



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 4, 2024 – 04:42 AM EST

PDB ID : 2A67  
Title : Crystal structure of Isochorismatase family protein  
Authors : Chang, C.; Hatzos, C.; Collart, F.; Moy, S.; Joachimiak, A.; Midwest Center  
for Structural Genomics (MCSG)  
Deposited on : 2005-07-01  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

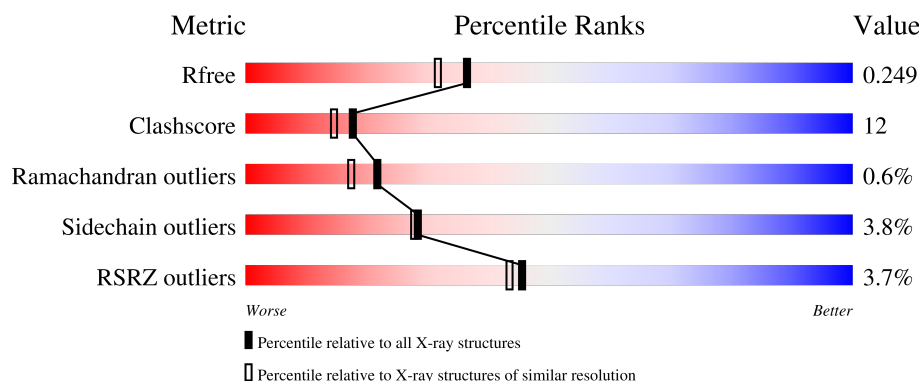
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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  $\geq 3$ , 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	167	<div> <div>4%</div> <div>81% 14% 5%</div> </div>
1	B	167	<div> <div>3%</div> <div>81% 13% 5%</div> </div>
1	C	167	<div> <div>4%</div> <div>83% 13%</div> </div>
1	D	167	<div> <div>4%</div> <div>80% 17%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5767 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 isochorismatase family protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	166	Total	C	N	O	S	Se	0	3	0
			1353	865	233	250	2	3			
1	B	167	Total	C	N	O	S	Se	0	2	0
			1358	868	234	251	2	3			
1	C	167	Total	C	N	O	S	Se	0	0	0
			1342	857	232	248	2	3			
1	D	167	Total	C	N	O	S	Se	0	5	0
			1378	877	237	259	2	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	cloning artifact	UNP Q82ZG7
A	1	MSE	MET	modified residue	UNP Q82ZG7
A	120	MSE	MET	modified residue	UNP Q82ZG7
A	130	MSE	MET	modified residue	UNP Q82ZG7
B	0	ALA	-	cloning artifact	UNP Q82ZG7
B	1	MSE	MET	modified residue	UNP Q82ZG7
B	120	MSE	MET	modified residue	UNP Q82ZG7
B	130	MSE	MET	modified residue	UNP Q82ZG7
C	0	ALA	-	cloning artifact	UNP Q82ZG7
C	1	MSE	MET	modified residue	UNP Q82ZG7
C	120	MSE	MET	modified residue	UNP Q82ZG7
C	130	MSE	MET	modified residue	UNP Q82ZG7
D	0	ALA	-	cloning artifact	UNP Q82ZG7
D	1	MSE	MET	modified residue	UNP Q82ZG7
D	120	MSE	MET	modified residue	UNP Q82ZG7
D	130	MSE	MET	modified residue	UNP Q82ZG7

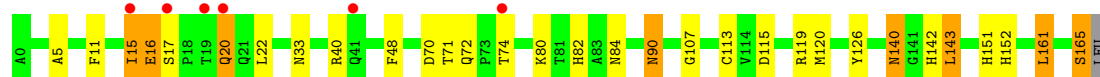
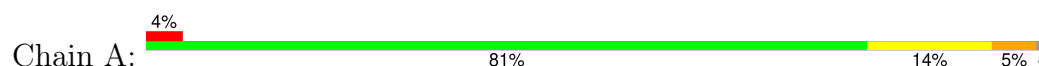
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	82	Total 82	O 82	0	0
2	B	80	Total 80	O 80	0	0
2	C	91	Total 91	O 91	0	0
2	D	83	Total 83	O 83	0	0

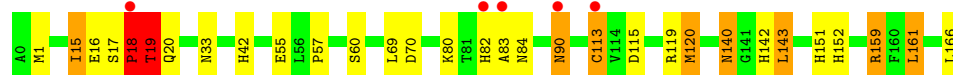
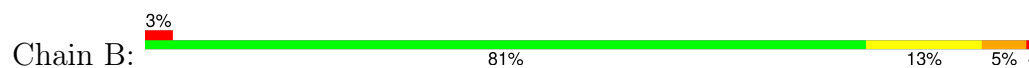
### 3 Residue-property plots [i](#)

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.

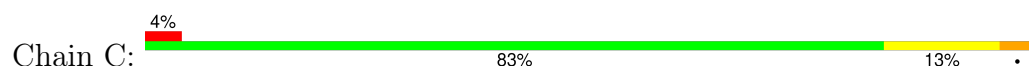
- Molecule 1: isochorismatase family protein



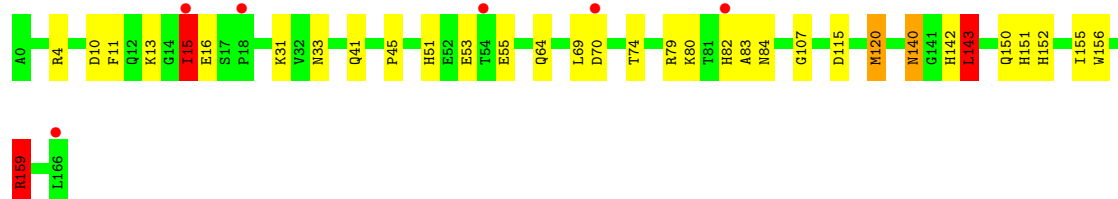
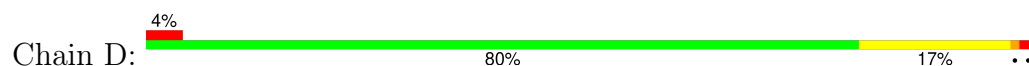
- Molecule 1: isochorismatase family protein



- Molecule 1: isochorismatase family protein



- Molecule 1: isochorismatase family protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.97Å 102.60Å 91.09Å 90.00° 116.93° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (50.00-2.00) 99.3 (50.00-2.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.74 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.190 , 0.231 0.211 , 0.249	Depositor DCC
$R_{free}$ test set	3196 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.5	Xtriage
Anisotropy	0.520	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 33.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5767	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.98	4/1390 (0.3%)	0.89	5/1885 (0.3%)
1	B	0.87	3/1392 (0.2%)	0.95	10/1886 (0.5%)
1	C	0.99	1/1370 (0.1%)	0.87	3/1858 (0.2%)
1	D	0.93	2/1412 (0.1%)	0.89	6/1914 (0.3%)
All	All	0.95	10/5564 (0.2%)	0.90	24/7543 (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	B	0	2
1	C	0	1
1	D	0	1
All	All	0	4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	113	CYS	CB-SG	8.26	1.96	1.82
1	D	120	MSE	SE-CE	-6.45	1.57	1.95
1	A	165	SER	CA-CB	-5.87	1.44	1.52
1	B	1	MSE	SE-CE	-5.82	1.61	1.95
1	B	120	MSE	SE-CE	-5.73	1.61	1.95
1	A	5	ALA	CA-CB	5.67	1.64	1.52
1	B	113	CYS	CB-SG	5.48	1.91	1.82
1	C	113	CYS	CB-SG	5.20	1.91	1.82
1	D	156	TRP	CZ3-CH2	5.20	1.48	1.40
1	A	126	TYR	CD2-CE2	5.12	1.47	1.39

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	LEU	CA-CB-CG	8.80	135.54	115.30
1	C	16	GLU	N-CA-C	7.84	132.16	111.00
1	B	161	LEU	CB-CG-CD2	7.71	124.11	111.00
1	B	161	LEU	CA-CB-CG	7.51	132.57	115.30
1	A	161	LEU	CB-CG-CD2	7.48	123.71	111.00
1	D	159	ARG	NE-CZ-NH2	-7.13	116.74	120.30
1	B	15	ILE	C-N-CA	6.92	139.00	121.70
1	B	159	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	D	159	ARG	NE-CZ-NH1	6.27	123.43	120.30
1	A	119	ARG	NE-CZ-NH1	6.03	123.31	120.30
1	B	159	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	B	15	ILE	CA-C-N	5.58	129.48	117.20
1	A	15	ILE	C-N-CA	5.38	135.14	121.70
1	D	16	GLU	N-CA-C	5.37	125.50	111.00
1	B	119	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	B	119	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	B	19	THR	N-CA-CB	5.30	120.36	110.30
1	D	143	LEU	CA-CB-CG	5.27	127.43	115.30
1	B	69	LEU	CB-CG-CD1	-5.23	102.11	111.00
1	C	15	ILE	CB-CA-C	-5.23	101.14	111.60
1	D	15	ILE	C-N-CA	5.18	134.64	121.70
1	D	79	ARG	NE-CZ-NH1	-5.05	117.78	120.30
1	A	15	ILE	N-CA-C	5.04	124.60	111.00
1	C	159	ARG	NE-CZ-NH1	5.04	122.82	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	15	ILE	Peptide
1	B	18	PRO	Peptide
1	C	15	ILE	Peptide
1	D	15	ILE	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1353	0	1338	33	0
1	B	1358	0	1348	38	1
1	C	1342	0	1323	36	0
1	D	1378	0	1352	36	0
2	A	82	0	0	1	0
2	B	80	0	0	4	1
2	C	91	0	0	12	1
2	D	83	0	0	4	2
All	All	5767	0	5361	132	3

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 12.

All (132) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:ASN:HB3	2:B:237:HOH:O	1.38	1.21
1:B:83:ALA:O	1:B:113:CYS:SG	2.21	0.98
1:D:82:HIS:HD2	1:D:84:ASN:H	1.13	0.92
1:C:90:ASN:HD22	1:C:90:ASN:H	1.19	0.91
1:D:82:HIS:CD2	1:D:84:ASN:H	1.88	0.91
1:D:150:GLN:HG2	2:D:232:HOH:O	1.72	0.89
1:A:82:HIS:HD2	1:A:84:ASN:H	1.21	0.85
1:C:82:HIS:HD2	1:C:84:ASN:H	1.26	0.82
1:D:150:GLN:CG	2:D:232:HOH:O	2.25	0.82
1:B:120:MSE:HA	1:C:120:MSE:HE1	1.63	0.81
1:A:115:ASP:OD2	1:A:152:HIS:HD2	1.64	0.81
1:C:113:CYS:HB3	2:C:217:HOH:O	1.84	0.77
1:A:140:ASN:ND2	1:A:143:LEU:H	1.82	0.77
1:B:17:SER:OG	1:B:19:THR:HG23	1.86	0.76
1:C:80:LYS:HE2	2:C:217:HOH:O	1.85	0.76
1:A:82:HIS:CD2	1:A:84:ASN:H	2.04	0.76
1:B:82:HIS:HD2	1:B:84:ASN:H	1.31	0.75
1:D:140:ASN:ND2	1:D:142:HIS:H	1.85	0.75
1:D:41:GLN:NE2	2:D:225:HOH:O	2.20	0.73
1:A:151:HIS:NE2	1:D:152:HIS:HE1	1.87	0.73
1:B:33:ASN:HD21	1:B:70:ASP:H	1.37	0.73
1:B:90:ASN:H	1:B:90:ASN:HD22	1.38	0.72
1:C:82:HIS:CD2	1:C:84:ASN:H	2.08	0.72
1:C:140:ASN:ND2	1:C:142:HIS:H	1.89	0.71
1:B:140:ASN:ND2	1:B:142:HIS:H	1.91	0.69
1:C:165:SER:N	2:C:244:HOH:O	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:HIS:HE1	1:D:151:HIS:NE2	1.92	0.68
1:B:20:GLN:HG2	2:B:205:HOH:O	1.94	0.68
1:D:115:ASP:OD2	1:D:152:HIS:HD2	1.77	0.67
1:A:90[A]:ASN:HD22	1:A:90[A]:ASN:H	1.43	0.67
1:B:152:HIS:HE1	1:C:151:HIS:NE2	1.93	0.66
1:D:140:ASN:C	1:D:140:ASN:HD22	1.98	0.66
1:A:84:ASN:ND2	1:A:120:MSE:HE3	2.10	0.66
1:C:90:ASN:H	1:C:90:ASN:ND2	1.94	0.65
1:A:140:ASN:HD21	1:A:143:LEU:H	1.43	0.64
1:C:33:ASN:HD21	1:C:70:ASP:H	1.44	0.64
1:B:151:HIS:NE2	1:C:152:HIS:HE1	1.95	0.63
1:C:115:ASP:OD2	1:C:152:HIS:HD2	1.82	0.63
1:B:140:ASN:HD22	1:B:142:HIS:H	1.46	0.63
1:C:140:ASN:ND2	1:C:143:LEU:H	1.95	0.63
1:D:33:ASN:HD21	1:D:70[A]:ASP:H	1.46	0.63
1:B:140:ASN:ND2	1:B:143:LEU:H	1.97	0.62
1:C:140:ASN:C	1:C:140:ASN:HD22	2.03	0.62
1:A:120:MSE:HE1	1:D:120:MSE:HA	1.82	0.61
1:A:140:ASN:ND2	1:A:142:HIS:H	1.99	0.61
1:D:140:ASN:HD22	1:D:142:HIS:H	1.47	0.61
1:B:140:ASN:HD22	1:B:140:ASN:C	2.04	0.61
1:B:83:ALA:HB2	2:B:216:HOH:O	2.02	0.60
1:C:164:LEU:C	2:C:244:HOH:O	2.38	0.60
1:B:18:PRO:HB2	1:B:19:THR:HG22	1.84	0.60
1:B:115:ASP:OD2	1:B:152:HIS:HD2	1.84	0.60
1:B:82:HIS:CD2	1:B:84:ASN:H	2.16	0.60
1:A:40:ARG:CZ	1:A:72:GLN:HG3	2.31	0.60
1:B:140:ASN:HD21	1:B:143:LEU:H	1.48	0.60
1:A:48:PHE:CZ	1:A:71:THR:HG22	2.37	0.59
1:C:140:ASN:HD21	1:C:143:LEU:H	1.49	0.59
1:B:18:PRO:CB	1:B:19:THR:HG22	2.32	0.59
1:A:120:MSE:HA	1:D:120:MSE:HE1	1.85	0.59
1:B:120:MSE:HE1	1:C:120:MSE:HA	1.85	0.58
1:B:33:ASN:ND2	1:B:70:ASP:H	2.02	0.58
1:D:140:ASN:ND2	1:D:143:LEU:H	2.01	0.58
1:B:17:SER:OG	1:B:19:THR:CG2	2.52	0.57
1:C:90:ASN:HD22	1:C:90:ASN:N	1.96	0.57
1:C:133:LYS:N	1:C:133:LYS:HD2	2.20	0.56
1:C:48:PHE:CZ	1:C:71:THR:HG22	2.41	0.56
1:C:140:ASN:HD22	1:C:142:HIS:H	1.51	0.56
1:C:164:LEU:HA	2:C:244:HOH:O	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:HIS:CD2	1:C:80:LYS:HZ1	2.24	0.55
1:C:113:CYS:SG	2:C:169:HOH:O	2.38	0.55
1:D:33:ASN:HD21	1:D:70[B]:ASP:H	1.53	0.55
1:B:159:ARG:O	1:C:82:HIS:HE1	1.89	0.54
1:D:51:HIS:HE1	1:D:53:GLU:OE1	1.91	0.54
1:A:140:ASN:HD22	1:A:142:HIS:H	1.55	0.54
1:D:140:ASN:HD21	1:D:143:LEU:H	1.55	0.54
1:A:165:SER:CB	2:C:229:HOH:O	2.57	0.53
1:B:80:LYS:NZ	1:B:113:CYS:SG	2.81	0.53
1:A:82:HIS:HE1	1:D:159:ARG:O	1.92	0.52
1:D:33:ASN:ND2	1:D:70[A]:ASP:H	2.08	0.52
1:A:165:SER:CB	2:C:244:HOH:O	2.56	0.52
1:D:11:PHE:CZ	1:D:107:GLY:HA2	2.44	0.52
1:A:84:ASN:HD21	1:A:120:MSE:HE3	1.75	0.52
1:D:13:LYS:HE3	1:D:64:GLN:HB2	1.92	0.51
1:C:33:ASN:ND2	1:C:70:ASP:H	2.09	0.51
1:C:83:ALA:O	2:C:217:HOH:O	2.19	0.51
1:A:16:GLU:O	1:A:17:SER:HB3	2.11	0.50
1:A:33:ASN:HD21	1:A:70:ASP:H	1.58	0.50
1:B:80:LYS:HE2	1:B:113:CYS:SG	2.52	0.49
1:C:120:MSE:HA	1:C:120:MSE:HE2	1.95	0.49
1:B:18:PRO:HB2	1:B:19:THR:CG2	2.43	0.49
1:D:82:HIS:HD2	1:D:84:ASN:N	1.95	0.49
1:D:140:ASN:ND2	1:D:140:ASN:C	2.66	0.48
1:B:17:SER:HB2	1:B:18:PRO:HD2	1.96	0.48
1:A:15:ILE:N	1:A:16:GLU:HB2	2.28	0.48
1:A:115:ASP:OD2	1:A:152:HIS:CD2	2.55	0.48
1:D:155:ILE:O	1:D:159:ARG:HG2	2.14	0.47
1:A:16:GLU:HG2	1:A:22:LEU:CD1	2.45	0.47
1:A:140:ASN:HD22	1:A:140:ASN:C	2.18	0.47
1:A:140:ASN:HD21	1:A:143:LEU:N	2.12	0.47
1:B:42:HIS:HE1	2:B:229:HOH:O	1.96	0.46
1:D:33:ASN:ND2	1:D:70[B]:ASP:H	2.14	0.46
1:C:42:HIS:CE1	2:C:252:HOH:O	2.67	0.46
1:C:90:ASN:ND2	2:C:191:HOH:O	2.48	0.46
1:D:150:GLN:HG3	2:D:232:HOH:O	2.03	0.46
1:B:18:PRO:N	1:B:19:THR:HG22	2.31	0.45
1:D:33:ASN:HD21	1:D:69:LEU:HA	1.81	0.45
1:C:11:PHE:HB3	1:C:69:LEU:HD11	1.98	0.45
1:A:11:PHE:CZ	1:A:107:GLY:HA2	2.52	0.45
1:B:120:MSE:HE2	1:C:120:MSE:HE2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:ASN:H	1:B:90:ASN:ND2	2.12	0.44
1:B:140:ASN:ND2	1:B:140:ASN:C	2.71	0.44
1:C:51:HIS:CD2	1:C:80:LYS:NZ	2.85	0.44
1:A:17:SER:OG	1:A:20[B]:GLN:HB3	2.18	0.43
1:D:10:ASP:OD1	1:D:80:LYS:HE3	2.18	0.43
1:A:80:LYS:HE2	2:A:217:HOH:O	2.18	0.43
1:B:18:PRO:HB2	1:B:19:THR:CB	2.49	0.43
1:D:53:GLU:OE2	1:D:55[B]:GLU:OE1	2.36	0.43
1:C:140:ASN:ND2	1:C:140:ASN:C	2.70	0.42
1:C:164:LEU:CA	2:C:244:HOH:O	2.64	0.42
1:B:80:LYS:CE	1:B:113:CYS:SG	3.08	0.42
1:D:159:ARG:HG2	1:D:159:ARG:HH11	1.85	0.42
1:B:18:PRO:HB2	1:B:19:THR:HB	2.00	0.42
1:D:82:HIS:CD2	1:D:83:ALA:N	2.88	0.42
1:B:57:PRO:HG2	1:B:60:SER:HB3	2.02	0.41
1:A:33:ASN:ND2	1:A:70:ASP:H	2.17	0.41
1:D:82:HIS:CG	1:D:83:ALA:N	2.88	0.41
1:B:84:ASN:ND2	1:B:120:MSE:HE3	2.36	0.40
1:A:16:GLU:HG2	1:A:22:LEU:HD12	2.03	0.40
1:D:33:ASN:HD22	1:D:33:ASN:HA	1.70	0.40
1:D:4:ARG:O	1:D:45:PRO:HD2	2.21	0.40
1:D:10:ASP:O	1:D:15:ILE:HD13	2.21	0.40

All (3) 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)
2:C:201:HOH:O	2:C:201:HOH:O[2_656]	1.40	0.80
1:B:166:LEU:O	2:D:169:HOH:O[1_556]	1.62	0.58
2:B:175:HOH:O	2:D:237:HOH:O[1_556]	2.18	0.02

## 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	167/167 (100%)	160 (96%)	6 (4%)	1 (1%)	22	17
1	B	167/167 (100%)	160 (96%)	4 (2%)	3 (2%)	7	3
1	C	165/167 (99%)	161 (98%)	4 (2%)	0	100	100
1	D	170/167 (102%)	166 (98%)	4 (2%)	0	100	100
All	All	669/668 (100%)	647 (97%)	18 (3%)	4 (1%)	22	17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	18	PRO
1	B	16	GLU
1	A	16	GLU
1	B	19	THR

### 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	147/143 (103%)	139 (95%)	8 (5%)	18	16
1	B	148/143 (104%)	143 (97%)	5 (3%)	32	32
1	C	145/143 (101%)	139 (96%)	6 (4%)	26	25
1	D	150/143 (105%)	145 (97%)	5 (3%)	33	33
All	All	590/572 (103%)	566 (96%)	24 (4%)	28	25

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

Mol	Chain	Res	Type
1	A	20[A]	GLN
1	A	20[B]	GLN
1	A	74	THR
1	A	90[A]	ASN
1	A	90[B]	ASN

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Mol	Chain	Res	Type
1	A	140	ASN
1	A	143	LEU
1	A	161	LEU
1	B	55	GLU
1	B	90	ASN
1	B	140	ASN
1	B	143	LEU
1	B	161	LEU
1	C	16	GLU
1	C	19	THR
1	C	90	ASN
1	C	133	LYS
1	C	140	ASN
1	C	143	LEU
1	D	31	LYS
1	D	74	THR
1	D	140	ASN
1	D	143	LEU
1	D	159	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	34	GLN
1	A	51	HIS
1	A	82	HIS
1	A	92	ASN
1	A	98	GLN
1	A	101	GLN
1	A	140	ASN
1	A	152	HIS
1	B	33	ASN
1	B	82	HIS
1	B	90	ASN
1	B	92	ASN
1	B	109	GLN
1	B	140	ASN
1	B	152	HIS
1	C	33	ASN
1	C	34	GLN
1	C	51	HIS

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Mol	Chain	Res	Type
1	C	82	HIS
1	C	90	ASN
1	C	92	ASN
1	C	140	ASN
1	C	152	HIS
1	D	33	ASN
1	D	42	HIS
1	D	51	HIS
1	D	82	HIS
1	D	92	ASN
1	D	101	GLN
1	D	140	ASN
1	D	152	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	163/167 (97%)	0.18	6 (3%)	45	43	17, 29, 43, 58	3 (1%)
1	B	164/167 (98%)	0.33	5 (3%)	52	51	17, 33, 48, 55	2 (1%)
1	C	164/167 (98%)	0.26	7 (4%)	40	38	23, 29, 40, 46	0
1	D	164/167 (98%)	0.05	6 (3%)	45	43	16, 30, 43, 54	5 (3%)
All	All	655/668 (98%)	0.21	24 (3%)	45	43	16, 30, 45, 58	10 (1%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	83	ALA	4.1
1	B	82	HIS	3.8
1	A	19	THR	3.1
1	C	0	ALA	3.0
1	D	70[A]	ASP	3.0
1	A	15	ILE	3.0
1	C	41	GLN	2.9
1	D	166	LEU	2.8
1	C	166	LEU	2.8
1	A	20[A]	GLN	2.7
1	B	90	ASN	2.7
1	A	74	THR	2.6
1	C	18	PRO	2.5
1	A	41	GLN	2.5
1	B	113	CYS	2.5
1	C	37	ALA	2.5
1	D	82	HIS	2.4
1	D	18	PRO	2.3
1	C	38	VAL	2.2
1	D	54[A]	THR	2.2
1	D	15	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	164	LEU	2.1
1	A	17	SER	2.1
1	B	18	PRO	2.1

## 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 monosaccharides 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.