



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:18 PM UTC

PDB ID : 6KRK / pdb_00006krk
Title : Peroxiredoxin from Aeropyrum pernix K1 (ApPrx) 0Cys mutant
Authors : Himiyama, T.; Nakamura, T.
Deposited on : 2019-08-22
Resolution : 1.80 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

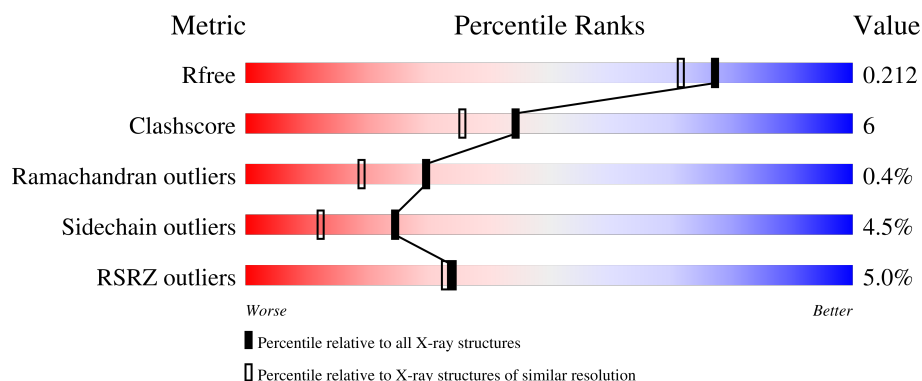
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	250	6% 80% 16% ..
1	B	250	4% 82% 14% ..
1	C	250	4% 81% 15% ...
1	D	250	4% 80% 16% ..
1	E	250	4% 82% 14% ...

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Mol	Chain	Length	Quality of chain
1	F	250	4% 82% 14% ...
1	G	250	6% 78% 17% ..
1	H	250	6% 82% 13% ..
1	I	250	4% 84% 12% ..
1	J	250	5% 82% 13% ...

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 21085 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 Peroxiredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	B	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	C	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	D	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	E	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	F	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	G	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	H	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	I	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0
1	J	244	Total 1973	C 1268	N 347	O 354	S 4	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

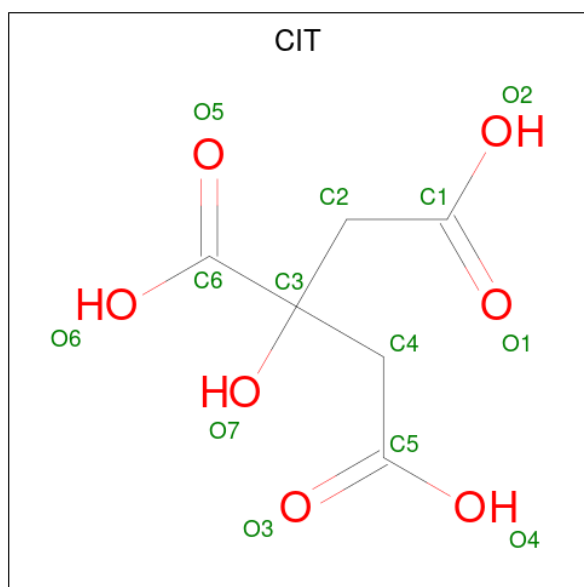
Chain	Residue	Modelled	Actual	Comment	Reference
A	50	SER	CYS	engineered mutation	UNP Q9Y9L0
A	207	SER	CYS	engineered mutation	UNP Q9Y9L0
A	213	SER	CYS	engineered mutation	UNP Q9Y9L0
B	50	SER	CYS	engineered mutation	UNP Q9Y9L0
B	207	SER	CYS	engineered mutation	UNP Q9Y9L0
B	213	SER	CYS	engineered mutation	UNP Q9Y9L0
C	50	SER	CYS	engineered mutation	UNP Q9Y9L0
C	207	SER	CYS	engineered mutation	UNP Q9Y9L0
C	213	SER	CYS	engineered mutation	UNP Q9Y9L0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	50	SER	CYS	engineered mutation	UNP Q9Y9L0
D	207	SER	CYS	engineered mutation	UNP Q9Y9L0
D	213	SER	CYS	engineered mutation	UNP Q9Y9L0
E	50	SER	CYS	engineered mutation	UNP Q9Y9L0
E	207	SER	CYS	engineered mutation	UNP Q9Y9L0
E	213	SER	CYS	engineered mutation	UNP Q9Y9L0
F	50	SER	CYS	engineered mutation	UNP Q9Y9L0
F	207	SER	CYS	engineered mutation	UNP Q9Y9L0
F	213	SER	CYS	engineered mutation	UNP Q9Y9L0
G	50	SER	CYS	engineered mutation	UNP Q9Y9L0
G	207	SER	CYS	engineered mutation	UNP Q9Y9L0
G	213	SER	CYS	engineered mutation	UNP Q9Y9L0
H	50	SER	CYS	engineered mutation	UNP Q9Y9L0
H	207	SER	CYS	engineered mutation	UNP Q9Y9L0
H	213	SER	CYS	engineered mutation	UNP Q9Y9L0
I	50	SER	CYS	engineered mutation	UNP Q9Y9L0
I	207	SER	CYS	engineered mutation	UNP Q9Y9L0
I	213	SER	CYS	engineered mutation	UNP Q9Y9L0
J	50	SER	CYS	engineered mutation	UNP Q9Y9L0
J	207	SER	CYS	engineered mutation	UNP Q9Y9L0
J	213	SER	CYS	engineered mutation	UNP Q9Y9L0

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 13 6 7	0	0
2	C	1	Total C O 13 6 7	0	0
2	D	1	Total C O 13 6 7	0	0
2	E	1	Total C O 13 6 7	0	0
2	F	1	Total C O 13 6 7	0	0
2	G	1	Total C O 13 6 7	0	0
2	H	1	Total C O 13 6 7	0	0
2	I	1	Total C O 13 6 7	0	0
2	J	1	Total C O 13 6 7	0	0

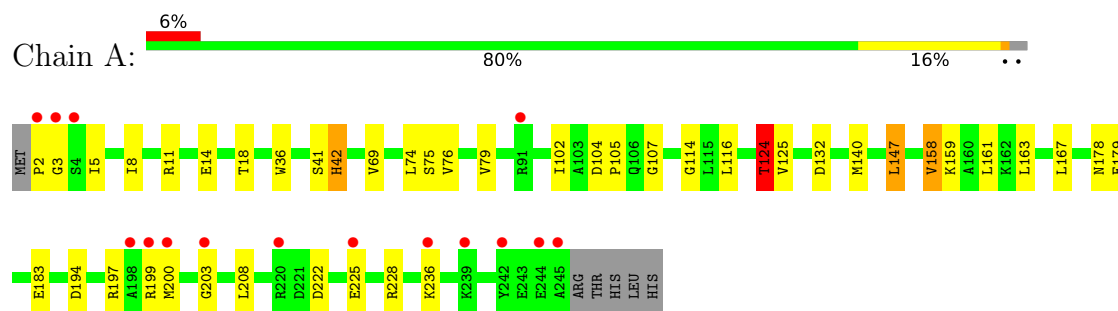
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	128	Total O 128 128	0	0
3	B	123	Total O 123 123	0	0
3	C	138	Total O 138 138	0	0
3	D	123	Total O 123 123	0	0
3	E	124	Total O 124 124	0	0
3	F	126	Total O 126 126	0	0
3	G	117	Total O 117 117	0	0
3	H	121	Total O 121 121	0	0
3	I	116	Total O 116 116	0	0
3	J	109	Total O 109 109	0	0

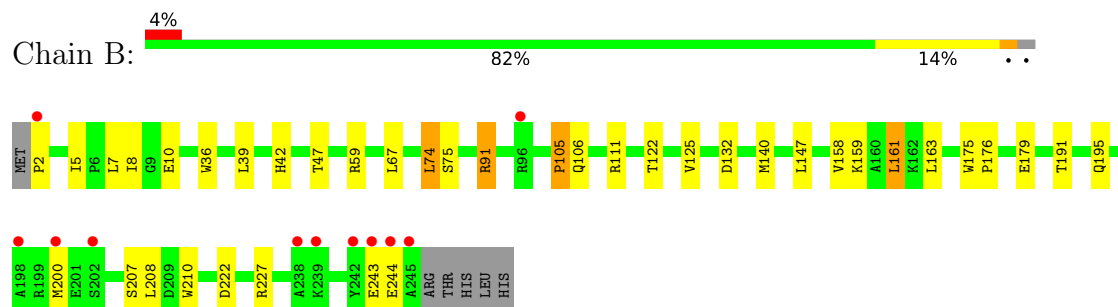
3 Residue-property plots [i](#)

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.

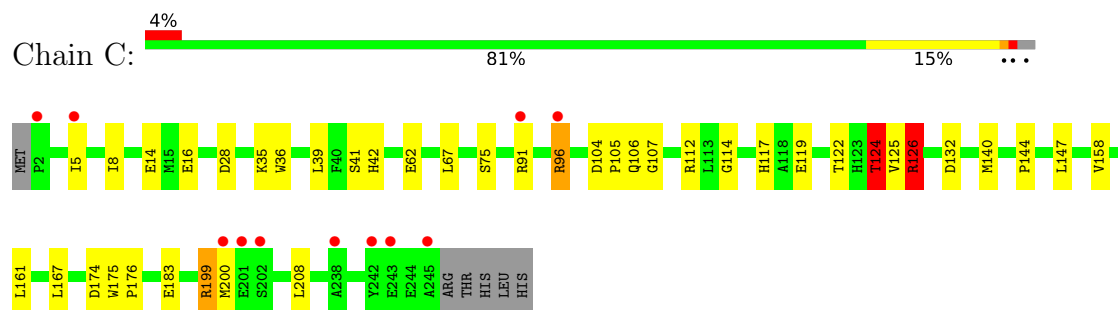
• Molecule 1: Peroxiredoxin



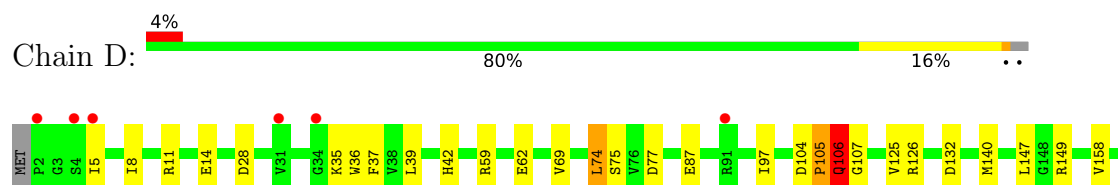
• Molecule 1: Peroxiredoxin

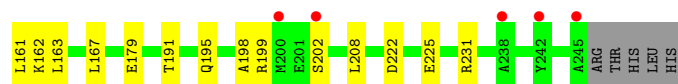


• Molecule 1: Peroxiredoxin

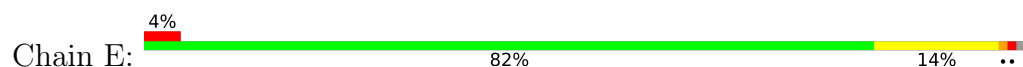


• Molecule 1: Peroxiredoxin

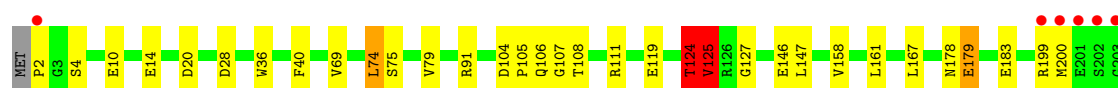
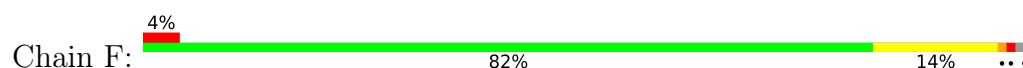




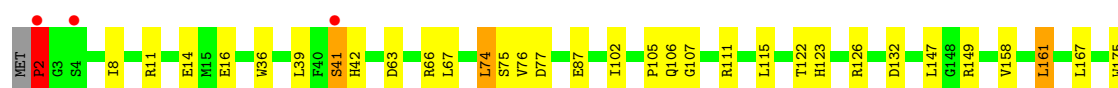
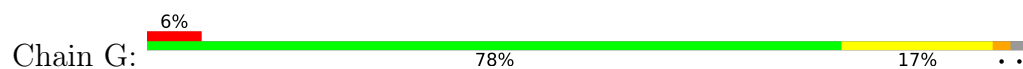
• Molecule 1: Peroxiredoxin



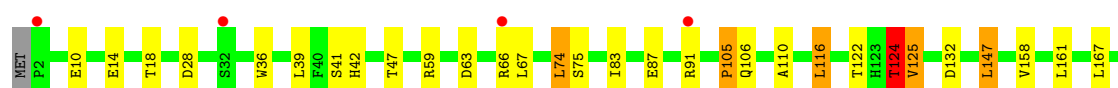
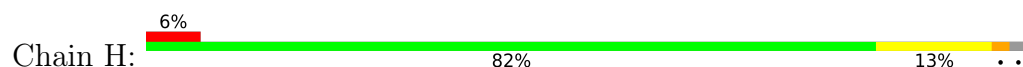
• Molecule 1: Peroxiredoxin



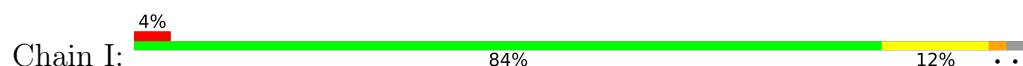
• Molecule 1: Peroxiredoxin

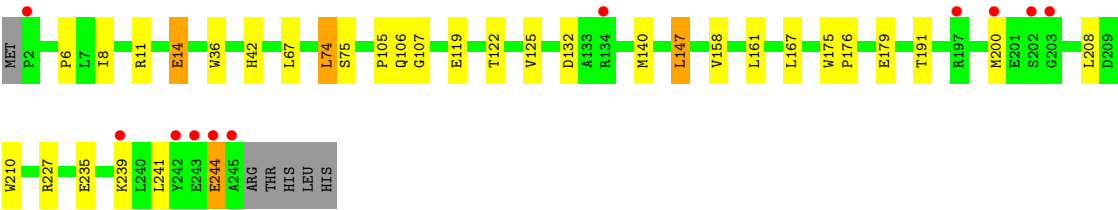


• Molecule 1: Peroxiredoxin

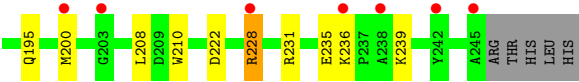
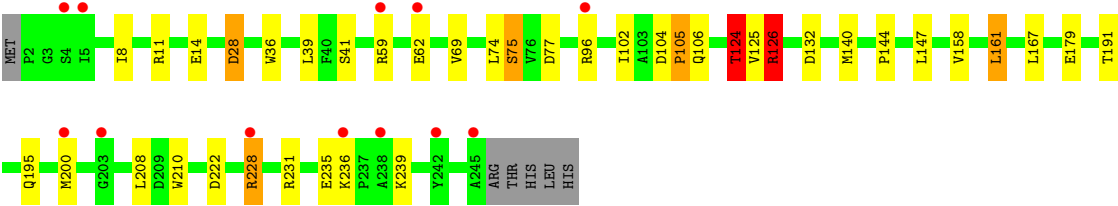
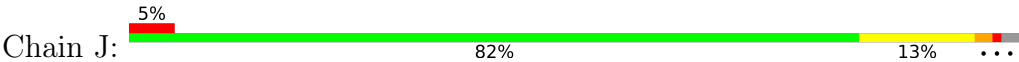


• Molecule 1: Peroxiredoxin





● Molecule 1: Peroxiredoxin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	75.83Å 102.79Å 104.44Å 105.88° 105.14° 92.46°	Depositor
Resolution (Å)	49.43 – 1.80 49.43 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.4 (49.43-1.80) 97.4 (49.43-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.159 , 0.194 (Not available) , 0.212	Depositor DCC
R_{free} test set	13261 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21085	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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: CIT

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	1.11	3/2028 (0.1%)	1.32	7/2757 (0.3%)
1	B	1.10	1/2028 (0.0%)	1.29	2/2757 (0.1%)
1	C	1.09	2/2028 (0.1%)	1.41	12/2757 (0.4%)
1	D	1.12	3/2028 (0.1%)	1.28	8/2757 (0.3%)
1	E	1.06	1/2028 (0.0%)	1.35	10/2757 (0.4%)
1	F	1.13	4/2028 (0.2%)	1.33	9/2757 (0.3%)
1	G	1.11	2/2028 (0.1%)	1.26	4/2757 (0.1%)
1	H	1.05	0/2028	1.29	6/2757 (0.2%)
1	I	1.07	0/2028	1.27	1/2757 (0.0%)
1	J	1.08	1/2028 (0.0%)	1.42	13/2757 (0.5%)
All	All	1.09	17/20280 (0.1%)	1.32	72/27570 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	E	0	1
1	J	0	1
All	All	0	3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	179	GLU	CD-OE2	10.35	1.45	1.25
1	F	179	GLU	CD-OE1	8.65	1.41	1.25
1	A	179	GLU	CD-OE2	8.28	1.41	1.25
1	D	179	GLU	CD-OE2	8.24	1.41	1.25
1	E	126	ARG	CD-NE	-7.64	1.35	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	126	ARG	CD-NE	-7.34	1.35	1.46
1	B	179	GLU	CD-OE2	6.44	1.37	1.25
1	J	126	ARG	CD-NE	-6.05	1.37	1.46
1	C	96	ARG	NE-CZ	5.54	1.39	1.33
1	F	125	VAL	C-O	5.41	1.30	1.24
1	A	42	HIS	CE1-NE2	5.34	1.37	1.32
1	F	36	TRP	C-O	5.32	1.31	1.23
1	D	77	ASP	CG-OD2	5.29	1.35	1.25
1	G	77	ASP	CG-OD1	5.28	1.35	1.25
1	G	8	ILE	C-O	5.20	1.29	1.24
1	D	198	ALA	C-O	5.08	1.30	1.24
1	A	158	VAL	C-O	5.00	1.29	1.24

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	126	ARG	NE-CZ-NH2	-18.66	102.41	119.20
1	J	126	ARG	NE-CZ-NH2	-14.38	106.26	119.20
1	E	126	ARG	NE-CZ-NH2	-13.89	106.69	119.20
1	C	126	ARG	CD-NE-CZ	13.87	143.82	124.40
1	C	126	ARG	NE-CZ-NH1	12.43	133.93	121.50
1	J	126	ARG	NE-CZ-NH1	10.69	132.19	121.50
1	E	126	ARG	CD-NE-CZ	10.48	139.07	124.40
1	E	126	ARG	NE-CZ-NH1	9.92	131.42	121.50
1	F	124	THR	N-CA-CB	-9.41	96.61	110.17
1	A	124	THR	N-CA-CB	-9.16	96.98	110.17
1	E	2	PRO	CA-N-CD	-9.10	99.26	112.00
1	C	124	THR	N-CA-CB	-8.92	96.36	109.83
1	G	2	PRO	CA-N-CD	-8.44	100.18	112.00
1	F	124	THR	CA-CB-OG1	8.41	122.21	109.60
1	H	124	THR	N-CA-CB	-8.41	98.06	110.17
1	J	124	THR	N-CA-CB	-8.36	98.13	110.17
1	E	126	ARG	CG-CD-NE	-8.31	93.72	112.00
1	J	126	ARG	CG-CD-NE	-8.28	93.79	112.00
1	J	126	ARG	CD-NE-CZ	8.22	135.91	124.40
1	D	106	GLN	CB-CG-CD	-7.84	99.26	112.60
1	F	179	GLU	CB-CG-CD	7.57	125.47	112.60
1	J	179	GLU	CB-CG-CD	7.18	124.80	112.60
1	J	124	THR	CB-CA-C	7.09	122.59	109.54
1	F	124	THR	CB-CA-C	7.06	122.54	109.54
1	A	124	THR	CB-CA-C	6.88	122.19	109.54
1	H	124	THR	CA-CB-OG1	6.79	119.78	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	124	THR	CB-CA-C	6.78	120.97	109.72
1	C	124	THR	CA-CB-OG1	6.73	119.69	109.60
1	D	62	GLU	CB-CG-CD	6.43	123.54	112.60
1	B	105	PRO	CA-C-N	-6.17	112.78	122.65
1	B	105	PRO	C-N-CA	-6.17	112.78	122.65
1	J	62	GLU	CB-CG-CD	6.08	122.94	112.60
1	D	231	ARG	NE-CZ-NH2	-6.05	113.75	119.20
1	D	199	ARG	CG-CD-NE	-6.05	98.69	112.00
1	E	28	ASP	CA-CB-CG	6.04	118.64	112.60
1	A	225	GLU	CB-CA-C	5.96	120.23	110.88
1	J	124	THR	OG1-CB-CG2	5.92	121.13	109.30
1	C	124	THR	OG1-CB-CG2	5.87	121.04	109.30
1	A	18	THR	CA-CB-OG1	-5.81	100.88	109.60
1	A	124	THR	OG1-CB-CG2	5.72	120.74	109.30
1	G	199	ARG	CG-CD-NE	-5.71	99.43	112.00
1	D	105	PRO	CA-C-N	-5.66	113.59	122.65
1	D	105	PRO	C-N-CA	-5.66	113.59	122.65
1	C	126	ARG	CG-CD-NE	-5.61	99.65	112.00
1	E	189	PRO	O-C-N	5.56	123.76	121.15
1	H	124	THR	CB-CA-C	5.52	119.69	109.54
1	E	132	ASP	CA-CB-CG	5.50	118.10	112.60
1	J	126	ARG	CB-CG-CD	5.49	123.92	111.30
1	A	178	ASN	CA-CB-CG	-5.47	107.13	112.60
1	G	215	ASP	CA-CB-CG	5.42	118.02	112.60
1	D	37	PHE	CA-CB-CG	5.41	119.21	113.80
1	E	227	ARG	CG-CD-NE	-5.41	100.09	112.00
1	F	108	THR	CA-CB-OG1	-5.40	101.50	109.60
1	H	18	THR	CA-CB-OG1	-5.37	101.54	109.60
1	D	97	ILE	CA-C-O	5.29	122.08	119.12
1	H	105	PRO	CA-C-N	-5.27	114.22	122.65
1	H	105	PRO	C-N-CA	-5.27	114.22	122.65
1	C	183	GLU	CA-C-N	5.26	125.10	120.10
1	C	183	GLU	C-N-CA	5.26	125.10	120.10
1	J	105	PRO	CA-C-N	-5.25	113.53	122.56
1	J	105	PRO	C-N-CA	-5.25	113.53	122.56
1	G	236	LYS	CB-CG-CD	5.21	123.28	111.30
1	F	124	THR	OG1-CB-CG2	5.21	119.72	109.30
1	F	178	ASN	CA-CB-CG	-5.20	107.40	112.60
1	J	222	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	199	ARG	CG-CD-NE	-5.14	100.70	112.00
1	C	199	ARG	CG-CD-NE	-5.10	100.77	112.00
1	I	6	PRO	N-CA-C	-5.09	104.09	111.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	96	ARG	NE-CZ-NH1	5.07	126.56	121.50
1	F	2	PRO	CA-N-CD	-5.04	104.95	112.00
1	E	37	PHE	CA-CB-CG	5.02	118.82	113.80
1	F	199	ARG	CG-CD-NE	-5.01	100.97	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	126	ARG	Sidechain
1	E	126	ARG	Sidechain
1	J	126	ARG	Sidechain

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	1973	0	1959	32	0
1	B	1973	0	1959	26	0
1	C	1973	0	1959	27	0
1	D	1973	0	1959	21	0
1	E	1973	0	1959	28	0
1	F	1973	0	1959	21	0
1	G	1973	0	1959	35	0
1	H	1973	0	1959	29	0
1	I	1973	0	1959	20	0
1	J	1973	0	1959	29	0
2	A	13	0	5	0	0
2	B	13	0	5	2	0
2	C	13	0	5	1	0
2	D	13	0	5	0	0
2	E	13	0	5	1	0
2	F	13	0	5	0	0
2	G	13	0	5	0	0
2	H	13	0	5	3	0
2	I	13	0	5	0	0
2	J	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	128	0	0	7	0
3	B	123	0	0	1	0
3	C	138	0	0	2	0
3	D	123	0	0	3	1
3	E	124	0	0	6	0
3	F	126	0	0	3	1
3	G	117	0	0	6	0
3	H	121	0	0	3	0
3	I	116	0	0	0	0
3	J	109	0	0	3	0
All	All	21085	0	19640	237	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 6.

All (237) 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:E:76:VAL:HG12	3:E:449:HOH:O	1.26	1.30
1:A:76:VAL:HG12	3:A:475:HOH:O	1.37	1.20
1:G:76:VAL:HB	3:G:488:HOH:O	1.01	1.18
1:E:126:ARG:HD2	1:E:144:PRO:O	1.67	0.92
1:I:11:ARG:NH1	1:I:14:GLU:OE1	2.04	0.90
1:H:222:ASP:OD2	3:H:401:HOH:O	1.90	0.90
1:H:245:ALA:HB1	3:H:407:HOH:O	1.74	0.87
1:D:11:ARG:NH1	1:D:14:GLU:OE2	2.09	0.85
1:C:105:PRO:O	1:H:105:PRO:O	1.96	0.83
1:E:11:ARG:NH1	1:E:14:GLU:OE1	2.10	0.82
1:D:14:GLU:OE1	1:D:28:ASP:OD1	1.99	0.80
1:A:11:ARG:NH1	1:A:14:GLU:OE1	2.13	0.80
1:E:76:VAL:CG1	3:E:449:HOH:O	1.96	0.78
1:A:236:LYS:HE2	3:A:415:HOH:O	1.82	0.78
1:C:126:ARG:HD2	1:C:144:PRO:O	1.84	0.78
1:G:63:ASP:OD2	1:G:228:ARG:NH2	2.19	0.76
1:B:91:ARG:NH1	3:B:401:HOH:O	2.19	0.75
1:J:11:ARG:NH1	1:J:14:GLU:OE2	2.18	0.75
1:H:14:GLU:OE1	1:H:28:ASP:OD1	2.06	0.73
1:H:47:THR:HB	2:H:301:CIT:H21	1.70	0.73
1:F:91:ARG:NH2	3:F:401:HOH:O	2.21	0.73
1:F:220:ARG:NH1	3:F:402:HOH:O	2.23	0.72
1:D:87:GLU:OE2	3:D:401:HOH:O	2.09	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:LEU:HD13	1:C:158:VAL:HG23	1.72	0.70
1:E:105:PRO:O	1:G:105:PRO:O	2.11	0.69
1:A:107:GLY:HA3	1:J:106:GLN:HE22	1.57	0.69
1:I:200:MET:HA	1:I:200:MET:HE2	1.75	0.69
1:D:8:ILE:HG13	1:D:140:MET:HE2	1.74	0.68
1:B:106:GLN:HE22	1:D:107:GLY:HA3	1.58	0.68
1:G:2:PRO:HB2	1:H:10:GLU:OE2	1.94	0.67
1:J:126:ARG:HD2	1:J:144:PRO:O	1.94	0.67
1:E:2:PRO:HB2	1:F:10:GLU:OE2	1.95	0.67
1:J:69:VAL:HG21	1:J:158:VAL:HG11	1.75	0.67
1:F:105:PRO:O	1:I:105:PRO:O	2.13	0.66
1:A:200:MET:HG2	3:A:519:HOH:O	1.94	0.66
1:B:105:PRO:O	1:D:105:PRO:O	2.14	0.66
1:J:200:MET:HE3	1:J:210:TRP:HA	1.79	0.64
1:A:236:LYS:CE	3:A:415:HOH:O	2.43	0.64
1:G:41:SER:OG	1:G:115:LEU:HD13	1.98	0.63
1:E:67:LEU:HD13	1:E:158:VAL:HG23	1.80	0.63
1:B:200:MET:HE3	1:B:210:TRP:HA	1.81	0.63
1:H:47:THR:HB	2:H:301:CIT:C2	2.29	0.63
1:J:236:LYS:HE3	3:J:416:HOH:O	1.97	0.63
1:A:2:PRO:O	1:B:5:ILE:O	2.16	0.63
1:G:122:THR:HG23	1:G:123:HIS:CD2	2.34	0.62
1:G:74:LEU:HD13	1:G:74:LEU:C	2.25	0.61
1:G:106:GLN:O	1:G:111:ARG:NH2	2.34	0.60
1:J:8:ILE:HG13	1:J:140:MET:HE2	1.83	0.60
1:J:236:LYS:CE	3:J:416:HOH:O	2.50	0.59
1:C:107:GLY:HA3	1:H:106:GLN:HE22	1.67	0.59
1:G:63:ASP:CG	1:G:228:ARG:HH22	2.10	0.58
1:G:76:VAL:CB	3:G:488:HOH:O	1.84	0.58
1:H:63:ASP:OD1	1:H:66:ARG:NH2	2.36	0.58
1:A:74:LEU:HD23	1:A:102:ILE:CG2	2.34	0.57
1:G:76:VAL:CG1	3:G:488:HOH:O	2.34	0.57
1:A:236:LYS:HD2	1:B:227:ARG:NH2	2.19	0.57
1:G:11:ARG:NH1	1:G:14:GLU:OE2	2.38	0.57
1:E:107:GLY:HA3	1:G:106:GLN:HE22	1.69	0.57
1:A:105:PRO:O	1:J:105:PRO:O	2.23	0.57
1:J:228:ARG:HH11	1:J:228:ARG:HB3	1.69	0.57
1:A:74:LEU:HD23	1:A:102:ILE:HB	1.86	0.56
1:E:105:PRO:HG2	1:G:122:THR:OG1	2.04	0.56
1:G:67:LEU:HD13	1:G:158:VAL:HG23	1.85	0.56
1:A:2:PRO:HB2	1:B:10:GLU:OE2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:41:SER:HB2	1:H:124:THR:HG21	1.88	0.56
1:C:200:MET:HE2	1:C:200:MET:HA	1.88	0.56
1:I:67:LEU:HD13	1:I:158:VAL:HG23	1.86	0.56
1:E:74:LEU:C	1:E:74:LEU:HD13	2.31	0.56
1:E:174:ASP:HB3	3:F:438:HOH:O	2.05	0.56
1:E:106:GLN:HE22	1:G:107:GLY:HA3	1.71	0.55
1:H:67:LEU:HD13	1:H:158:VAL:HG23	1.89	0.55
1:F:106:GLN:HE22	1:I:107:GLY:HA3	1.72	0.55
1:J:74:LEU:HD23	1:J:102:ILE:HB	1.89	0.55
1:G:200:MET:HA	1:G:200:MET:HE2	1.88	0.54
1:A:200:MET:CG	3:A:519:HOH:O	2.55	0.54
1:H:91:ARG:NH1	3:H:402:HOH:O	2.39	0.54
1:H:200:MET:HE3	1:H:210:TRP:HA	1.89	0.54
1:F:69:VAL:HG21	1:F:158:VAL:HG11	1.89	0.54
1:J:74:LEU:HD23	1:J:102:ILE:CG2	2.37	0.53
1:B:47:THR:HB	2:B:301:CIT:H42	1.90	0.53
1:I:227:ARG:NH2	1:J:236:LYS:HD2	2.22	0.53
1:B:200:MET:HA	1:B:200:MET:HE2	1.90	0.53
1:H:74:LEU:C	1:H:74:LEU:HD13	2.33	0.53
1:F:107:GLY:HA3	1:I:106:GLN:HE22	1.74	0.53
1:B:39:LEU:C	1:B:39:LEU:HD23	2.33	0.53
1:B:74:LEU:HD13	1:B:74:LEU:C	2.34	0.53
1:J:14:GLU:OE1	1:J:28:ASP:OD1	2.26	0.53
1:C:199:ARG:HG3	1:C:200:MET:HE3	1.91	0.53
1:A:69:VAL:HG21	1:A:158:VAL:HG11	1.91	0.53
1:J:96:ARG:NH2	3:J:403:HOH:O	2.42	0.52
1:J:231:ARG:O	1:J:235:GLU:HG3	2.08	0.52
1:G:220:ARG:HB3	1:G:220:ARG:NH1	2.25	0.52
3:E:446:HOH:O	1:F:206:ARG:HD3	2.09	0.52
1:F:74:LEU:HD13	1:F:74:LEU:C	2.35	0.52
1:H:59:ARG:NH2	1:H:241:LEU:HD21	2.24	0.52
1:B:106:GLN:O	1:B:111:ARG:NH2	2.43	0.52
1:A:8:ILE:HG13	1:A:140:MET:HE2	1.92	0.51
1:E:126:ARG:CD	1:E:144:PRO:O	2.50	0.51
1:D:74:LEU:HD13	1:D:74:LEU:C	2.36	0.51
1:D:39:LEU:C	1:D:39:LEU:HD23	2.36	0.51
1:J:200:MET:HE2	1:J:200:MET:HA	1.93	0.50
1:A:74:LEU:HD13	1:A:74:LEU:C	2.36	0.50
1:A:79:VAL:HG11	1:I:191:THR:O	2.12	0.50
1:I:74:LEU:HD13	1:I:75:SER:N	2.27	0.50
1:E:104:ASP:N	1:E:105:PRO:HD3	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:236:LYS:NZ	3:E:402:HOH:O	2.39	0.49
1:G:200:MET:HE3	1:G:210:TRP:HA	1.94	0.49
1:A:41:SER:HB2	1:A:124:THR:HG21	1.94	0.49
1:I:8:ILE:HG13	1:I:140:MET:HE2	1.94	0.49
1:G:228:ARG:HH21	1:G:232:ARG:NH1	2.11	0.49
1:C:199:ARG:HG3	1:C:200:MET:CE	2.42	0.49
1:D:69:VAL:HG21	1:D:158:VAL:HG11	1.94	0.49
1:D:191:THR:H	1:D:195:GLN:NE2	2.11	0.49
1:A:2:PRO:CB	1:B:10:GLU:OE2	2.61	0.48
1:G:39:LEU:C	1:G:39:LEU:HD23	2.37	0.48
1:H:39:LEU:C	1:H:39:LEU:HD23	2.37	0.48
1:H:83:ILE:O	1:H:87:GLU:HG3	2.14	0.48
1:B:163:LEU:HD21	1:B:222:ASP:OD2	2.13	0.48
1:F:179:GLU:CD	1:F:179:GLU:H	2.21	0.48
1:B:36:TRP:CD2	1:B:132:ASP:HA	2.49	0.48
1:I:36:TRP:CD2	1:I:132:ASP:HA	2.48	0.48
1:A:42:HIS:CE1	1:A:75:SER:HB3	2.48	0.48
1:B:67:LEU:HD13	1:B:158:VAL:HG23	1.96	0.48
1:H:191:THR:H	1:H:195:GLN:NE2	2.12	0.48
1:B:191:THR:H	1:B:195:GLN:NE2	2.11	0.47
1:C:5:ILE:HD13	1:D:5:ILE:HD13	1.95	0.47
1:D:225:GLU:HG2	3:D:444:HOH:O	2.13	0.47
1:E:200:MET:HG2	1:E:210:TRP:HB3	1.97	0.47
1:I:147:LEU:HG	1:J:161:LEU:HD13	1.96	0.47
1:C:39:LEU:C	1:C:39:LEU:HD23	2.39	0.47
1:J:75:SER:HB3	1:J:77:ASP:H	1.79	0.47
1:E:228:ARG:HD3	3:E:505:HOH:O	2.14	0.47
2:C:301:CIT:O5	2:C:301:CIT:O1	2.33	0.47
1:D:36:TRP:CD2	1:D:132:ASP:HA	2.50	0.47
1:C:104:ASP:N	1:C:105:PRO:HD3	2.30	0.46
3:E:402:HOH:O	1:F:183:GLU:HG2	2.15	0.46
1:F:14:GLU:OE1	1:F:28:ASP:OD1	2.32	0.46
1:A:74:LEU:HD21	1:A:104:ASP:HB2	1.98	0.46
1:J:104:ASP:N	1:J:105:PRO:HD3	2.31	0.46
1:A:36:TRP:CD2	1:A:132:ASP:HA	2.50	0.46
1:D:163:LEU:HD11	1:D:222:ASP:HB3	1.98	0.46
1:J:74:LEU:HD21	1:J:104:ASP:HB2	1.98	0.46
1:A:200:MET:HA	3:A:519:HOH:O	2.15	0.46
1:C:91:ARG:NH2	3:C:404:HOH:O	2.49	0.46
1:C:117:HIS:CE1	1:D:140:MET:HE1	2.51	0.46
1:G:161:LEU:HD13	1:H:147:LEU:HG	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:THR:HA	1:D:106:GLN:OE1	2.16	0.46
1:G:36:TRP:CD2	1:G:132:ASP:HA	2.51	0.46
1:J:39:LEU:HD23	1:J:39:LEU:C	2.41	0.46
1:E:74:LEU:HD13	1:E:75:SER:N	2.31	0.45
1:E:36:TRP:CD2	1:E:132:ASP:HA	2.52	0.45
1:H:36:TRP:CD2	1:H:132:ASP:HA	2.51	0.45
1:I:74:LEU:HD13	1:I:74:LEU:C	2.41	0.45
1:A:159:LYS:NZ	1:A:222:ASP:OD1	2.49	0.45
1:D:42:HIS:CE1	1:D:75:SER:HB3	2.51	0.45
1:G:42:HIS:CE1	1:G:75:SER:HB3	2.51	0.45
1:J:74:LEU:C	1:J:74:LEU:HD13	2.41	0.45
1:B:47:THR:HB	2:B:301:CIT:C4	2.46	0.45
1:C:36:TRP:CD2	1:C:132:ASP:HA	2.52	0.45
1:I:227:ARG:NH2	1:J:236:LYS:CD	2.79	0.45
1:A:3:GLY:HA3	1:B:7:LEU:HD21	1.99	0.45
1:D:74:LEU:HD13	1:D:75:SER:N	2.32	0.45
1:G:74:LEU:HD23	1:G:102:ILE:CG2	2.47	0.44
1:A:104:ASP:N	1:A:105:PRO:HD3	2.32	0.44
1:E:208:LEU:HD13	1:E:214:TRP:CZ3	2.52	0.44
1:F:119:GLU:OE2	1:F:146:GLU:OE2	2.35	0.44
1:J:191:THR:H	1:J:195:GLN:NE2	2.15	0.44
1:B:59:ARG:HD3	1:B:59:ARG:HA	1.84	0.44
1:A:194:ASP:OD1	1:A:197:ARG:NH2	2.50	0.44
1:E:67:LEU:CD1	1:E:158:VAL:HG23	2.46	0.44
1:A:5:ILE:HG22	1:A:114:GLY:HA3	2.00	0.44
1:J:41:SER:HB2	1:J:124:THR:HG21	2.00	0.44
1:B:42:HIS:CE1	1:B:75:SER:HB3	2.52	0.44
1:E:67:LEU:O	1:E:162:LYS:HE3	2.18	0.44
1:H:67:LEU:CD1	1:H:158:VAL:HG23	2.47	0.44
1:A:76:VAL:CG1	3:A:475:HOH:O	2.20	0.43
1:F:106:GLN:O	1:F:111:ARG:NH2	2.51	0.43
1:G:175:TRP:CG	1:G:176:PRO:HA	2.53	0.43
1:H:42:HIS:CE1	1:H:75:SER:HB3	2.53	0.43
1:B:8:ILE:HG13	1:B:140:MET:HE2	1.99	0.43
1:H:41:SER:HB2	1:H:124:THR:CG2	2.47	0.43
1:A:69:VAL:CG2	1:A:158:VAL:HG11	2.48	0.43
1:G:87:GLU:OE2	3:G:401:HOH:O	2.21	0.43
3:G:432:HOH:O	1:H:174:ASP:HB3	2.17	0.43
1:A:147:LEU:HG	1:B:161:LEU:HD13	2.00	0.43
2:E:301:CIT:O3	2:E:301:CIT:O2	2.37	0.43
1:G:188:PRO:O	1:G:199:ARG:NH2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:LEU:HD23	1:A:102:ILE:CB	2.48	0.43
1:F:74:LEU:HD13	1:F:75:SER:N	2.34	0.43
1:G:244:GLU:O	1:G:245:ALA:C	2.62	0.43
1:I:67:LEU:CD1	1:I:158:VAL:HG23	2.48	0.43
1:C:42:HIS:O	1:C:124:THR:HG22	2.19	0.43
1:D:126:ARG:HB3	1:D:149:ARG:CZ	2.48	0.43
1:I:200:MET:HE3	1:I:210:TRP:HA	2.01	0.43
1:E:5:ILE:HG22	1:E:114:GLY:HA3	2.01	0.43
1:F:20:ASP:HA	1:F:79:VAL:CG2	2.49	0.42
1:C:8:ILE:HG13	1:C:140:MET:HE2	2.02	0.42
1:G:126:ARG:HB3	1:G:149:ARG:CZ	2.50	0.42
1:G:106:GLN:NE2	3:G:409:HOH:O	2.53	0.42
1:C:124:THR:HG23	1:C:125:VAL:O	2.20	0.42
1:E:11:ARG:HG2	1:E:11:ARG:HH11	1.85	0.42
1:F:40:PHE:HA	1:F:127:GLY:O	2.20	0.42
1:F:105:PRO:HG2	1:I:122:THR:HB	2.02	0.42
1:B:175:TRP:CG	1:B:176:PRO:HA	2.55	0.42
1:C:14:GLU:OE2	1:C:28:ASP:OD1	2.37	0.42
1:E:74:LEU:C	1:E:74:LEU:CD1	2.92	0.42
1:I:42:HIS:CE1	1:I:75:SER:HB3	2.55	0.42
1:J:124:THR:HG23	1:J:125:VAL:O	2.20	0.42
1:C:106:GLN:HG3	1:H:122:THR:HA	2.01	0.41
1:C:5:ILE:HG22	1:C:114:GLY:HA3	2.02	0.41
1:C:175:TRP:CG	1:C:176:PRO:HA	2.55	0.41
1:G:63:ASP:OD1	1:G:66:ARG:NH1	2.54	0.41
1:H:110:ALA:HB1	1:H:116:LEU:HD22	2.02	0.41
1:C:67:LEU:CD1	1:C:158:VAL:HG23	2.46	0.41
1:E:8:ILE:HG13	1:E:140:MET:HE2	2.03	0.41
1:F:104:ASP:N	1:F:105:PRO:CD	2.83	0.41
1:G:74:LEU:C	1:G:74:LEU:CD1	2.93	0.41
1:C:41:SER:HB2	1:C:124:THR:HG21	2.03	0.41
1:E:103:ALA:C	1:E:105:PRO:HD3	2.46	0.41
1:C:112:ARG:NH1	3:C:406:HOH:O	2.53	0.41
1:D:104:ASP:N	1:D:105:PRO:HD3	2.35	0.41
1:C:122:THR:HB	1:H:105:PRO:HG2	2.02	0.41
1:F:124:THR:HG23	1:F:125:VAL:O	2.21	0.41
1:J:69:VAL:CG2	1:J:158:VAL:HG11	2.47	0.41
1:B:67:LEU:HD21	1:B:159:LYS:HD3	2.03	0.41
1:C:174:ASP:HB3	3:D:425:HOH:O	2.20	0.41
1:H:124:THR:HG23	1:H:125:VAL:O	2.21	0.41
1:I:241:LEU:HA	1:I:244:GLU:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:74:LEU:HD23	1:G:102:ILE:HB	2.03	0.40
1:I:175:TRP:CG	1:I:176:PRO:HA	2.56	0.40
1:C:5:ILE:HG21	1:D:5:ILE:HD11	2.03	0.40
1:C:42:HIS:CE1	1:C:75:SER:HB3	2.56	0.40
1:F:200:MET:HG2	1:F:210:TRP:HB3	2.02	0.40
1:J:36:TRP:CD2	1:J:132:ASP:HA	2.56	0.40
1:E:208:LEU:HD13	1:E:214:TRP:HZ3	1.85	0.40
1:G:215:ASP:OD1	1:G:217:PRO:HD3	2.21	0.40
1:H:47:THR:HB	2:H:301:CIT:C1	2.51	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)
3:D:444:HOH:O	3:F:492:HOH:O[1_544]	2.16	0.04

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	242/250 (97%)	232 (96%)	8 (3%)	2 (1%)	16	6
1	B	242/250 (97%)	239 (99%)	2 (1%)	1 (0%)	30	19
1	C	242/250 (97%)	238 (98%)	4 (2%)	0	100	100
1	D	242/250 (97%)	237 (98%)	4 (2%)	1 (0%)	30	19
1	E	242/250 (97%)	237 (98%)	4 (2%)	1 (0%)	30	19
1	F	242/250 (97%)	237 (98%)	4 (2%)	1 (0%)	30	19
1	G	242/250 (97%)	238 (98%)	4 (2%)	0	100	100
1	H	242/250 (97%)	237 (98%)	3 (1%)	2 (1%)	16	6
1	I	242/250 (97%)	237 (98%)	4 (2%)	1 (0%)	30	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	242/250 (97%)	238 (98%)	4 (2%)	0	100	100
All	All	2420/2500 (97%)	2370 (98%)	41 (2%)	9 (0%)	30	19

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	244	GLU
1	A	203	GLY
1	E	125	VAL
1	F	125	VAL
1	A	125	VAL
1	D	125	VAL
1	I	125	VAL
1	B	125	VAL
1	H	125	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	210/216 (97%)	201 (96%)	9 (4%)	26	13
1	B	210/216 (97%)	201 (96%)	9 (4%)	26	13
1	C	210/216 (97%)	200 (95%)	10 (5%)	23	11
1	D	210/216 (97%)	200 (95%)	10 (5%)	23	11
1	E	210/216 (97%)	202 (96%)	8 (4%)	29	17
1	F	210/216 (97%)	200 (95%)	10 (5%)	23	11
1	G	210/216 (97%)	201 (96%)	9 (4%)	26	13
1	H	210/216 (97%)	202 (96%)	8 (4%)	29	17
1	I	210/216 (97%)	199 (95%)	11 (5%)	21	9
1	J	210/216 (97%)	200 (95%)	10 (5%)	23	11
All	All	2100/2160 (97%)	2006 (96%)	94 (4%)	24	12

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	LEU
1	A	124	THR
1	A	147	LEU
1	A	161	LEU
1	A	163	LEU
1	A	167	LEU
1	A	183	GLU
1	A	208	LEU
1	A	228	ARG
1	B	2	PRO
1	B	74	LEU
1	B	91	ARG
1	B	147	LEU
1	B	161	LEU
1	B	207	SER
1	B	208	LEU
1	B	243	GLU
1	B	244	GLU
1	C	16	GLU
1	C	35	LYS
1	C	62	GLU
1	C	96	ARG
1	C	119	GLU
1	C	124	THR
1	C	147	LEU
1	C	161	LEU
1	C	167	LEU
1	C	208	LEU
1	D	35	LYS
1	D	59	ARG
1	D	74	LEU
1	D	106	GLN
1	D	147	LEU
1	D	161	LEU
1	D	162	LYS
1	D	167	LEU
1	D	202	SER
1	D	208	LEU
1	E	2	PRO
1	E	16	GLU
1	E	74	LEU
1	E	116	LEU

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Mol	Chain	Res	Type
1	E	147	LEU
1	E	167	LEU
1	E	204	GLN
1	E	208	LEU
1	F	4	SER
1	F	74	LEU
1	F	124	THR
1	F	147	LEU
1	F	161	LEU
1	F	167	LEU
1	F	207	SER
1	F	208	LEU
1	F	228	ARG
1	F	244	GLU
1	G	2	PRO
1	G	16	GLU
1	G	41	SER
1	G	74	LEU
1	G	147	LEU
1	G	161	LEU
1	G	167	LEU
1	G	179	GLU
1	G	208	LEU
1	H	74	LEU
1	H	116	LEU
1	H	124	THR
1	H	147	LEU
1	H	161	LEU
1	H	167	LEU
1	H	208	LEU
1	H	244	GLU
1	I	14	GLU
1	I	74	LEU
1	I	119	GLU
1	I	147	LEU
1	I	161	LEU
1	I	167	LEU
1	I	179	GLU
1	I	208	LEU
1	I	235	GLU
1	I	239	LYS
1	I	244	GLU

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Mol	Chain	Res	Type
1	J	28	ASP
1	J	59	ARG
1	J	75	SER
1	J	124	THR
1	J	147	LEU
1	J	161	LEU
1	J	167	LEU
1	J	208	LEU
1	J	228	ARG
1	J	239	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	204	GLN
1	B	106	GLN
1	B	123	HIS
1	B	195	GLN
1	B	204	GLN
1	C	33	GLN
1	C	65	GLN
1	D	33	GLN
1	D	195	GLN
1	E	65	GLN
1	E	106	GLN
1	F	106	GLN
1	F	195	GLN
1	G	65	GLN
1	G	106	GLN
1	G	123	HIS
1	H	106	GLN
1	H	195	GLN
1	H	204	GLN
1	I	106	GLN
1	J	106	GLN
1	J	123	HIS
1	J	195	GLN
1	J	204	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

10 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	CIT	B	301	-	12,12,12	1.74	4 (33%)	17,17,17	1.29	3 (17%)
2	CIT	A	301	-	12,12,12	1.81	4 (33%)	17,17,17	1.18	1 (5%)
2	CIT	G	301	-	12,12,12	1.46	2 (16%)	17,17,17	1.52	2 (11%)
2	CIT	I	301	-	12,12,12	1.55	1 (8%)	17,17,17	1.90	4 (23%)
2	CIT	C	301	-	12,12,12	1.36	1 (8%)	17,17,17	1.76	5 (29%)
2	CIT	F	301	-	12,12,12	1.48	1 (8%)	17,17,17	1.48	4 (23%)
2	CIT	H	301	-	12,12,12	1.26	2 (16%)	17,17,17	1.90	4 (23%)
2	CIT	E	301	-	12,12,12	1.71	3 (25%)	17,17,17	1.55	3 (17%)
2	CIT	D	301	-	12,12,12	1.72	2 (16%)	17,17,17	1.53	2 (11%)
2	CIT	J	301	-	12,12,12	1.76	2 (16%)	17,17,17	1.67	5 (29%)

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	CIT	B	301	-	-	9/16/16/16	-
2	CIT	A	301	-	-	3/16/16/16	-
2	CIT	G	301	-	-	8/16/16/16	-
2	CIT	I	301	-	-	6/16/16/16	-
2	CIT	C	301	-	-	5/16/16/16	-
2	CIT	F	301	-	-	5/16/16/16	-
2	CIT	H	301	-	-	6/16/16/16	-
2	CIT	E	301	-	-	6/16/16/16	-
2	CIT	D	301	-	-	3/16/16/16	-
2	CIT	J	301	-	-	6/16/16/16	-

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	301	CIT	C3-C6	4.87	1.58	1.53
2	I	301	CIT	C3-C6	4.27	1.57	1.53
2	C	301	CIT	C3-C6	3.94	1.57	1.53
2	A	301	CIT	C3-C6	3.84	1.57	1.53
2	E	301	CIT	C3-C6	3.84	1.57	1.53
2	F	301	CIT	C3-C6	3.66	1.57	1.53
2	D	301	CIT	O4-C5	-3.23	1.20	1.30
2	B	301	CIT	O3-C5	3.22	1.32	1.22
2	D	301	CIT	C3-C6	3.21	1.56	1.53
2	G	301	CIT	C3-C6	2.96	1.56	1.53
2	A	301	CIT	O2-C1	-2.66	1.22	1.30
2	E	301	CIT	O3-C5	2.61	1.30	1.22
2	B	301	CIT	O2-C1	-2.53	1.22	1.30
2	E	301	CIT	O4-C5	-2.43	1.22	1.30
2	B	301	CIT	C3-C6	2.36	1.55	1.53
2	A	301	CIT	O1-C1	2.23	1.29	1.22
2	J	301	CIT	O4-C5	-2.21	1.23	1.30
2	A	301	CIT	C2-C3	-2.19	1.51	1.54
2	H	301	CIT	C2-C3	-2.16	1.51	1.54
2	B	301	CIT	O4-C5	-2.14	1.23	1.30
2	H	301	CIT	O4-C5	-2.11	1.23	1.30
2	G	301	CIT	O2-C1	-2.03	1.24	1.30

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	301	CIT	O1-C1-C2	-4.50	110.22	122.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	301	CIT	O3-C5-C4	-4.36	110.61	122.95
2	G	301	CIT	O3-C5-C4	-4.01	111.60	122.95
2	I	301	CIT	O4-C5-C4	3.75	126.23	114.35
2	C	301	CIT	O1-C1-C2	-3.72	112.42	122.95
2	D	301	CIT	O6-C6-C3	3.57	119.98	113.14
2	D	301	CIT	O5-C6-C3	-3.49	115.33	122.09
2	J	301	CIT	O6-C6-C3	3.40	119.66	113.14
2	F	301	CIT	O1-C1-C2	-3.37	113.42	122.95
2	C	301	CIT	C2-C3-C6	3.36	117.46	110.03
2	E	301	CIT	O6-C6-C3	3.07	119.03	113.14
2	G	301	CIT	O4-C5-C4	2.98	123.79	114.35
2	H	301	CIT	O2-C1-C2	2.83	123.32	114.35
2	C	301	CIT	O2-C1-C2	2.82	123.30	114.35
2	E	301	CIT	O5-C6-C3	-2.82	116.62	122.09
2	F	301	CIT	O3-C5-C4	-2.76	115.14	122.95
2	I	301	CIT	O1-C1-C2	-2.66	115.42	122.95
2	J	301	CIT	O7-C3-C4	-2.62	103.40	109.38
2	E	301	CIT	O1-C1-C2	-2.57	115.66	122.95
2	J	301	CIT	O1-C1-C2	-2.57	115.67	122.95
2	J	301	CIT	C4-C3-C6	2.55	115.67	110.03
2	H	301	CIT	O5-C6-C3	-2.51	117.24	122.09
2	B	301	CIT	O7-C3-C4	-2.49	103.70	109.38
2	F	301	CIT	O2-C1-C2	2.47	122.16	114.35
2	A	301	CIT	O3-C5-C4	-2.44	116.03	122.95
2	H	301	CIT	O7-C3-C2	-2.44	103.81	109.38
2	C	301	CIT	O3-C5-C4	-2.23	116.64	122.95
2	J	301	CIT	O5-C6-C3	-2.20	117.83	122.09
2	B	301	CIT	C3-C2-C1	2.19	119.92	113.92
2	F	301	CIT	C4-C3-C6	2.18	114.85	110.03
2	B	301	CIT	O5-C6-C3	-2.17	117.88	122.09
2	C	301	CIT	O7-C3-C2	-2.11	104.57	109.38
2	I	301	CIT	O2-C1-C2	2.07	120.92	114.35

There are no chirality outliers.

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	CIT	C2-C3-C4-C5
2	A	301	CIT	O7-C3-C4-C5
2	A	301	CIT	C6-C3-C4-C5
2	B	301	CIT	C1-C2-C3-O7
2	B	301	CIT	O7-C3-C6-O5

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Mol	Chain	Res	Type	Atoms
2	C	301	CIT	C2-C3-C6-O5
2	C	301	CIT	C2-C3-C6-O6
2	C	301	CIT	O7-C3-C6-O5
2	C	301	CIT	O7-C3-C6-O6
2	D	301	CIT	C1-C2-C3-O7
2	D	301	CIT	C1-C2-C3-C6
2	E	301	CIT	C1-C2-C3-O7
2	E	301	CIT	C1-C2-C3-C4
2	E	301	CIT	C1-C2-C3-C6
2	F	301	CIT	O7-C3-C4-C5
2	F	301	CIT	C6-C3-C4-C5
2	G	301	CIT	C1-C2-C3-O7
2	G	301	CIT	C1-C2-C3-C6
2	H	301	CIT	O7-C3-C6-O6
2	H	301	CIT	C4-C3-C6-O6
2	I	301	CIT	C1-C2-C3-O7
2	I	301	CIT	C1-C2-C3-C4
2	I	301	CIT	C1-C2-C3-C6
2	J	301	CIT	C2-C3-C6-O5
2	J	301	CIT	C2-C3-C6-O6
2	J	301	CIT	O7-C3-C6-O5
2	J	301	CIT	O7-C3-C6-O6
2	D	301	CIT	C1-C2-C3-C4
2	F	301	CIT	C2-C3-C4-C5
2	G	301	CIT	C1-C2-C3-C4
2	E	301	CIT	C2-C3-C4-C5
2	H	301	CIT	C4-C3-C6-O5
2	E	301	CIT	C6-C3-C4-C5
2	F	301	CIT	O2-C1-C2-C3
2	F	301	CIT	O1-C1-C2-C3
2	G	301	CIT	C3-C4-C5-O3
2	I	301	CIT	C3-C4-C5-O3
2	B	301	CIT	C1-C2-C3-C4
2	C	301	CIT	C2-C3-C4-C5
2	G	301	CIT	C3-C4-C5-O4
2	B	301	CIT	C2-C3-C6-O6
2	B	301	CIT	C4-C3-C6-O5
2	I	301	CIT	C3-C4-C5-O4
2	B	301	CIT	C1-C2-C3-C6
2	E	301	CIT	O7-C3-C4-C5
2	H	301	CIT	O7-C3-C6-O5
2	B	301	CIT	C2-C3-C6-O5

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Mol	Chain	Res	Type	Atoms
2	G	301	CIT	C4-C3-C6-O5
2	H	301	CIT	C2-C3-C6-O5
2	G	301	CIT	C2-C3-C6-O5
2	J	301	CIT	C3-C4-C5-O3
2	H	301	CIT	O7-C3-C4-C5
2	B	301	CIT	O7-C3-C6-O6
2	G	301	CIT	O7-C3-C6-O5
2	B	301	CIT	C4-C3-C6-O6
2	I	301	CIT	C2-C3-C6-O6
2	J	301	CIT	C3-C4-C5-O4

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	CIT	2	0
2	C	301	CIT	1	0
2	H	301	CIT	3	0
2	E	301	CIT	1	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	244/250 (97%)	0.17	15 (6%) 27 25	17, 23, 47, 82	0
1	B	244/250 (97%)	0.01	11 (4%) 38 37	15, 22, 45, 84	0
1	C	244/250 (97%)	-0.06	11 (4%) 38 37	14, 21, 43, 81	0
1	D	244/250 (97%)	0.02	11 (4%) 38 37	14, 21, 41, 84	0
1	E	244/250 (97%)	0.03	10 (4%) 41 41	16, 22, 45, 90	0
1	F	244/250 (97%)	0.03	10 (4%) 41 41	16, 23, 43, 75	0
1	G	244/250 (97%)	0.14	15 (6%) 27 25	17, 23, 48, 84	0
1	H	244/250 (97%)	0.13	15 (6%) 27 25	16, 24, 47, 87	0
1	I	244/250 (97%)	0.13	11 (4%) 38 37	16, 23, 46, 87	0
1	J	244/250 (97%)	0.23	12 (4%) 35 33	16, 24, 47, 87	0
All	All	2440/2500 (97%)	0.08	121 (4%) 34 33	14, 23, 46, 90	0

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	PRO	7.0
1	E	245	ALA	6.6
1	I	245	ALA	6.3
1	D	245	ALA	6.3
1	B	245	ALA	5.6
1	G	245	ALA	5.5
1	H	245	ALA	5.5
1	J	245	ALA	5.5
1	A	245	ALA	5.3
1	E	2	PRO	4.7
1	F	245	ALA	4.6
1	C	245	ALA	4.5
1	I	200	MET	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	200	MET	4.2
1	G	2	PRO	4.2
1	C	96	ARG	4.1
1	F	200	MET	4.1
1	J	200	MET	3.8
1	E	200	MET	3.7
1	G	236	LYS	3.7
1	H	200	MET	3.6
1	H	201	GLU	3.4
1	G	202	SER	3.4
1	G	200	MET	3.4
1	A	236	LYS	3.3
1	D	200	MET	3.3
1	J	4	SER	3.3
1	G	242	TYR	3.2
1	J	96	ARG	3.2
1	G	203	GLY	3.2
1	H	242	TYR	3.1
1	A	220	ARG	3.1
1	F	244	GLU	3.1
1	J	5	ILE	3.0
1	B	96	ARG	3.0
1	B	202	SER	3.0
1	J	242	TYR	3.0
1	H	2	PRO	3.0
1	D	34	GLY	2.9
1	G	198	ALA	2.9
1	E	202	SER	2.9
1	D	2	PRO	2.9
1	J	236	LYS	2.9
1	F	203	GLY	2.9
1	I	197	ARG	2.8
1	I	2	PRO	2.8
1	I	244	GLU	2.8
1	C	2	PRO	2.8
1	C	201	GLU	2.8
1	C	243	GLU	2.8
1	G	220	ARG	2.7
1	A	198	ALA	2.7
1	B	200	MET	2.7
1	D	242	TYR	2.7
1	A	244	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	G	239	LYS	2.6
1	I	239	LYS	2.6
1	A	242	TYR	2.6
1	H	243	GLU	2.6
1	J	62	GLU	2.6
1	F	201	GLU	2.5
1	E	198	ALA	2.5
1	F	202	SER	2.5
1	C	202	SER	2.5
1	E	244	GLU	2.5
1	A	239	LYS	2.5
1	B	239	LYS	2.5
1	G	243	GLU	2.5
1	F	2	PRO	2.5
1	A	3	GLY	2.4
1	E	203	GLY	2.4
1	I	243	GLU	2.4
1	H	32	SER	2.4
1	E	220	ARG	2.4
1	C	200	MET	2.4
1	I	202	SER	2.4
1	A	203	GLY	2.3
1	D	31	VAL	2.3
1	C	91	ARG	2.3
1	D	91	ARG	2.3
1	B	238	ALA	2.3
1	A	91	ARG	2.3
1	G	244	GLU	2.3
1	F	242	TYR	2.3
1	E	201	GLU	2.3
1	H	244	GLU	2.3
1	D	4	SER	2.2
1	H	202	SER	2.2
1	J	238	ALA	2.2
1	B	242	TYR	2.2
1	A	199	ARG	2.2
1	H	66	ARG	2.2
1	J	228	ARG	2.2
1	B	243	GLU	2.2
1	A	4	SER	2.2
1	G	41	SER	2.2
1	H	91	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	203	GLY	2.2
1	H	220	ARG	2.2
1	J	59	ARG	2.2
1	I	242	TYR	2.1
1	B	2	PRO	2.1
1	E	134	ARG	2.1
1	F	220	ARG	2.1
1	C	238	ALA	2.1
1	H	238	ALA	2.1
1	D	5	ILE	2.1
1	F	199	ARG	2.1
1	I	203	GLY	2.1
1	H	239	LYS	2.1
1	B	198	ALA	2.1
1	A	225	GLU	2.1
1	G	201	GLU	2.1
1	D	238	ALA	2.1
1	G	4	SER	2.0
1	C	242	TYR	2.0
1	B	244	GLU	2.0
1	D	202	SER	2.0
1	C	5	ILE	2.0
1	H	203	GLY	2.0
1	I	134	ARG	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
2	CIT	B	301	13/13	0.90	0.15	21,39,56,63	0
2	CIT	C	301	13/13	0.91	0.12	18,33,47,54	0
2	CIT	H	301	13/13	0.91	0.13	18,36,54,64	0
2	CIT	I	301	13/13	0.91	0.11	21,33,43,45	0
2	CIT	D	301	13/13	0.92	0.11	18,31,46,52	0
2	CIT	F	301	13/13	0.92	0.11	20,32,46,51	0
2	CIT	J	301	13/13	0.92	0.11	20,39,48,49	0
2	CIT	E	301	13/13	0.93	0.10	22,36,48,49	0
2	CIT	G	301	13/13	0.94	0.10	21,37,52,58	0
2	CIT	A	301	13/13	0.94	0.09	21,33,42,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.