



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:36 AM UTC

PDB ID : 1R15 / pdb_00001r15
Title : Aplysia ADP ribosyl cyclase with bound nicotinamide and R5P
Authors : Love, M.L.; Szebenyi, D.M.E.; Kriksunov, I.A.; Thiel, D.J.; Munshi, C.; Graeff, R.; Lee, H.C.; Hao, Q.
Deposited on : 2003-09-23
Resolution : 2.40 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:

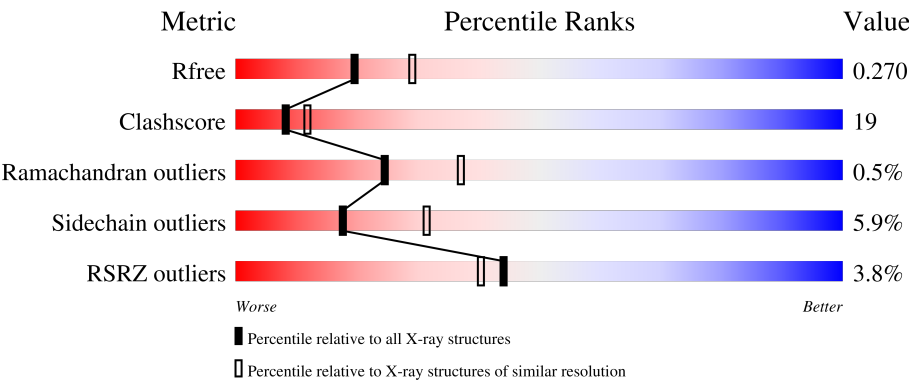
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (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 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	258	4% 61% 32% . .
1	B	258	3% 61% 32% . .
1	C	258	3% 61% 32% . .
1	D	258	2% 64% 29% . . .
1	E	258	6% 59% 33% 5% .

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Mol	Chain	Length	Quality of chain
1	F	258	
1	G	258	
1	H	258	

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
2	N	A	1179	X	-	-	-
2	N	B	1179	X	-	-	-
2	N	C	1179	X	-	-	-
2	N	D	1179	X	-	-	-
2	N	E	1179	X	-	-	-
2	N	F	1179	X	-	-	-
2	N	G	1179	X	-	-	-
2	N	H	1179	X	-	-	-
3	NCA	B	329	-	X	-	-
3	NCA	B	429	-	X	-	-
3	NCA	E	459	-	-	X	-
3	NCA	F	469	-	X	-	-
3	NCA	G	379	-	-	X	-
3	NCA	G	479	-	X	-	-
3	NCA	H	389	-	X	-	-
3	NCA	H	489	-	-	X	-

2 Entry composition

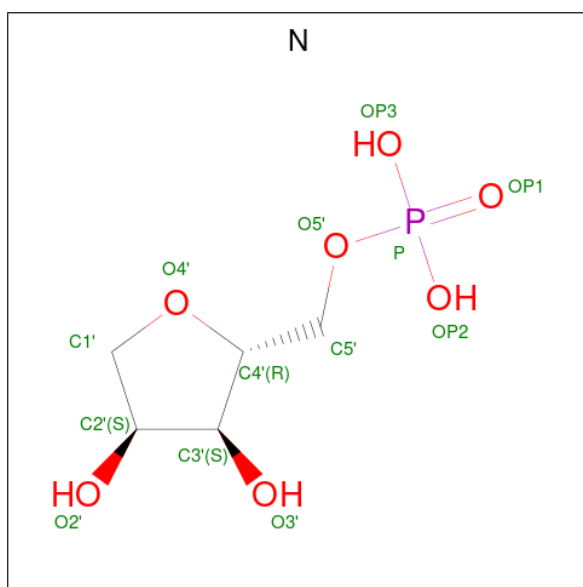
There are 3 unique types of molecules in this entry. The entry contains 16344 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ADP-ribosyl cyclase.

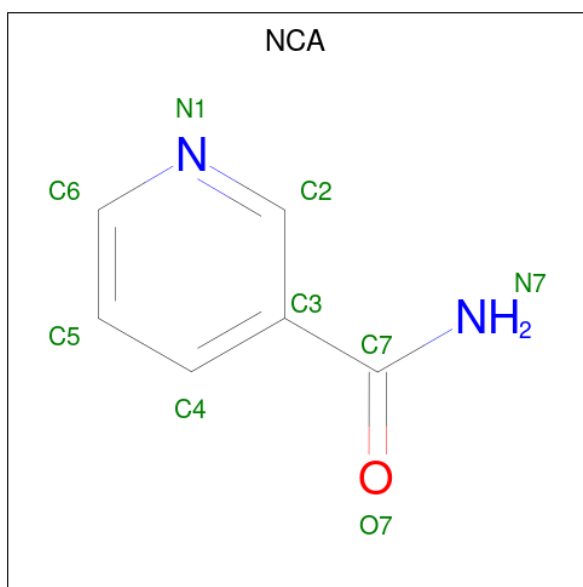
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0
1	B	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0
1	C	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0
1	D	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0
1	E	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0
1	F	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0
1	G	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0
1	H	251	Total 2012	C 1288	N 342	O 368	S 14	0	0	0

- Molecule 2 is ANY 5'-MONOPHOSPHATE NUCLEOTIDE (CCD ID: N) (formula: C₅H₁₁O₇P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			13	5	7	1		
2	B	1	Total	C	O	P	0	0
			13	5	7	1		
2	C	1	Total	C	O	P	0	0
			13	5	7	1		
2	D	1	Total	C	O	P	0	0
			13	5	7	1		
2	E	1	Total	C	O	P	0	0
			13	5	7	1		
2	F	1	Total	C	O	P	0	0
			13	5	7	1		
2	G	1	Total	C	O	P	0	0
			13	5	7	1		
2	H	1	Total	C	O	P	0	0
			13	5	7	1		

- Molecule 3 is NICOTINAMIDE (CCD ID: NCA) (formula: $C_6H_6N_2O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	6	2	1		
3	A	1	Total	C	N	O	0	0
			9	6	2	1		
3	B	1	Total	C	N	O	0	0
			9	6	2	1		
3	B	1	Total	C	N	O	0	0
			9	6	2	1		
3	C	1	Total	C	N	O	0	0
			9	6	2	1		
3	C	1	Total	C	N	O	0	0
			9	6	2	1		
3	D	1	Total	C	N	O	0	0
			9	6	2	1		
3	D	1	Total	C	N	O	0	0
			9	6	2	1		
3	E	1	Total	C	N	O	0	0
			9	6	2	1		
3	E	1	Total	C	N	O	0	0
			9	6	2	1		
3	F	1	Total	C	N	O	0	0
			9	6	2	1		
3	F	1	Total	C	N	O	0	0
			9	6	2	1		
3	G	1	Total	C	N	O	0	0
			9	6	2	1		
3	G	1	Total	C	N	O	0	0
			9	6	2	1		

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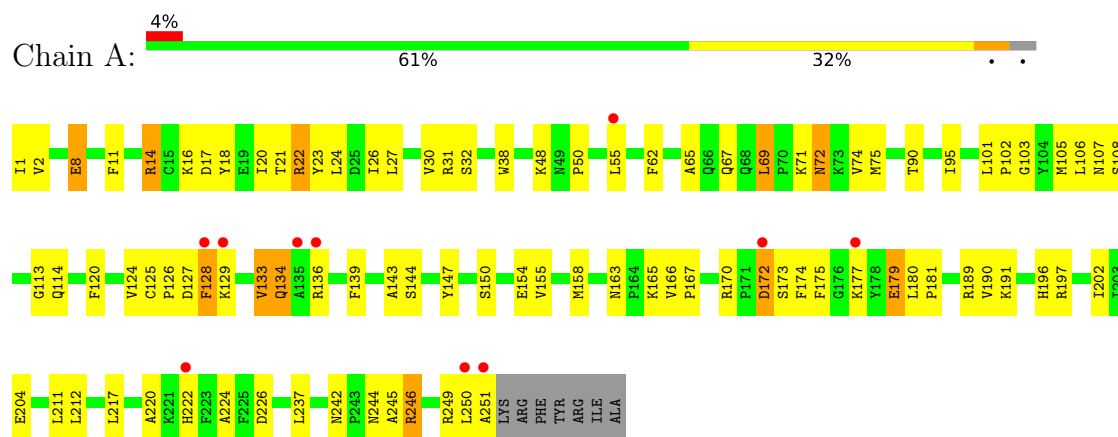
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total	C	N	O	0	0
			9	6	2	1		
3	H	1	Total	C	N	O	0	0
			9	6	2	1		

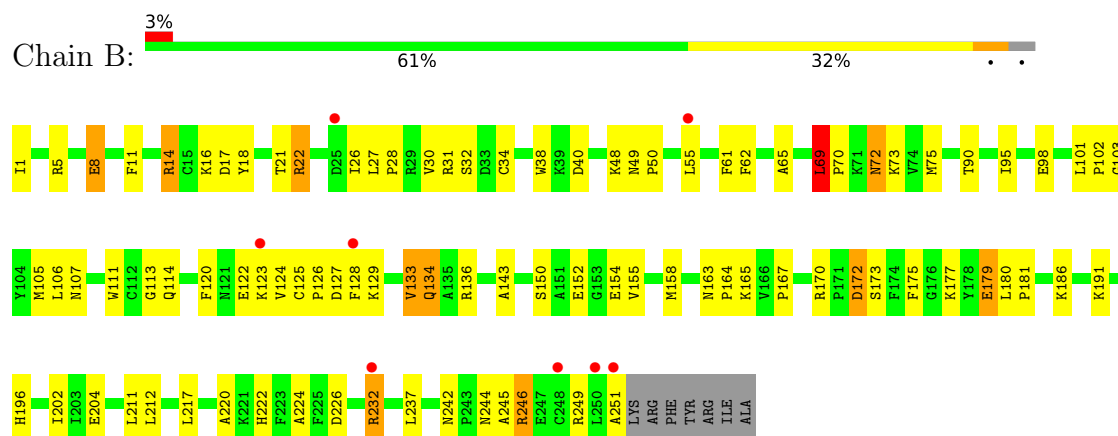
3 Residue-property plots [i](#)

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.

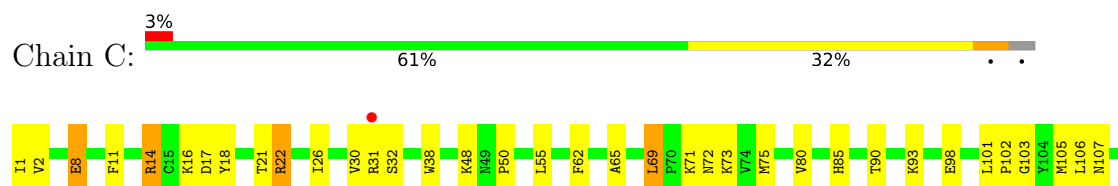
• Molecule 1: ADP-ribosyl cyclase

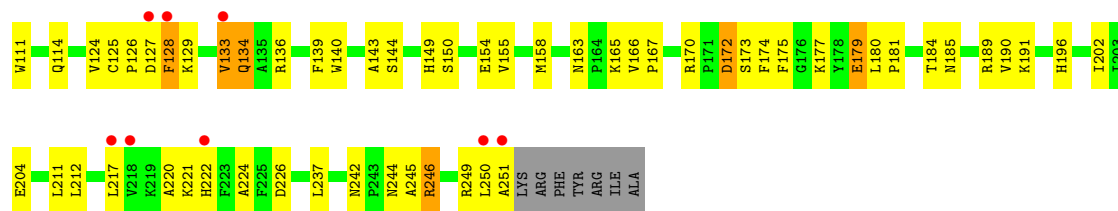


• Molecule 1: ADP-ribosyl cyclase

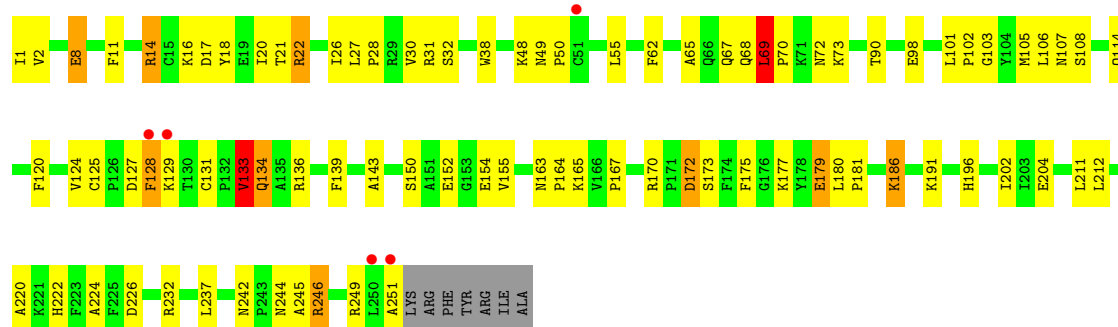


• Molecule 1: ADP-ribosyl cyclase

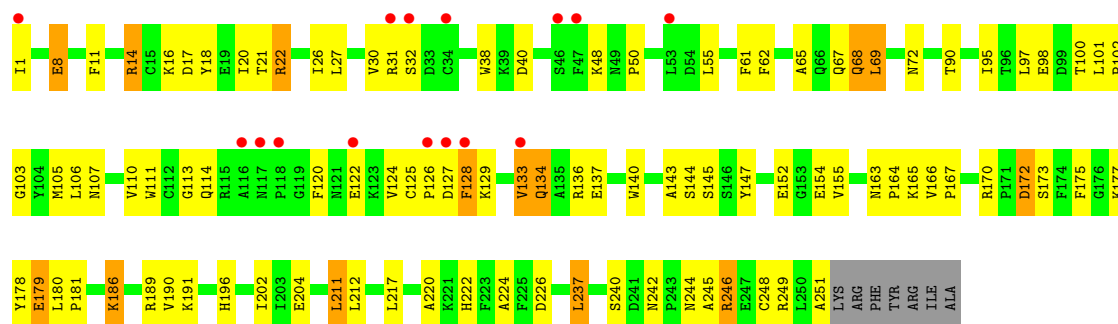




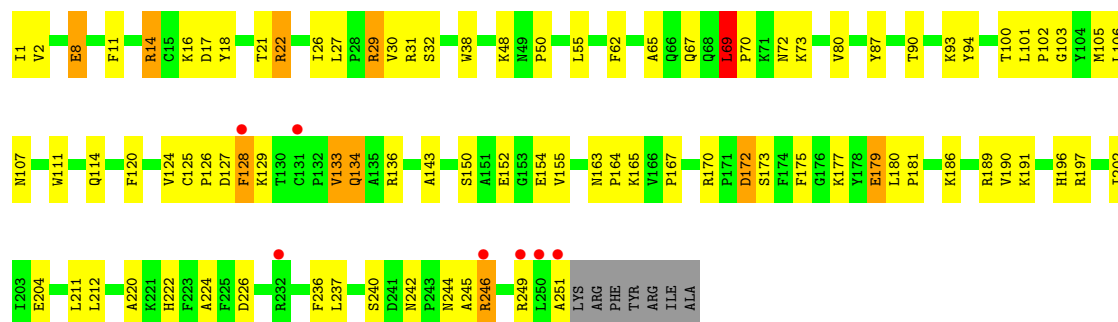
• Molecule 1: ADP-ribosyl cyclase



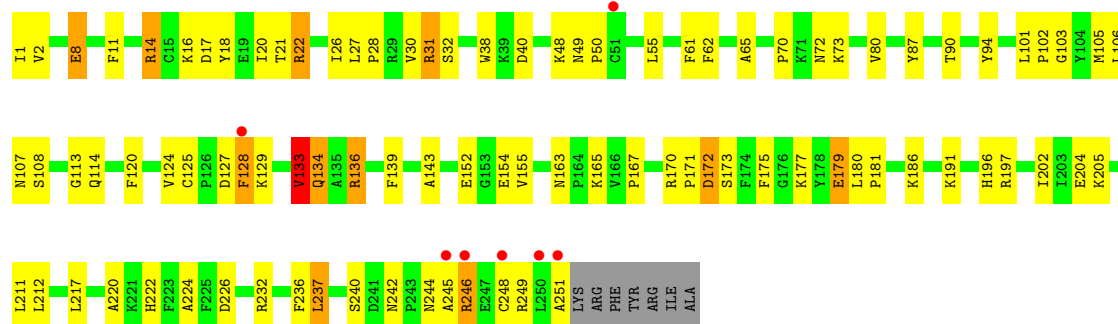
• Molecule 1: ADP-ribosyl cyclase



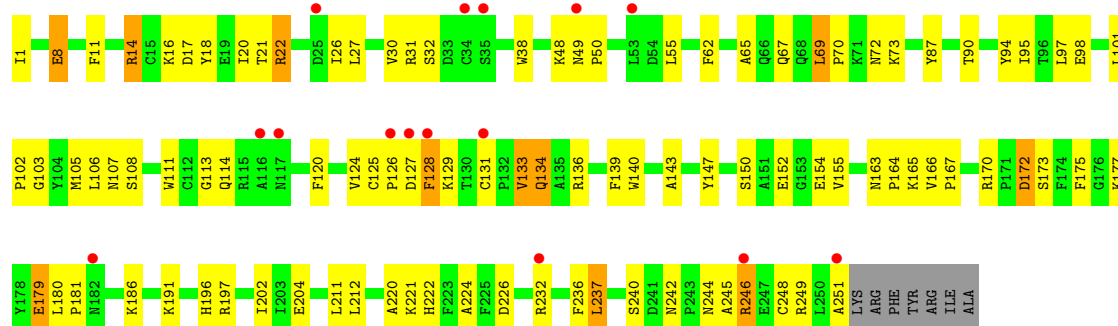
• Molecule 1: ADP-ribosyl cyclase



• Molecule 1: ADP-ribosyl cyclase



• Molecule 1: ADP-ribosyl cyclase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.40Å 75.32Å 138.13Å 88.16° 89.22° 89.09°	Depositor
Resolution (Å)	33.00 – 2.40 33.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (33.00-2.40) 60.1 (33.00-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.244 , 0.269 0.244 , 0.270	Depositor DCC
R_{free} test set	2873 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	33.0	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.085 for h,-k,-l 0.022 for -h,k,-l 0.008 for -h,-k,l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	16344	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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: NCA

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	0.80	1/2064 (0.0%)	1.15	14/2793 (0.5%)
1	B	0.87	1/2064 (0.0%)	1.16	16/2793 (0.6%)
1	C	0.81	1/2064 (0.0%)	1.14	13/2793 (0.5%)
1	D	0.84	1/2064 (0.0%)	1.16	17/2793 (0.6%)
1	E	0.80	1/2064 (0.0%)	1.13	13/2793 (0.5%)
1	F	0.87	1/2064 (0.0%)	1.18	16/2793 (0.6%)
1	G	0.86	2/2064 (0.1%)	1.27	17/2793 (0.6%)
1	H	0.78	1/2064 (0.0%)	1.15	16/2793 (0.6%)
All	All	0.83	9/16512 (0.1%)	1.17	122/22344 (0.5%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	GLU	CD-OE2	13.78	1.51	1.25
1	E	179	GLU	CD-OE2	13.51	1.51	1.25
1	C	179	GLU	CD-OE2	13.47	1.50	1.25
1	H	179	GLU	CD-OE2	13.38	1.50	1.25
1	G	179	GLU	CD-OE2	13.24	1.50	1.25
1	F	179	GLU	CD-OE2	13.11	1.50	1.25
1	D	179	GLU	CD-OE2	12.64	1.49	1.25
1	B	179	GLU	CD-OE2	12.57	1.49	1.25
1	G	136	ARG	CD-NE	-6.94	1.36	1.46

All (122) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	136	ARG	NE-CZ-NH2	17.52	134.96	119.20
1	G	136	ARG	NE-CZ-NH1	-16.14	105.36	121.50
1	B	22	ARG	N-CA-C	14.33	129.72	111.24
1	D	22	ARG	N-CA-C	14.13	129.47	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	22	ARG	N-CA-C	13.79	129.03	111.24
1	H	22	ARG	N-CA-C	13.76	128.99	111.24
1	A	22	ARG	N-CA-C	13.57	128.75	111.24
1	G	22	ARG	N-CA-C	13.51	128.67	111.24
1	C	22	ARG	N-CA-C	13.45	128.59	111.24
1	F	22	ARG	N-CA-C	13.23	128.31	111.24
1	G	136	ARG	CD-NE-CZ	12.89	142.44	124.40
1	C	242	ASN	CA-C-N	10.01	130.16	119.05
1	C	242	ASN	C-N-CA	10.01	130.16	119.05
1	B	173	SER	N-CA-C	-9.98	95.75	110.52
1	E	173	SER	N-CA-C	-9.95	96.16	110.59
1	D	242	ASN	CA-C-N	9.75	129.88	119.05
1	D	242	ASN	C-N-CA	9.75	129.88	119.05
1	A	242	ASN	CA-C-N	9.75	129.87	119.05
1	A	242	ASN	C-N-CA	9.75	129.87	119.05
1	C	173	SER	N-CA-C	-9.70	96.53	110.59
1	A	173	SER	N-CA-C	-9.65	96.60	110.59
1	H	242	ASN	CA-C-N	9.59	129.69	119.05
1	H	242	ASN	C-N-CA	9.59	129.69	119.05
1	G	242	ASN	CA-C-N	9.51	129.60	119.05
1	G	242	ASN	C-N-CA	9.51	129.60	119.05
1	F	242	ASN	CA-C-N	9.47	129.56	119.05
1	F	242	ASN	C-N-CA	9.47	129.56	119.05
1	H	173	SER	N-CA-C	-9.39	96.98	110.59
1	E	242	ASN	CA-C-N	9.32	129.40	119.05
1	E	242	ASN	C-N-CA	9.32	129.40	119.05
1	F	173	SER	N-CA-C	-9.32	96.73	110.52
1	D	173	SER	N-CA-C	-9.30	96.75	110.52
1	B	242	ASN	CA-C-N	9.14	129.19	119.05
1	B	242	ASN	C-N-CA	9.14	129.19	119.05
1	G	173	SER	N-CA-C	-9.04	97.48	110.59
1	G	136	ARG	CG-CD-NE	7.83	129.23	112.00
1	F	69	LEU	CA-C-N	7.79	128.27	119.93
1	F	69	LEU	C-N-CA	7.79	128.27	119.93
1	F	224	ALA	N-CA-C	-6.93	101.59	110.53
1	B	69	LEU	N-CA-C	6.90	119.62	109.62
1	G	224	ALA	N-CA-C	-6.83	101.72	110.53
1	B	224	ALA	N-CA-C	-6.71	101.87	110.53
1	B	114	GLN	N-CA-C	-6.65	98.96	109.07
1	E	224	ALA	N-CA-C	-6.61	102.00	110.53
1	C	2	VAL	N-CA-C	6.60	115.84	108.05
1	H	224	ALA	N-CA-C	-6.55	102.08	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	133	VAL	CB-CA-C	-6.54	103.51	111.88
1	G	133	VAL	CB-CA-C	-6.42	103.67	111.88
1	F	2	VAL	N-CA-C	6.38	115.57	108.05
1	E	114	GLN	N-CA-C	-6.31	99.48	109.07
1	B	133	VAL	CB-CA-C	-6.30	103.81	111.88
1	C	114	GLN	N-CA-C	-6.27	99.54	109.07
1	B	72	ASN	N-CA-C	6.26	120.71	113.38
1	A	2	VAL	N-CA-C	6.23	115.40	108.05
1	D	224	ALA	N-CA-C	-6.22	102.50	110.53
1	D	133	VAL	CB-CA-C	-6.17	103.98	111.88
1	H	133	VAL	CB-CA-C	-6.15	104.00	111.88
1	F	114	GLN	N-CA-C	-6.13	99.76	109.07
1	D	48	LYS	N-CA-C	-6.11	101.16	110.14
1	E	133	VAL	CB-CA-C	-6.11	104.06	111.88
1	C	21	THR	N-CA-C	6.07	123.50	114.09
1	A	224	ALA	N-CA-C	-6.06	102.37	110.55
1	C	224	ALA	N-CA-C	-6.05	102.72	110.53
1	H	114	GLN	N-CA-C	-6.05	99.88	109.07
1	H	48	LYS	N-CA-C	-6.03	101.27	110.14
1	G	114	GLN	N-CA-C	-6.02	99.91	109.07
1	E	48	LYS	N-CA-C	-6.01	101.30	110.14
1	F	48	LYS	N-CA-C	-5.99	101.33	110.14
1	B	172	ASP	N-CA-C	5.99	119.86	111.30
1	C	133	VAL	CB-CA-C	-5.93	104.29	111.88
1	C	48	LYS	N-CA-C	-5.92	101.44	110.14
1	G	172	ASP	N-CA-C	5.92	119.77	111.30
1	A	133	VAL	CB-CA-C	-5.90	104.33	111.88
1	A	20	ILE	N-CA-C	5.89	118.45	111.09
1	D	114	GLN	N-CA-C	-5.86	99.79	108.99
1	B	48	LYS	N-CA-C	-5.80	101.62	110.14
1	A	114	GLN	N-CA-C	-5.78	99.91	108.99
1	A	48	LYS	N-CA-C	-5.74	101.71	110.14
1	D	69	LEU	N-CA-C	5.74	117.76	109.04
1	D	2	VAL	N-CA-C	5.71	114.79	108.05
1	D	68	GLN	N-CA-C	-5.71	101.83	110.28
1	E	21	THR	N-CA-C	5.66	122.86	114.09
1	G	2	VAL	N-CA-C	5.62	114.69	108.05
1	A	21	THR	N-CA-C	5.61	122.78	114.09
1	F	172	ASP	N-CA-C	5.59	119.29	111.30
1	A	72	ASN	N-CA-CB	-5.58	107.81	114.17
1	H	67	GLN	CA-C-N	-5.54	115.24	123.11
1	H	67	GLN	C-N-CA	-5.54	115.24	123.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	21	THR	N-CA-C	5.52	122.65	114.09
1	E	20	ILE	N-CA-C	5.50	118.81	111.44
1	A	133	VAL	N-CA-C	5.50	116.13	110.36
1	D	20	ILE	N-CA-C	5.45	118.75	111.44
1	B	232	ARG	N-CA-C	5.45	117.64	111.11
1	H	133	VAL	N-CA-C	5.38	116.00	110.36
1	D	21	THR	N-CA-C	5.36	122.40	114.09
1	D	69	LEU	CA-C-N	5.35	126.53	119.84
1	D	69	LEU	C-N-CA	5.35	126.53	119.84
1	H	232	ARG	N-CA-C	5.35	117.81	111.33
1	D	172	ASP	N-CA-C	5.34	118.94	111.30
1	B	21	THR	N-CA-C	5.33	122.35	114.09
1	A	172	ASP	N-CA-C	5.32	118.91	111.30
1	H	172	ASP	N-CA-C	5.30	118.88	111.30
1	G	21	THR	N-CA-C	5.28	122.27	114.09
1	H	20	ILE	N-CA-C	5.27	118.50	111.44
1	F	29	ARG	N-CA-C	-5.25	103.47	110.55
1	F	21	THR	N-CA-C	5.24	122.21	114.09
1	E	172	ASP	N-CA-C	5.22	118.77	111.30
1	G	48	LYS	N-CA-C	-5.14	102.58	110.14
1	B	69	LEU	CA-C-N	5.13	125.42	119.93
1	B	69	LEU	C-N-CA	5.13	125.42	119.93
1	C	2	VAL	CA-C-O	5.12	122.52	119.19
1	D	186	LYS	N-CA-C	-5.11	106.55	112.89
1	G	31	ARG	N-CA-C	5.10	116.65	111.14
1	E	133	VAL	N-CA-C	5.09	115.71	110.36
1	B	34	CYS	N-CA-C	5.06	116.80	111.28
1	C	133	VAL	N-CA-C	5.04	115.65	110.36
1	G	20	ILE	N-CA-C	5.04	118.19	111.44
1	C	172	ASP	N-CA-C	5.03	118.49	111.30
1	F	27	LEU	CA-C-N	5.03	125.01	120.03
1	F	27	LEU	C-N-CA	5.03	125.01	120.03
1	H	131	CYS	N-CA-C	5.02	117.09	110.36
1	E	186	LYS	N-CA-C	-5.01	106.68	112.89

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2012	0	1968	85	0
1	B	2012	0	1968	85	0
1	C	2012	0	1968	91	0
1	D	2012	0	1968	84	0
1	E	2012	0	1968	84	1
1	F	2012	0	1968	70	0
1	G	2012	0	1968	88	0
1	H	2012	0	1968	89	1
2	A	13	0	8	2	0
2	B	13	0	8	0	0
2	C	13	0	8	2	0
2	D	13	0	8	0	0
2	E	13	0	8	1	0
2	F	13	0	8	1	0
2	G	13	0	8	3	0
2	H	13	0	8	0	0
3	A	18	0	12	3	0
3	B	18	0	12	3	0
3	C	18	0	12	4	0
3	D	18	0	12	2	0
3	E	18	0	12	7	0
3	F	18	0	12	3	0
3	G	18	0	12	5	0
3	H	18	0	12	7	0
All	All	16344	0	15904	622	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (622) 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:123:LYS:HD2	1:C:149:HIS:CE1	1.86	1.10
1:B:123:LYS:HD2	1:C:149:HIS:ND1	1.76	0.99
1:D:152:GLU:HG2	1:D:186:LYS:HB3	1.40	0.97
1:A:139:PHE:HB3	3:A:419:NCA:H6	1.42	0.97
1:G:152:GLU:HG2	1:G:186:LYS:HB3	1.46	0.96
1:B:111:TRP:H	3:B:429:NCA:HN72	1.11	0.96
1:D:101:LEU:HG	1:D:105:MET:HE2	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:LEU:HG	1:B:105:MET:HE2	1.49	0.94
1:B:123:LYS:HG2	1:C:184:THR:HG22	1.50	0.93
1:E:101:LEU:HG	1:E:105:MET:HE2	1.50	0.93
1:F:101:LEU:HG	1:F:105:MET:HE2	1.49	0.93
1:A:17:ASP:OD1	1:B:14:ARG:HD2	1.70	0.91
1:H:101:LEU:HG	1:H:105:MET:HE2	1.52	0.91
1:G:101:LEU:HG	1:G:105:MET:HE2	1.50	0.91
1:B:123:LYS:CD	1:C:149:HIS:CE1	2.54	0.90
1:H:140:TRP:CD1	3:H:489:NCA:H5	2.06	0.90
1:A:101:LEU:HG	1:A:105:MET:HE2	1.54	0.89
1:C:101:LEU:HG	1:C:105:MET:HE2	1.55	0.89
1:G:17:ASP:OD1	1:H:14:ARG:HD2	1.73	0.88
1:D:133:VAL:HG22	1:G:177:LYS:HB3	1.56	0.87
2:F:1179:N:H1'	3:F:369:NCA:H6	1.54	0.87
1:C:69:LEU:CD2	1:C:150:SER:HB2	2.06	0.86
1:D:69:LEU:HD22	1:D:150:SER:HB2	1.57	0.86
1:F:69:LEU:HD22	1:F:150:SER:HB2	1.58	0.85
1:H:108:SER:H	3:H:389:NCA:HN72	1.23	0.85
1:E:128:PHE:HB3	1:E:129:LYS:HD2	1.58	0.85
1:H:152:GLU:HG2	1:H:186:LYS:HB3	1.57	0.85
1:E:17:ASP:OD1	1:F:14:ARG:HD2	1.77	0.84
1:A:128:PHE:HB3	1:A:129:LYS:HD2	1.60	0.84
1:H:128:PHE:HB3	1:H:129:LYS:HD2	1.59	0.83
1:G:14:ARG:HD2	1:H:17:ASP:OD1	1.79	0.83
1:A:128:PHE:CE2	1:A:136:ARG:HD3	2.12	0.83
1:E:129:LYS:CD	1:E:129:LYS:H	1.91	0.83
1:G:128:PHE:HB3	1:G:129:LYS:HD2	1.62	0.82
1:C:17:ASP:OD1	1:D:14:ARG:HD2	1.80	0.82
1:E:128:PHE:CE2	1:E:136:ARG:HD3	2.14	0.82
1:E:129:LYS:HD2	1:E:129:LYS:H	1.45	0.81
1:C:128:PHE:HB3	1:C:129:LYS:HD2	1.62	0.81
1:A:129:LYS:H	1:A:129:LYS:CD	1.94	0.81
1:F:128:PHE:HB3	1:F:129:LYS:HD2	1.63	0.81
1:H:129:LYS:HD2	1:H:129:LYS:H	1.46	0.80
1:H:129:LYS:H	1:H:129:LYS:CD	1.94	0.80
1:C:128:PHE:CE2	1:C:136:ARG:HD3	2.15	0.79
1:C:129:LYS:CD	1:C:129:LYS:H	1.96	0.79
1:F:128:PHE:CE2	1:F:136:ARG:HD3	2.18	0.79
1:B:128:PHE:HB3	1:B:129:LYS:HD2	1.65	0.79
1:B:123:LYS:CG	1:C:184:THR:HG22	2.13	0.78
1:H:128:PHE:CE2	1:H:136:ARG:HD3	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:129:LYS:CD	1:G:129:LYS:H	1.97	0.78
1:B:128:PHE:CE2	1:B:136:ARG:HD3	2.19	0.78
1:A:129:LYS:HD2	1:A:129:LYS:H	1.49	0.77
1:C:129:LYS:HD2	1:C:129:LYS:H	1.49	0.77
1:F:129:LYS:H	1:F:129:LYS:CD	1.97	0.77
1:E:14:ARG:HD2	1:F:17:ASP:OD1	1.85	0.77
1:C:71:LYS:HG2	1:C:72:ASN:ND2	2.00	0.77
1:B:5:ARG:HD2	1:C:185:ASN:O	1.85	0.77
1:E:163:ASN:C	1:E:163:ASN:HD22	1.91	0.77
1:D:133:VAL:HG13	1:G:177:LYS:HG2	1.67	0.77
1:D:133:VAL:CG2	1:G:177:LYS:HB3	2.14	0.76
1:B:129:LYS:CD	1:B:129:LYS:H	1.99	0.76
1:D:128:PHE:HB3	1:D:129:LYS:HD2	1.67	0.76
1:F:111:TRP:O	3:F:469:NCA:N7	2.19	0.76
1:A:167:PRO:HG2	1:A:170:ARG:HG2	1.68	0.76
1:B:123:LYS:CD	1:C:149:HIS:HE1	1.97	0.75
1:H:8:GLU:HG2	1:H:38:TRP:CZ2	2.22	0.75
1:B:111:TRP:N	3:B:429:NCA:HN72	1.84	0.75
1:H:69:LEU:HD13	1:H:69:LEU:H	1.52	0.74
1:E:167:PRO:HG2	1:E:170:ARG:HG2	1.70	0.74
1:F:129:LYS:HD2	1:F:129:LYS:H	1.53	0.74
1:D:128:PHE:CE2	1:D:136:ARG:HD3	2.23	0.73
1:G:129:LYS:HD2	1:G:129:LYS:H	1.52	0.73
1:B:129:LYS:HD2	1:B:129:LYS:H	1.53	0.73
1:C:167:PRO:HG2	1:C:170:ARG:HG2	1.70	0.72
1:H:167:PRO:HG2	1:H:170:ARG:HG2	1.71	0.72
1:A:69:LEU:CD2	1:A:150:SER:HB2	2.19	0.72
1:E:240:SER:OG	1:F:237:LEU:HD13	1.90	0.72
1:B:101:LEU:HB3	1:B:102:PRO:HD3	1.72	0.71
1:C:8:GLU:HG2	1:C:38:TRP:CZ2	2.25	0.71
1:A:8:GLU:HG2	1:A:38:TRP:CZ2	2.26	0.71
1:G:246:ARG:O	1:G:249:ARG:HG3	1.91	0.71
1:D:129:LYS:H	1:D:129:LYS:CD	2.04	0.71
1:C:101:LEU:HB3	1:C:102:PRO:HD3	1.72	0.70
1:B:163:ASN:C	1:B:163:ASN:HD22	1.98	0.70
1:E:8:GLU:HG2	1:E:38:TRP:CZ2	2.26	0.70
1:F:246:ARG:O	1:F:249:ARG:HG3	1.91	0.70
1:D:129:LYS:HD2	1:D:129:LYS:H	1.57	0.70
1:G:237:LEU:HD13	1:H:240:SER:OG	1.92	0.70
1:H:163:ASN:C	1:H:163:ASN:HD22	1.99	0.70
1:C:14:ARG:HD2	1:D:17:ASP:OD1	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:72:ASN:HA	1:F:154:GLU:O	1.92	0.70
1:A:163:ASN:C	1:A:163:ASN:HD22	1.98	0.69
1:C:163:ASN:C	1:C:163:ASN:HD22	1.99	0.69
1:C:31:ARG:HG3	1:C:31:ARG:HH11	1.57	0.69
1:E:69:LEU:HG	1:E:95:ILE:HD11	1.73	0.69
1:D:129:LYS:HG3	1:G:171:PRO:HG3	1.74	0.69
1:E:101:LEU:HB3	1:E:102:PRO:HD3	1.74	0.69
1:G:240:SER:OG	1:H:237:LEU:HD13	1.93	0.68
1:B:8:GLU:HG2	1:B:38:TRP:CZ2	2.28	0.68
1:D:129:LYS:HB3	1:G:217:LEU:HD21	1.75	0.68
1:B:167:PRO:HG2	1:B:170:ARG:HG2	1.74	0.68
1:D:163:ASN:HD22	1:D:163:ASN:C	2.00	0.68
1:F:8:GLU:HG2	1:F:38:TRP:CZ2	2.29	0.68
1:D:101:LEU:HB3	1:D:102:PRO:HD3	1.76	0.68
1:E:134:GLN:H	1:E:134:GLN:HE21	1.42	0.68
1:H:134:GLN:H	1:H:134:GLN:HE21	1.42	0.67
1:D:167:PRO:HG2	1:D:170:ARG:HG2	1.75	0.67
1:A:31:ARG:HG3	1:A:31:ARG:HH11	1.59	0.67
1:A:69:LEU:HD22	1:A:150:SER:HB2	1.76	0.67
1:H:70:PRO:HG2	1:H:73:LYS:HB2	1.77	0.67
1:E:237:LEU:HD13	1:F:240:SER:OG	1.95	0.67
1:A:31:ARG:NH2	1:C:191:LYS:NZ	2.42	0.67
1:F:101:LEU:HB3	1:F:102:PRO:HD3	1.76	0.67
1:E:111:TRP:O	3:E:459:NCA:N7	2.27	0.67
1:D:246:ARG:O	1:D:249:ARG:HG3	1.95	0.67
1:A:251:ALA:HA	1:B:251:ALA:HA	1.75	0.66
1:D:8:GLU:HG2	1:D:38:TRP:CZ2	2.30	0.66
1:G:8:GLU:HG2	1:G:38:TRP:CZ2	2.30	0.66
1:A:14:ARG:HD2	1:B:17:ASP:OD1	1.95	0.66
1:F:163:ASN:C	1:F:163:ASN:HD22	2.03	0.66
1:H:107:ASN:OD1	3:H:389:NCA:N7	2.27	0.66
1:G:134:GLN:HE21	1:G:134:GLN:H	1.43	0.66
1:H:31:ARG:HG3	1:H:31:ARG:HH11	1.60	0.66
1:H:101:LEU:HB3	1:H:102:PRO:HD3	1.77	0.66
1:A:65:ALA:HB1	1:A:102:PRO:HG3	1.79	0.65
1:G:191:LYS:HE3	1:G:226:ASP:OD2	1.96	0.65
1:B:127:ASP:OD1	1:B:129:LYS:HD3	1.97	0.65
1:C:111:TRP:H	3:C:439:NCA:HN72	1.44	0.65
1:B:191:LYS:HE3	1:B:226:ASP:OD2	1.96	0.65
1:A:101:LEU:HB3	1:A:102:PRO:HD3	1.78	0.65
1:F:191:LYS:HE3	1:F:226:ASP:OD2	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:ALA:HB1	1:B:102:PRO:HG3	1.79	0.65
1:E:31:ARG:HG3	1:E:31:ARG:HH11	1.61	0.65
1:A:69:LEU:HD22	1:A:150:SER:CB	2.27	0.65
1:F:167:PRO:HG2	1:F:170:ARG:HG2	1.79	0.65
1:B:246:ARG:O	1:B:249:ARG:HG3	1.97	0.64
1:C:31:ARG:HG3	1:C:31:ARG:NH1	2.12	0.64
1:F:134:GLN:H	1:F:134:GLN:HE21	1.43	0.64
1:F:134:GLN:H	1:F:134:GLN:NE2	1.96	0.64
1:B:69:LEU:HG	1:B:95:ILE:HD11	1.79	0.64
1:G:163:ASN:C	1:G:163:ASN:HD22	2.05	0.64
1:G:167:PRO:HG2	1:G:170:ARG:HG2	1.79	0.64
1:B:134:GLN:HE21	1:B:134:GLN:H	1.45	0.64
1:C:134:GLN:H	1:C:134:GLN:HE21	1.45	0.64
1:E:110:VAL:HA	3:E:459:NCA:O7	1.98	0.64
1:A:31:ARG:HG3	1:A:31:ARG:NH1	2.12	0.64
1:H:31:ARG:HG3	1:H:31:ARG:NH1	2.13	0.64
1:A:134:GLN:H	1:A:134:GLN:HE21	1.44	0.63
1:G:70:PRO:HG2	1:G:73:LYS:HB2	1.80	0.63
1:H:108:SER:N	3:H:389:NCA:HN72	1.95	0.63
1:G:101:LEU:HB3	1:G:102:PRO:HD3	1.79	0.63
1:E:140:TRP:CD1	3:E:459:NCA:H5	2.34	0.63
1:E:251:ALA:HA	1:F:251:ALA:HA	1.79	0.63
1:H:127:ASP:OD1	1:H:129:LYS:HD3	1.98	0.63
1:D:191:LYS:HE3	1:D:226:ASP:OD2	1.99	0.62
1:D:133:VAL:HG11	1:G:177:LYS:CD	2.30	0.62
1:B:26:ILE:HD12	1:B:26:ILE:N	2.13	0.62
1:G:152:GLU:HG2	1:G:186:LYS:CB	2.26	0.62
1:H:69:LEU:HD13	1:H:69:LEU:N	2.14	0.62
1:D:133:VAL:CG1	1:G:177:LYS:HG2	2.28	0.62
1:H:65:ALA:HB1	1:H:102:PRO:HG3	1.82	0.62
1:H:191:LYS:HE3	1:H:226:ASP:OD2	2.00	0.62
1:C:65:ALA:HB1	1:C:102:PRO:HG3	1.82	0.62
1:D:26:ILE:HD12	1:D:26:ILE:N	2.15	0.62
1:D:65:ALA:HB1	1:D:102:PRO:HG3	1.83	0.61
1:E:65:ALA:HB1	1:E:102:PRO:HG3	1.82	0.61
1:H:134:GLN:H	1:H:134:GLN:NE2	1.98	0.61
1:E:31:ARG:HG3	1:E:31:ARG:NH1	2.14	0.61
1:H:246:ARG:O	1:H:249:ARG:HG3	2.01	0.61
1:C:72:ASN:HA	1:C:154:GLU:O	2.01	0.60
1:B:152:GLU:HG2	1:B:186:LYS:HB3	1.83	0.60
1:C:127:ASP:OD1	1:C:129:LYS:HD3	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:ASP:HA	1:C:177:LYS:HG3	1.84	0.60
1:D:31:ARG:HH11	1:D:31:ARG:HG3	1.64	0.60
1:A:108:SER:H	3:A:319:NCA:HN72	1.48	0.60
1:A:246:ARG:O	1:A:249:ARG:HG3	2.01	0.60
1:D:134:GLN:H	1:D:134:GLN:HE21	1.49	0.60
1:E:127:ASP:OD1	1:E:129:LYS:HD3	2.00	0.60
1:F:31:ARG:HG3	1:F:31:ARG:HH11	1.66	0.60
1:F:111:TRP:H	3:F:469:NCA:HN72	1.49	0.60
1:E:134:GLN:H	1:E:134:GLN:NE2	1.99	0.60
1:G:134:GLN:H	1:G:134:GLN:NE2	2.00	0.60
1:A:31:ARG:NH2	1:C:191:LYS:HZ1	1.99	0.60
1:E:191:LYS:HE3	1:E:226:ASP:OD2	2.02	0.60
1:D:127:ASP:OD1	1:D:129:LYS:HD3	2.02	0.60
1:C:69:LEU:CD2	1:C:150:SER:CB	2.79	0.60
1:G:127:ASP:OD1	1:G:129:LYS:HD3	2.02	0.60
1:C:251:ALA:HA	1:D:251:ALA:HA	1.84	0.59
1:H:26:ILE:N	1:H:26:ILE:HD12	2.17	0.59
1:E:163:ASN:C	1:E:163:ASN:ND2	2.60	0.59
1:H:140:TRP:HD1	3:H:489:NCA:H5	1.66	0.59
1:A:191:LYS:HE3	1:A:226:ASP:OD2	2.02	0.59
1:B:55:LEU:HD22	1:B:55:LEU:H	1.68	0.59
1:G:65:ALA:HB1	1:G:102:PRO:HG3	1.83	0.59
1:F:26:ILE:N	1:F:26:ILE:HD12	2.17	0.59
1:B:134:GLN:H	1:B:134:GLN:NE2	1.99	0.59
1:E:1:ILE:HG22	1:E:125:CYS:O	2.02	0.59
1:E:129:LYS:HD2	1:E:129:LYS:N	2.17	0.59
1:E:172:ASP:HA	1:E:177:LYS:HG3	1.85	0.59
1:F:127:ASP:OD1	1:F:129:LYS:HD3	2.03	0.59
1:G:31:ARG:HG3	1:G:31:ARG:HH11	1.68	0.59
1:H:172:ASP:HA	1:H:177:LYS:HG3	1.85	0.59
1:B:122:GLU:O	1:C:185:ASN:OD1	2.20	0.59
1:B:31:ARG:HG3	1:B:31:ARG:HH11	1.66	0.58
1:A:127:ASP:OD1	1:A:129:LYS:HD3	2.03	0.58
1:H:111:TRP:O	3:H:489:NCA:N7	2.36	0.58
1:H:129:LYS:HD2	1:H:129:LYS:N	2.18	0.58
1:C:246:ARG:O	1:C:249:ARG:HG3	2.02	0.58
1:A:172:ASP:HA	1:A:177:LYS:HG3	1.86	0.58
1:B:55:LEU:HD22	1:B:55:LEU:N	2.19	0.58
1:C:128:PHE:CD2	1:C:136:ARG:HD3	2.38	0.58
2:C:1179:N:H1'	3:C:339:NCA:H6	1.85	0.58
1:A:71:LYS:O	1:A:72:ASN:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:ASN:HA	1:B:154:GLU:O	2.04	0.58
1:D:177:LYS:HB3	1:G:133:VAL:HG22	1.86	0.58
1:A:134:GLN:H	1:A:134:GLN:NE2	2.02	0.57
1:D:152:GLU:HG2	1:D:186:LYS:CB	2.26	0.57
1:D:196:HIS:CE1	1:D:202:ILE:HG23	2.39	0.57
1:D:134:GLN:H	1:D:134:GLN:NE2	2.02	0.57
1:B:31:ARG:HG3	1:B:31:ARG:NH1	2.19	0.57
1:E:26:ILE:HD12	1:E:26:ILE:N	2.19	0.57
1:D:129:LYS:CB	1:G:217:LEU:HD21	2.35	0.57
1:H:69:LEU:N	1:H:69:LEU:CD1	2.67	0.57
1:C:69:LEU:HD22	1:C:150:SER:CB	2.35	0.57
1:D:31:ARG:HG3	1:D:31:ARG:NH1	2.18	0.57
1:E:101:LEU:CG	1:E:105:MET:HE2	2.31	0.57
1:A:128:PHE:CD2	1:A:136:ARG:HD3	2.39	0.57
1:C:134:GLN:H	1:C:134:GLN:NE2	2.01	0.56
1:F:31:ARG:HG3	1:F:31:ARG:NH1	2.19	0.56
1:D:129:LYS:HG3	1:G:171:PRO:CG	2.35	0.56
1:G:108:SER:H	3:G:379:NCA:HN72	1.52	0.55
1:G:31:ARG:HG3	1:G:31:ARG:NH1	2.20	0.55
1:C:191:LYS:HE3	1:C:226:ASP:OD2	2.06	0.55
1:D:177:LYS:HB3	1:G:133:VAL:CG2	2.36	0.55
1:E:144:SER:HB3	1:E:179:GLU:HG3	1.88	0.55
1:B:196:HIS:CE1	1:B:202:ILE:HG23	2.42	0.55
1:H:175:PHE:HA	1:H:179:GLU:HB2	1.89	0.55
1:C:163:ASN:ND2	1:C:165:LYS:H	2.05	0.55
1:E:27:LEU:HD21	1:E:95:ILE:HD13	1.89	0.54
1:E:196:HIS:CE1	1:E:202:ILE:HG23	2.41	0.54
1:H:167:PRO:HG2	1:H:170:ARG:CG	2.37	0.54
1:E:175:PHE:HA	1:E:179:GLU:HB2	1.90	0.54
1:F:175:PHE:HA	1:F:179:GLU:HB2	1.88	0.54
1:E:69:LEU:CD1	1:E:69:LEU:N	2.70	0.54
1:A:26:ILE:N	1:A:26:ILE:HD12	2.22	0.54
1:D:55:LEU:N	1:D:55:LEU:HD22	2.22	0.54
1:E:152:GLU:HG2	1:E:186:LYS:HB3	1.90	0.54
1:G:26:ILE:HD12	1:G:26:ILE:N	2.22	0.54
1:H:101:LEU:CG	1:H:105:MET:HE2	2.34	0.54
1:C:26:ILE:N	1:C:26:ILE:HD12	2.22	0.54
1:E:67:GLN:OE1	1:E:100:THR:HB	2.08	0.54
1:H:55:LEU:N	1:H:55:LEU:HD22	2.23	0.54
1:E:55:LEU:N	1:E:55:LEU:HD22	2.23	0.54
1:E:246:ARG:O	1:E:249:ARG:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:PHE:CZ	1:B:143:ALA:HB2	2.43	0.53
1:C:129:LYS:HD2	1:C:129:LYS:N	2.20	0.53
1:D:55:LEU:HD22	1:D:55:LEU:H	1.74	0.53
1:D:72:ASN:HA	1:D:154:GLU:O	2.08	0.53
1:F:65:ALA:HB1	1:F:102:PRO:HG3	1.89	0.53
1:C:18:TYR:HA	1:C:22:ARG:CG	2.39	0.53
1:E:128:PHE:CD2	1:E:136:ARG:HD3	2.42	0.53
1:G:251:ALA:HA	1:H:251:ALA:HA	1.88	0.53
1:H:69:LEU:H	1:H:69:LEU:CD1	2.21	0.53
1:H:128:PHE:CD2	1:H:136:ARG:HD3	2.42	0.53
1:B:172:ASP:HA	1:B:177:LYS:HG3	1.91	0.53
1:A:55:LEU:N	1:A:55:LEU:HD22	2.23	0.53
1:C:167:PRO:HG2	1:C:170:ARG:CG	2.38	0.53
1:F:172:ASP:HA	1:F:177:LYS:HG3	1.90	0.53
1:B:163:ASN:ND2	1:B:165:LYS:H	2.07	0.53
1:D:175:PHE:HA	1:D:179:GLU:HB2	1.91	0.53
1:E:167:PRO:HG2	1:E:170:ARG:CG	2.38	0.53
1:G:139:PHE:H	3:G:479:NCA:C6	2.22	0.53
1:A:167:PRO:HG2	1:A:170:ARG:CG	2.38	0.53
1:D:172:ASP:HA	1:D:177:LYS:HG3	1.91	0.53
1:C:18:TYR:HA	1:C:22:ARG:HG2	1.91	0.53
1:C:196:HIS:CE1	1:C:202:ILE:HG23	2.44	0.53
1:G:101:LEU:CG	1:G:105:MET:HE2	2.32	0.53
1:H:163:ASN:C	1:H:163:ASN:ND2	2.67	0.52
1:A:129:LYS:HD2	1:A:129:LYS:N	2.20	0.52
1:F:129:LYS:HD2	1:F:129:LYS:N	2.22	0.52
1:H:103:GLY:O	1:H:107:ASN:HB2	2.10	0.52
1:A:163:ASN:ND2	1:A:165:LYS:H	2.07	0.52
1:B:129:LYS:HD2	1:B:129:LYS:N	2.22	0.52
1:A:31:ARG:HH21	1:C:191:LYS:NZ	2.06	0.52
1:F:128:PHE:CD2	1:F:136:ARG:HD3	2.43	0.52
1:G:72:ASN:HA	1:G:154:GLU:O	2.10	0.52
1:B:103:GLY:O	1:B:107:ASN:HB2	2.10	0.52
1:E:145:SER:OG	1:E:178:TYR:HB3	2.08	0.52
1:H:97:LEU:HD13	1:H:147:TYR:HB2	1.92	0.52
1:C:175:PHE:HA	1:C:179:GLU:HB2	1.92	0.52
1:G:152:GLU:CD	1:G:186:LYS:HD3	2.34	0.52
1:E:55:LEU:HD22	1:E:55:LEU:H	1.75	0.52
1:F:18:TYR:HA	1:F:22:ARG:CG	2.40	0.52
1:H:196:HIS:CE1	1:H:202:ILE:HG23	2.44	0.52
1:A:175:PHE:HA	1:A:179:GLU:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:163:ASN:ND2	1:E:165:LYS:H	2.07	0.51
1:F:101:LEU:CG	1:F:105:MET:HE2	2.33	0.51
1:A:196:HIS:CE1	1:A:202:ILE:HG23	2.46	0.51
1:G:172:ASP:HA	1:G:177:LYS:HG3	1.91	0.51
1:G:196:HIS:CE1	1:G:202:ILE:HG23	2.45	0.51
1:B:5:ARG:HG2	1:C:185:ASN:HB2	1.91	0.51
1:H:55:LEU:HD22	1:H:55:LEU:H	1.74	0.51
2:E:1179:N:H1'	3:E:359:NCA:H2	1.92	0.51
1:E:27:LEU:HB3	1:E:67:GLN:NE2	2.25	0.51
1:A:62:PHE:CZ	1:A:143:ALA:HB2	2.45	0.51
1:D:163:ASN:C	1:D:163:ASN:ND2	2.69	0.51
1:D:129:LYS:HB3	1:G:217:LEU:CD2	2.40	0.51
1:A:55:LEU:HD22	1:A:55:LEU:H	1.74	0.51
1:D:101:LEU:CG	1:D:105:MET:HE2	2.32	0.50
1:G:129:LYS:HD2	1:G:129:LYS:N	2.23	0.50
1:A:163:ASN:C	1:A:163:ASN:ND2	2.66	0.50
1:B:123:LYS:HD3	1:C:149:HIS:HE1	1.75	0.50
1:G:244:ASN:O	1:G:245:ALA:C	2.54	0.50
1:G:180:LEU:HB3	1:G:181:PRO:HD3	1.94	0.50
1:H:163:ASN:ND2	1:H:165:LYS:H	2.08	0.50
1:D:133:VAL:HG11	1:G:177:LYS:HD2	1.93	0.50
1:E:196:HIS:HE1	1:E:204:GLU:O	1.94	0.50
1:B:98:GLU:H	1:B:98:GLU:CD	2.20	0.50
1:C:62:PHE:CZ	1:C:143:ALA:HB2	2.46	0.50
1:C:163:ASN:C	1:C:163:ASN:ND2	2.67	0.50
1:D:62:PHE:CZ	1:D:143:ALA:HB2	2.46	0.50
1:F:55:LEU:H	1:F:55:LEU:HD22	1.77	0.50
1:A:69:LEU:N	1:A:69:LEU:HD13	2.26	0.50
1:B:128:PHE:CD2	1:B:136:ARG:HD3	2.47	0.50
1:B:136:ARG:O	3:B:429:NCA:H5	2.12	0.50
1:G:62:PHE:CZ	1:G:143:ALA:HB2	2.47	0.50
1:E:103:GLY:O	1:E:107:ASN:HB2	2.12	0.50
1:C:55:LEU:N	1:C:55:LEU:HD22	2.26	0.49
1:C:85:HIS:NE2	1:C:98:GLU:OE1	2.42	0.49
1:E:97:LEU:HD13	1:E:147:TYR:HB2	1.93	0.49
1:F:220:ALA:C	1:F:222:HIS:H	2.21	0.49
1:H:72:ASN:OD1	1:H:154:GLU:N	2.25	0.49
1:D:129:LYS:CG	1:G:171:PRO:HG3	2.41	0.49
1:E:106:LEU:HD22	1:E:106:LEU:N	2.27	0.49
1:B:69:LEU:HD22	1:B:150:SER:HB2	1.95	0.49
1:G:163:ASN:ND2	1:G:165:LYS:H	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:TYR:HA	1:D:22:ARG:CG	2.41	0.49
1:H:196:HIS:HE1	1:H:204:GLU:O	1.95	0.49
1:A:129:LYS:CD	1:A:129:LYS:N	2.70	0.49
1:A:18:TYR:HA	1:A:22:ARG:CG	2.43	0.49
1:B:196:HIS:HE1	1:B:204:GLU:O	1.96	0.49
1:D:129:LYS:CB	1:G:217:LEU:CD2	2.91	0.49
1:D:163:ASN:ND2	1:D:165:LYS:H	2.10	0.49
1:H:18:TYR:HA	1:H:22:ARG:CG	2.42	0.49
1:B:5:ARG:CD	1:C:185:ASN:O	2.58	0.49
1:C:69:LEU:HD22	1:C:150:SER:HB2	1.91	0.49
1:G:175:PHE:HA	1:G:179:GLU:HB2	1.94	0.49
1:A:1:ILE:HG22	1:A:125:CYS:O	2.12	0.48
1:B:124:VAL:HG22	1:B:125:CYS:N	2.27	0.48
1:C:55:LEU:HD22	1:C:55:LEU:H	1.77	0.48
1:H:1:ILE:HG22	1:H:125:CYS:O	2.13	0.48
1:H:106:LEU:N	1:H:106:LEU:HD22	2.28	0.48
1:G:18:TYR:HA	1:G:22:ARG:CG	2.44	0.48
1:B:55:LEU:H	1:B:55:LEU:CD2	2.26	0.48
1:E:98:GLU:OE2	3:E:359:NCA:N7	2.46	0.48
1:F:55:LEU:HD22	1:F:55:LEU:N	2.26	0.48
1:F:180:LEU:HB3	1:F:181:PRO:HD3	1.95	0.48
1:A:101:LEU:CG	1:A:105:MET:HE2	2.37	0.48
1:C:103:GLY:O	1:C:107:ASN:HB2	2.14	0.48
1:A:27:LEU:HD21	1:A:95:ILE:HD13	1.96	0.48
1:A:220:ALA:C	1:A:222:HIS:H	2.22	0.48
1:D:196:HIS:HE1	1:D:204:GLU:O	1.97	0.48
1:C:1:ILE:HG22	1:C:125:CYS:O	2.13	0.48
1:E:137:GLU:OE1	1:E:177:LYS:NZ	2.44	0.48
2:G:1179:N:H1'	3:G:379:NCA:C6	2.43	0.48
1:E:165:LYS:HG2	1:G:202:ILE:HG13	1.95	0.48
1:C:129:LYS:CD	1:C:129:LYS:N	2.72	0.48
1:F:67:GLN:O	1:F:69:LEU:HD13	2.13	0.48
1:C:101:LEU:CG	1:C:105:MET:HE2	2.38	0.48
1:C:106:LEU:N	1:C:106:LEU:HD22	2.29	0.48
1:D:139:PHE:HB3	3:D:449:NCA:C6	2.44	0.47
1:D:220:ALA:C	1:D:222:HIS:H	2.22	0.47
1:D:1:ILE:HG22	1:D:125:CYS:O	2.14	0.47
1:F:196:HIS:CE1	1:F:202:ILE:HG23	2.49	0.47
1:C:250:LEU:CD1	1:D:232:ARG:HD2	2.45	0.47
1:F:18:TYR:HA	1:F:22:ARG:HG2	1.96	0.47
1:B:18:TYR:HA	1:B:22:ARG:CG	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:ASN:O	1:B:245:ALA:C	2.57	0.47
1:F:196:HIS:HE1	1:F:204:GLU:O	1.97	0.47
1:A:250:LEU:CD1	1:B:232:ARG:HD2	2.45	0.47
1:B:18:TYR:HA	1:B:22:ARG:HG2	1.95	0.47
1:B:175:PHE:HA	1:B:179:GLU:HB2	1.96	0.47
1:C:69:LEU:HD22	1:C:150:SER:HB3	1.96	0.47
1:D:27:LEU:HD23	1:D:70:PRO:HD3	1.96	0.47
1:E:11:PHE:CD1	1:E:11:PHE:C	2.93	0.47
1:A:103:GLY:O	1:A:107:ASN:HB2	2.15	0.47
1:A:106:LEU:N	1:A:106:LEU:HD22	2.29	0.47
1:A:180:LEU:HB3	1:A:181:PRO:HD3	1.95	0.47
1:D:106:LEU:N	1:D:106:LEU:HD22	2.30	0.47
1:D:129:LYS:HD2	1:D:129:LYS:N	2.28	0.47
1:G:1:ILE:HG22	1:G:125:CYS:O	2.15	0.47
1:G:103:GLY:O	1:G:107:ASN:HB2	2.14	0.47
1:C:180:LEU:HB3	1:C:181:PRO:HD3	1.95	0.47
1:E:180:LEU:HB3	1:E:181:PRO:HD3	1.96	0.47
1:D:139:PHE:HB3	3:D:449:NCA:C5	2.45	0.47
1:E:62:PHE:CZ	1:E:143:ALA:HB2	2.50	0.47
1:F:62:PHE:CZ	1:F:143:ALA:HB2	2.50	0.47
1:G:128:PHE:CD2	1:G:136:ARG:HD2	2.50	0.47
1:G:236:PHE:CZ	1:H:248:CYS:HB3	2.50	0.47
1:H:98:GLU:CD	1:H:98:GLU:H	2.23	0.47
1:F:103:GLY:O	1:F:107:ASN:HB2	2.15	0.47
1:F:244:ASN:O	1:F:245:ALA:C	2.58	0.47
2:G:1179:N:H1'	3:G:379:NCA:H6	1.97	0.47
1:A:144:SER:HB3	1:A:179:GLU:HG3	1.97	0.46
1:A:196:HIS:HE1	1:A:204:GLU:O	1.98	0.46
1:D:244:ASN:O	1:D:245:ALA:C	2.58	0.46
1:E:18:TYR:HA	1:E:22:ARG:CG	2.44	0.46
1:H:69:LEU:CD2	1:H:150:SER:HB2	2.45	0.46
1:E:50:PRO:HB2	1:E:126:PRO:HG3	1.97	0.46
1:H:55:LEU:H	1:H:55:LEU:CD2	2.28	0.46
1:D:103:GLY:O	1:D:107:ASN:HB2	2.15	0.46
1:E:110:VAL:HG13	3:E:459:NCA:O7	2.16	0.46
1:E:220:ALA:C	1:E:222:HIS:H	2.22	0.46
1:C:221:LYS:O	1:C:222:HIS:HB2	2.16	0.46
1:G:55:LEU:HD22	1:G:55:LEU:H	1.81	0.46
1:A:55:LEU:H	1:A:55:LEU:CD2	2.29	0.46
1:E:163:ASN:HD22	1:E:164:PRO:N	2.14	0.46
1:F:163:ASN:ND2	1:F:165:LYS:H	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:72:ASN:HA	1:H:154:GLU:O	2.16	0.46
1:H:220:ALA:C	1:H:222:HIS:H	2.24	0.46
1:D:124:VAL:HG22	1:D:125:CYS:N	2.29	0.46
1:D:128:PHE:CD2	1:D:136:ARG:HD3	2.51	0.46
1:G:220:ALA:C	1:G:222:HIS:H	2.23	0.46
1:B:220:ALA:C	1:B:222:HIS:H	2.23	0.46
1:D:167:PRO:HG2	1:D:170:ARG:CG	2.45	0.46
1:F:152:GLU:HG2	1:F:186:LYS:HB3	1.98	0.46
1:F:69:LEU:HA	1:F:70:PRO:HD2	1.70	0.46
1:C:50:PRO:HB2	1:C:126:PRO:HG3	1.98	0.46
1:E:246:ARG:O	1:E:246:ARG:HD3	2.16	0.46
1:H:49:ASN:O	1:H:50:PRO:C	2.59	0.46
1:H:62:PHE:CZ	1:H:143:ALA:HB2	2.51	0.46
1:H:124:VAL:HG22	1:H:125:CYS:N	2.30	0.46
1:B:167:PRO:HG2	1:B:170:ARG:CG	2.46	0.45
1:C:139:PHE:HB3	3:C:439:NCA:N1	2.31	0.45
1:C:140:TRP:HD1	3:C:439:NCA:C5	2.28	0.45
1:D:90:THR:HG22	1:D:90:THR:O	2.16	0.45
1:A:31:ARG:NH2	1:C:191:LYS:HZ2	2.13	0.45
1:A:69:LEU:HD22	1:A:150:SER:HB3	1.98	0.45
1:A:17:ASP:CG	1:B:14:ARG:HD2	2.39	0.45
1:A:217:LEU:O	1:A:220:ALA:HB3	2.16	0.45
1:B:65:ALA:CB	1:B:102:PRO:HG3	2.46	0.45
1:C:196:HIS:HE1	1:C:204:GLU:O	2.00	0.45
1:B:70:PRO:HB2	1:B:73:LYS:CG	2.47	0.45
1:D:107:ASN:O	1:D:108:SER:HB2	2.16	0.45
1:G:18:TYR:HA	1:G:22:ARG:HG2	1.98	0.45
1:G:196:HIS:HE1	1:G:204:GLU:O	1.99	0.45
1:C:124:VAL:HG22	1:C:125:CYS:N	2.31	0.45
1:D:55:LEU:H	1:D:55:LEU:CD2	2.29	0.45
1:H:69:LEU:HD22	1:H:150:SER:CB	2.47	0.45
1:E:68:GLN:HE21	1:E:68:GLN:HB2	1.50	0.45
1:F:167:PRO:HG2	1:F:170:ARG:CG	2.45	0.45
1:H:163:ASN:HA	1:H:164:PRO:HD2	1.85	0.45
1:H:246:ARG:O	1:H:246:ARG:HD3	2.17	0.45
1:A:18:TYR:HA	1:A:22:ARG:HG2	1.99	0.45
1:A:124:VAL:HG22	1:A:125:CYS:N	2.32	0.45
1:D:18:TYR:HA	1:D:22:ARG:HG2	1.97	0.45
1:D:177:LYS:HG2	1:G:133:VAL:HG13	1.99	0.45
1:E:18:TYR:HA	1:E:22:ARG:HG2	1.98	0.45
1:E:140:TRP:HD1	3:E:459:NCA:H5	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:124:VAL:HG22	1:G:125:CYS:N	2.32	0.45
1:B:27:LEU:HD21	1:B:95:ILE:HD13	1.98	0.45
1:D:180:LEU:HB3	1:D:181:PRO:HD3	1.98	0.45
1:F:69:LEU:HD22	1:F:150:SER:CB	2.39	0.45
1:B:246:ARG:O	1:B:246:ARG:HD3	2.16	0.45
1:F:14:ARG:NH2	1:F:107:ASN:O	2.49	0.45
1:H:196:HIS:O	1:H:197:ARG:C	2.59	0.45
1:C:62:PHE:CE1	1:C:143:ALA:HA	2.52	0.44
1:E:163:ASN:HA	1:E:164:PRO:HD2	1.85	0.44
1:H:27:LEU:HD21	1:H:95:ILE:HD13	1.99	0.44
1:B:70:PRO:HB2	1:B:73:LYS:HG2	2.00	0.44
1:B:180:LEU:HB3	1:B:181:PRO:HD3	1.98	0.44
1:H:180:LEU:HB3	1:H:181:PRO:HD3	1.99	0.44
1:A:244:ASN:O	1:A:245:ALA:C	2.59	0.44
1:C:71:LYS:HG2	1:C:72:ASN:HD21	1.77	0.44
1:E:55:LEU:H	1:E:55:LEU:CD2	2.29	0.44
1:E:55:LEU:HA	1:E:55:LEU:HD13	1.84	0.44
1:H:244:ASN:O	1:H:245:ALA:C	2.60	0.44
1:A:75:MET:CE	1:A:158:MET:HE3	2.48	0.44
1:B:22:ARG:HA	1:B:22:ARG:HD3	1.83	0.44
1:H:18:TYR:HA	1:H:22:ARG:HG2	1.99	0.44
1:A:74:VAL:HG13	1:A:147:TYR:CZ	2.52	0.44
1:G:167:PRO:HG2	1:G:170:ARG:CG	2.45	0.44
1:E:244:ASN:O	1:E:245:ALA:C	2.59	0.44
1:H:11:PHE:CD1	1:H:11:PHE:C	2.96	0.44
1:H:69:LEU:HD22	1:H:150:SER:HB2	1.99	0.44
1:C:163:ASN:HD22	1:C:165:LYS:H	1.66	0.44
1:D:127:ASP:O	1:D:128:PHE:C	2.60	0.44
1:D:133:VAL:CG1	1:G:177:LYS:CG	2.96	0.44
1:F:106:LEU:N	1:F:106:LEU:HD22	2.32	0.44
1:A:166:VAL:HG13	1:A:170:ARG:HD3	2.00	0.44
1:C:69:LEU:HD21	1:C:150:SER:HB2	1.96	0.44
1:D:163:ASN:HA	1:D:164:PRO:HD2	1.83	0.44
1:B:90:THR:HG22	1:B:90:THR:O	2.18	0.43
1:G:55:LEU:HD22	1:G:55:LEU:N	2.32	0.43
1:G:127:ASP:O	1:G:128:PHE:C	2.61	0.43
1:C:220:ALA:C	1:C:222:HIS:H	2.25	0.43
1:G:11:PHE:CD1	1:G:11:PHE:C	2.96	0.43
1:H:98:GLU:CD	1:H:98:GLU:N	2.76	0.43
1:A:14:ARG:NH2	1:A:107:ASN:O	2.51	0.43
1:A:50:PRO:HB2	1:A:126:PRO:HG3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:LEU:H	1:C:55:LEU:CD2	2.32	0.43
1:D:11:PHE:C	1:D:11:PHE:CD1	2.96	0.43
1:B:11:PHE:CD1	1:B:11:PHE:C	2.96	0.43
1:G:106:LEU:N	1:G:106:LEU:HD22	2.33	0.43
2:G:1179:N:C1'	3:G:379:NCA:H6	2.47	0.43
1:A:71:LYS:O	1:A:72:ASN:CB	2.63	0.43
1:C:75:MET:CE	1:C:158:MET:HE3	2.49	0.43
1:E:127:ASP:O	1:E:128:PHE:C	2.62	0.43
1:F:55:LEU:H	1:F:55:LEU:CD2	2.32	0.43
1:F:73:LYS:HE2	1:F:93:LYS:O	2.18	0.43
1:B:49:ASN:O	1:B:50:PRO:C	2.62	0.43
1:C:144:SER:HB3	1:C:179:GLU:HG3	2.01	0.43
1:E:124:VAL:HG22	1:E:125:CYS:N	2.33	0.43
1:H:14:ARG:NH2	1:H:107:ASN:O	2.51	0.43
1:C:90:THR:O	1:C:90:THR:HG22	2.18	0.43
1:C:217:LEU:O	1:C:220:ALA:HB3	2.19	0.43
1:F:120:PHE:CD1	1:F:120:PHE:N	2.87	0.43
1:G:246:ARG:O	1:G:246:ARG:HD3	2.19	0.43
1:B:26:ILE:N	1:B:26:ILE:CD1	2.81	0.43
1:B:163:ASN:HA	1:B:164:PRO:HD2	1.82	0.42
1:E:14:ARG:NH2	1:E:107:ASN:O	2.49	0.42
1:E:204:GLU:HB3	1:E:211:LEU:HD22	2.01	0.42
1:B:217:LEU:O	1:B:220:ALA:HB3	2.19	0.42
1:C:11:PHE:CD1	1:C:11:PHE:C	2.97	0.42
1:G:62:PHE:CE1	1:G:143:ALA:HA	2.54	0.42
1:A:62:PHE:CE1	1:A:143:ALA:HA	2.54	0.42
1:C:244:ASN:O	1:C:245:ALA:C	2.61	0.42
1:E:72:ASN:HA	1:E:154:GLU:O	2.18	0.42
1:G:90:THR:O	1:G:90:THR:HG22	2.19	0.42
1:D:246:ARG:O	1:D:246:ARG:HD3	2.19	0.42
1:E:65:ALA:CB	1:E:102:PRO:HG3	2.49	0.42
1:F:1:ILE:HG22	1:F:125:CYS:O	2.20	0.42
1:F:62:PHE:CE1	1:F:143:ALA:HA	2.54	0.42
1:F:246:ARG:O	1:F:246:ARG:HD3	2.20	0.42
1:A:113:GLY:HA2	1:A:120:PHE:HA	2.00	0.42
1:D:67:GLN:O	1:D:69:LEU:HD13	2.19	0.42
1:H:221:LYS:O	1:H:222:HIS:HB2	2.19	0.42
1:B:1:ILE:HG22	1:B:125:CYS:O	2.19	0.42
1:D:65:ALA:CB	1:D:102:PRO:HG3	2.49	0.42
1:E:128:PHE:HB3	1:E:129:LYS:CD	2.41	0.42
1:C:189:ARG:HG2	1:C:190:VAL:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:196:HIS:O	1:F:197:ARG:C	2.63	0.42
1:H:90:THR:O	1:H:90:THR:HG22	2.19	0.42
1:B:106:LEU:N	1:B:106:LEU:HD22	2.33	0.42
1:F:124:VAL:HG22	1:F:125:CYS:N	2.35	0.42
1:A:246:ARG:O	1:A:246:ARG:HD3	2.20	0.42
1:A:127:ASP:O	1:A:128:PHE:C	2.63	0.42
1:H:55:LEU:HD13	1:H:55:LEU:HA	1.90	0.42
1:C:246:ARG:O	1:C:246:ARG:HD3	2.20	0.41
1:A:55:LEU:HD13	1:A:55:LEU:HA	1.87	0.41
1:A:65:ALA:CB	1:A:102:PRO:HG3	2.48	0.41
1:A:174:PHE:HB2	2:A:1179:N:O5'	2.20	0.41
1:F:87:TYR:CE2	1:F:94:TYR:HE2	2.39	0.41
1:H:50:PRO:HB2	1:H:126:PRO:HG3	2.02	0.41
1:G:152:GLU:OE2	1:G:186:LYS:HD3	2.21	0.41
1:G:202:ILE:HG21	1:G:205:LYS:HE3	2.02	0.41
1:H:113:GLY:HA2	1:H:120:PHE:HA	2.03	0.41
1:E:90:THR:O	1:E:90:THR:HG22	2.20	0.41
1:F:50:PRO:HB2	1:F:126:PRO:HG3	2.01	0.41
1:F:90:THR:O	1:F:90:THR:HG22	2.21	0.41
1:F:128:PHE:HB3	1:F:129:LYS:CD	2.43	0.41
1:F:189:ARG:HG2	1:F:190:VAL:N	2.35	0.41
1:G:40:ASP:HB3	1:G:61:PHE:HA	2.01	0.41
1:H:166:VAL:HG13	1:H:170:ARG:HD3	2.03	0.41
1:C:174:PHE:HB2	2:C:1179:N:O5'	2.20	0.41
1:D:69:LEU:HD22	1:D:150:SER:CB	2.40	0.41
1:G:27:LEU:HA	1:G:28:PRO:HD3	1.91	0.41
1:A:23:TYR:O	1:A:24:LEU:C	2.64	0.41
1:A:128:PHE:HB3	1:A:129:LYS:CD	2.42	0.41
1:B:50:PRO:HB2	1:B:126:PRO:HG3	2.01	0.41
1:C:127:ASP:O	1:C:128:PHE:C	2.64	0.41
1:G:251:ALA:HB3	1:H:249:ARG:HB2	2.02	0.41
1:H:65:ALA:CB	1:H:102:PRO:HG3	2.50	0.41
1:A:72:ASN:HA	1:A:154:GLU:O	2.21	0.41
1:A:90:THR:HG22	1:A:90:THR:O	2.20	0.41
1:E:40:ASP:HB3	1:E:61:PHE:HA	2.03	0.41
1:E:113:GLY:HA2	1:E:120:PHE:HA	2.03	0.41
1:F:67:GLN:OE1	1:F:100:THR:HB	2.21	0.41
1:G:17:ASP:CG	1:H:14:ARG:HD2	2.44	0.41
1:G:49:ASN:O	1:G:50:PRO:C	2.64	0.41
1:G:107:ASN:O	1:G:108:SER:HB2	2.20	0.41
1:G:113:GLY:HA2	1:G:120:PHE:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:163:ASN:HD22	1:H:165:LYS:H	1.68	0.41
1:A:11:PHE:CD1	1:A:11:PHE:C	2.99	0.41
1:A:67:GLN:O	1:A:69:LEU:HD13	2.20	0.41
1:A:163:ASN:HD22	1:A:165:LYS:H	1.69	0.41
1:A:196:HIS:O	1:A:197:ARG:C	2.62	0.41
1:C:22:ARG:HD3	1:C:22:ARG:HA	1.78	0.41
1:C:250:LEU:HD12	1:D:232:ARG:HD2	2.03	0.41
1:E:166:VAL:HG13	1:E:170:ARG:HD3	2.03	0.41
1:E:189:ARG:HG2	1:E:190:VAL:N	2.36	0.41
1:F:11:PHE:CD1	1:F:11:PHE:C	2.98	0.41
1:F:18:TYR:O	1:F:29:ARG:NH1	2.54	0.41
1:H:139:PHE:HB3	3:H:489:NCA:C6	2.51	0.41
1:A:189:ARG:HG2	1:A:190:VAL:N	2.36	0.41
1:D:131:CYS:C	1:G:181:PRO:HB3	2.46	0.41
1:E:1:ILE:HG23	1:E:125:CYS:HB2	2.03	0.41
1:F:127:ASP:O	1:F:128:PHE:C	2.64	0.41
1:D:98:GLU:CD	1:D:98:GLU:N	2.79	0.40
1:D:120:PHE:CD1	1:D:120:PHE:N	2.89	0.40
1:F:163:ASN:HA	1:F:164:PRO:HD2	1.81	0.40
1:B:14:ARG:NH2	1:B:107:ASN:O	2.52	0.40
1:G:87:TYR:CE2	1:G:94:TYR:HE2	2.39	0.40
1:G:196:HIS:O	1:G:197:ARG:C	2.63	0.40
1:B:27:LEU:HA	1:B:28:PRO:HD3	1.86	0.40
1:B:113:GLY:HA2	1:B:120:PHE:HA	2.02	0.40
1:B:163:ASN:HD22	1:B:165:LYS:H	1.68	0.40
1:H:87:TYR:CE2	1:H:94:TYR:HE2	2.39	0.40
2:A:1179:N:H1'	3:A:319:NCA:H6	2.03	0.40
1:B:75:MET:CE	1:B:158:MET:HE3	2.52	0.40
1:B:98:GLU:CD	1:B:98:GLU:N	2.79	0.40
1:B:127:ASP:O	1:B:128:PHE:C	2.64	0.40
1:C:73:LYS:HD3	1:C:93:LYS:O	2.21	0.40
1:D:27:LEU:HA	1:D:28:PRO:HD3	1.89	0.40
1:E:248:CYS:HB3	1:F:236:PHE:CZ	2.56	0.40
1:A:251:ALA:HA	1:B:251:ALA:CA	2.47	0.40
1:B:40:ASP:HB3	1:B:61:PHE:HA	2.03	0.40
1:C:166:VAL:HG13	1:C:170:ARG:HD3	2.04	0.40
1:D:49:ASN:O	1:D:50:PRO:C	2.65	0.40
1:E:217:LEU:O	1:E:220:ALA:HB3	2.21	0.40
1:G:232:ARG:HH22	1:H:244:ASN:HA	1.86	0.40
1:G:248:CYS:HB3	1:H:236:PHE:CZ	2.56	0.40
1:H:22:ARG:HA	1:H:22:ARG:HD3	1.78	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:122:GLU:OE1	1:H:31:ARG:NH2[1_545]	1.99	0.21

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	249/258 (96%)	233 (94%)	15 (6%)	1 (0%)	30	43
1	B	249/258 (96%)	235 (94%)	14 (6%)	0	100	100
1	C	249/258 (96%)	232 (93%)	15 (6%)	2 (1%)	16	25
1	D	249/258 (96%)	230 (92%)	18 (7%)	1 (0%)	30	43
1	E	249/258 (96%)	234 (94%)	14 (6%)	1 (0%)	30	43
1	F	249/258 (96%)	234 (94%)	13 (5%)	2 (1%)	16	25
1	G	249/258 (96%)	234 (94%)	13 (5%)	2 (1%)	16	25
1	H	249/258 (96%)	232 (93%)	16 (6%)	1 (0%)	30	43
All	All	1992/2064 (96%)	1864 (94%)	118 (6%)	10 (0%)	24	37

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	128	PHE
1	E	128	PHE
1	F	128	PHE
1	G	128	PHE
1	H	128	PHE
1	A	128	PHE
1	C	128	PHE
1	G	80	VAL
1	C	80	VAL

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Mol	Chain	Res	Type
1	F	80	VAL

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	220/226 (97%)	207 (94%)	13 (6%)	18	31
1	B	220/226 (97%)	207 (94%)	13 (6%)	18	31
1	C	220/226 (97%)	207 (94%)	13 (6%)	18	31
1	D	220/226 (97%)	206 (94%)	14 (6%)	16	28
1	E	220/226 (97%)	206 (94%)	14 (6%)	16	28
1	F	220/226 (97%)	208 (94%)	12 (6%)	19	34
1	G	220/226 (97%)	208 (94%)	12 (6%)	19	34
1	H	220/226 (97%)	207 (94%)	13 (6%)	18	31
All	All	1760/1808 (97%)	1656 (94%)	104 (6%)	18	31

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	GLU
1	A	14	ARG
1	A	16	LYS
1	A	30	VAL
1	A	32	SER
1	A	69	LEU
1	A	133	VAL
1	A	134	GLN
1	A	155	VAL
1	A	211	LEU
1	A	212	LEU
1	A	237	LEU
1	A	246	ARG
1	B	8	GLU

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Mol	Chain	Res	Type
1	B	14	ARG
1	B	16	LYS
1	B	30	VAL
1	B	32	SER
1	B	69	LEU
1	B	133	VAL
1	B	134	GLN
1	B	155	VAL
1	B	211	LEU
1	B	212	LEU
1	B	237	LEU
1	B	246	ARG
1	C	8	GLU
1	C	14	ARG
1	C	16	LYS
1	C	30	VAL
1	C	32	SER
1	C	69	LEU
1	C	133	VAL
1	C	134	GLN
1	C	155	VAL
1	C	211	LEU
1	C	212	LEU
1	C	237	LEU
1	C	246	ARG
1	D	8	GLU
1	D	14	ARG
1	D	16	LYS
1	D	30	VAL
1	D	32	SER
1	D	69	LEU
1	D	73	LYS
1	D	133	VAL
1	D	134	GLN
1	D	155	VAL
1	D	211	LEU
1	D	212	LEU
1	D	237	LEU
1	D	246	ARG
1	E	8	GLU
1	E	14	ARG
1	E	16	LYS

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Mol	Chain	Res	Type
1	E	30	VAL
1	E	32	SER
1	E	68	GLN
1	E	69	LEU
1	E	133	VAL
1	E	134	GLN
1	E	155	VAL
1	E	211	LEU
1	E	212	LEU
1	E	237	LEU
1	E	246	ARG
1	F	8	GLU
1	F	14	ARG
1	F	16	LYS
1	F	30	VAL
1	F	32	SER
1	F	69	LEU
1	F	133	VAL
1	F	134	GLN
1	F	155	VAL
1	F	211	LEU
1	F	212	LEU
1	F	246	ARG
1	G	8	GLU
1	G	14	ARG
1	G	16	LYS
1	G	30	VAL
1	G	32	SER
1	G	133	VAL
1	G	134	GLN
1	G	155	VAL
1	G	211	LEU
1	G	212	LEU
1	G	237	LEU
1	G	246	ARG
1	H	8	GLU
1	H	14	ARG
1	H	16	LYS
1	H	30	VAL
1	H	32	SER
1	H	69	LEU
1	H	133	VAL

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Mol	Chain	Res	Type
1	H	134	GLN
1	H	155	VAL
1	H	211	LEU
1	H	212	LEU
1	H	237	LEU
1	H	246	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	68	GLN
1	A	89	ASN
1	A	134	GLN
1	A	163	ASN
1	A	196	HIS
1	A	242	ASN
1	B	66	GLN
1	B	89	ASN
1	B	134	GLN
1	B	163	ASN
1	B	196	HIS
1	B	242	ASN
1	C	66	GLN
1	C	89	ASN
1	C	134	GLN
1	C	149	HIS
1	C	163	ASN
1	C	196	HIS
1	C	242	ASN
1	D	66	GLN
1	D	89	ASN
1	D	134	GLN
1	D	163	ASN
1	D	196	HIS
1	D	242	ASN
1	E	66	GLN
1	E	68	GLN
1	E	89	ASN
1	E	134	GLN
1	E	163	ASN
1	E	196	HIS

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Mol	Chain	Res	Type
1	E	242	ASN
1	F	66	GLN
1	F	89	ASN
1	F	134	GLN
1	F	163	ASN
1	F	196	HIS
1	F	242	ASN
1	G	66	GLN
1	G	68	GLN
1	G	89	ASN
1	G	134	GLN
1	G	163	ASN
1	G	196	HIS
1	G	242	ASN
1	H	66	GLN
1	H	89	ASN
1	H	134	GLN
1	H	163	ASN
1	H	196	HIS
1	H	242	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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](#)

24 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
2	N	G	1179	1	13,13,13	3.32	6 (46%)	16,19,19	2.72	9 (56%)
3	NCA	D	449	-	9,9,9	2.99	5 (55%)	11,11,11	1.88	3 (27%)
3	NCA	H	389	-	9,9,9	3.58	5 (55%)	11,11,11	2.12	5 (45%)
3	NCA	C	339	-	9,9,9	2.96	4 (44%)	11,11,11	2.02	4 (36%)
3	NCA	F	469	-	9,9,9	3.41	7 (77%)	11,11,11	1.96	4 (36%)
2	N	E	1179	1	13,13,13	3.63	6 (46%)	16,19,19	2.61	9 (56%)
3	NCA	E	359	-	9,9,9	2.65	5 (55%)	11,11,11	1.73	3 (27%)
3	NCA	D	349	-	9,9,9	2.90	5 (55%)	11,11,11	1.92	4 (36%)
2	N	B	1179	1	13,13,13	3.71	6 (46%)	16,19,19	2.77	9 (56%)
3	NCA	B	329	-	9,9,9	2.79	6 (66%)	11,11,11	1.89	4 (36%)
2	N	A	1179	1	13,13,13	3.55	6 (46%)	16,19,19	2.53	9 (56%)
3	NCA	A	419	-	9,9,9	2.38	3 (33%)	11,11,11	1.92	3 (27%)
3	NCA	E	459	-	9,9,9	2.59	4 (44%)	11,11,11	1.96	3 (27%)
3	NCA	F	369	-	9,9,9	3.09	5 (55%)	11,11,11	1.92	4 (36%)
3	NCA	G	479	-	9,9,9	3.74	8 (88%)	11,11,11	2.17	4 (36%)
3	NCA	A	319	-	9,9,9	3.24	5 (55%)	11,11,11	2.03	4 (36%)
2	N	H	1179	1	13,13,13	3.46	6 (46%)	16,19,19	2.55	10 (62%)
2	N	F	1179	1	13,13,13	3.60	6 (46%)	16,19,19	2.68	9 (56%)
3	NCA	B	429	-	9,9,9	3.07	5 (55%)	11,11,11	1.97	5 (45%)
3	NCA	G	379	-	9,9,9	3.13	5 (55%)	11,11,11	2.16	3 (27%)
2	N	C	1179	1	13,13,13	3.66	6 (46%)	16,19,19	2.61	10 (62%)
3	NCA	C	439	-	9,9,9	2.93	4 (44%)	11,11,11	2.11	4 (36%)
3	NCA	H	489	-	9,9,9	2.31	4 (44%)	11,11,11	1.55	2 (18%)
2	N	D	1179	1	13,13,13	3.49	6 (46%)	16,19,19	2.58	9 (56%)

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
2	N	G	1179	1	1/1/4/4	0/6/19/19	0/1/1/1
3	NCA	D	449	-	-	0/4/4/4	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NCA	H	389	-	-	0/4/4/4	0/1/1/1
3	NCA	C	339	-	-	0/4/4/4	0/1/1/1
3	NCA	F	469	-	-	0/4/4/4	0/1/1/1
2	N	E	1179	1	1/1/4/4	0/6/19/19	0/1/1/1
3	NCA	E	359	-	-	0/4/4/4	0/1/1/1
3	NCA	D	349	-	-	0/4/4/4	0/1/1/1
2	N	B	1179	1	1/1/4/4	0/6/19/19	0/1/1/1
3	NCA	B	329	-	-	0/4/4/4	0/1/1/1
2	N	A	1179	1	1/1/4/4	0/6/19/19	0/1/1/1
3	NCA	A	419	-	-	0/4/4/4	0/1/1/1
3	NCA	E	459	-	-	0/4/4/4	0/1/1/1
3	NCA	F	369	-	-	0/4/4/4	0/1/1/1
3	NCA	G	479	-	-	0/4/4/4	0/1/1/1
3	NCA	A	319	-	-	0/4/4/4	0/1/1/1
2	N	H	1179	1	1/1/4/4	0/6/19/19	0/1/1/1
2	N	F	1179	1	1/1/4/4	0/6/19/19	0/1/1/1
3	NCA	B	429	-	-	0/4/4/4	0/1/1/1
3	NCA	G	379	-	-	0/4/4/4	0/1/1/1
2	N	C	1179	1	1/1/4/4	0/6/19/19	0/1/1/1
3	NCA	C	439	-	-	0/4/4/4	0/1/1/1
3	NCA	H	489	-	-	0/4/4/4	0/1/1/1
2	N	D	1179	1	1/1/4/4	0/6/19/19	0/1/1/1

All (128) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1179	N	O4'-C4'	7.28	1.56	1.44
2	C	1179	N	C1'-C2'	7.18	1.64	1.51
2	F	1179	N	O4'-C4'	7.15	1.56	1.44
2	C	1179	N	O4'-C4'	7.10	1.56	1.44
3	H	389	NCA	C3-C7	7.02	1.61	1.50
2	E	1179	N	C1'-C2'	6.88	1.63	1.51
2	A	1179	N	C1'-C2'	6.87	1.63	1.51
2	G	1179	N	O4'-C4'	6.87	1.55	1.44
2	B	1179	N	C1'-C2'	6.85	1.63	1.51
2	D	1179	N	O4'-C4'	6.81	1.55	1.44
2	E	1179	N	O4'-C4'	6.77	1.55	1.44
2	H	1179	N	O4'-C4'	6.75	1.55	1.44
3	G	479	NCA	C2-N1	6.72	1.48	1.34
2	A	1179	N	O4'-C4'	6.70	1.55	1.44
2	H	1179	N	C1'-C2'	6.61	1.63	1.51
2	D	1179	N	C1'-C2'	6.57	1.63	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1179	N	C1'-C2'	6.31	1.62	1.51
3	F	469	NCA	C2-N1	6.25	1.47	1.34
2	A	1179	N	P-O5'	6.17	1.79	1.60
2	C	1179	N	P-O5'	6.13	1.79	1.60
2	E	1179	N	P-O5'	6.04	1.79	1.60
3	F	369	NCA	C3-C7	5.99	1.59	1.50
2	H	1179	N	P-O5'	5.91	1.79	1.60
2	G	1179	N	C1'-C2'	5.89	1.62	1.51
3	C	339	NCA	C3-C7	5.87	1.59	1.50
3	A	319	NCA	C3-C7	5.82	1.59	1.50
2	F	1179	N	P-O5'	5.66	1.78	1.60
2	D	1179	N	P-O5'	5.60	1.78	1.60
2	G	1179	N	P-O5'	5.57	1.77	1.60
2	B	1179	N	P-O5'	5.50	1.77	1.60
2	B	1179	N	C2'-C3'	5.49	1.62	1.53
3	D	449	NCA	C2-N1	5.47	1.45	1.34
3	D	349	NCA	C2-N1	5.37	1.45	1.34
3	G	379	NCA	C3-C7	5.31	1.58	1.50
3	E	359	NCA	C2-N1	5.13	1.45	1.34
3	C	439	NCA	C3-C7	5.09	1.58	1.50
3	A	319	NCA	C4-C3	5.02	1.47	1.39
3	B	329	NCA	C2-N1	5.02	1.44	1.34
2	F	1179	N	C2'-C3'	5.02	1.62	1.53
3	B	429	NCA	C2-N1	4.95	1.44	1.34
3	H	389	NCA	C2-N1	4.93	1.44	1.34
3	C	439	NCA	C2-N1	4.89	1.44	1.34
3	H	489	NCA	C2-N1	4.89	1.44	1.34
3	G	379	NCA	C4-C3	4.85	1.46	1.39
2	E	1179	N	C2'-C3'	4.75	1.61	1.53
3	E	459	NCA	C2-N1	4.70	1.44	1.34
3	G	379	NCA	C2-N1	4.54	1.43	1.34
3	H	389	NCA	C4-C3	4.52	1.46	1.39
3	G	479	NCA	C4-C3	4.49	1.46	1.39
3	A	319	NCA	C2-N1	4.45	1.43	1.34
3	A	419	NCA	C2-N1	4.44	1.43	1.34
2	D	1179	N	C2'-C3'	4.36	1.61	1.53
3	A	419	NCA	C3-C7	4.27	1.57	1.50
3	F	369	NCA	C2-N1	4.27	1.43	1.34
3	F	369	NCA	C4-C3	4.27	1.45	1.39
3	B	329	NCA	C4-C3	4.26	1.45	1.39
3	C	339	NCA	C4-C3	4.25	1.45	1.39
3	D	449	NCA	C3-C7	4.22	1.56	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	429	NCA	C4-C3	4.21	1.45	1.39
3	D	349	NCA	C4-C3	4.15	1.45	1.39
3	C	339	NCA	C2-N1	4.15	1.43	1.34
2	C	1179	N	C2'-C3'	4.10	1.60	1.53
3	C	439	NCA	C4-C3	4.06	1.45	1.39
3	G	479	NCA	C3-C7	4.01	1.56	1.50
2	A	1179	N	C2'-C3'	3.93	1.60	1.53
2	G	1179	N	C2'-C3'	3.91	1.60	1.53
3	B	429	NCA	C3-C7	3.76	1.56	1.50
3	D	349	NCA	C3-C7	3.76	1.56	1.50
3	B	429	NCA	C7-N7	-3.72	1.26	1.33
2	H	1179	N	C2'-C3'	3.71	1.59	1.53
3	D	449	NCA	C2-C3	3.69	1.45	1.39
3	F	469	NCA	C2-C3	3.58	1.44	1.39
3	E	459	NCA	C3-C7	3.54	1.55	1.50
3	F	469	NCA	C4-C3	3.51	1.44	1.39
3	G	479	NCA	C2-C3	3.34	1.44	1.39
3	E	359	NCA	C4-C3	3.33	1.44	1.39
3	E	459	NCA	C4-C3	3.25	1.44	1.39
3	F	469	NCA	C7-N7	-3.23	1.27	1.33
3	G	479	NCA	C7-N7	-3.19	1.27	1.33
3	F	469	NCA	O7-C7	-3.16	1.18	1.24
3	H	389	NCA	C2-C3	3.12	1.44	1.39
3	E	359	NCA	C3-C7	3.12	1.55	1.50
3	F	469	NCA	C3-C7	3.04	1.55	1.50
2	F	1179	N	C3'-C4'	2.99	1.60	1.53
2	H	1179	N	C3'-C4'	2.94	1.60	1.53
3	D	449	NCA	C4-C3	2.90	1.43	1.39
2	E	1179	N	C3'-C4'	2.89	1.60	1.53
3	G	479	NCA	C6-N1	2.86	1.41	1.33
2	C	1179	N	C3'-C4'	2.85	1.60	1.53
3	F	369	NCA	C2-C3	2.82	1.43	1.39
3	G	479	NCA	O7-C7	-2.80	1.18	1.24
3	B	329	NCA	C3-C7	2.78	1.54	1.50
2	D	1179	N	C3'-C4'	2.72	1.59	1.53
3	F	469	NCA	C6-N1	2.63	1.41	1.33
2	B	1179	N	C3'-C4'	2.61	1.59	1.53
3	A	419	NCA	C2-C3	2.60	1.43	1.39
3	A	319	NCA	C6-N1	2.58	1.41	1.33
3	G	379	NCA	C2-C3	2.57	1.43	1.39
2	A	1179	N	C3'-C4'	2.57	1.59	1.53
3	B	329	NCA	C2-C3	2.53	1.43	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1179	N	O5'-C5'	2.50	1.54	1.44
3	G	379	NCA	C6-N1	2.47	1.40	1.33
3	G	479	NCA	C5-C4	2.46	1.43	1.38
3	H	389	NCA	C6-N1	2.43	1.40	1.33
3	H	489	NCA	C2-C3	2.43	1.43	1.39
3	A	319	NCA	C2-C3	2.38	1.42	1.39
3	B	329	NCA	C6-N1	2.35	1.40	1.33
3	E	459	NCA	C6-N1	2.33	1.40	1.33
2	F	1179	N	O5'-C5'	2.33	1.53	1.44
2	H	1179	N	O5'-C5'	2.32	1.53	1.44
2	C	1179	N	O5'-C5'	2.31	1.53	1.44
3	E	359	NCA	C2-C3	2.30	1.42	1.39
3	D	449	NCA	C6-N1	2.30	1.40	1.33
2	E	1179	N	O5'-C5'	2.30	1.53	1.44
3	D	349	NCA	C2-C3	2.29	1.42	1.39
2	G	1179	N	C3'-C4'	2.26	1.58	1.53
3	B	429	NCA	O7-C7	-2.24	1.20	1.24
2	G	1179	N	O5'-C5'	2.22	1.53	1.44
2	B	1179	N	O5'-C5'	2.21	1.53	1.44
2	D	1179	N	O5'-C5'	2.21	1.53	1.44
3	H	489	NCA	O7-C7	-2.14	1.20	1.24
3	E	359	NCA	C6-N1	2.12	1.39	1.33
3	C	439	NCA	C6-N1	2.10	1.39	1.33
3	D	349	NCA	C6-N1	2.10	1.39	1.33
3	F	369	NCA	C6-N1	2.10	1.39	1.33
3	H	489	NCA	C6-N1	2.09	1.39	1.33
3	C	339	NCA	C6-N1	2.04	1.39	1.33
3	B	329	NCA	C5-C4	2.01	1.42	1.38

All (133) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1179	N	OP2-P-O5'	-5.12	93.31	106.67
2	G	1179	N	O4'-C1'-C2'	-5.06	97.05	105.76
2	B	1179	N	O4'-C1'-C2'	-5.05	97.06	105.76
2	F	1179	N	O4'-C1'-C2'	-4.97	97.19	105.76
2	E	1179	N	O4'-C1'-C2'	-4.89	97.33	105.76
2	C	1179	N	O4'-C1'-C2'	-4.89	97.34	105.76
2	H	1179	N	O4'-C1'-C2'	-4.88	97.35	105.76
2	G	1179	N	OP2-P-O5'	-4.86	94.00	106.67
2	D	1179	N	O4'-C1'-C2'	-4.76	97.56	105.76
2	F	1179	N	OP2-P-O5'	-4.76	94.27	106.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1179	N	OP2-P-O5'	-4.71	94.38	106.67
2	A	1179	N	O4'-C1'-C2'	-4.67	97.72	105.76
2	C	1179	N	OP2-P-O5'	-4.43	95.11	106.67
2	A	1179	N	OP2-P-O5'	-4.33	95.37	106.67
2	E	1179	N	OP2-P-O5'	-4.30	95.46	106.67
2	B	1179	N	C1'-O4'-C4'	4.22	117.37	108.06
3	G	379	NCA	C5-C4-C3	4.18	124.47	120.36
3	G	479	NCA	C5-C4-C3	4.15	124.44	120.36
2	F	1179	N	C1'-O4'-C4'	4.01	116.90	108.06
3	H	389	NCA	C5-C4-C3	4.00	124.30	120.36
3	C	339	NCA	C5-C4-C3	4.00	124.29	120.36
2	H	1179	N	OP2-P-O5'	-3.98	96.29	106.67
2	E	1179	N	C1'-O4'-C4'	3.96	116.80	108.06
3	C	439	NCA	C5-C4-C3	3.88	124.18	120.36
3	A	319	NCA	C5-C4-C3	3.87	124.17	120.36
2	D	1179	N	C1'-O4'-C4'	3.87	116.59	108.06
2	G	1179	N	C1'-O4'-C4'	3.86	116.57	108.06
2	H	1179	N	C1'-O4'-C4'	3.85	116.57	108.06
2	C	1179	N	C1'-O4'-C4'	3.85	116.56	108.06
3	D	449	NCA	C5-C4-C3	3.73	124.03	120.36
2	A	1179	N	C1'-O4'-C4'	3.69	116.21	108.06
3	F	369	NCA	C5-C4-C3	3.69	123.99	120.36
3	D	349	NCA	C5-C4-C3	3.60	123.91	120.36
2	E	1179	N	O5'-C5'-C4'	3.59	121.22	108.99
3	E	459	NCA	C5-C4-C3	3.59	123.89	120.36
2	C	1179	N	O5'-C5'-C4'	3.55	121.08	108.99
3	B	329	NCA	C5-C4-C3	3.51	123.81	120.36
2	F	1179	N	O5'-C5'-C4'	3.50	120.91	108.99
2	B	1179	N	O5'-C5'-C4'	3.50	120.89	108.99
2	H	1179	N	O5'-C5'-C4'	3.48	120.85	108.99
3	F	469	NCA	C5-C4-C3	3.45	123.76	120.36
3	G	479	NCA	C3-C7-N7	3.44	121.97	117.74
3	A	419	NCA	C5-C4-C3	3.42	123.73	120.36
3	B	429	NCA	C5-C4-C3	3.41	123.72	120.36
2	A	1179	N	O5'-C5'-C4'	3.41	120.61	108.99
2	G	1179	N	O5'-C5'-C4'	3.39	120.54	108.99
3	G	379	NCA	C3-C7-N7	3.38	121.90	117.74
2	D	1179	N	O5'-C5'-C4'	3.37	120.45	108.99
3	F	469	NCA	C3-C7-N7	3.32	121.83	117.74
3	H	389	NCA	C4-C3-C2	-3.32	113.92	117.61
3	C	439	NCA	C4-C3-C2	-3.32	113.92	117.61
2	G	1179	N	O4'-C4'-C3'	-3.24	101.64	104.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	459	NCA	C3-C7-N7	3.24	121.73	117.74
3	A	419	NCA	C4-C3-C2	-3.20	114.05	117.61
3	G	479	NCA	C4-C3-C2	-3.19	114.06	117.61
3	C	339	NCA	C4-C3-C2	-3.16	114.09	117.61
3	D	449	NCA	C4-C3-C2	-3.10	114.16	117.61
2	B	1179	N	O5'-P-OP1	3.09	114.78	106.44
3	E	359	NCA	C5-C4-C3	3.07	123.38	120.36
3	G	379	NCA	C4-C3-C2	-3.06	114.21	117.61
3	D	349	NCA	C4-C3-C2	-3.04	114.22	117.61
3	B	429	NCA	C4-C3-C2	-3.02	114.25	117.61
3	A	319	NCA	C3-C7-N7	2.98	121.41	117.74
3	C	439	NCA	C3-C7-N7	2.97	121.40	117.74
3	A	419	NCA	C3-C7-N7	2.96	121.38	117.74
3	F	369	NCA	C4-C3-C2	-2.95	114.32	117.61
3	A	319	NCA	C4-C3-C2	-2.94	114.33	117.61
3	B	329	NCA	C4-C3-C2	-2.81	114.48	117.61
2	A	1179	N	O5'-P-OP1	2.76	113.90	106.44
2	D	1179	N	O5'-P-OP1	2.75	113.88	106.44
2	C	1179	N	O5'-P-OP1	2.74	113.86	106.44
2	E	1179	N	O5'-P-OP1	2.73	113.81	106.44
2	H	1179	N	O5'-P-OP1	2.73	113.81	106.44
2	F	1179	N	O4'-C4'-C3'	-2.68	102.15	104.63
3	H	489	NCA	C5-C4-C3	2.67	122.99	120.36
2	B	1179	N	O2'-C2'-C3'	2.66	116.67	111.43
3	F	469	NCA	C4-C3-C2	-2.66	114.65	117.61
3	E	359	NCA	C4-C3-C2	-2.64	114.68	117.61
3	B	329	NCA	C3-C7-N7	2.63	120.97	117.74
2	B	1179	N	O4'-C4'-C3'	-2.62	102.22	104.63
2	F	1179	N	O5'-P-OP1	2.61	113.49	106.44
2	G	1179	N	O2'-C2'-C3'	2.60	116.55	111.43
2	G	1179	N	O5'-P-OP1	2.60	113.46	106.44
3	H	389	NCA	C3-C7-N7	2.58	120.92	117.74
3	F	369	NCA	C3-C7-N7	2.57	120.91	117.74
2	F	1179	N	O2'-C2'-C3'	2.56	116.47	111.43
3	E	359	NCA	C3-C7-N7	2.51	120.83	117.74
3	B	429	NCA	C3-C7-N7	2.48	120.79	117.74
2	E	1179	N	O2'-C2'-C3'	2.47	116.30	111.43
3	B	429	NCA	C6-N1-C2	2.47	121.17	116.85
3	E	459	NCA	C4-C3-C2	-2.44	114.90	117.61
3	C	339	NCA	C3-C7-N7	2.43	120.74	117.74
3	G	479	NCA	O7-C7-N7	-2.43	119.10	122.62
3	H	389	NCA	O7-C7-N7	-2.40	119.15	122.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	339	NCA	C6-N1-C2	2.40	121.05	116.85
3	D	349	NCA	C6-N1-C2	2.39	121.03	116.85
3	F	469	NCA	O7-C7-N7	-2.38	119.17	122.62
2	H	1179	N	C5'-C4'-C3'	2.38	123.77	115.21
2	D	1179	N	O2'-C2'-C3'	2.37	116.09	111.43
2	A	1179	N	O2'-C2'-C3'	2.36	116.08	111.43
2	G	1179	N	OP2-P-OP1	2.34	119.97	110.83
2	F	1179	N	OP2-P-OP1	2.34	119.94	110.83
3	C	439	NCA	C6-N1-C2	2.34	120.94	116.85
3	D	349	NCA	C3-C7-N7	2.33	120.61	117.74
2	D	1179	N	OP2-P-OP1	2.32	119.89	110.83
2	F	1179	N	C5'-C4'-C3'	2.32	123.57	115.21
3	B	429	NCA	O7-C7-N7	-2.32	119.26	122.62
2	D	1179	N	O4'-C4'-C3'	-2.30	102.50	104.63
2	C	1179	N	OP2-P-OP1	2.30	119.81	110.83
2	B	1179	N	OP2-P-OP1	2.30	119.79	110.83
2	G	1179	N	C5'-C4'-C3'	2.30	123.47	115.21
2	E	1179	N	C5'-C4'-C3'	2.29	123.45	115.21
3	H	389	NCA	C6-N1-C2	2.29	120.86	116.85
2	H	1179	N	O4'-C4'-C3'	-2.27	102.53	104.63
2	C	1179	N	C5'-C4'-C3'	2.26	123.36	115.21
2	D	1179	N	C5'-C4'-C3'	2.26	123.35	115.21
3	D	449	NCA	C3-C7-N7	2.26	120.52	117.74
2	A	1179	N	C5'-C4'-C3'	2.26	123.33	115.21
2	A	1179	N	OP2-P-OP1	2.22	119.50	110.83
2	H	1179	N	C1'-C2'-C3'	2.21	105.17	101.63
2	E	1179	N	O4'-C4'-C3'	-2.21	102.60	104.63
2	B	1179	N	C5'-C4'-C3'	2.20	123.12	115.21
3	B	329	NCA	C6-N1-C2	2.18	120.67	116.85
2	E	1179	N	OP2-P-OP1	2.17	119.29	110.83
2	C	1179	N	O4'-C4'-C3'	-2.17	102.63	104.63
2	H	1179	N	O2'-C2'-C3'	2.17	115.70	111.43
3	H	489	NCA	C4-C3-C2	-2.14	115.23	117.61
3	F	369	NCA	C6-N1-C2	2.11	120.56	116.85
2	C	1179	N	O2'-C2'-C3'	2.11	115.59	111.43
3	A	319	NCA	C6-N1-C2	2.10	120.53	116.85
2	H	1179	N	OP2-P-OP1	2.08	118.94	110.83
2	C	1179	N	C1'-C2'-C3'	2.04	104.89	101.63
2	A	1179	N	O4'-C4'-C3'	-2.01	102.77	104.63

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1179	N	C3'
2	B	1179	N	C3'
2	C	1179	N	C3'
2	D	1179	N	C3'
2	E	1179	N	C3'
2	F	1179	N	C3'
2	G	1179	N	C3'
2	H	1179	N	C3'

There are no torsion outliers.

There are no ring outliers.

19 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1179	N	3	0
3	D	449	NCA	2	0
3	H	389	NCA	3	0
3	C	339	NCA	1	0
3	F	469	NCA	2	0
2	E	1179	N	1	0
3	E	359	NCA	2	0
2	A	1179	N	2	0
3	A	419	NCA	1	0
3	E	459	NCA	5	0
3	F	369	NCA	1	0
3	G	479	NCA	1	0
3	A	319	NCA	2	0
2	F	1179	N	1	0
3	B	429	NCA	3	0
3	G	379	NCA	4	0
2	C	1179	N	2	0
3	C	439	NCA	3	0
3	H	489	NCA	4	0

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	251/258 (97%)	0.50	10 (3%) 42 38	21, 41, 63, 72	0
1	B	251/258 (97%)	0.24	8 (3%) 50 46	15, 35, 55, 68	0
1	C	251/258 (97%)	0.38	9 (3%) 46 42	19, 39, 60, 73	0
1	D	251/258 (97%)	0.20	5 (1%) 65 60	14, 34, 53, 75	0
1	E	251/258 (97%)	0.67	15 (5%) 27 24	23, 46, 63, 71	0
1	F	251/258 (97%)	0.22	7 (2%) 55 51	14, 34, 54, 75	0
1	G	251/258 (97%)	0.21	7 (2%) 55 51	12, 35, 55, 78	0
1	H	251/258 (97%)	0.78	15 (5%) 27 24	26, 49, 63, 74	0
All	All	2008/2064 (97%)	0.40	76 (3%) 44 40	12, 39, 61, 78	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	128	PHE	5.2
1	E	128	PHE	5.2
1	D	128	PHE	4.9
1	C	128	PHE	4.5
1	B	251	ALA	4.5
1	H	127	ASP	4.2
1	A	251	ALA	4.0
1	H	128	PHE	3.9
1	E	117	ASN	3.9
1	D	251	ALA	3.9
1	F	128	PHE	3.7
1	G	128	PHE	3.6
1	E	116	ALA	3.5
1	B	250	LEU	3.5
1	C	250	LEU	3.5
1	B	128	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	H	117	ASN	3.3
1	H	34	CYS	3.3
1	G	250	LEU	3.3
1	G	251	ALA	3.3
1	E	46	SER	3.2
1	A	250	LEU	3.1
1	F	251	ALA	2.9
1	E	118	PRO	2.9
1	D	250	LEU	2.9
1	F	250	LEU	2.9
1	G	51	CYS	2.9
1	D	51	CYS	2.8
1	E	53	LEU	2.8
1	E	126	PRO	2.7
1	C	31	ARG	2.7
1	H	116	ALA	2.7
1	F	246	ARG	2.7
1	H	35	SER	2.7
1	G	245	ALA	2.7
1	F	232	ARG	2.6
1	E	133	VAL	2.6
1	C	127	ASP	2.5
1	E	127	ASP	2.5
1	H	49	ASN	2.5
1	A	55	LEU	2.4
1	B	232	ARG	2.4
1	C	133	VAL	2.4
1	A	135	ALA	2.4
1	E	47	PHE	2.4
1	C	251	ALA	2.4
1	E	34	CYS	2.3
1	H	131	CYS	2.3
1	A	136	ARG	2.3
1	G	248	CYS	2.3
1	H	53	LEU	2.3
1	A	177	LYS	2.3
1	C	218	VAL	2.3
1	H	251	ALA	2.3
1	B	25	ASP	2.3
1	D	129	LYS	2.3
1	B	248	CYS	2.3
1	H	246	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	249	ARG	2.2
1	A	129	LYS	2.2
1	C	217	LEU	2.1
1	C	222	HIS	2.1
1	H	25	ASP	2.1
1	H	182	ASN	2.1
1	E	31	ARG	2.1
1	E	122	GLU	2.1
1	E	32	SER	2.1
1	A	222	HIS	2.1
1	F	131	CYS	2.0
1	G	246	ARG	2.0
1	H	232	ARG	2.0
1	B	55	LEU	2.0
1	B	123	LYS	2.0
1	E	1	ILE	2.0
1	A	172	ASP	2.0
1	H	126	PRO	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
3	NCA	H	389	9/9	0.48	0.23	57,58,60,62	0
3	NCA	B	329	9/9	0.55	0.22	35,39,40,41	0
3	NCA	E	359	9/9	0.56	0.26	54,54,55,55	0
2	N	A	1179	13/13	0.60	0.26	69,71,85,86	0
3	NCA	D	349	9/9	0.62	0.26	67,67,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NCA	G	379	9/9	0.65	0.20	61,62,62,63	0
3	NCA	F	369	9/9	0.71	0.21	49,52,52,53	0
3	NCA	A	319	9/9	0.71	0.17	59,61,62,62	0
2	N	C	1179	13/13	0.71	0.22	71,74,82,84	0
2	N	G	1179	13/13	0.73	0.18	59,60,66,66	0
2	N	E	1179	13/13	0.75	0.19	69,72,79,80	0
2	N	F	1179	13/13	0.76	0.20	59,61,68,68	0
3	NCA	H	489	9/9	0.76	0.22	48,49,54,54	0
2	N	H	1179	13/13	0.77	0.18	69,71,74,74	0
2	N	B	1179	13/13	0.78	0.18	58,61,66,67	0
3	NCA	F	469	9/9	0.79	0.23	48,49,53,55	0
2	N	D	1179	13/13	0.79	0.17	53,54,68,68	0
3	NCA	G	479	9/9	0.81	0.21	38,40,44,44	0
3	NCA	C	339	9/9	0.82	0.16	53,54,54,55	0
3	NCA	A	419	9/9	0.83	0.23	58,59,60,61	0
3	NCA	C	439	9/9	0.85	0.14	52,54,55,56	0
3	NCA	E	459	9/9	0.85	0.13	52,53,55,55	0
3	NCA	D	449	9/9	0.86	0.18	41,44,46,47	0
3	NCA	B	429	9/9	0.87	0.17	43,45,49,49	0

6.5 Other polymers

There are no such residues in this entry.