



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:29 AM UTC

PDB ID : 4IC5 / pdb_00004ic5
Title : Crystal structure of Deg5
Authors : Gong, W.; Sun, W.; Fan, H.; Gao, F.; Liu, L.
Deposited on : 2012-12-10
Resolution : 2.61 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

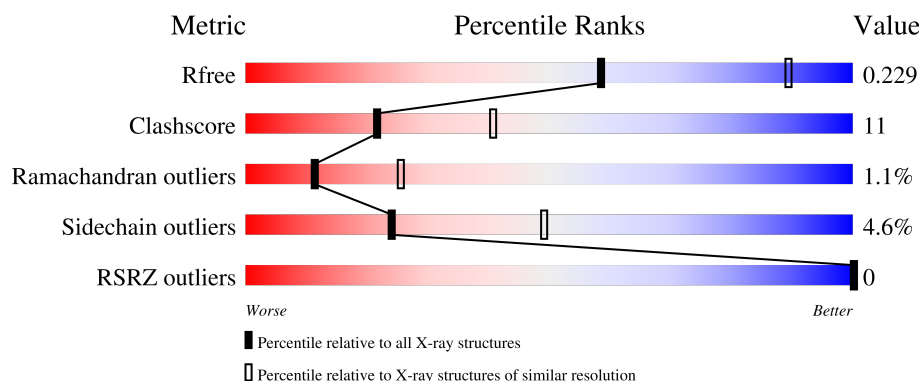
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	291	
1	B	291	
1	C	291	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4946 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 Protease Do-like 5, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	3	0
			1609	1015	271	321	2			
1	B	210	Total	C	N	O	S	0	2	0
			1601	1010	268	321	2			
1	C	209	Total	C	N	O	S	0	3	0
			1600	1010	270	318	2			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	MET	-	expression tag	UNP Q9SEL7
A	51	GLY	-	expression tag	UNP Q9SEL7
A	52	SER	-	expression tag	UNP Q9SEL7
A	53	SER	-	expression tag	UNP Q9SEL7
A	54	HIS	-	expression tag	UNP Q9SEL7
A	55	HIS	-	expression tag	UNP Q9SEL7
A	56	HIS	-	expression tag	UNP Q9SEL7
A	57	HIS	-	expression tag	UNP Q9SEL7
A	58	HIS	-	expression tag	UNP Q9SEL7
A	59	HIS	-	expression tag	UNP Q9SEL7
A	60	SER	-	expression tag	UNP Q9SEL7
A	61	SER	-	expression tag	UNP Q9SEL7
A	62	GLY	-	expression tag	UNP Q9SEL7
A	63	LEU	-	expression tag	UNP Q9SEL7
A	64	VAL	-	expression tag	UNP Q9SEL7
A	65	PRO	-	expression tag	UNP Q9SEL7
A	66	ARG	-	expression tag	UNP Q9SEL7
A	67	GLY	-	expression tag	UNP Q9SEL7
A	68	SER	-	expression tag	UNP Q9SEL7
A	69	HIS	-	expression tag	UNP Q9SEL7
A	70	MET	-	expression tag	UNP Q9SEL7
A	71	ALA	-	expression tag	UNP Q9SEL7
A	72	SER	-	expression tag	UNP Q9SEL7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	266	ALA	SER	engineered mutation	UNP Q9SEL7
A	323	LEU	-	expression tag	UNP Q9SEL7
A	324	SER	-	expression tag	UNP Q9SEL7
A	325	SER	-	expression tag	UNP Q9SEL7
A	326	VAL	-	expression tag	UNP Q9SEL7
A	327	ASP	-	expression tag	UNP Q9SEL7
A	328	LYS	-	expression tag	UNP Q9SEL7
A	329	LEU	-	expression tag	UNP Q9SEL7
A	330	ALA	-	expression tag	UNP Q9SEL7
A	331	ALA	-	expression tag	UNP Q9SEL7
A	332	ALA	-	expression tag	UNP Q9SEL7
A	333	LEU	-	expression tag	UNP Q9SEL7
A	334	GLU	-	expression tag	UNP Q9SEL7
A	335	HIS	-	expression tag	UNP Q9SEL7
A	336	HIS	-	expression tag	UNP Q9SEL7
A	337	HIS	-	expression tag	UNP Q9SEL7
A	338	HIS	-	expression tag	UNP Q9SEL7
A	339	HIS	-	expression tag	UNP Q9SEL7
A	340	HIS	-	expression tag	UNP Q9SEL7
B	50	MET	-	expression tag	UNP Q9SEL7
B	51	GLY	-	expression tag	UNP Q9SEL7
B	52	SER	-	expression tag	UNP Q9SEL7
B	53	SER	-	expression tag	UNP Q9SEL7
B	54	HIS	-	expression tag	UNP Q9SEL7
B	55	HIS	-	expression tag	UNP Q9SEL7
B	56	HIS	-	expression tag	UNP Q9SEL7
B	57	HIS	-	expression tag	UNP Q9SEL7
B	58	HIS	-	expression tag	UNP Q9SEL7
B	59	HIS	-	expression tag	UNP Q9SEL7
B	60	SER	-	expression tag	UNP Q9SEL7
B	61	SER	-	expression tag	UNP Q9SEL7
B	62	GLY	-	expression tag	UNP Q9SEL7
B	63	LEU	-	expression tag	UNP Q9SEL7
B	64	VAL	-	expression tag	UNP Q9SEL7
B	65	PRO	-	expression tag	UNP Q9SEL7
B	66	ARG	-	expression tag	UNP Q9SEL7
B	67	GLY	-	expression tag	UNP Q9SEL7
B	68	SER	-	expression tag	UNP Q9SEL7
B	69	HIS	-	expression tag	UNP Q9SEL7
B	70	MET	-	expression tag	UNP Q9SEL7
B	71	ALA	-	expression tag	UNP Q9SEL7
B	72	SER	-	expression tag	UNP Q9SEL7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	266	ALA	SER	engineered mutation	UNP Q9SEL7
B	323	LEU	-	expression tag	UNP Q9SEL7
B	324	SER	-	expression tag	UNP Q9SEL7
B	325	SER	-	expression tag	UNP Q9SEL7
B	326	VAL	-	expression tag	UNP Q9SEL7
B	327	ASP	-	expression tag	UNP Q9SEL7
B	328	LYS	-	expression tag	UNP Q9SEL7
B	329	LEU	-	expression tag	UNP Q9SEL7
B	330	ALA	-	expression tag	UNP Q9SEL7
B	331	ALA	-	expression tag	UNP Q9SEL7
B	332	ALA	-	expression tag	UNP Q9SEL7
B	333	LEU	-	expression tag	UNP Q9SEL7
B	334	GLU	-	expression tag	UNP Q9SEL7
B	335	HIS	-	expression tag	UNP Q9SEL7
B	336	HIS	-	expression tag	UNP Q9SEL7
B	337	HIS	-	expression tag	UNP Q9SEL7
B	338	HIS	-	expression tag	UNP Q9SEL7
B	339	HIS	-	expression tag	UNP Q9SEL7
B	340	HIS	-	expression tag	UNP Q9SEL7
C	50	MET	-	expression tag	UNP Q9SEL7
C	51	GLY	-	expression tag	UNP Q9SEL7
C	52	SER	-	expression tag	UNP Q9SEL7
C	53	SER	-	expression tag	UNP Q9SEL7
C	54	HIS	-	expression tag	UNP Q9SEL7
C	55	HIS	-	expression tag	UNP Q9SEL7
C	56	HIS	-	expression tag	UNP Q9SEL7
C	57	HIS	-	expression tag	UNP Q9SEL7
C	58	HIS	-	expression tag	UNP Q9SEL7
C	59	HIS	-	expression tag	UNP Q9SEL7
C	60	SER	-	expression tag	UNP Q9SEL7
C	61	SER	-	expression tag	UNP Q9SEL7
C	62	GLY	-	expression tag	UNP Q9SEL7
C	63	LEU	-	expression tag	UNP Q9SEL7
C	64	VAL	-	expression tag	UNP Q9SEL7
C	65	PRO	-	expression tag	UNP Q9SEL7
C	66	ARG	-	expression tag	UNP Q9SEL7
C	67	GLY	-	expression tag	UNP Q9SEL7
C	68	SER	-	expression tag	UNP Q9SEL7
C	69	HIS	-	expression tag	UNP Q9SEL7
C	70	MET	-	expression tag	UNP Q9SEL7
C	71	ALA	-	expression tag	UNP Q9SEL7
C	72	SER	-	expression tag	UNP Q9SEL7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	266	ALA	SER	engineered mutation	UNP Q9SEL7
C	323	LEU	-	expression tag	UNP Q9SEL7
C	324	SER	-	expression tag	UNP Q9SEL7
C	325	SER	-	expression tag	UNP Q9SEL7
C	326	VAL	-	expression tag	UNP Q9SEL7
C	327	ASP	-	expression tag	UNP Q9SEL7
C	328	LYS	-	expression tag	UNP Q9SEL7
C	329	LEU	-	expression tag	UNP Q9SEL7
C	330	ALA	-	expression tag	UNP Q9SEL7
C	331	ALA	-	expression tag	UNP Q9SEL7
C	332	ALA	-	expression tag	UNP Q9SEL7
C	333	LEU	-	expression tag	UNP Q9SEL7
C	334	GLU	-	expression tag	UNP Q9SEL7
C	335	HIS	-	expression tag	UNP Q9SEL7
C	336	HIS	-	expression tag	UNP Q9SEL7
C	337	HIS	-	expression tag	UNP Q9SEL7
C	338	HIS	-	expression tag	UNP Q9SEL7
C	339	HIS	-	expression tag	UNP Q9SEL7
C	340	HIS	-	expression tag	UNP Q9SEL7

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total Ca 3 3	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

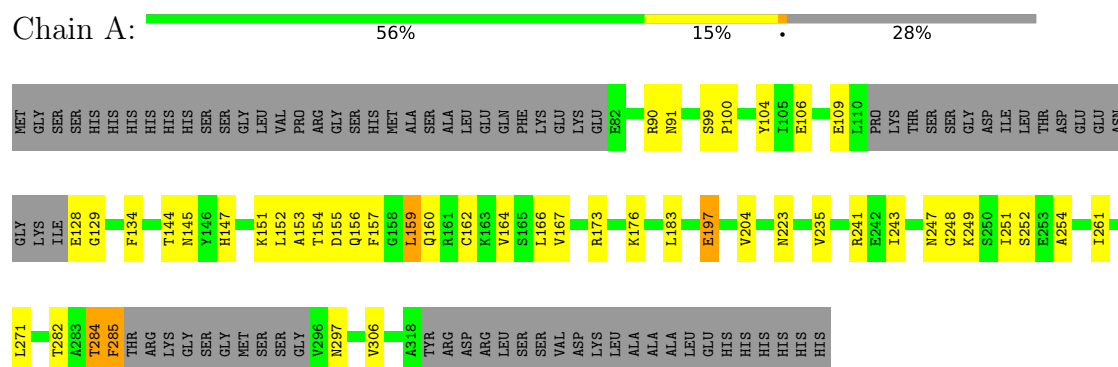
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	37	Total O 37 37	0	0
3	B	45	Total O 45 45	0	0
3	C	49	Total O 49 49	0	0

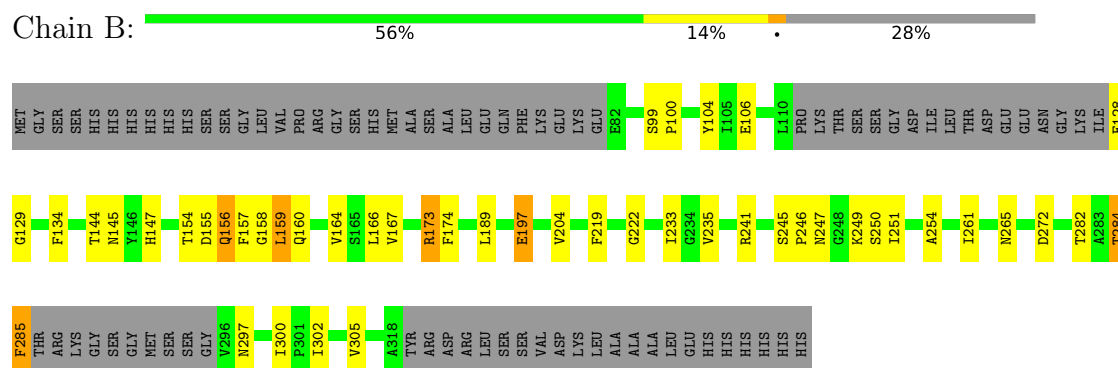
3 Residue-property plots

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

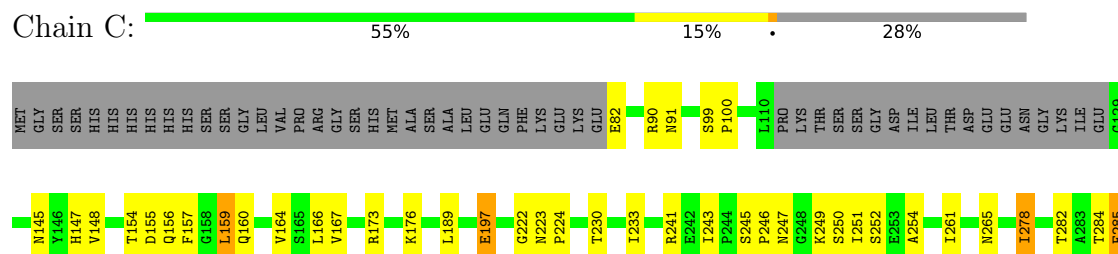
- Molecule 1: Protease Do-like 5, chloroplastic



- Molecule 1: Protease Do-like 5, chloroplastic



- Molecule 1: Protease Do-like 5, chloroplastic



THR	ARG	LYS	GLY	SER	GLY	MET	SER	SER	GLY	V296	M297	I300	P301	I302	V305	V309	P310	A318	TYR	ARG	ASP	ARG	ARG	LEU	SER	SER	VAL	ASP	LYS	LEU	ALA	ALA	ALA	LEU	GLU	HIS	HIS	HIS	HIS	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	109.09Å 125.95Å 83.33Å 90.00° 102.91° 90.00°	Depositor
Resolution (Å)	49.88 – 2.61 49.88 – 2.61	Depositor EDS
% Data completeness (in resolution range)	98.7 (49.88-2.61) 98.7 (49.88-2.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.182 , 0.232 0.179 , 0.229	Depositor DCC
R_{free} test set	1675 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	39.3	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.448 for -1/2*h+1/2*k-l,1/2*h-1/2*k-l,-1/2 *h-1/2*k 0.457 for -1/2*h-1/2*k-l,-1/2*h-1/2*k+l,-1/ 2*h+1/2*k	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4946	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.48	0/1641	0.78	0/2229
1	B	0.47	0/1630	0.80	2/2215 (0.1%)
1	C	0.48	0/1632	0.82	3/2217 (0.1%)
All	All	0.48	0/4903	0.80	5/6661 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	278	ILE	CB-CA-C	-5.71	104.65	110.93
1	B	245	SER	CA-C-N	5.69	125.16	119.24
1	B	245	SER	C-N-CA	5.69	125.16	119.24
1	C	245	SER	CA-C-N	5.65	125.11	119.24
1	C	245	SER	C-N-CA	5.65	125.11	119.24

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1609	0	1589	33	0
1	B	1601	0	1576	34	0
1	C	1600	0	1583	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	3	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	37	0	0	0	0
3	B	45	0	0	0	0
3	C	49	0	0	1	0
All	All	4946	0	4748	103	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 11.

All (103) 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:C:197:GLU:HG2	1:C:197:GLU:O	1.61	0.97
1:B:197:GLU:O	1:B:197:GLU:HG2	1.68	0.91
1:A:197:GLU:O	1:A:197:GLU:HG2	1.70	0.87
1:A:249:LYS:HA	1:A:285:PHE:HE1	1.48	0.78
1:C:249:LYS:HA	1:C:285:PHE:HE1	1.50	0.77
1:C:251:ILE:HB	1:C:254:ALA:HB2	1.67	0.77
1:B:251:ILE:HB	1:B:254:ALA:HB2	1.70	0.74
1:C:82:GLU:OE2	3:C:541:HOH:O	2.05	0.73
1:B:249:LYS:HA	1:B:285:PHE:HE1	1.54	0.73
1:A:90[B]:ARG:HG3	1:A:91:ASN:N	2.02	0.72
1:A:251:ILE:HB	1:A:254:ALA:HB2	1.70	0.71
1:A:249:LYS:HA	1:A:285:PHE:CE1	2.26	0.71
1:A:147[B]:HIS:ND1	1:A:284:THR:HB	2.06	0.70
1:C:147[B]:HIS:ND1	1:C:284:THR:HB	2.07	0.70
1:A:128:GLU:HG2	1:A:129:GLY:H	1.57	0.70
1:B:145:ASN:HD21	1:B:282:THR:HA	1.62	0.65
1:C:90[B]:ARG:HG3	1:C:91:ASN:N	2.11	0.65
1:B:249:LYS:HA	1:B:285:PHE:CE1	2.31	0.65
1:C:249:LYS:HA	1:C:285:PHE:CE1	2.32	0.63
1:C:249:LYS:HG3	1:C:285:PHE:HD1	1.63	0.62
1:A:159:LEU:HD12	1:A:160:GLN:H	1.65	0.62
1:A:147[B]:HIS:CE1	1:A:284:THR:HB	2.34	0.62
1:C:154:THR:HG23	1:C:155:ASP:N	2.16	0.61
1:B:147[B]:HIS:ND1	1:B:284:THR:HB	2.15	0.60
1:A:197:GLU:O	1:A:197:GLU:CG	2.48	0.59
1:C:147[B]:HIS:CE1	1:C:284:THR:HB	2.39	0.58
1:C:164:VAL:HG12	1:C:166:LEU:HD22	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:THR:HG23	1:B:155:ASP:N	2.19	0.57
1:A:104:TYR:CE2	1:A:106:GLU:HG3	2.40	0.57
1:B:154:THR:CG2	1:B:155:ASP:N	2.67	0.57
1:A:99:SER:N	1:A:100:PRO:CD	2.70	0.56
1:A:154:THR:HG23	1:A:155:ASP:N	2.21	0.55
1:C:155:ASP:O	1:C:157:PHE:N	2.39	0.55
1:B:147[B]:HIS:CE1	1:B:284:THR:HB	2.41	0.55
1:C:222:GLY:HA3	1:C:265:ASN:CB	2.36	0.55
1:A:109:GLU:HG3	1:A:159:LEU:HD13	1.88	0.54
1:C:166:LEU:HD23	1:C:166:LEU:N	2.23	0.54
1:C:154:THR:CG2	1:C:155:ASP:N	2.70	0.53
1:C:251:ILE:HD11	1:C:285:PHE:CE2	2.42	0.53
1:C:197:GLU:O	1:C:197:GLU:CG	2.47	0.53
1:B:235:VAL:HG11	1:C:233:ILE:HD12	1.91	0.53
1:C:159:LEU:HD12	1:C:160:GLN:H	1.74	0.53
1:C:249:LYS:HG3	1:C:285:PHE:CD1	2.44	0.52
1:A:144:THR:OG1	1:A:145:ASN:N	2.41	0.52
1:A:166:LEU:HD23	1:A:166:LEU:N	2.25	0.52
1:A:153:ALA:HB1	1:A:183:LEU:HD11	1.93	0.51
1:C:145:ASN:HD21	1:C:282:THR:HA	1.75	0.51
1:A:145:ASN:HD21	1:A:282:THR:HA	1.75	0.51
1:A:154:THR:CG2	1:A:155:ASP:N	2.75	0.49
1:A:155:ASP:O	1:A:157:PHE:N	2.46	0.49
1:B:164:VAL:HG12	1:B:166:LEU:HD22	1.94	0.48
1:B:251:ILE:HD11	1:B:285:PHE:CE2	2.47	0.48
1:B:99:SER:N	1:B:100:PRO:CD	2.76	0.48
1:B:159:LEU:HD12	1:B:160:GLN:H	1.78	0.48
1:A:164:VAL:HG12	1:A:166:LEU:HD22	1.95	0.48
1:B:128:GLU:HG2	1:B:129:GLY:H	1.79	0.48
1:B:261:ILE:HB	1:B:297:ASN:HB3	1.95	0.48
1:C:99:SER:N	1:C:100:PRO:CD	2.77	0.48
1:B:144:THR:OG1	1:B:145:ASN:N	2.44	0.47
1:C:154:THR:CG2	1:C:155:ASP:H	2.27	0.47
1:B:222:GLY:HA3	1:B:265:ASN:CB	2.44	0.47
1:C:145:ASN:HB2	1:C:148:VAL:HG23	1.96	0.47
1:C:261:ILE:HB	1:C:297:ASN:HB3	1.97	0.47
1:A:261:ILE:HB	1:A:297:ASN:HB3	1.97	0.47
1:A:243:ILE:HG12	1:A:252:SER:HA	1.96	0.46
1:B:189:LEU:HD11	1:B:305:VAL:HG22	1.96	0.46
1:B:166:LEU:N	1:B:166:LEU:HD23	2.30	0.46
1:A:128:GLU:HG2	1:A:129:GLY:N	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:LEU:HD22	1:A:162:CYS:HB2	1.97	0.46
1:C:147[B]:HIS:CG	1:C:284:THR:HB	2.51	0.46
1:A:235:VAL:HG11	1:B:233:ILE:HD12	1.98	0.46
1:A:159:LEU:HD12	1:A:160:GLN:N	2.31	0.45
1:A:249:LYS:HE3	1:A:284:THR:O	2.16	0.45
1:C:222:GLY:HA3	1:C:265:ASN:HB3	1.98	0.45
1:B:104:TYR:CE2	1:B:106:GLU:HG3	2.52	0.45
1:B:246:PRO:HB3	1:B:250:SER:O	2.16	0.44
1:C:278:ILE:C	1:C:302:ILE:HB	2.41	0.44
1:B:302:ILE:HD12	1:B:302:ILE:HA	1.84	0.44
1:B:154:THR:CG2	1:B:155:ASP:H	2.30	0.43
1:B:282:THR:HG21	1:B:300:ILE:HD11	2.00	0.43
1:A:128:GLU:CG	1:A:129:GLY:H	2.27	0.43
1:B:155:ASP:O	1:B:157:PHE:N	2.51	0.43
1:C:282:THR:HG21	1:C:300:ILE:HD11	2.00	0.43
1:B:156:GLN:C	1:B:158:GLY:H	2.26	0.43
1:C:302:ILE:HD12	1:C:302:ILE:HA	1.85	0.43
1:B:134:PHE:CD1	1:B:204:VAL:HG11	2.54	0.42
1:C:224:PRO:HG3	1:C:230:THR:HG21	2.02	0.42
1:C:284:THR:HG22	1:C:285:PHE:CE2	2.54	0.42
1:C:176:LYS:HD3	1:C:176:LYS:HA	1.93	0.42
1:A:151:LYS:O	1:A:155:ASP:HB3	2.20	0.42
1:B:222:GLY:HA3	1:B:265:ASN:HB3	2.02	0.41
1:C:189:LEU:HD11	1:C:305:VAL:HG22	2.02	0.41
1:A:176:LYS:HA	1:A:176:LYS:HD3	1.91	0.41
1:B:219:PHE:CD2	1:B:219:PHE:N	2.89	0.41
1:B:284:THR:HG22	1:B:285:PHE:CE2	2.56	0.41
1:C:243:ILE:HG12	1:C:252:SER:HA	2.02	0.41
1:C:309:VAL:N	1:C:310:PRO:CD	2.84	0.41
1:A:134:PHE:CD1	1:A:204:VAL:HG11	2.56	0.40
1:C:246:PRO:HB3	1:C:250:SER:O	2.21	0.40
1:B:173:ARG:HD3	1:B:174:PHE:H	1.86	0.40
1:B:272:ASP:C	1:B:272:ASP:OD2	2.64	0.40
1:C:145:ASN:OD1	1:C:282:THR:HG22	2.22	0.40
1:A:251:ILE:HD11	1:A:285:PHE:CE2	2.56	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	207/291 (71%)	189 (91%)	15 (7%)	3 (1%)	9	19
1	B	206/291 (71%)	190 (92%)	14 (7%)	2 (1%)	12	28
1	C	206/291 (71%)	194 (94%)	10 (5%)	2 (1%)	12	28
All	All	619/873 (71%)	573 (93%)	39 (6%)	7 (1%)	11	25

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	GLN
1	A	247	ASN
1	C	156	GLN
1	B	156	GLN
1	B	247	ASN
1	C	247	ASN
1	A	248	GLY

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	177/243 (73%)	167 (94%)	10 (6%)	19	40
1	B	176/243 (72%)	169 (96%)	7 (4%)	28	55
1	C	176/243 (72%)	169 (96%)	7 (4%)	28	55
All	All	529/729 (73%)	505 (96%)	24 (4%)	24	50

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	LEU
1	A	167	VAL
1	A	173	ARG
1	A	197	GLU
1	A	223	ASN
1	A	241	ARG
1	A	271	LEU
1	A	284	THR
1	A	285	PHE
1	A	306	VAL
1	B	159	LEU
1	B	167	VAL
1	B	173	ARG
1	B	197	GLU
1	B	241	ARG
1	B	284	THR
1	B	285	PHE
1	C	159	LEU
1	C	167	VAL
1	C	173	ARG
1	C	197	GLU
1	C	223	ASN
1	C	241	ARG
1	C	285	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	187	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	210/291 (72%)	-1.59	0 100 100	16, 42, 109, 158	4 (1%)
1	B	210/291 (72%)	-1.57	0 100 100	15, 42, 112, 150	4 (1%)
1	C	209/291 (71%)	-1.56	0 100 100	16, 43, 103, 147	4 (1%)
All	All	629/873 (72%)	-1.57	0 100 100	15, 42, 109, 158	12 (1%)

There are no RSRZ outliers to report.

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(Å ²)	Q<0.9
2	CA	A	401	1/1	1.00	0.02	33,33,33,33	0
2	CA	A	402	1/1	1.00	0.02	64,64,64,64	0
2	CA	A	403	1/1	1.00	0.07	88,88,88,88	0
2	CA	B	401	1/1	1.00	0.02	36,36,36,36	0
2	CA	C	401	1/1	1.00	0.01	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.