1:C:167:ILE:H	1:C:167:ILE:HD13	1.76	0.49
2:R:25:U:H2'	2:R:26:U:C5	2.47	0.49
1:C:31:TYR:CD1	1:C:31:TYR:C	2.86	0.49
1:E:171:PHE:O	1:E:172:GLU:OE2	2.31	0.49
1:C:374:ASP:O	1:C:378:TRP:HD1	1.94	0.49
1:C:14:ILE:HD12	1:D:259:VAL:HG22	1.94	0.49
2:R:34:U:H2'	2:R:35:U:O4'	2.12	0.49
1:B:182:PHE:C	1:B:184:VAL:H	2.15	0.49
1:B:143:ARG:CD	1:B:216:GLY:HA2	2.40	0.49
1:C:128:SER:HA	1:C:130:ASP:HB2	1.94	0.49
1:C:182:PHE:CD2	1:C:182:PHE:C	2.86	0.49
1:A:240:MET:HE3	1:A:244:ASP:HB3	1.95	0.49
1:B:317:ARG:O	1:B:319:PRO:HD3	2.13	0.49
1:C:227:ALA:HA	1:C:230:THR:HG23	1.95	0.49
1:D:22:GLU:O	1:D:23:ASP:C	2.51	0.49
1:D:143:ARG:HH21	2:R:8:U:C5'	2.24	0.49
1:D:283:LEU:HD23	1:D:283:LEU:N	2.27	0.49
1:B:240:MET:HE3	1:B:244:ASP:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:129:ALA:HA	1:C:132:LYS:NZ	2.28	0.49
1:D:172:GLU:CB	1:D:173:PRO:HD3	2.42	0.49
1:E:52:ARG:HD3	1:E:127:THR:O	2.13	0.49
1:E:45:THR:H	1:E:46:LYS:NZ	2.11	0.49
1:A:160:LEU:C	1:A:162:ASN:N	2.66	0.48
1:A:342:ALA:CB	1:A:344:LEU:HD23	2.41	0.48
1:E:117:LEU:HB3	1:E:118:PRO:HD3	1.86	0.48
1:B:172:GLU:CB	1:B:173:PRO:HD3	2.43	0.48
1:B:177:GLU:CG	1:B:178:GLY:H	2.26	0.48
1:C:119:ASP:O	1:C:121:VAL:N	2.46	0.48
1:C:143:ARG:HH21	2:R:17:U:H5''	1.77	0.48
1:A:163:GLN:C	1:A:165:LYS:N	2.64	0.48
1:A:171:PHE:O	1:A:172:GLU:OE2	2.30	0.48
1:A:214:ARG:O	1:A:217:THR:HG22	2.12	0.48
1:A:324:TYR:O	1:A:328:THR:CG2	2.61	0.48
1:B:316:ALA:HA	2:R:23:U:H5'	1.95	0.48
1:B:356:THR:N	1:B:357:PRO:CD	2.76	0.48
1:C:158:ASP:HA	1:C:161:THR:OG1	2.13	0.48
1:C:45:THR:C	1:C:46:LYS:HE3	2.34	0.48
1:D:153:ARG:NH2	1:D:176:PRO:HA	2.28	0.48
1:D:143:ARG:CD	1:D:216:GLY:HA2	2.43	0.48
1:E:31:TYR:C	1:E:31:TYR:CD1	2.87	0.48
2:R:29:U:H2'	2:R:29:U:O2	2.12	0.48
1:D:130:ASP:O	1:D:131:ASP:C	2.52	0.48
1:E:342:ALA:CB	1:E:344:LEU:HD23	2.40	0.48
1:A:221:ARG:O	1:A:222:PHE:HB2	2.14	0.48
1:B:317:ARG:HH21	1:B:410:LYS:HE2	1.79	0.48
1:D:66:ILE:HD12	1:D:69:VAL:CG1	2.44	0.48
1:E:158:ASP:HA	1:E:161:THR:OG1	2.13	0.48
1:E:22:GLU:O	1:E:23:ASP:C	2.51	0.48
1:E:257:GLU:CG	1:E:294:ASN:HA	2.43	0.48
1:A:177:GLU:HA	1:A:181:ILE:CD1	2.37	0.48
1:C:55:VAL:HG23	1:C:56:TYR:H	1.77	0.48
1:E:295:PRO:HB2	1:E:322:ILE:CG2	2.43	0.48
1:B:171:PHE:O	1:B:172:GLU:OE2	2.31	0.48
1:C:324:TYR:O	1:C:328:THR:HG22	2.13	0.48
1:C:44:THR:HG22	1:C:46:LYS:HZ2	1.79	0.48
1:D:248:TRP:O	1:D:250:LEU:HG	2.13	0.48
1:E:180:ASP:N	1:E:183:ASP:OD2	2.40	0.48
1:B:45:THR:H	1:B:46:LYS:HZ2	1.60	0.48
1:C:273:SER:OG	1:C:274:TYR:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:ASP:HA	1:D:161:THR:OG1	2.14	0.48
1:A:382:PHE:CE2	1:A:387:ARG:HA	2.48	0.48
1:A:388:LYS:HE2	1:A:389:PRO:HD2	1.94	0.48
1:C:317:ARG:HD3	2:R:13:U:C2	2.49	0.48
1:E:317:ARG:O	1:E:319:PRO:HD3	2.14	0.48
1:A:119:ASP:O	1:A:121:VAL:N	2.46	0.47
1:A:44:THR:HG22	1:A:46:LYS:NZ	2.28	0.47
1:A:55:VAL:HG23	1:A:56:TYR:H	1.78	0.47
1:A:79:ASP:OD2	1:A:81:ARG:HB2	2.14	0.47
1:C:163:GLN:C	1:C:165:LYS:H	2.17	0.47
1:C:182:PHE:C	1:C:184:VAL:H	2.16	0.47
1:D:303:LEU:HD22	1:D:328:THR:HB	1.96	0.47
1:E:182:PHE:CD2	1:E:182:PHE:C	2.87	0.47
1:A:137:TYR:HB2	1:A:163:GLN:NE2	2.29	0.47
2:R:37:U:C5	2:R:38:U:C5	3.02	0.47
1:A:143:ARG:HE	1:A:155:LYS:HZ1	1.61	0.47
1:B:257:GLU:CG	1:B:294:ASN:HA	2.44	0.47
1:C:180:ASP:N	1:C:183:ASP:OD1	2.47	0.47
1:A:228:LEU:HD23	1:A:228:LEU:HA	1.69	0.47
1:A:28:PRO:O	1:A:29:ALA:C	2.53	0.47
1:A:379:LEU:CD1	1:B:346:GLN:HB2	2.44	0.47
1:B:251:ASN:OD1	1:B:251:ASN:N	2.48	0.47
1:B:345:ALA:O	1:B:347:GLN:HG2	2.13	0.47
1:D:132:LYS:HB3	1:D:167:ILE:HD11	1.97	0.47
1:E:182:PHE:C	1:E:184:VAL:H	2.16	0.47
1:B:149:MET:HG3	2:R:24:U:O4'	2.15	0.47
1:C:55:VAL:O	1:C:56:TYR:C	2.53	0.47
1:D:149:MET:HG3	2:R:6:U:N1	2.29	0.47
1:A:44:THR:HG22	1:A:46:LYS:HZ2	1.80	0.47
1:C:167:ILE:CD1	1:C:167:ILE:H	2.28	0.47
1:D:43:ASN:O	1:D:44:THR:O	2.33	0.47
1:E:160:LEU:C	1:E:162:ASN:N	2.68	0.47
1:A:158:ASP:HA	1:A:161:THR:OG1	2.15	0.47
1:B:79:ASP:O	1:B:79:ASP:CG	2.52	0.47
1:C:317:ARG:HH21	1:C:410:LYS:HE2	1.80	0.47
1:D:165:LYS:CB	1:D:166:MET:SD	3.02	0.47
1:D:27:TYR:HB3	1:D:266:GLN:NE2	2.29	0.47
1:E:143:ARG:HB2	1:E:216:GLY:HA2	1.95	0.47
1:B:163:GLN:C	1:B:165:LYS:H	2.16	0.47
1:B:167:ILE:HD13	1:B:168:ASN:CA	2.33	0.47
1:B:179:ARG:O	1:B:180:ASP:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:LEU:HB2	1:C:19:PRO:HD2	1.97	0.47
1:D:182:PHE:C	1:D:182:PHE:CD2	2.88	0.47
1:D:342:ALA:CB	1:D:344:LEU:HD23	2.42	0.47
1:B:142:TYR:CD1	1:B:195:VAL:HG11	2.50	0.47
1:E:220:SER:HB2	1:E:280:ASP:OD2	2.15	0.47
2:R:17:U:H2'	2:R:18:U:C5'	2.42	0.47
1:A:324:TYR:O	1:A:328:THR:HG22	2.15	0.47
1:A:46:LYS:HD2	1:A:46:LYS:N	2.30	0.47
1:B:350:VAL:HG13	1:E:4:THR:O	2.15	0.47
1:A:162:ASN:O	1:A:164:CYS:N	2.48	0.47
1:A:167:ILE:N	1:A:167:ILE:HD12	2.27	0.47
1:A:178:GLY:O	1:A:179:ARG:CB	2.63	0.47
1:B:79:ASP:C	1:B:79:ASP:OD2	2.54	0.47
1:C:184:VAL:CG2	1:D:166:MET:HE3	2.45	0.47
1:E:48:LEU:CD2	1:E:48:LEU:N	2.74	0.47
1:B:234:LEU:O	1:B:238:THR:HG23	2.15	0.46
1:A:344:LEU:CD1	1:E:250:LEU:HD13	2.45	0.46
1:A:87:ASP:OD2	1:A:98:ALA:N	2.48	0.46
1:B:182:PHE:C	1:B:182:PHE:CD2	2.89	0.46
1:B:250:LEU:HB3	1:C:344:LEU:HD13	1.96	0.46
1:D:263:LEU:HA	1:D:264:PRO:HD3	1.75	0.46
1:D:317:ARG:HH21	1:D:410:LYS:HE2	1.79	0.46
1:D:45:THR:H	1:D:46:LYS:NZ	2.12	0.46
1:D:52:ARG:HD3	1:D:127:THR:O	2.14	0.46
1:E:409:GLU:O	1:E:410:LYS:HB2	2.16	0.46
1:B:151:GLU:HA	1:B:154:LYS:HZ2	1.80	0.46
1:C:160:LEU:C	1:C:162:ASN:N	2.68	0.46
1:D:251:ASN:N	1:D:251:ASN:OD1	2.49	0.46
1:E:55:VAL:HG23	1:E:56:TYR:H	1.79	0.46
2:R:21:U:C4	2:R:22:U:C4	3.04	0.46
2:R:7:U:H2'	2:R:8:U:O4'	2.16	0.46
1:A:167:ILE:HD13	1:A:167:ILE:N	2.13	0.46
1:B:181:ILE:N	1:B:183:ASP:OD2	2.48	0.46
1:B:379:LEU:HB3	1:C:354:LYS:HD2	1.98	0.46
1:C:44:THR:HG22	1:C:46:LYS:NZ	2.31	0.46
1:C:79:ASP:O	1:C:79:ASP:CG	2.53	0.46
1:D:160:LEU:C	1:D:162:ASN:N	2.68	0.46
1:D:177:GLU:CG	1:D:178:GLY:H	2.28	0.46
1:E:142:TYR:CD1	1:E:195:VAL:HG11	2.51	0.46
1:E:181:ILE:N	1:E:183:ASP:OD2	2.48	0.46
1:A:344:LEU:HD11	1:E:250:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:THR:HG22	1:D:46:LYS:NZ	2.31	0.46
1:D:45:THR:C	1:D:46:LYS:HE3	2.36	0.46
2:R:17:U:H2'	2:R:18:U:O4'	2.16	0.46
1:A:137:TYR:O	1:A:141:LEU:HG	2.16	0.46
1:A:52:ARG:HD3	1:A:127:THR:O	2.16	0.46
1:B:160:LEU:C	1:B:162:ASN:N	2.68	0.46
1:C:22:GLU:O	1:C:23:ASP:C	2.54	0.46
1:C:388:LYS:HE2	1:C:389:PRO:HD2	1.97	0.46
1:E:240:MET:HE3	1:E:244:ASP:HB3	1.96	0.46
2:R:31:U:H3'	2:R:31:U:C6	2.51	0.46
1:A:182:PHE:C	1:A:184:VAL:H	2.19	0.46
1:B:143:ARG:HB2	1:B:216:GLY:HA2	1.98	0.46
1:C:249:ILE:HD13	1:C:254:VAL:HG12	1.98	0.46
1:D:182:PHE:C	1:D:184:VAL:H	2.19	0.46
1:E:291:SER:HB3	2:R:40:U:O5'	2.15	0.46
1:A:130:ASP:O	1:A:131:ASP:C	2.54	0.46
1:A:143:ARG:NE	1:A:155:LYS:HZ2	2.14	0.46
1:B:214:ARG:O	1:B:215:TYR:C	2.54	0.46
1:D:143:ARG:HB2	1:D:216:GLY:HA2	1.98	0.46
1:E:66:ILE:O	1:E:70:ASN:ND2	2.47	0.46
1:A:422:LYS:HD3	1:A:422:LYS:HA	1.63	0.46
1:A:74:TYR:CD1	1:A:78:LYS:HD3	2.49	0.46
1:B:233:HIS:NE2	1:B:312:ARG:NH1	2.63	0.46
1:C:152:TYR:CE1	1:C:153:ARG:CZ	2.99	0.46
1:C:175:VAL:HG13	1:C:181:ILE:CG1	2.46	0.46
1:C:184:VAL:CB	1:D:166:MET:HE1	2.33	0.46
1:D:324:TYR:O	1:D:328:THR:CG2	2.64	0.46
1:E:69:VAL:HG21	1:E:138:LEU:HD22	1.98	0.46
1:A:97:LYS:NZ	1:A:97:LYS:HB2	2.30	0.45
1:C:184:VAL:HB	1:D:166:MET:CE	2.33	0.45
1:E:152:TYR:HE1	1:E:153:ARG:NH1	2.12	0.45
1:A:128:SER:C	1:A:130:ASP:N	2.70	0.45
1:D:178:GLY:O	1:D:179:ARG:CB	2.64	0.45
1:D:368:ALA:HA	1:D:369:PRO:HD3	1.79	0.45
1:A:364:LEU:CD1	1:A:364:LEU:H	2.27	0.45
1:C:228:LEU:HA	1:C:228:LEU:HD23	1.74	0.45
1:A:177:GLU:CG	1:A:178:GLY:H	2.28	0.45
1:A:45:THR:C	1:A:46:LYS:HE3	2.36	0.45
1:B:303:LEU:HD22	1:B:328:THR:HB	1.99	0.45
1:C:171:PHE:O	1:C:172:GLU:OE2	2.34	0.45
1:C:324:TYR:O	1:C:328:THR:HG23	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:152:TYR:CE1	1:E:153:ARG:CZ	3.00	0.45
1:E:302:GLN:HG3	1:E:313:ALA:HB1	1.98	0.45
1:B:143:ARG:NH2	2:R:26:U:H2'	2.32	0.45
1:A:162:ASN:HB3	1:A:163:GLN:H	1.59	0.45
1:C:167:ILE:CD1	1:C:168:ASN:N	2.78	0.45
1:D:18:LEU:HB2	1:D:19:PRO:HD2	1.98	0.45
1:B:212:SER:HA	2:R:27:U:C5	2.51	0.45
1:A:31:TYR:CD1	1:A:31:TYR:C	2.89	0.45
1:C:142:TYR:CD1	1:C:195:VAL:HG11	2.52	0.45
1:C:175:VAL:HA	1:C:176:PRO:HD2	1.69	0.45
1:E:143:ARG:NH2	2:R:44:U:H5''	2.32	0.45
1:E:178:GLY:O	1:E:179:ARG:CB	2.62	0.45
1:E:233:HIS:NE2	1:E:312:ARG:NH1	2.64	0.45
1:E:83:LYS:HD2	1:E:99:GLY:O	2.16	0.45
1:A:214:ARG:O	1:A:215:TYR:C	2.54	0.45
1:B:422:LYS:HA	1:B:422:LYS:HD3	1.63	0.45
1:C:178:GLY:O	1:C:179:ARG:CB	2.65	0.45
1:C:302:GLN:HG2	1:C:316:ALA:HB2	1.98	0.45
1:D:97:LYS:O	1:D:98:ALA:C	2.55	0.45
1:E:70:ASN:H	1:E:70:ASN:ND2	2.14	0.45
1:E:72:TYR:CE1	1:E:134:LEU:HD13	2.51	0.45
1:C:285:SER:OG	1:D:207:LYS:HE3	2.17	0.45
1:C:233:HIS:NE2	1:C:312:ARG:NH1	2.65	0.45
1:C:317:ARG:O	1:C:319:PRO:HD3	2.17	0.45
1:C:345:ALA:O	1:C:347:GLN:HG2	2.16	0.45
1:E:66:ILE:HD13	1:E:185:TRP:CD1	2.51	0.45
1:E:18:LEU:HB2	1:E:19:PRO:HD2	1.99	0.45
1:A:356:THR:N	1:A:357:PRO:CD	2.80	0.45
1:B:365:THR:CG2	1:B:366:THR:N	2.73	0.45
1:D:119:ASP:O	1:D:121:VAL:N	2.49	0.45
1:D:162:ASN:HB3	1:D:163:GLN:H	1.61	0.45
1:D:142:TYR:CD1	1:D:195:VAL:HG11	2.51	0.45
1:A:160:LEU:HA	1:A:163:GLN:CG	2.46	0.45
1:D:181:ILE:N	1:D:183:ASP:OD2	2.50	0.45
1:D:324:TYR:O	1:D:328:THR:HG23	2.16	0.45
1:E:55:VAL:O	1:E:56:TYR:C	2.55	0.45
1:B:158:ASP:HA	1:B:161:THR:OG1	2.17	0.44
1:B:46:LYS:HD2	1:B:46:LYS:N	2.32	0.44
1:C:137:TYR:O	1:C:141:LEU:HG	2.17	0.44
1:E:180:ASP:HB3	1:E:181:ILE:HD12	1.99	0.44
1:A:66:ILE:HG23	1:A:67:ILE:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:TYR:HE1	1:B:153:ARG:NH1	2.15	0.44
1:B:180:ASP:N	1:B:183:ASP:CG	2.66	0.44
1:C:177:GLU:HA	1:C:181:ILE:CD1	2.39	0.44
1:C:203:HIS:HA	1:C:214:ARG:NH1	2.32	0.44
1:B:2:SER:HB2	1:C:243:GLU:HG3	1.99	0.44
1:B:368:ALA:HA	1:B:369:PRO:HD3	1.82	0.44
1:C:177:GLU:CG	1:C:178:GLY:H	2.28	0.44
1:C:422:LYS:HA	1:C:422:LYS:HD3	1.63	0.44
1:B:50:ASP:OD1	1:B:121:VAL:HG22	2.17	0.44
1:B:90:SER:HG	1:B:91:PHE:HD1	1.64	0.44
1:D:137:TYR:HD1	1:D:163:GLN:NE2	2.02	0.44
1:D:141:LEU:HD12	1:D:185:TRP:CZ3	2.52	0.44
1:D:180:ASP:HB3	1:D:181:ILE:HD12	1.99	0.44
1:B:72:TYR:CE1	1:B:134:LEU:HD13	2.52	0.44
1:C:127:THR:OG1	1:C:128:SER:N	2.49	0.44
1:C:45:THR:H	1:C:46:LYS:NZ	2.15	0.44
1:D:160:LEU:HA	1:D:163:GLN:HB2	1.98	0.44
2:R:44:U:H5'	2:R:45:U:OP2	2.17	0.44
1:A:152:TYR:CE1	1:A:153:ARG:CZ	3.01	0.44
1:C:224:ASP:OD1	2:R:12:U:H4'	2.18	0.44
1:C:72:TYR:CE1	1:C:134:LEU:HD13	2.53	0.44
1:D:45:THR:H	1:D:46:LYS:HZ2	1.65	0.44
1:E:127:THR:OG1	1:E:128:SER:N	2.49	0.44
1:E:130:ASP:O	1:E:131:ASP:C	2.56	0.44
2:R:27:U:H2'	2:R:28:U:O4'	2.17	0.44
2:R:8:U:H5'	2:R:9:U:OP2	2.18	0.44
1:D:175:VAL:HG13	1:D:181:ILE:HG12	1.99	0.44
1:D:44:THR:HG21	1:D:116:VAL:HG11	1.99	0.44
1:A:143:ARG:HB2	1:A:216:GLY:HA2	1.98	0.44
1:B:379:LEU:HD23	1:B:379:LEU:HA	1.89	0.44
1:C:151:GLU:HA	1:C:154:LYS:HZ2	1.83	0.44
1:C:376:VAL:HG13	1:D:354:LYS:CB	2.35	0.44
1:C:45:THR:O	1:C:46:LYS:HE3	2.18	0.44
1:A:45:THR:H	1:A:46:LYS:HZ2	1.65	0.44
1:C:251:ASN:OD1	1:C:251:ASN:N	2.50	0.44
1:D:38:ILE:HA	1:D:39:PRO:HD2	1.90	0.44
1:A:161:THR:HB	1:E:179:ARG:CB	2.43	0.43
1:B:175:VAL:HG13	1:B:181:ILE:CG1	2.48	0.43
1:B:249:ILE:HD13	1:B:254:VAL:HG12	2.00	0.43
1:C:214:ARG:O	1:C:215:TYR:C	2.53	0.43
1:C:291:SER:HB3	2:R:13:U:P	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:303:LEU:HD22	1:E:328:THR:HB	2.00	0.43
1:D:70:ASN:ND2	1:D:70:ASN:H	2.14	0.43
1:E:79:ASP:O	1:E:79:ASP:CG	2.56	0.43
1:A:317:ARG:HH21	1:A:410:LYS:HE2	1.83	0.43
1:B:180:ASP:HB3	1:B:181:ILE:HD12	2.01	0.43
1:B:199:ASP:OD1	1:B:218:ILE:HA	2.18	0.43
1:C:38:ILE:HA	1:C:39:PRO:HD2	1.90	0.43
1:E:107:LEU:C	1:E:108:VAL:HG23	2.38	0.43
1:E:175:VAL:HG13	1:E:181:ILE:CG1	2.48	0.43
1:E:251:ASN:OD1	1:E:251:ASN:N	2.51	0.43
1:E:84:LEU:HA	1:E:84:LEU:HD23	1.78	0.43
1:A:199:ASP:OD1	1:A:218:ILE:HA	2.18	0.43
1:B:152:TYR:CE1	1:B:153:ARG:CZ	3.01	0.43
1:B:45:THR:O	1:B:46:LYS:HE3	2.19	0.43
1:E:27:TYR:HB3	1:E:266:GLN:NE2	2.33	0.43
1:E:422:LYS:HA	1:E:422:LYS:HD3	1.62	0.43
2:R:17:U:C2'	2:R:18:U:H5''	2.42	0.43
1:B:151:GLU:HG2	1:B:151:GLU:O	2.18	0.43
1:B:215:TYR:O	1:B:217:THR:N	2.51	0.43
1:B:324:TYR:O	1:B:328:THR:CG2	2.66	0.43
1:D:220:SER:HB2	1:D:280:ASP:OD2	2.19	0.43
1:E:162:ASN:ND2	1:E:165:LYS:NZ	2.67	0.43
1:E:44:THR:HG21	1:E:116:VAL:HG11	2.00	0.43
1:E:79:ASP:OD2	1:E:81:ARG:HB2	2.19	0.43
2:R:21:U:C4	2:R:22:U:C5	3.07	0.43
2:R:36:U:O2'	2:R:37:U:H5'	2.18	0.43
1:E:149:MET:HG3	2:R:42:U:C6	2.54	0.43
1:B:84:LEU:HD11	1:B:96:GLY:HA3	2.01	0.43
1:D:72:TYR:CE1	1:D:134:LEU:HD13	2.53	0.43
1:E:199:ASP:OD1	1:E:218:ILE:HA	2.19	0.43
1:A:69:VAL:HG21	1:A:138:LEU:HD22	2.01	0.43
1:C:130:ASP:O	1:C:131:ASP:C	2.57	0.43
1:C:152:TYR:HE1	1:C:153:ARG:NH1	2.17	0.43
1:D:162:ASN:O	1:D:164:CYS:N	2.51	0.43
1:D:55:VAL:O	1:D:56:TYR:C	2.55	0.43
1:E:45:THR:H	1:E:46:LYS:HZ2	1.67	0.43
1:A:152:TYR:HE1	1:A:153:ARG:NH1	2.16	0.43
1:A:45:THR:O	1:A:46:LYS:HE3	2.19	0.43
1:C:199:ASP:OD1	1:C:218:ILE:HA	2.18	0.43
1:C:257:GLU:CG	1:C:294:ASN:HA	2.45	0.43
1:D:160:LEU:HA	1:D:163:GLN:CG	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:HIS:NE2	1:D:312:ARG:NH1	2.67	0.43
1:A:163:GLN:OE1	1:A:163:GLN:CA	2.67	0.43
1:B:162:ASN:HB3	1:B:163:GLN:H	1.63	0.43
1:C:151:GLU:HG2	1:C:151:GLU:O	2.18	0.43
1:C:175:VAL:HG13	1:C:181:ILE:HG12	2.00	0.43
1:D:137:TYR:HB2	1:D:163:GLN:NE2	2.33	0.43
1:E:46:LYS:N	1:E:46:LYS:HD2	2.34	0.43
1:A:66:ILE:HD12	1:A:69:VAL:HG11	2.01	0.42
1:B:175:VAL:HG13	1:B:181:ILE:HG12	2.00	0.42
1:B:38:ILE:HA	1:B:39:PRO:HD2	1.89	0.42
1:B:69:VAL:HG21	1:B:138:LEU:HD22	2.01	0.42
1:E:249:ILE:HD13	1:E:254:VAL:HG12	2.01	0.42
1:E:317:ARG:HH21	1:E:410:LYS:HE2	1.84	0.42
1:B:295:PRO:HB2	1:B:322:ILE:CG2	2.49	0.42
1:B:382:PHE:CE2	1:B:387:ARG:HA	2.54	0.42
1:D:175:VAL:HA	1:D:176:PRO:HD2	1.67	0.42
1:D:382:PHE:CE2	1:D:387:ARG:HA	2.54	0.42
1:E:200:MET:HB2	1:E:277:TYR:CE2	2.54	0.42
1:E:45:THR:O	1:E:46:LYS:HE3	2.19	0.42
2:R:11:U:H2'	2:R:12:U:O4'	2.18	0.42
1:A:180:ASP:N	1:A:183:ASP:CG	2.62	0.42
1:A:251:ASN:N	1:A:251:ASN:OD1	2.52	0.42
1:B:44:THR:HG21	1:B:116:VAL:HG11	2.01	0.42
1:C:52:ARG:HD3	1:C:127:THR:O	2.18	0.42
1:C:20:ALA:HB2	1:D:269:ASP:O	2.20	0.42
1:D:163:GLN:O	1:D:165:LYS:N	2.52	0.42
1:D:249:ILE:HD13	1:D:254:VAL:HG12	2.00	0.42
1:D:286:LYS:HZ1	2:R:2:U:P	2.42	0.42
1:A:31:TYR:C	1:A:33:ARG:N	2.73	0.42
1:C:47:SER:HB3	1:C:50:ASP:OD2	2.19	0.42
1:D:127:THR:OG1	1:D:128:SER:N	2.51	0.42
1:D:152:TYR:HE1	1:D:153:ARG:NH1	2.17	0.42
1:D:221:ARG:O	1:D:222:PHE:HB2	2.19	0.42
1:C:249:ILE:HD12	1:D:348:PHE:CE1	2.54	0.42
1:B:347:GLN:HE21	1:B:347:GLN:HB3	1.71	0.42
1:C:136:LEU:HB2	1:C:213:PHE:CE2	2.55	0.42
1:D:180:ASP:N	1:D:183:ASP:CG	2.62	0.42
1:D:44:THR:HG22	1:D:46:LYS:HZ2	1.84	0.42
1:E:252:ARG:NH2	1:E:256:ASP:OD1	2.52	0.42
1:E:356:THR:N	1:E:357:PRO:CD	2.81	0.42
1:E:80:ILE:HG12	1:E:80:ILE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ASP:OD1	1:A:121:VAL:HG22	2.20	0.42
1:A:182:PHE:HD2	1:A:182:PHE:C	2.19	0.42
1:A:31:TYR:C	1:A:33:ARG:H	2.23	0.42
1:B:167:ILE:CD1	1:B:167:ILE:C	2.71	0.42
1:C:285:SER:OG	1:D:207:LYS:CE	2.67	0.42
1:E:228:LEU:HA	1:E:228:LEU:HD23	1.76	0.42
1:E:272:ASP:OD2	1:E:272:ASP:N	2.53	0.42
1:E:358:ASP:CG	1:E:359:ASP:N	2.69	0.42
1:E:382:PHE:CE2	1:E:387:ARG:HA	2.55	0.42
1:A:302:GLN:HG2	1:A:316:ALA:HB2	2.01	0.42
1:B:83:LYS:HD2	1:B:99:GLY:O	2.20	0.42
1:D:263:LEU:HD12	1:D:263:LEU:HA	1.89	0.42
1:E:29:ALA:H	1:E:266:GLN:HE22	1.67	0.42
1:E:273:SER:OG	1:E:274:TYR:N	2.52	0.42
1:C:294:ASN:N	1:C:295:PRO:HD3	2.34	0.42
1:C:382:PHE:CE2	1:C:387:ARG:HA	2.54	0.42
1:C:44:THR:HG21	1:C:116:VAL:HG11	2.02	0.42
1:C:97:LYS:O	1:C:98:ALA:O	2.37	0.42
1:D:152:TYR:CE1	1:D:153:ARG:CZ	3.03	0.42
1:D:295:PRO:HB2	1:D:322:ILE:CG2	2.49	0.42
1:E:151:GLU:HG2	1:E:151:GLU:O	2.19	0.42
1:A:136:LEU:HB2	1:A:213:PHE:CE2	2.55	0.42
1:B:137:TYR:O	1:B:141:LEU:HG	2.20	0.42
1:C:162:ASN:HB3	1:C:163:GLN:H	1.61	0.42
1:D:177:GLU:HA	1:D:181:ILE:CD1	2.36	0.42
1:D:83:LYS:HD2	1:D:99:GLY:O	2.20	0.42
1:E:136:LEU:HB2	1:E:213:PHE:CE2	2.54	0.42
1:E:302:GLN:CB	1:E:412:ILE:HD11	2.46	0.42
1:A:142:TYR:CD1	1:A:195:VAL:HG11	2.55	0.42
1:A:275:MET:C	1:A:275:MET:SD	2.98	0.42
1:A:303:LEU:HD22	1:A:328:THR:HB	2.02	0.42
1:C:263:LEU:HA	1:C:263:LEU:HD12	1.92	0.42
1:C:79:ASP:C	1:C:79:ASP:OD2	2.58	0.42
1:E:141:LEU:HD12	1:E:185:TRP:CZ3	2.55	0.42
1:E:175:VAL:HG13	1:E:181:ILE:HG12	2.01	0.42
2:R:31:U:C3'	2:R:31:U:C6	3.03	0.42
1:A:55:VAL:O	1:A:56:TYR:C	2.56	0.41
1:B:25:VAL:HG11	1:B:288:PRO:HA	2.02	0.41
1:B:44:THR:HG22	1:B:46:LYS:HZ2	1.85	0.41
1:C:234:LEU:O	1:C:238:THR:HG23	2.19	0.41
1:C:69:VAL:HG21	1:C:138:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:107:LEU:CD2	1:D:274:TYR:OH	2.65	0.41
1:C:250:LEU:HD13	1:D:344:LEU:CD1	2.49	0.41
1:D:356:THR:N	1:D:357:PRO:CD	2.78	0.41
1:D:38:ILE:O	1:D:38:ILE:CG1	2.68	0.41
1:D:55:VAL:HG23	1:D:56:TYR:N	2.33	0.41
1:C:317:ARG:HD3	2:R:13:U:O2	2.20	0.41
1:A:317:ARG:HG3	2:R:32:U:OP2	2.19	0.41
1:E:149:MET:CG	2:R:42:U:O4'	2.55	0.41
1:A:79:ASP:CG	1:A:79:ASP:O	2.57	0.41
1:B:72:TYR:CE1	1:B:134:LEU:CD1	3.03	0.41
1:B:182:PHE:C	1:B:184:VAL:N	2.73	0.41
1:B:302:GLN:CB	1:B:412:ILE:HD11	2.46	0.41
1:B:55:VAL:HG23	1:B:56:TYR:N	2.34	0.41
1:B:84:LEU:HA	1:B:84:LEU:HD23	1.76	0.41
1:A:72:TYR:CE1	1:A:134:LEU:HD13	2.55	0.41
1:A:151:GLU:HA	1:A:154:LYS:HZ2	1.84	0.41
1:A:169:GLU:HB3	1:A:170:GLN:H	1.70	0.41
1:B:74:TYR:CD1	1:B:78:LYS:HD3	2.53	0.41
1:B:80:ILE:HG12	1:B:80:ILE:O	2.20	0.41
1:D:175:VAL:HG13	1:D:181:ILE:CG1	2.49	0.41
1:D:199:ASP:OD1	1:D:218:ILE:HA	2.20	0.41
1:D:272:ASP:N	1:D:272:ASP:OD2	2.53	0.41
1:E:66:ILE:HG23	1:E:67:ILE:N	2.35	0.41
2:R:4:U:O2'	2:R:5:U:H5'	2.20	0.41
2:R:9:U:O3'	2:R:10:U:C6	2.70	0.41
1:A:175:VAL:HG13	1:A:181:ILE:CG1	2.50	0.41
1:A:364:LEU:HD12	1:A:364:LEU:N	2.28	0.41
1:A:97:LYS:HG3	1:A:98:ALA:H	1.80	0.41
1:C:19:PRO:HA	1:D:268:ILE:O	2.21	0.41
1:C:263:LEU:HA	1:C:264:PRO:HD3	1.78	0.41
1:C:18:LEU:HD12	1:D:232:GLY:HA2	2.03	0.41
1:D:275:MET:SD	1:D:275:MET:C	2.98	0.41
1:D:317:ARG:O	1:D:319:PRO:HD3	2.20	0.41
1:D:379:LEU:HA	1:D:379:LEU:HD23	1.87	0.41
1:E:203:HIS:HA	1:E:214:ARG:NH1	2.36	0.41
1:B:141:LEU:HD12	1:B:185:TRP:CZ3	2.56	0.41
1:B:55:VAL:O	1:B:56:TYR:C	2.58	0.41
1:C:109:SER:O	1:C:110:LEU:HD23	2.20	0.41
1:C:128:SER:C	1:C:130:ASP:N	2.73	0.41
1:D:128:SER:C	1:D:130:ASP:N	2.73	0.41
1:D:302:GLN:HG3	1:D:313:ALA:HB1	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:84:LEU:HD11	1:E:96:GLY:HA3	2.02	0.41
2:R:5:U:O2	2:R:5:U:H2'	2.20	0.41
1:A:175:VAL:HA	1:A:176:PRO:HD2	1.70	0.41
1:B:149:MET:HG3	2:R:24:U:C6	2.55	0.41
1:B:79:ASP:OD2	1:B:81:ARG:HB2	2.20	0.41
1:C:181:ILE:HD13	1:C:183:ASP:OD1	2.20	0.41
1:C:182:PHE:O	1:C:184:VAL:N	2.54	0.41
1:D:116:VAL:HB	1:D:117:LEU:H	1.68	0.41
1:D:214:ARG:O	1:D:215:TYR:C	2.58	0.41
1:D:422:LYS:HA	1:D:422:LYS:HD3	1.63	0.41
1:E:379:LEU:HD23	1:E:379:LEU:HA	1.95	0.41
1:C:224:ASP:CG	2:R:12:U:H4'	2.41	0.41
1:A:66:ILE:HD13	1:A:185:TRP:CD1	2.56	0.41
1:A:295:PRO:HB2	1:A:322:ILE:CG2	2.51	0.41
1:B:263:LEU:HA	1:B:264:PRO:HD3	1.78	0.41
1:B:409:GLU:O	1:B:410:LYS:HB2	2.21	0.41
1:C:182:PHE:C	1:C:184:VAL:N	2.73	0.41
1:E:182:PHE:N	1:E:182:PHE:CD2	2.84	0.41
1:A:47:SER:HB3	1:A:50:ASP:OD2	2.20	0.41
1:C:250:LEU:HB3	1:D:344:LEU:HD13	2.02	0.41
1:C:66:ILE:HD12	1:C:69:VAL:HG11	2.03	0.41
1:D:133:TRP:CD1	1:D:167:ILE:HG21	2.55	0.41
1:D:228:LEU:HD23	1:D:228:LEU:HA	1.69	0.41
1:E:50:ASP:OD1	1:E:121:VAL:HG22	2.21	0.41
1:E:182:PHE:C	1:E:184:VAL:N	2.74	0.41
1:A:10:ASP:OD2	1:A:12:THR:HG23	2.21	0.41
1:A:116:VAL:HB	1:A:117:LEU:H	1.66	0.41
1:B:136:LEU:HB2	1:B:213:PHE:CE2	2.56	0.41
1:B:273:SER:OG	1:B:274:TYR:N	2.54	0.41
1:C:10:ASP:OD2	1:C:10:ASP:C	2.58	0.41
1:D:137:TYR:O	1:D:141:LEU:HG	2.21	0.41
1:D:176:PRO:HB2	1:D:177:GLU:H	1.69	0.41
1:E:324:TYR:O	1:E:328:THR:CG2	2.69	0.41
1:A:263:LEU:HA	1:A:264:PRO:HD3	1.80	0.41
1:A:70:ASN:ND2	1:A:70:ASN:H	2.15	0.41
1:B:175:VAL:O	1:B:176:PRO:O	2.39	0.41
1:B:18:LEU:HB2	1:B:19:PRO:HD2	2.02	0.41
1:D:294:ASN:N	1:D:295:PRO:HD3	2.36	0.41
1:B:152:TYR:OH	1:B:176:PRO:CB	2.63	0.41
1:B:150:PRO:O	1:B:154:LYS:HE3	2.21	0.41
1:C:50:ASP:OD1	1:C:121:VAL:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:150:PRO:O	1:C:154:LYS:HE3	2.21	0.41
1:C:187:ASN:HD22	1:C:187:ASN:HA	1.63	0.41
1:D:200:MET:HB2	1:D:277:TYR:CE2	2.55	0.41
1:D:45:THR:O	1:D:46:LYS:HE3	2.21	0.41
1:D:79:ASP:O	1:D:79:ASP:CG	2.58	0.41
1:E:287:SER:HA	1:E:288:PRO:HD3	1.83	0.41
1:A:127:THR:OG1	1:A:128:SER:N	2.54	0.40
1:A:233:HIS:NE2	1:A:312:ARG:NH1	2.68	0.40
1:B:342:ALA:O	1:B:343:ASP:C	2.58	0.40
1:C:66:ILE:HD13	1:C:185:TRP:CD1	2.56	0.40
1:A:409:GLU:O	1:A:410:LYS:HB2	2.20	0.40
1:A:412:ILE:HG21	1:A:412:ILE:HD13	1.75	0.40
1:B:22:GLU:HG2	1:C:206:LYS:NZ	2.36	0.40
1:C:80:ILE:HG12	1:C:80:ILE:O	2.20	0.40
1:C:79:ASP:OD2	1:C:81:ARG:HB2	2.21	0.40
1:D:180:ASP:N	1:D:183:ASP:OD1	2.54	0.40
1:D:412:ILE:HG21	1:D:412:ILE:HD13	1.62	0.40
1:D:66:ILE:O	1:D:70:ASN:ND2	2.48	0.40
1:E:177:GLU:CG	1:E:183:ASP:HB3	2.52	0.40
2:R:8:U:H2'	2:R:9:U:H5''	2.03	0.40
1:A:18:LEU:HB2	1:A:19:PRO:HD2	2.02	0.40
1:A:358:ASP:O	1:A:359:ASP:HB2	2.21	0.40
1:C:272:ASP:OD2	1:C:272:ASP:N	2.54	0.40
1:C:84:LEU:HA	1:C:84:LEU:HD23	1.77	0.40
1:E:109:SER:O	1:E:110:LEU:HD23	2.22	0.40
1:A:151:GLU:HG2	1:A:151:GLU:O	2.21	0.40
1:B:38:ILE:O	1:B:38:ILE:CG1	2.68	0.40
1:C:342:ALA:O	1:C:343:ASP:C	2.59	0.40
1:E:263:LEU:HA	1:E:264:PRO:HD3	1.80	0.40
1:E:66:ILE:HD12	1:E:69:VAL:HG11	2.02	0.40
1:A:203:HIS:HA	1:A:214:ARG:NH1	2.37	0.40
1:A:25:VAL:HG11	1:A:288:PRO:HA	2.04	0.40
1:A:368:ALA:HA	1:A:369:PRO:HD3	1.79	0.40
1:B:130:ASP:O	1:B:131:ASP:C	2.60	0.40
1:C:356:THR:N	1:C:357:PRO:CD	2.81	0.40
1:E:167:ILE:HD13	1:E:167:ILE:H	1.87	0.40
1:E:295:PRO:HB2	1:E:322:ILE:HG21	2.02	0.40
1:E:226:ALA:HB2	2:R:40:U:OP1	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	419/421 (100%)	316 (75%)	70 (17%)	33 (8%)	1	5
1	B	411/421 (98%)	315 (77%)	67 (16%)	29 (7%)	1	6
1	C	409/421 (97%)	318 (78%)	62 (15%)	29 (7%)	1	6
1	D	412/421 (98%)	319 (77%)	61 (15%)	32 (8%)	1	5
1	E	419/421 (100%)	317 (76%)	67 (16%)	35 (8%)	1	4
All	All	2070/2105 (98%)	1585 (77%)	327 (16%)	158 (8%)	1	6

All (158) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	A	99	GLY
1	A	117	LEU
1	A	120	GLY
1	A	132	LYS
1	A	163	GLN
1	A	176	PRO
1	A	177	GLU
1	A	180	ASP
1	A	344	LEU
1	A	358	ASP
1	B	30	ASP
1	B	34	LYS
1	B	117	LEU
1	B	120	GLY
1	B	163	GLN
1	B	176	PRO
1	B	180	ASP
1	B	344	LEU
1	C	34	LYS
1	C	117	LEU

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Mol	Chain	Res	Type
1	C	120	GLY
1	C	132	LYS
1	C	163	GLN
1	C	176	PRO
1	C	177	GLU
1	C	180	ASP
1	C	344	LEU
1	D	30	ASP
1	D	34	LYS
1	D	117	LEU
1	D	120	GLY
1	D	163	GLN
1	D	165	LYS
1	D	176	PRO
1	D	177	GLU
1	D	180	ASP
1	D	344	LEU
1	E	30	ASP
1	E	34	LYS
1	E	117	LEU
1	E	120	GLY
1	E	163	GLN
1	E	165	LYS
1	E	176	PRO
1	E	344	LEU
1	E	360	SER
1	E	362	GLY
1	A	30	ASP
1	A	44	THR
1	A	108	VAL
1	A	113	LEU
1	A	171	PHE
1	A	181	ILE
1	A	309	ARG
1	B	44	THR
1	B	108	VAL
1	B	113	LEU
1	B	132	LYS
1	B	171	PHE
1	B	177	GLU
1	B	181	ILE
1	B	309	ARG

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Mol	Chain	Res	Type
1	C	30	ASP
1	C	44	THR
1	C	98	ALA
1	C	108	VAL
1	C	113	LEU
1	C	171	PHE
1	C	181	ILE
1	C	309	ARG
1	D	44	THR
1	D	108	VAL
1	D	113	LEU
1	D	132	LYS
1	D	164	CYS
1	D	171	PHE
1	D	181	ILE
1	D	309	ARG
1	E	44	THR
1	E	100	ASP
1	E	108	VAL
1	E	113	LEU
1	E	132	LYS
1	E	171	PHE
1	E	180	ASP
1	E	181	ILE
1	E	359	ASP
1	A	43	ASN
1	A	122	SER
1	A	164	CYS
1	A	172	GLU
1	A	179	ARG
1	A	183	ASP
1	B	122	SER
1	B	172	GLU
1	B	183	ASP
1	C	122	SER
1	C	125	SER
1	C	172	GLU
1	C	179	ARG
1	C	183	ASP
1	C	387	ARG
1	D	43	ASN
1	D	98	ALA

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Mol	Chain	Res	Type
1	D	122	SER
1	D	168	ASN
1	D	172	GLU
1	D	183	ASP
1	E	43	ASN
1	E	122	SER
1	E	162	ASN
1	E	172	GLU
1	E	179	ARG
1	E	183	ASP
1	E	309	ARG
1	A	125	SER
1	A	162	ASN
1	A	357	PRO
1	A	362	GLY
1	A	387	ARG
1	B	43	ASN
1	B	118	PRO
1	B	125	SER
1	C	43	ASN
1	C	118	PRO
1	C	162	ASN
1	D	118	PRO
1	D	125	SER
1	D	162	ASN
1	D	179	ARG
1	D	357	PRO
1	E	118	PRO
1	E	125	SER
1	A	118	PRO
1	B	162	ASN
1	B	179	ARG
1	E	363	GLY
1	E	387	ARG
1	B	357	PRO
1	B	387	ARG
1	A	116	VAL
1	B	80	ILE
1	B	116	VAL
1	C	80	ILE
1	C	116	VAL
1	D	80	ILE

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Mol	Chain	Res	Type
1	D	116	VAL
1	D	370	PRO
1	E	80	ILE
1	E	116	VAL
1	E	357	PRO
1	E	370	PRO
1	A	80	ILE
1	A	28	PRO
1	B	216	GLY
1	C	216	GLY
1	E	216	GLY

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	362/362 (100%)	301 (83%)	61 (17%)	2	12
1	B	358/362 (99%)	296 (83%)	62 (17%)	2	12
1	C	356/362 (98%)	298 (84%)	58 (16%)	3	13
1	D	359/362 (99%)	296 (82%)	63 (18%)	2	11
1	E	362/362 (100%)	298 (82%)	64 (18%)	2	11
All	All	1797/1810 (99%)	1489 (83%)	308 (17%)	2	12

All (308) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ILE
1	A	9	ILE
1	A	13	VAL
1	A	18	LEU
1	A	22	GLU
1	A	34	LYS
1	A	38	ILE
1	A	40	LEU

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Mol	Chain	Res	Type
1	A	44	THR
1	A	46	LYS
1	A	47	SER
1	A	48	LEU
1	A	55	VAL
1	A	61	SER
1	A	63	ASN
1	A	79	ASP
1	A	83	LYS
1	A	85	ASP
1	A	100	ASP
1	A	101	THR
1	A	107	LEU
1	A	113	LEU
1	A	134	LEU
1	A	149	MET
1	A	154	LYS
1	A	156	LEU
1	A	162	ASN
1	A	165	LYS
1	A	166	MET
1	A	167	ILE
1	A	168	ASN
1	A	171	PHE
1	A	172	GLU
1	A	174	LEU
1	A	181	ILE
1	A	182	PHE
1	A	183	ASP
1	A	187	ASN
1	A	230	THR
1	A	237	ILE
1	A	251	ASN
1	A	257	GLU
1	A	270	LYS
1	A	272	ASP
1	A	273	SER
1	A	292	VAL
1	A	307	LEU
1	A	308	LEU
1	A	327	LEU
1	A	328	THR

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Mol	Chain	Res	Type
1	A	332	LEU
1	A	344	LEU
1	A	353	ASN
1	A	354	LYS
1	A	356	THR
1	A	364	LEU
1	A	365	THR
1	A	388	LYS
1	A	394	MET
1	A	410	LYS
1	A	412	ILE
1	B	8	ILE
1	B	9	ILE
1	B	13	VAL
1	B	18	LEU
1	B	22	GLU
1	B	31	TYR
1	B	34	LYS
1	B	38	ILE
1	B	40	LEU
1	B	44	THR
1	B	46	LYS
1	B	47	SER
1	B	48	LEU
1	B	55	VAL
1	B	61	SER
1	B	63	ASN
1	B	79	ASP
1	B	83	LYS
1	B	85	ASP
1	B	97	LYS
1	B	100	ASP
1	B	101	THR
1	B	107	LEU
1	B	113	LEU
1	B	134	LEU
1	B	149	MET
1	B	154	LYS
1	B	155	LYS
1	B	156	LEU
1	B	162	ASN
1	B	163	GLN

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Mol	Chain	Res	Type
1	B	165	LYS
1	B	166	MET
1	B	167	ILE
1	B	168	ASN
1	B	171	PHE
1	B	172	GLU
1	B	174	LEU
1	B	181	ILE
1	B	182	PHE
1	B	183	ASP
1	B	187	ASN
1	B	230	THR
1	B	237	ILE
1	B	251	ASN
1	B	257	GLU
1	B	270	LYS
1	B	272	ASP
1	B	273	SER
1	B	292	VAL
1	B	307	LEU
1	B	308	LEU
1	B	327	LEU
1	B	328	THR
1	B	332	LEU
1	B	344	LEU
1	B	353	ASN
1	B	354	LYS
1	B	356	THR
1	B	388	LYS
1	B	410	LYS
1	B	412	ILE
1	C	8	ILE
1	C	9	ILE
1	C	13	VAL
1	C	18	LEU
1	C	22	GLU
1	C	34	LYS
1	C	38	ILE
1	C	40	LEU
1	C	44	THR
1	C	46	LYS
1	C	47	SER

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Mol	Chain	Res	Type
1	C	48	LEU
1	C	63	ASN
1	C	79	ASP
1	C	83	LYS
1	C	85	ASP
1	C	100	ASP
1	C	101	THR
1	C	107	LEU
1	C	113	LEU
1	C	134	LEU
1	C	149	MET
1	C	154	LYS
1	C	156	LEU
1	C	162	ASN
1	C	163	GLN
1	C	165	LYS
1	C	166	MET
1	C	167	ILE
1	C	168	ASN
1	C	171	PHE
1	C	172	GLU
1	C	174	LEU
1	C	181	ILE
1	C	182	PHE
1	C	183	ASP
1	C	187	ASN
1	C	230	THR
1	C	237	ILE
1	C	251	ASN
1	C	257	GLU
1	C	270	LYS
1	C	272	ASP
1	C	273	SER
1	C	291	SER
1	C	292	VAL
1	C	307	LEU
1	C	308	LEU
1	C	327	LEU
1	C	328	THR
1	C	332	LEU
1	C	344	LEU
1	C	353	ASN

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Mol	Chain	Res	Type
1	C	354	LYS
1	C	356	THR
1	C	388	LYS
1	C	410	LYS
1	C	412	ILE
1	D	8	ILE
1	D	9	ILE
1	D	13	VAL
1	D	18	LEU
1	D	22	GLU
1	D	31	TYR
1	D	38	ILE
1	D	40	LEU
1	D	44	THR
1	D	46	LYS
1	D	47	SER
1	D	48	LEU
1	D	55	VAL
1	D	61	SER
1	D	63	ASN
1	D	79	ASP
1	D	83	LYS
1	D	85	ASP
1	D	100	ASP
1	D	101	THR
1	D	107	LEU
1	D	113	LEU
1	D	134	LEU
1	D	149	MET
1	D	154	LYS
1	D	155	LYS
1	D	156	LEU
1	D	162	ASN
1	D	165	LYS
1	D	166	MET
1	D	168	ASN
1	D	171	PHE
1	D	172	GLU
1	D	174	LEU
1	D	181	ILE
1	D	182	PHE
1	D	183	ASP

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Mol	Chain	Res	Type
1	D	187	ASN
1	D	230	THR
1	D	237	ILE
1	D	251	ASN
1	D	257	GLU
1	D	270	LYS
1	D	272	ASP
1	D	273	SER
1	D	291	SER
1	D	292	VAL
1	D	307	LEU
1	D	308	LEU
1	D	326	SER
1	D	327	LEU
1	D	328	THR
1	D	332	LEU
1	D	344	LEU
1	D	353	ASN
1	D	354	LYS
1	D	356	THR
1	D	364	LEU
1	D	365	THR
1	D	376	VAL
1	D	388	LYS
1	D	410	LYS
1	D	412	ILE
1	E	8	ILE
1	E	9	ILE
1	E	13	VAL
1	E	18	LEU
1	E	22	GLU
1	E	31	TYR
1	E	34	LYS
1	E	38	ILE
1	E	40	LEU
1	E	44	THR
1	E	46	LYS
1	E	47	SER
1	E	48	LEU
1	E	61	SER
1	E	63	ASN
1	E	79	ASP

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Mol	Chain	Res	Type
1	E	83	LYS
1	E	85	ASP
1	E	97	LYS
1	E	100	ASP
1	E	101	THR
1	E	107	LEU
1	E	113	LEU
1	E	134	LEU
1	E	149	MET
1	E	154	LYS
1	E	155	LYS
1	E	156	LEU
1	E	162	ASN
1	E	163	GLN
1	E	165	LYS
1	E	166	MET
1	E	167	ILE
1	E	168	ASN
1	E	171	PHE
1	E	172	GLU
1	E	174	LEU
1	E	181	ILE
1	E	182	PHE
1	E	183	ASP
1	E	187	ASN
1	E	230	THR
1	E	237	ILE
1	E	251	ASN
1	E	257	GLU
1	E	270	LYS
1	E	272	ASP
1	E	273	SER
1	E	292	VAL
1	E	307	LEU
1	E	308	LEU
1	E	326	SER
1	E	327	LEU
1	E	328	THR
1	E	332	LEU
1	E	344	LEU
1	E	353	ASN
1	E	354	LYS

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Mol	Chain	Res	Type
1	E	356	THR
1	E	364	LEU
1	E	388	LYS
1	E	394	MET
1	E	410	LYS
1	E	412	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	70	ASN
1	A	162	ASN
1	A	168	ASN
1	A	187	ASN
1	A	203	HIS
1	A	260	GLN
1	A	266	GLN
1	A	347	GLN
1	A	395	GLN
1	A	405	GLN
1	B	57	GLN
1	B	70	ASN
1	B	162	ASN
1	B	168	ASN
1	B	187	ASN
1	B	203	HIS
1	B	266	GLN
1	B	347	GLN
1	B	395	GLN
1	C	57	GLN
1	C	70	ASN
1	C	162	ASN
1	C	168	ASN
1	C	187	ASN
1	C	203	HIS
1	C	266	GLN
1	C	347	GLN
1	C	395	GLN
1	C	405	GLN
1	D	57	GLN
1	D	70	ASN

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Mol	Chain	Res	Type
1	D	187	ASN
1	D	203	HIS
1	D	266	GLN
1	D	347	GLN
1	D	395	GLN
1	E	57	GLN
1	E	70	ASN
1	E	162	ASN
1	E	187	ASN
1	E	203	HIS
1	E	266	GLN
1	E	347	GLN
1	E	395	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	44/45 (97%)	27 (61%)	0

All (27) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	R	2	U
2	R	3	U
2	R	5	U
2	R	9	U
2	R	10	U
2	R	12	U
2	R	13	U
2	R	14	U
2	R	17	U
2	R	18	U
2	R	19	U
2	R	20	U
2	R	23	U
2	R	24	U
2	R	25	U
2	R	27	U
2	R	29	U
2	R	31	U
2	R	32	U

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Mol	Chain	Res	Type
2	R	33	U
2	R	38	U
2	R	39	U
2	R	40	U
2	R	41	U
2	R	42	U
2	R	44	U
2	R	45	U

There are no RNA pucker outliers to report.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 20 are modelled with single atom - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	421/421 (100%)	-0.08	16 (3%) 41 17	50, 81, 131, 148	0
1	B	415/421 (98%)	-0.15	9 (2%) 62 33	50, 81, 130, 140	0
1	C	413/421 (98%)	-0.08	13 (3%) 49 22	50, 81, 129, 141	0
1	D	416/421 (98%)	0.06	20 (4%) 31 12	50, 81, 129, 141	0
1	E	421/421 (100%)	-0.07	17 (4%) 39 16	49, 82, 131, 145	0
2	R	45/45 (100%)	1.86	19 (42%) 0 0	106, 124, 140, 151	0
All	All	2131/2150 (99%)	-0.02	94 (4%) 35 14	49, 82, 131, 151	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	361	THR	7.9
1	C	2	SER	7.7
1	E	2	SER	6.9
1	D	166	MET	6.8
1	B	2	SER	6.5
2	R	19	U	6.3
1	D	43	ASN	5.5
1	E	364	LEU	5.3
1	C	171	PHE	4.8
1	E	174	LEU	4.8
1	A	2	SER	4.7
1	D	98	ALA	4.7
1	A	362	GLY	4.7
1	D	364	LEU	4.6
1	A	148	GLN	4.6
1	C	174	LEU	4.3
1	B	118	PRO	4.3
1	E	99	GLY	4.3
1	C	161	THR	4.3

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Mol	Chain	Res	Type	RSRZ
2	R	27	U	4.2
2	R	36	U	4.2
1	E	365	THR	4.2
1	A	363	GLY	4.1
1	E	180	ASP	4.0
1	D	2	SER	4.0
2	R	10	U	4.0
1	D	122	SER	3.9
2	R	15	U	3.9
1	D	119	ASP	3.9
1	B	119	ASP	3.8
1	D	371	GLN	3.6
2	R	45	U	3.6
1	D	167	ILE	3.6
1	C	164	CYS	3.6
1	C	177	GLU	3.5
2	R	42	U	3.5
1	E	362	GLY	3.3
2	R	37	U	3.3
1	B	386	ASN	3.3
1	D	44	THR	3.2
1	A	171	PHE	3.2
2	R	33	U	3.2
1	B	122	SER	3.2
1	E	118	PRO	3.2
2	R	41	U	3.1
1	D	177	GLU	3.1
1	C	158	ASP	3.1
2	R	11	U	3.0
1	B	180	ASP	3.0
1	A	359	ASP	3.0
1	D	422	LYS	3.0
1	A	173	PRO	3.0
1	C	179	ARG	2.8
2	R	20	U	2.8
1	E	112	ALA	2.8
1	A	122	SER	2.8
1	A	177	GLU	2.8
1	E	363	GLY	2.8
2	R	6	U	2.7
1	D	113	LEU	2.7
1	E	113	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	149	MET	2.6
1	C	175	VAL	2.6
1	D	174	LEU	2.6
1	D	60	LYS	2.5
1	A	149	MET	2.5
1	D	147	THR	2.5
1	E	176	PRO	2.5
1	E	149	MET	2.4
1	B	124	ALA	2.4
2	R	1	U	2.4
1	C	122	SER	2.4
1	B	422	LYS	2.3
2	R	14	U	2.3
1	E	148	GLN	2.3
1	E	175	VAL	2.3
2	R	24	U	2.3
1	C	173	PRO	2.3
1	A	59	LEU	2.3
1	A	152	TYR	2.2
1	D	355	TYR	2.2
1	B	371	GLN	2.2
2	R	23	U	2.2
1	C	149	MET	2.2
2	R	40	U	2.2
1	D	164	CYS	2.2
1	E	359	ASP	2.1
1	A	57	GLN	2.1
1	C	176	PRO	2.1
1	E	114	ASP	2.1
1	A	170	GLN	2.0
1	D	13	VAL	2.0
1	A	174	LEU	2.0
2	R	2	U	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	IUM	E	534	1/3	0.99	0.12	-0.94	105,105,105,105	0
3	IUM	B	526	1/3	0.99	0.12	-1.16	104,104,104,104	0
3	IUM	D	532	1/3	1.00	0.11	-1.60	100,100,100,100	0
3	IUM	A	522	1/3	0.99	0.10	-1.64	109,109,109,109	0
3	IUM	C	529	1/3	0.99	0.09	-2.67	105,105,105,105	0
3	IUM	A	521	1/3	0.96	0.04	-	162,162,162,162	0
3	IUM	E	535	1/3	0.98	0.06	-	186,186,186,186	0
3	IUM	R	540	1/3	0.69	0.20	-	257,257,257,257	0
3	IUM	B	527	1/3	0.94	0.05	-	199,199,199,199	0
3	IUM	A	523	1/3	0.95	0.04	-	174,174,174,174	0
3	IUM	C	528	1/3	0.97	0.03	-	138,138,138,138	0
3	IUM	C	530	1/3	0.99	0.04	-	151,151,151,151	0
3	IUM	R	538	1/3	0.56	0.07	-	272,272,272,272	0
3	IUM	R	536	1/3	0.91	0.04	-	245,245,245,245	0
3	IUM	A	524	1/3	0.99	0.04	-	158,158,158,158	0
3	IUM	R	537	1/3	0.90	0.12	-	258,258,258,258	0
3	IUM	B	525	1/3	0.90	0.09	-	187,187,187,187	0
3	IUM	D	531	1/3	0.89	0.08	-	188,188,188,188	0
3	IUM	E	533	1/3	0.91	0.03	-	173,173,173,173	0
3	IUM	R	539	1/3	0.88	0.14	-	265,265,265,265	0

6.5 Other polymers [i](#)

There are no such residues in this entry.