



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:56 AM UTC

PDB ID : 1WOH / pdb_00001woh
Title : Crystal Structure of Agmatinase Reveals Structural Conservation and Inhibition Mechanism of the Ureohydrolase Superfamily
Authors : Ahn, H.J.; Kim, K.H.; Lee, J.; Ha, J.-Y.; Lee, H.H.; Kim, D.; Yoon, H.-J.; Kwon, A.-R.; Suh, S.W.
Deposited on : 2004-08-18
Resolution : 1.75 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
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

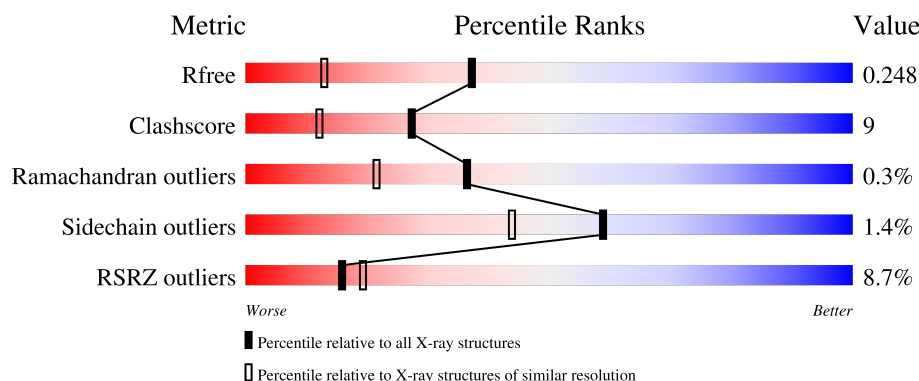
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	305	6% 78% 20% ..
1	B	305	13% 75% 23% ..
1	C	305	8% 80% 18% ..
1	D	305	12% 80% 18% ..
1	E	305	9% 81% 17% ..

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Mol	Chain	Length	Quality of chain
1	F	305	5% 81% 17% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14622 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 agmatinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2287	1446	409	425	7			
1	B	303	Total	C	N	O	S	0	0	0
			2287	1446	409	425	7			
1	C	303	Total	C	N	O	S	0	0	0
			2287	1446	409	425	7			
1	D	303	Total	C	N	O	S	0	0	0
			2287	1446	409	425	7			
1	E	303	Total	C	N	O	S	0	0	0
			2287	1446	409	425	7			
1	F	303	Total	C	N	O	S	0	0	0
			2287	1446	409	425	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	LEU	-	cloning artifact	UNP Q9RZ04
B	305	LEU	-	cloning artifact	UNP Q9RZ04
C	305	LEU	-	cloning artifact	UNP Q9RZ04
D	305	LEU	-	cloning artifact	UNP Q9RZ04
E	305	LEU	-	cloning artifact	UNP Q9RZ04
F	305	LEU	-	cloning artifact	UNP Q9RZ04

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	199	Total	O	0	0
			199	199		
2	B	118	Total	O	0	0
			118	118		
2	C	160	Total	O	0	0
			160	160		

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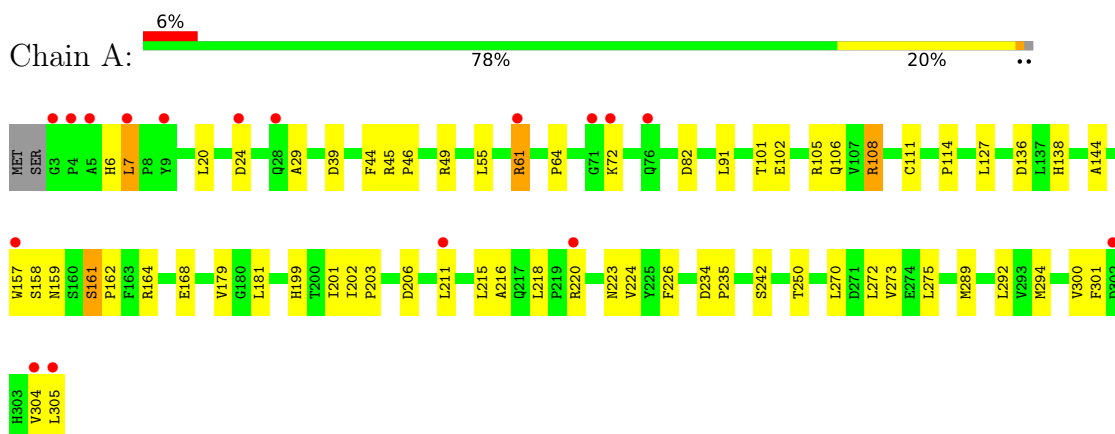
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	120	Total 120	O 120	0	0
2	E	148	Total 148	O 148	0	0
2	F	155	Total 155	O 155	0	0

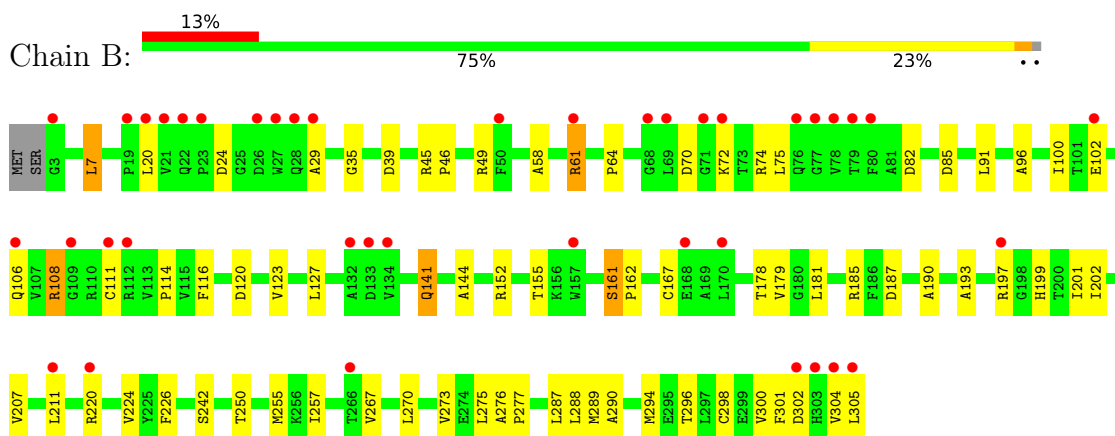
3 Residue-property plots [i](#)

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.

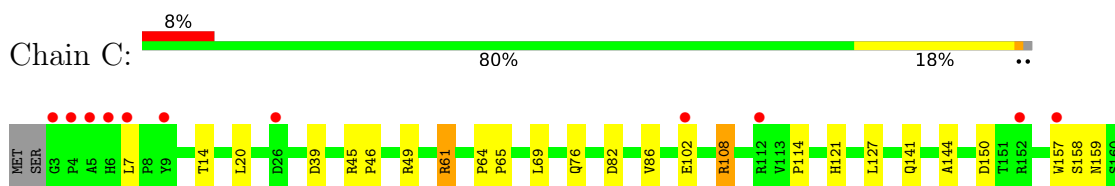
- Molecule 1: agmatinase

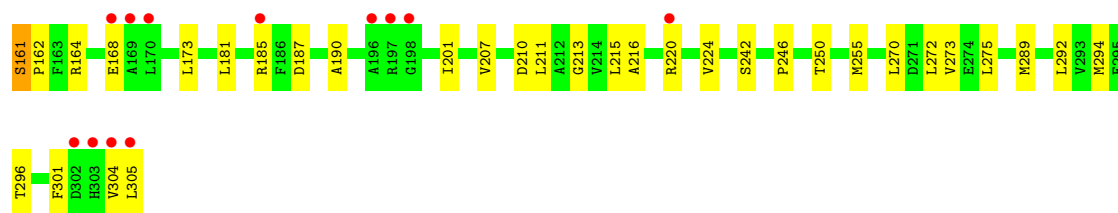


- Molecule 1: agmatinase

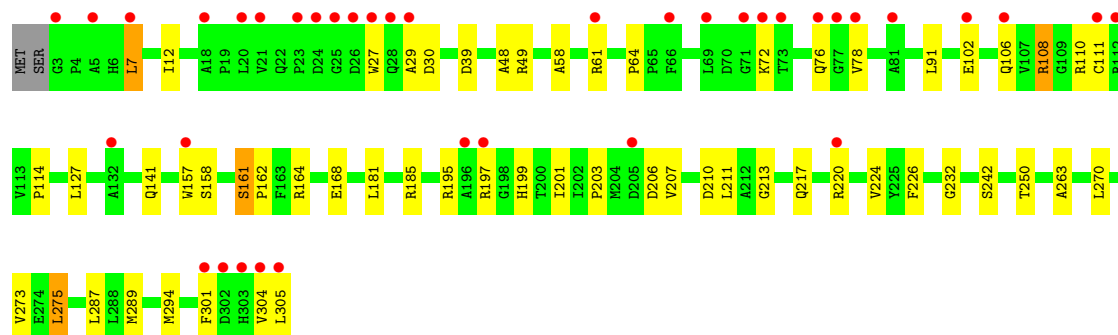
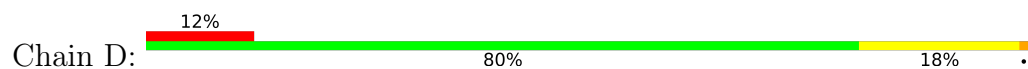


- Molecule 1: agmatinase

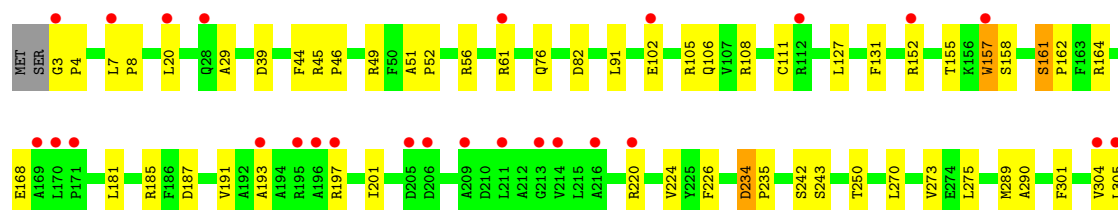
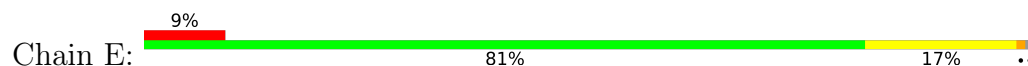




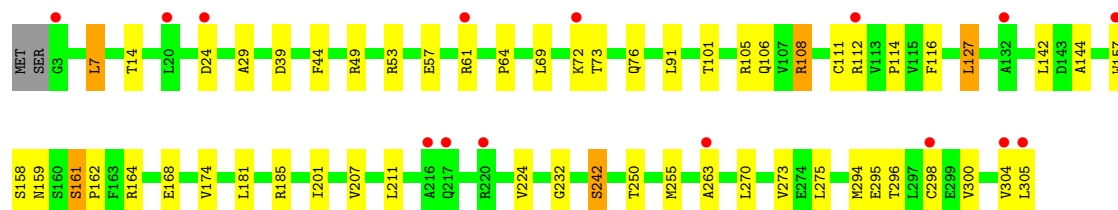
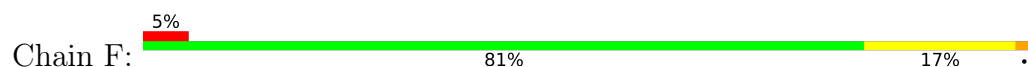
• Molecule 1: agmatinase



• Molecule 1: agmatinase



• Molecule 1: agmatinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.88Å 130.54Å 168.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.84 – 1.75 29.84 – 1.75	Depositor EDS
% Data completeness (in resolution range)	96.2 (29.84-1.75) 96.4 (29.84-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.72 (at 1.75Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.219 , 0.248 0.219 , 0.248	Depositor DCC
R_{free} test set	17423 reflections (9.93%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.443	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14622	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% 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

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	0.55	2/2342 (0.1%)	0.95	7/3202 (0.2%)
1	B	0.37	0/2342	0.93	9/3202 (0.3%)
1	C	0.48	2/2342 (0.1%)	0.93	9/3202 (0.3%)
1	D	0.38	1/2342 (0.0%)	0.93	7/3202 (0.2%)
1	E	0.40	1/2342 (0.0%)	0.94	10/3202 (0.3%)
1	F	0.49	2/2342 (0.1%)	0.94	10/3202 (0.3%)
All	All	0.45	8/14052 (0.1%)	0.94	52/19212 (0.3%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	SER	C-N	-14.70	1.11	1.33
1	F	158	SER	C-N	-13.74	1.15	1.33
1	C	158	SER	C-N	-12.55	1.17	1.33
1	A	159	ASN	C-N	-11.38	1.16	1.33
1	E	158	SER	C-N	-8.29	1.20	1.33
1	F	159	ASN	C-N	-6.32	1.24	1.33
1	C	159	ASN	C-N	6.11	1.43	1.33
1	D	158	SER	C-N	-5.71	1.24	1.33

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	250	THR	N-CA-C	-8.15	100.01	110.53
1	C	158	SER	O-C-N	-8.02	113.65	122.79
1	F	7	LEU	N-CA-C	-8.00	100.93	110.13
1	E	7	LEU	N-CA-C	-8.00	100.93	110.13
1	D	250	THR	N-CA-C	-7.80	100.46	110.53
1	A	250	THR	N-CA-C	-7.80	100.47	110.53
1	C	250	THR	N-CA-C	-7.62	100.70	110.53
1	E	250	THR	N-CA-C	-7.62	100.70	110.53
1	B	250	THR	N-CA-C	-7.42	100.96	110.53
1	C	224	VAL	N-CA-C	7.13	118.15	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	LEU	N-CA-C	-7.00	102.08	110.13
1	F	242	SER	N-CA-C	6.67	118.24	110.97
1	A	242	SER	N-CA-C	6.61	118.14	111.07
1	C	7	LEU	N-CA-C	-6.57	102.57	110.13
1	A	273	VAL	N-CA-C	6.45	118.11	108.96
1	D	224	VAL	N-CA-C	6.39	117.06	108.11
1	B	276	ALA	CA-C-N	6.39	126.60	119.32
1	B	276	ALA	C-N-CA	6.39	126.60	119.32
1	E	273	VAL	N-CA-C	6.32	117.93	108.96
1	D	7	LEU	N-CA-C	-6.27	101.95	110.36
1	C	242	SER	N-CA-C	6.19	118.54	111.11
1	D	242	SER	N-CA-C	6.19	118.54	111.11
1	B	242	SER	N-CA-C	5.88	118.20	111.02
1	B	224	VAL	N-CA-C	5.86	116.31	108.11
1	A	224	VAL	N-CA-C	5.80	116.84	108.48
1	C	273	VAL	N-CA-C	5.79	117.18	108.96
1	E	242	SER	N-CA-C	5.75	118.00	111.11
1	E	157	TRP	N-CA-C	5.72	119.25	112.72
1	B	7	LEU	N-CA-C	-5.71	101.74	110.07
1	F	273	VAL	N-CA-C	5.70	117.12	108.80
1	D	232	GLY	N-CA-C	-5.70	105.74	113.37
1	B	290	ALA	N-CA-C	-5.68	105.17	111.36
1	F	142	LEU	N-CA-C	-5.64	100.05	109.24
1	D	157	TRP	N-CA-C	5.60	119.42	112.59
1	D	273	VAL	N-CA-C	5.56	116.85	108.96
1	E	234	ASP	CA-C-N	5.55	125.38	119.28
1	E	234	ASP	C-N-CA	5.55	125.38	119.28
1	C	14	THR	N-CA-C	-5.46	101.68	110.14
1	F	232	GLY	N-CA-C	-5.44	106.09	113.37
1	E	224	VAL	N-CA-C	5.43	116.30	108.48
1	F	224	VAL	N-CA-C	5.42	116.28	108.48
1	E	91	LEU	CB-CA-C	-5.35	110.42	116.63
1	A	223	ASN	N-CA-C	-5.27	100.58	108.96
1	F	174	VAL	N-CA-C	5.25	119.80	112.50
1	B	273	VAL	N-CA-C	5.25	116.42	108.96
1	C	144	ALA	N-CA-C	-5.19	106.80	113.23
1	E	290	ALA	N-CA-C	-5.14	105.75	111.36
1	A	144	ALA	N-CA-C	-5.12	106.55	112.89
1	C	86	VAL	N-CA-C	-5.12	102.98	109.58
1	F	144	ALA	N-CA-C	-5.11	106.89	113.23
1	F	14	THR	N-CA-C	-5.10	102.23	110.14
1	B	144	ALA	N-CA-C	-5.06	106.61	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	2287	0	2265	48	0
1	B	2287	0	2266	57	0
1	C	2287	0	2265	42	0
1	D	2287	0	2266	46	0
1	E	2287	0	2266	42	0
1	F	2287	0	2265	35	0
2	A	199	0	0	3	0
2	B	118	0	0	3	0
2	C	160	0	0	4	0
2	D	120	0	0	7	0
2	E	148	0	0	4	0
2	F	155	0	0	4	0
All	All	14622	0	13593	249	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (249) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:LEU:HD21	1:A:289:MET:HE2	1.31	1.07
1:C:272:LEU:HD21	1:C:289:MET:HE2	1.42	1.00
1:C:272:LEU:HD21	1:C:289:MET:CE	2.00	0.90
1:F:300:VAL:O	1:F:304:VAL:HG23	1.72	0.89
1:B:181:LEU:HD12	1:B:201:ILE:HG23	1.59	0.84
1:D:61:ARG:HE	1:D:61:ARG:HA	1.42	0.84
1:E:181:LEU:HD12	1:E:201:ILE:HG23	1.59	0.83
1:B:46:PRO:HG3	1:E:49:ARG:NH1	1.99	0.78
1:A:181:LEU:HD12	1:A:201:ILE:HG23	1.66	0.78
1:C:181:LEU:HD12	1:C:201:ILE:HG23	1.67	0.74
1:A:300:VAL:O	1:A:304:VAL:HG23	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:ARG:HE	1:B:61:ARG:HA	1.58	0.68
1:A:289:MET:HE3	1:A:289:MET:HA	1.75	0.68
1:A:289:MET:HE1	1:A:292:LEU:HD22	1.75	0.67
1:D:301:PHE:HA	1:D:304:VAL:HG23	1.75	0.66
1:D:181:LEU:HD12	1:D:201:ILE:HG23	1.77	0.64
1:B:24:ASP:HB3	1:B:106:GLN:NE2	2.13	0.64
1:B:181:LEU:CD1	1:B:201:ILE:HG23	2.27	0.64
1:A:164:ARG:O	1:A:168:GLU:HG2	1.98	0.64
1:D:61:ARG:HD3	2:D:372:HOH:O	2.00	0.62
1:F:181:LEU:HD12	1:F:201:ILE:HG23	1.80	0.62
1:C:39:ASP:OD2	1:C:49:ARG:HD2	2.00	0.61
1:A:289:MET:HE1	1:A:292:LEU:CD2	2.31	0.60
1:E:61:ARG:HD3	2:E:379:HOH:O	2.01	0.60
1:C:216:ALA:HA	1:C:220:ARG:HH22	1.65	0.59
1:A:216:ALA:HA	1:A:220:ARG:HH22	1.67	0.59
1:A:39:ASP:OD2	1:A:49:ARG:HD2	2.02	0.58
1:D:289:MET:HA	1:D:289:MET:HE2	1.85	0.58
1:C:301:PHE:HA	1:C:304:VAL:HG23	1.85	0.58
1:A:61:ARG:HE	1:A:61:ARG:HA	1.69	0.58
1:D:197:ARG:HD2	2:D:386:HOH:O	2.04	0.58
1:D:72:LYS:NZ	1:D:72:LYS:HB3	2.19	0.57
1:B:298:CYS:O	1:B:302:ASP:HB2	2.03	0.57
1:E:102:GLU:O	1:E:106:GLN:HG3	2.04	0.57
1:B:181:LEU:HD12	1:B:201:ILE:CG2	2.33	0.57
1:E:161:SER:N	1:E:162:PRO:HD2	2.19	0.57
1:E:270:LEU:C	1:E:270:LEU:HD23	2.30	0.56
1:D:164:ARG:O	1:D:168:GLU:HG2	2.05	0.56
1:B:185:ARG:HG3	2:B:348:HOH:O	2.06	0.56
1:A:136:ASP:O	1:A:138:HIS:HD2	1.87	0.56
1:E:181:LEU:CD1	1:E:201:ILE:HG23	2.35	0.56
1:C:46:PRO:HG2	1:D:49:ARG:HD3	1.87	0.56
1:C:157:TRP:HB2	1:D:91:LEU:CD1	2.36	0.56
1:B:167:CYS:HB3	1:B:197:ARG:NH1	2.21	0.55
1:B:211:LEU:HD13	1:B:211:LEU:C	2.32	0.55
1:E:161:SER:N	1:E:162:PRO:CD	2.70	0.55
1:A:272:LEU:HD21	1:A:289:MET:CE	2.20	0.55
1:C:65:PRO:HG3	1:C:76:GLN:HE22	1.71	0.55
1:E:8:PRO:HG2	1:E:61:ARG:NE	2.21	0.55
1:E:220:ARG:HG3	1:E:220:ARG:HH11	1.72	0.55
1:C:301:PHE:HA	1:C:304:VAL:CG2	2.36	0.55
1:F:7:LEU:HD23	2:F:352:HOH:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:29:ALA:O	1:B:111:CYS:HA	2.07	0.55
1:F:164:ARG:O	1:F:168:GLU:HG2	2.06	0.54
1:B:46:PRO:HG2	1:E:49:ARG:HD3	1.90	0.54
1:F:185:ARG:HG3	2:F:386:HOH:O	2.06	0.54
1:B:91:LEU:CD1	1:E:157:TRP:HB2	2.38	0.54
1:F:211:LEU:C	1:F:211:LEU:HD13	2.33	0.54
1:B:220:ARG:HG3	1:B:220:ARG:HH11	1.73	0.54
1:B:49:ARG:HD3	1:E:46:PRO:HG2	1.89	0.54
1:B:289:MET:HE2	1:B:289:MET:HA	1.90	0.53
1:C:270:LEU:HD23	1:C:270:LEU:C	2.33	0.53
1:D:61:ARG:HA	1:D:61:ARG:NE	2.19	0.53
1:D:270:LEU:C	1:D:270:LEU:HD23	2.32	0.53
1:A:44:PHE:CD1	1:C:61:ARG:HD2	2.44	0.53
1:D:207:VAL:HG13	1:D:211:LEU:HD23	1.89	0.53
1:C:102:GLU:HA	1:C:102:GLU:OE2	2.08	0.53
1:A:29:ALA:O	1:A:111:CYS:HA	2.09	0.53
1:D:102:GLU:O	1:D:106:GLN:HG3	2.08	0.53
1:A:199:HIS:HD2	2:A:391:HOH:O	1.91	0.53
1:B:116:PHE:CB	1:B:127:LEU:HD21	2.39	0.52
1:E:305:LEU:N	1:E:305:LEU:HD12	2.24	0.52
1:B:7:LEU:HD23	2:B:379:HOH:O	2.08	0.52
1:C:108:ARG:HG2	1:C:114:PRO:HG3	1.91	0.52
1:F:270:LEU:HD23	1:F:270:LEU:C	2.34	0.52
1:D:301:PHE:HA	1:D:304:VAL:CG2	2.39	0.52
1:A:270:LEU:HD23	1:A:270:LEU:C	2.34	0.52
1:B:116:PHE:HB3	1:B:127:LEU:HD21	1.92	0.52
1:B:141:GLN:HG2	1:B:178:THR:HG23	1.92	0.52
2:D:372:HOH:O	1:E:243:SER:HB3	2.10	0.52
1:B:102:GLU:O	1:B:106:GLN:HG3	2.10	0.51
1:C:39:ASP:CG	1:C:49:ARG:HD2	2.35	0.51
1:B:193:ALA:O	1:B:197:ARG:HG3	2.09	0.51
1:D:263:ALA:HB2	2:D:393:HOH:O	2.10	0.51
1:D:61:ARG:HD2	1:E:44:PHE:CD1	2.46	0.51
1:C:207:VAL:HG13	1:C:211:LEU:HD23	1.92	0.51
1:F:207:VAL:HG13	1:F:211:LEU:HD23	1.91	0.51
1:D:161:SER:N	1:D:162:PRO:HD2	2.26	0.51
1:A:6:HIS:HA	2:E:376:HOH:O	2.10	0.51
1:A:72:LYS:NZ	1:A:72:LYS:HB3	2.26	0.51
1:B:161:SER:N	1:B:162:PRO:CD	2.74	0.51
1:D:76:GLN:HA	1:D:76:GLN:HE21	1.76	0.51
1:C:164:ARG:O	1:C:168:GLU:HG2	2.12	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:PRO:HD2	1:D:206:ASP:OD2	2.11	0.51
1:E:105:ARG:HD2	2:E:425:HOH:O	2.11	0.50
1:F:29:ALA:O	1:F:111:CYS:HA	2.12	0.50
1:B:270:LEU:C	1:B:270:LEU:HD23	2.36	0.50
1:B:275:LEU:CD1	1:B:277:PRO:HG3	2.42	0.50
1:C:211:LEU:HD13	1:C:211:LEU:C	2.36	0.50
1:F:263:ALA:HB2	2:F:427:HOH:O	2.12	0.50
1:A:101:THR:HG22	1:A:105:ARG:NH1	2.27	0.50
1:F:72:LYS:NZ	1:F:72:LYS:HB3	2.25	0.50
1:B:123:VAL:O	1:B:127:LEU:HB2	2.12	0.50
1:E:29:ALA:O	1:E:111:CYS:HA	2.12	0.50
1:D:226:PHE:O	1:D:270:LEU:HA	2.12	0.50
1:B:199:HIS:HE1	2:B:338:HOH:O	1.95	0.49
1:C:216:ALA:HA	1:C:220:ARG:NH2	2.28	0.49
1:D:220:ARG:HG3	1:D:220:ARG:HH11	1.78	0.49
1:E:61:ARG:HD2	1:F:44:PHE:CD1	2.47	0.49
1:D:304:VAL:C	1:D:305:LEU:HD12	2.37	0.49
1:F:61:ARG:HA	1:F:61:ARG:HE	1.78	0.48
1:C:161:SER:N	1:C:162:PRO:CD	2.76	0.48
1:F:108:ARG:HG2	1:F:114:PRO:HG3	1.95	0.48
1:A:24:ASP:HB3	1:A:106:GLN:NE2	2.29	0.48
1:F:161:SER:N	1:F:162:PRO:CD	2.76	0.48
1:A:211:LEU:C	1:A:211:LEU:HD13	2.39	0.48
1:E:164:ARG:O	1:E:168:GLU:HG2	2.13	0.48
1:F:305:LEU:HD12	1:F:305:LEU:N	2.29	0.48
1:B:49:ARG:NH1	1:E:46:PRO:HG3	2.29	0.48
1:C:150:ASP:HB3	2:C:446:HOH:O	2.12	0.48
1:D:141:GLN:HG3	2:D:350:HOH:O	2.14	0.48
1:E:3:GLY:N	1:E:4:PRO:HD2	2.29	0.48
1:E:108:ARG:HD3	1:E:131:PHE:CE2	2.49	0.48
1:B:255:MET:HE1	1:B:296:THR:HA	1.96	0.47
1:B:301:PHE:HA	1:B:304:VAL:HG23	1.95	0.47
1:A:64:PRO:HD3	1:A:294:MET:HE2	1.96	0.47
1:A:46:PRO:HG2	1:F:49:ARG:HD3	1.97	0.47
1:D:161:SER:N	1:D:162:PRO:CD	2.77	0.47
1:A:39:ASP:CG	1:A:49:ARG:HD2	2.40	0.47
1:C:289:MET:HE1	1:C:292:LEU:CD2	2.45	0.47
1:D:30:ASP:HB2	1:D:78:VAL:HG13	1.97	0.47
1:B:96:ALA:O	1:B:100:ILE:HG13	2.15	0.47
1:B:187:ASP:HB3	1:B:190:ALA:HB3	1.96	0.47
1:C:211:LEU:HD13	1:C:215:LEU:HG	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:39:ASP:OD2	1:F:49:ARG:HD2	2.15	0.47
1:E:45:ARG:HA	1:E:46:PRO:HD3	1.79	0.47
1:C:65:PRO:HG3	1:C:76:GLN:NE2	2.29	0.47
1:D:39:ASP:CG	1:D:49:ARG:HD2	2.39	0.47
1:B:305:LEU:N	1:B:305:LEU:HD12	2.29	0.46
1:F:39:ASP:CG	1:F:49:ARG:HD2	2.40	0.46
1:E:181:LEU:HD12	1:E:201:ILE:CG2	2.39	0.46
1:A:181:LEU:CD1	1:A:201:ILE:HG23	2.41	0.46
1:D:48:ALA:HA	1:D:275:LEU:O	2.16	0.46
1:E:289:MET:HE2	1:E:289:MET:HA	1.96	0.46
1:B:39:ASP:OD2	1:B:49:ARG:HD2	2.16	0.46
1:E:20:LEU:HD12	1:E:82:ASP:O	2.16	0.46
1:A:46:PRO:HG3	1:F:49:ARG:CZ	2.46	0.46
1:C:45:ARG:HA	1:C:46:PRO:HD3	1.85	0.46
1:D:181:LEU:HD12	1:D:201:ILE:CG2	2.46	0.46
1:E:76:GLN:HA	1:E:76:GLN:NE2	2.31	0.46
1:A:161:SER:N	1:A:162:PRO:CD	2.79	0.45
1:A:305:LEU:HD12	1:A:305:LEU:N	2.31	0.45
1:B:120:ASP:O	1:B:123:VAL:HG22	2.16	0.45
1:D:210:ASP:OD2	1:D:213:GLY:HA3	2.15	0.45
1:A:157:TRP:HB2	1:F:91:LEU:CD1	2.46	0.45
1:B:226:PHE:O	1:B:270:LEU:HA	2.15	0.45
1:E:39:ASP:CG	1:E:49:ARG:HD2	2.42	0.45
1:C:121:HIS:HE1	2:C:348:HOH:O	1.99	0.45
1:E:301:PHE:HA	1:E:304:VAL:HG23	1.98	0.45
1:A:179:VAL:HG22	1:A:202:ILE:HD12	1.97	0.45
1:A:203:PRO:HD2	1:A:206:ASP:OD2	2.17	0.45
1:A:102:GLU:O	1:A:106:GLN:HG3	2.16	0.45
1:A:108:ARG:HG2	1:A:114:PRO:HG3	1.98	0.45
1:C:255:MET:HE1	1:C:296:THR:HA	1.97	0.45
1:A:289:MET:HE3	1:A:289:MET:CA	2.42	0.45
1:B:64:PRO:HD3	1:B:294:MET:HE2	1.98	0.45
1:E:193:ALA:O	1:E:197:ARG:HG3	2.17	0.45
1:B:20:LEU:HD12	1:B:82:ASP:O	2.17	0.45
1:B:74:ARG:O	1:B:75:LEU:HB2	2.17	0.45
1:E:152:ARG:O	1:E:155:THR:HG22	2.16	0.45
1:B:267:VAL:HG21	1:B:300:VAL:HG22	1.98	0.45
1:D:7:LEU:N	1:D:7:LEU:HD22	2.31	0.45
1:D:108:ARG:HG2	1:D:114:PRO:HG3	1.99	0.44
1:E:39:ASP:OD2	1:E:49:ARG:HD2	2.17	0.44
1:F:211:LEU:HD13	1:F:211:LEU:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:210:ASP:OD2	1:C:213:GLY:HA3	2.17	0.44
1:D:76:GLN:HA	1:D:76:GLN:NE2	2.32	0.44
1:D:58:ALA:HB1	1:D:287:LEU:HA	2.00	0.44
1:A:211:LEU:HD13	1:A:215:LEU:HG	2.00	0.44
1:C:181:LEU:HD12	1:C:201:ILE:CG2	2.43	0.44
1:D:185:ARG:HG3	2:D:371:HOH:O	2.17	0.44
1:F:255:MET:HE1	1:F:296:THR:HA	2.00	0.44
1:E:76:GLN:HA	1:E:76:GLN:HE21	1.83	0.44
1:F:295:GLU:O	1:F:298:CYS:SG	2.68	0.44
1:A:20:LEU:HD12	1:A:82:ASP:O	2.18	0.44
1:B:301:PHE:HA	1:B:304:VAL:CG2	2.48	0.44
1:C:46:PRO:HG3	1:D:49:ARG:CZ	2.48	0.43
1:D:39:ASP:OD1	1:D:49:ARG:HD2	2.17	0.43
1:E:234:ASP:HA	1:E:235:PRO:HD3	1.86	0.43
1:F:64:PRO:HD3	1:F:294:MET:HE2	1.99	0.43
1:E:51:ALA:HB3	1:E:52:PRO:HD3	1.99	0.43
1:B:161:SER:N	1:B:162:PRO:HD2	2.33	0.43
1:E:226:PHE:O	1:E:270:LEU:HA	2.18	0.43
1:F:44:PHE:HB3	1:F:242:SER:OG	2.18	0.43
1:D:199:HIS:HE1	2:D:354:HOH:O	2.02	0.43
1:A:220:ARG:HH11	1:A:220:ARG:HG3	1.82	0.43
1:C:305:LEU:N	1:C:305:LEU:HD12	2.33	0.43
1:D:195:ARG:HH11	1:D:195:ARG:HG2	1.84	0.43
1:F:24:ASP:HB3	1:F:106:GLN:NE2	2.34	0.43
1:A:199:HIS:HE1	2:A:336:HOH:O	2.01	0.43
1:B:35:GLY:HA3	1:B:85:ASP:OD1	2.18	0.43
1:E:187:ASP:O	1:E:191:VAL:HG23	2.18	0.43
1:C:289:MET:HE1	1:C:292:LEU:HD22	2.01	0.43
1:A:91:LEU:CD1	1:F:157:TRP:HB2	2.49	0.43
1:D:29:ALA:O	1:D:111:CYS:HA	2.18	0.43
1:F:53:ARG:O	1:F:57:GLU:HG3	2.19	0.43
1:F:112:ARG:HD3	2:F:406:HOH:O	2.19	0.43
1:A:7:LEU:HD23	2:E:376:HOH:O	2.19	0.43
1:B:20:LEU:HD13	1:D:12:ILE:HG13	2.00	0.43
1:B:46:PRO:CG	1:E:49:ARG:HD3	2.48	0.43
1:B:58:ALA:HB1	1:B:287:LEU:HA	2.01	0.42
1:B:70:ASP:OD2	1:B:72:LYS:HD3	2.19	0.42
1:B:152:ARG:O	1:B:155:THR:HG22	2.19	0.42
1:C:108:ARG:HD3	2:C:339:HOH:O	2.18	0.42
1:F:73:THR:HG22	1:F:76:GLN:HG3	2.01	0.42
1:B:207:VAL:HG13	1:B:211:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:211:LEU:C	1:D:211:LEU:HD13	2.44	0.42
1:B:288:LEU:HG	1:C:246:PRO:HB3	2.02	0.42
1:D:203:PRO:HG3	1:F:69:LEU:CD2	2.50	0.42
1:F:101:THR:HG22	1:F:105:ARG:NH1	2.34	0.42
1:A:105:ARG:NH1	2:A:446:HOH:O	2.52	0.42
1:B:179:VAL:HG11	1:B:257:ILE:HD13	2.00	0.42
1:D:64:PRO:HD3	1:D:294:MET:HE2	2.01	0.42
1:C:141:GLN:HG3	2:C:348:HOH:O	2.20	0.42
1:B:39:ASP:CG	1:B:49:ARG:HD2	2.45	0.42
1:C:76:GLN:NE2	1:C:76:GLN:HA	2.34	0.42
1:C:187:ASP:HB3	1:C:190:ALA:HB3	2.02	0.42
1:D:27:TRP:CE2	1:D:110:ARG:HD3	2.55	0.42
1:B:49:ARG:CZ	1:E:46:PRO:HG3	2.49	0.42
1:A:301:PHE:HA	1:A:304:VAL:HG23	2.02	0.41
1:B:108:ARG:HG2	1:B:114:PRO:HG3	2.02	0.41
1:A:234:ASP:HA	1:A:235:PRO:HD3	1.93	0.41
1:B:45:ARG:HA	1:B:46:PRO:HD3	1.82	0.41
1:E:185:ARG:HH11	1:E:185:ARG:HG3	1.85	0.41
1:E:52:PRO:O	1:E:56:ARG:HG3	2.21	0.41
1:C:64:PRO:HD3	1:C:294:MET:HE2	2.03	0.41
1:D:213:GLY:O	1:D:217:GLN:HG3	2.21	0.41
1:F:116:PHE:CD1	1:F:127:LEU:HG	2.56	0.41
1:A:203:PRO:HG3	1:C:69:LEU:HD21	2.03	0.41
1:A:218:LEU:O	1:A:220:ARG:NH1	2.54	0.41
1:C:161:SER:N	1:C:162:PRO:HD2	2.35	0.41
1:C:185:ARG:HG3	1:C:185:ARG:HH11	1.85	0.41
1:A:45:ARG:HA	1:A:46:PRO:HD3	1.86	0.41
1:F:305:LEU:HD12	1:F:305:LEU:H	1.86	0.41
1:B:226:PHE:HB2	1:B:270:LEU:HB2	2.03	0.40
1:A:55:LEU:HD11	1:A:272:LEU:HD12	2.03	0.40
1:A:226:PHE:O	1:A:270:LEU:HA	2.21	0.40
1:B:179:VAL:HG22	1:B:202:ILE:HD12	2.03	0.40
1:C:20:LEU:HD12	1:C:82:ASP:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	301/305 (99%)	291 (97%)	9 (3%)	1 (0%)	36	21
1	B	301/305 (99%)	289 (96%)	11 (4%)	1 (0%)	36	21
1	C	301/305 (99%)	291 (97%)	9 (3%)	1 (0%)	36	21
1	D	301/305 (99%)	290 (96%)	10 (3%)	1 (0%)	36	21
1	E	301/305 (99%)	293 (97%)	7 (2%)	1 (0%)	36	21
1	F	301/305 (99%)	292 (97%)	8 (3%)	1 (0%)	36	21
All	All	1806/1830 (99%)	1746 (97%)	54 (3%)	6 (0%)	36	21

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	161	SER
1	C	161	SER
1	F	161	SER
1	A	161	SER
1	D	161	SER
1	E	161	SER

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	240/242 (99%)	236 (98%)	4 (2%)	53	36
1	B	240/242 (99%)	237 (99%)	3 (1%)	61	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	240/242 (99%)	235 (98%)	5 (2%)	47 27
1	D	240/242 (99%)	237 (99%)	3 (1%)	61 46
1	E	240/242 (99%)	238 (99%)	2 (1%)	73 64
1	F	240/242 (99%)	237 (99%)	3 (1%)	61 46
All	All	1440/1452 (99%)	1420 (99%)	20 (1%)	59 44

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	ARG
1	A	108	ARG
1	A	127	LEU
1	A	275	LEU
1	B	61	ARG
1	B	108	ARG
1	B	141	GLN
1	C	61	ARG
1	C	108	ARG
1	C	127	LEU
1	C	173	LEU
1	C	275	LEU
1	D	108	ARG
1	D	127	LEU
1	D	275	LEU
1	E	127	LEU
1	E	275	LEU
1	F	108	ARG
1	F	127	LEU
1	F	275	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	76	GLN
1	A	106	GLN
1	A	121	HIS
1	A	199	HIS
1	B	76	GLN
1	B	121	HIS

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Mol	Chain	Res	Type
1	B	138	HIS
1	B	145	HIS
1	B	199	HIS
1	C	76	GLN
1	C	106	GLN
1	C	121	HIS
1	C	199	HIS
1	C	222	GLN
1	D	22	GLN
1	D	76	GLN
1	D	121	HIS
1	D	138	HIS
1	D	145	HIS
1	D	175	HIS
1	D	199	HIS
1	D	222	GLN
1	D	223	ASN
1	E	76	GLN
1	E	121	HIS
1	E	175	HIS
1	E	199	HIS
1	F	106	GLN
1	F	121	HIS
1	F	138	HIS
1	F	145	HIS
1	F	199	HIS
1	F	303	HIS

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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
1	C	1
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	158:SER	C	159:ASN	N	1.17
1	A	159:ASN	C	160:SER	N	1.16
1	F	158:SER	C	159:ASN	N	1.14
1	A	158:SER	C	159:ASN	N	1.11

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	303/305 (99%)	0.19	17 (5%) 30 34	7, 15, 34, 47	0
1	B	303/305 (99%)	0.91	40 (13%) 7 8	10, 23, 43, 87	0
1	C	303/305 (99%)	0.41	23 (7%) 20 23	8, 17, 35, 95	0
1	D	303/305 (99%)	0.79	38 (12%) 8 9	11, 22, 41, 91	0
1	E	303/305 (99%)	0.71	26 (8%) 16 19	12, 21, 38, 60	0
1	F	303/305 (99%)	0.36	15 (4%) 34 39	9, 17, 34, 66	0
All	All	1818/1830 (99%)	0.56	159 (8%) 16 19	7, 19, 38, 95	0

All (159) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	305	LEU	10.3
1	D	304	VAL	7.5
1	C	305	LEU	7.5
1	C	304	VAL	7.1
1	D	305	LEU	6.2
1	E	305	LEU	6.2
1	B	305	LEU	6.1
1	A	304	VAL	6.1
1	B	304	VAL	6.1
1	F	298	CYS	5.4
1	C	303	HIS	5.3
1	C	102	GLU	5.2
1	A	305	LEU	4.9
1	F	304	VAL	4.5
1	F	220	ARG	4.4
1	E	304	VAL	4.4
1	D	157	TRP	4.2
1	A	220	ARG	4.1
1	C	157	TRP	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	157	TRP	3.9
1	B	72	LYS	3.9
1	D	302	ASP	3.8
1	D	81	ALA	3.7
1	C	198	GLY	3.7
1	D	72	LYS	3.6
1	B	20	LEU	3.6
1	B	28	GLN	3.5
1	C	3	GLY	3.5
1	D	3	GLY	3.5
1	F	112	ARG	3.4
1	A	3	GLY	3.4
1	F	72	LYS	3.4
1	B	27	TRP	3.4
1	C	170	LEU	3.4
1	D	27	TRP	3.4
1	E	157	TRP	3.3
1	D	26	ASP	3.2
1	F	20	LEU	3.2
1	D	220	ARG	3.2
1	B	112	ARG	3.1
1	A	157	TRP	3.1
1	B	21	VAL	3.1
1	B	132	ALA	3.1
1	F	157	TRP	3.1
1	C	220	ARG	3.1
1	B	26	ASP	3.1
1	C	4	PRO	3.0
1	B	3	GLY	3.0
1	B	77	GLY	3.0
1	C	9	TYR	3.0
1	D	7	LEU	3.0
1	E	171	PRO	3.0
1	B	78	VAL	3.0
1	F	3	GLY	3.0
1	E	220	ARG	3.0
1	D	20	LEU	3.0
1	D	102	GLU	2.9
1	E	152	ARG	2.9
1	E	197	ARG	2.9
1	D	303	HIS	2.9
1	A	28	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	29	ALA	2.8
1	C	302	ASP	2.8
1	B	69	LEU	2.8
1	B	303	HIS	2.8
1	D	106	GLN	2.8
1	C	6	HIS	2.8
1	A	61	ARG	2.8
1	E	112	ARG	2.8
1	D	76	GLN	2.8
1	A	72	LYS	2.8
1	C	197	ARG	2.7
1	B	197	ARG	2.7
1	C	169	ALA	2.7
1	E	206	ASP	2.7
1	D	197	ARG	2.7
1	D	71	GLY	2.7
1	E	211	LEU	2.7
1	B	71	GLY	2.7
1	D	23	PRO	2.6
1	D	73	THR	2.6
1	B	220	ARG	2.6
1	A	5	ALA	2.6
1	B	302	ASP	2.6
1	D	24	ASP	2.6
1	A	7	LEU	2.6
1	B	211	LEU	2.6
1	C	112	ARG	2.5
1	D	61	ARG	2.5
1	D	78	VAL	2.5
1	A	4	PRO	2.5
1	C	5	ALA	2.5
1	D	196	ALA	2.5
1	B	61	ARG	2.5
1	E	102	GLU	2.5
1	D	5	ALA	2.5
1	E	61	ARG	2.5
1	D	111	CYS	2.5
1	A	302	ASP	2.5
1	C	7	LEU	2.5
1	D	21	VAL	2.5
1	D	25	GLY	2.5
1	E	28	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	168	GLU	2.4
1	C	152	ARG	2.4
1	B	109	GLY	2.4
1	E	170	LEU	2.4
1	D	132	ALA	2.4
1	E	196	ALA	2.4
1	B	106	GLN	2.4
1	E	205	ASP	2.4
1	D	112	ARG	2.4
1	E	3	GLY	2.4
1	D	28	GLN	2.3
1	B	79	THR	2.3
1	C	196	ALA	2.3
1	D	18	ALA	2.3
1	D	29	ALA	2.3
1	D	205	ASP	2.3
1	E	216	ALA	2.3
1	B	134	VAL	2.3
1	F	217	GLN	2.3
1	D	69	LEU	2.3
1	C	185	ARG	2.3
1	F	24	ASP	2.3
1	B	19	PRO	2.2
1	E	214	VAL	2.2
1	E	169	ALA	2.2
1	F	132	ALA	2.2
1	B	170	LEU	2.2
1	D	77	GLY	2.2
1	B	22	GLN	2.2
1	B	76	GLN	2.2
1	A	24	ASP	2.2
1	E	209	ALA	2.2
1	E	7	LEU	2.2
1	B	80	PHE	2.2
1	B	68	GLY	2.1
1	A	211	LEU	2.1
1	B	50	PHE	2.1
1	C	26	ASP	2.1
1	D	66	PHE	2.1
1	D	301	PHE	2.1
1	A	9	TYR	2.1
1	E	195	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	193	ALA	2.1
1	F	216	ALA	2.1
1	F	263	ALA	2.1
1	B	111	CYS	2.1
1	E	20	LEU	2.1
1	B	266	THR	2.1
1	B	102	GLU	2.1
1	F	61	ARG	2.1
1	E	213	GLY	2.0
1	A	76	GLN	2.0
1	B	133	ASP	2.0
1	B	23	PRO	2.0
1	B	168	GLU	2.0
1	A	71	GLY	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.