



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 22, 2024 – 01:07 AM EDT

PDB ID : 3HB7  
Title : The Crystal Structure of an Isochorismatase-like Hydrolase from *Alkaliphilus metalliredigens* to 2.3Å  
Authors : Stein, A.J.; Xu, X.; Cui, H.; Ng, J.; Edwards, A.; Savchenko, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2009-05-04  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

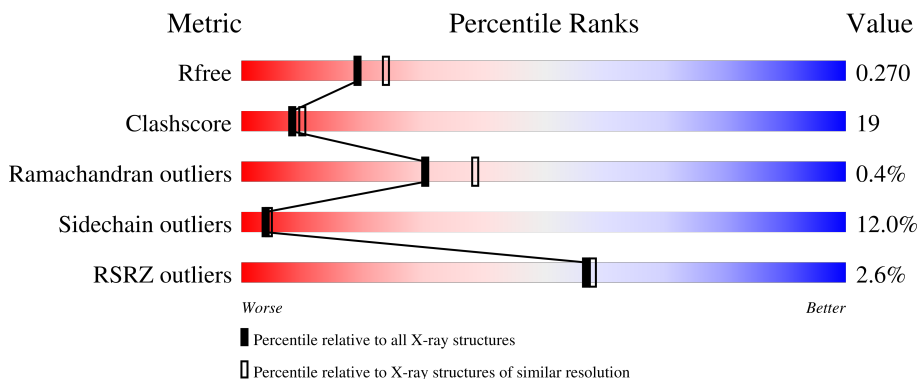
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	204	 2% 67% 22% 8%
1	B	204	 3% 66% 19% 12%
1	C	204	 0% 54% 29% 13%
1	D	204	 0% 59% 26% 12%
1	E	204	 3% 64% 24% 5% 7%

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Mol	Chain	Length	Quality of chain
1	F	204	<div><div><div></div><div></div><div></div><div></div></div><div>3%64%24%10%</div></div>
1	G	204	<div><div><div></div><div></div><div></div><div></div></div><div>%60%24%5%11%</div></div>
1	H	204	<div><div><div></div><div></div><div></div><div></div></div><div>3%39%34%11%16%</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11682 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 hydrolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	Se	0	2	0
			1478	945	254	274	2	3			
1	C	178	Total	C	N	O	S	Se	0	0	0
			1396	887	240	264	2	3			
1	B	179	Total	C	N	O	S	Se	0	1	0
			1419	908	239	267	2	3			
1	D	179	Total	C	N	O	S	Se	0	0	0
			1398	890	241	262	2	3			
1	E	189	Total	C	N	O	S	Se	0	0	0
			1474	935	253	281	2	3			
1	F	183	Total	C	N	O	S	Se	0	0	0
			1437	914	246	272	2	3			
1	G	182	Total	C	N	O	S	Se	0	0	0
			1423	907	242	269	2	3			
1	H	171	Total	C	N	O	S	Se	0	0	0
			1309	835	226	243	2	3			

There are 32 discrepancies between the modelled and reference sequences:

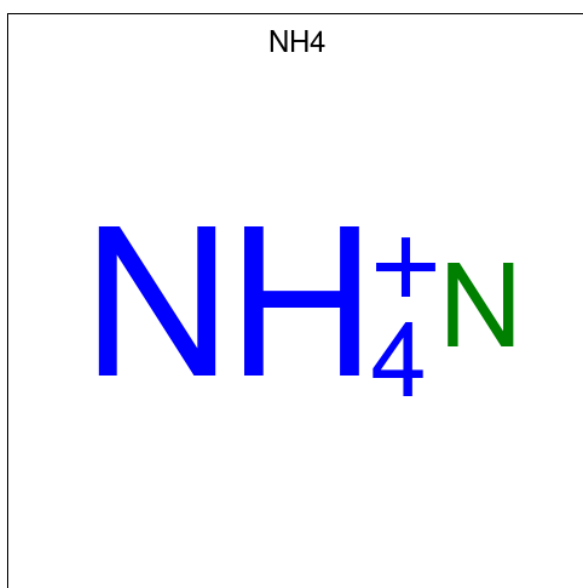
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	TYR	-	expression tag	UNP A6TWT6
A	-2	PHE	-	expression tag	UNP A6TWT6
A	-1	GLN	-	expression tag	UNP A6TWT6
A	0	GLY	-	expression tag	UNP A6TWT6
C	-3	TYR	-	expression tag	UNP A6TWT6
C	-2	PHE	-	expression tag	UNP A6TWT6
C	-1	GLN	-	expression tag	UNP A6TWT6
C	0	GLY	-	expression tag	UNP A6TWT6
B	-3	TYR	-	expression tag	UNP A6TWT6
B	-2	PHE	-	expression tag	UNP A6TWT6
B	-1	GLN	-	expression tag	UNP A6TWT6
B	0	GLY	-	expression tag	UNP A6TWT6
D	-3	TYR	-	expression tag	UNP A6TWT6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	PHE	-	expression tag	UNP A6TWT6
D	-1	GLN	-	expression tag	UNP A6TWT6
D	0	GLY	-	expression tag	UNP A6TWT6
E	-3	TYR	-	expression tag	UNP A6TWT6
E	-2	PHE	-	expression tag	UNP A6TWT6
E	-1	GLN	-	expression tag	UNP A6TWT6
E	0	GLY	-	expression tag	UNP A6TWT6
F	-3	TYR	-	expression tag	UNP A6TWT6
F	-2	PHE	-	expression tag	UNP A6TWT6
F	-1	GLN	-	expression tag	UNP A6TWT6
F	0	GLY	-	expression tag	UNP A6TWT6
G	-3	TYR	-	expression tag	UNP A6TWT6
G	-2	PHE	-	expression tag	UNP A6TWT6
G	-1	GLN	-	expression tag	UNP A6TWT6
G	0	GLY	-	expression tag	UNP A6TWT6
H	-3	TYR	-	expression tag	UNP A6TWT6
H	-2	PHE	-	expression tag	UNP A6TWT6
H	-1	GLN	-	expression tag	UNP A6TWT6
H	0	GLY	-	expression tag	UNP A6TWT6

- Molecule 2 is AMMONIUM ION (three-letter code: NH4) (formula: H<sub>4</sub>N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total N 1 1	0	0
2	C	1	Total N 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total N 1 1	0	0
2	D	1	Total N 1 1	0	0
2	E	1	Total N 1 1	0	0
2	H	1	Total N 1 1	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0
3	B	1	Total Na 1 1	0	0
3	E	1	Total Na 1 1	0	0
3	F	1	Total Na 1 1	0	0
3	G	1	Total Na 1 1	0	0

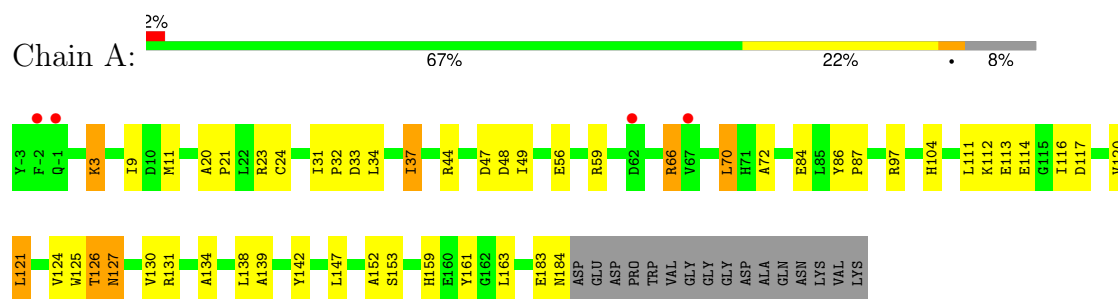
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	69	Total O 69 69	0	0
4	C	52	Total O 52 52	0	0
4	B	67	Total O 67 67	0	0
4	D	38	Total O 38 38	0	0
4	E	19	Total O 19 19	0	0
4	F	44	Total O 44 44	0	0
4	G	35	Total O 35 35	0	0
4	H	13	Total O 13 13	0	0

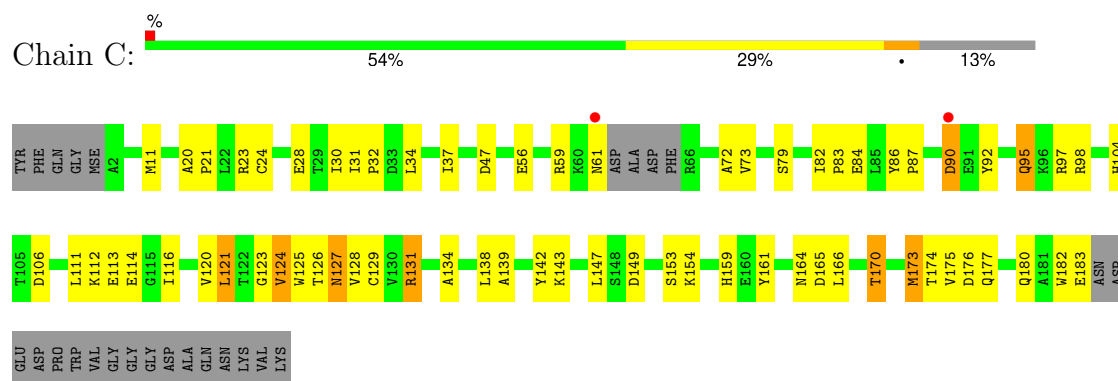
### 3 Residue-property plots [i](#)

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.

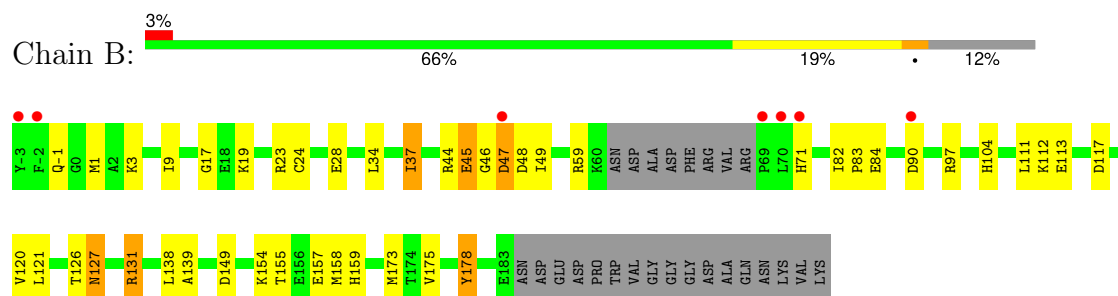
#### • Molecule 1: Isochorismatase hydrolase



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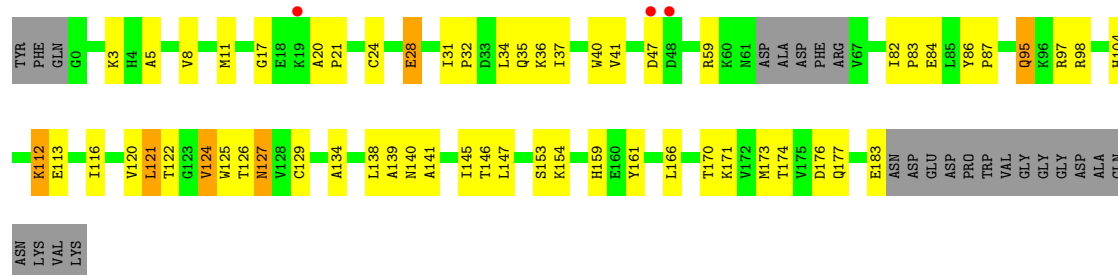


#### • Molecule 1: Isochorismatase hydrolase

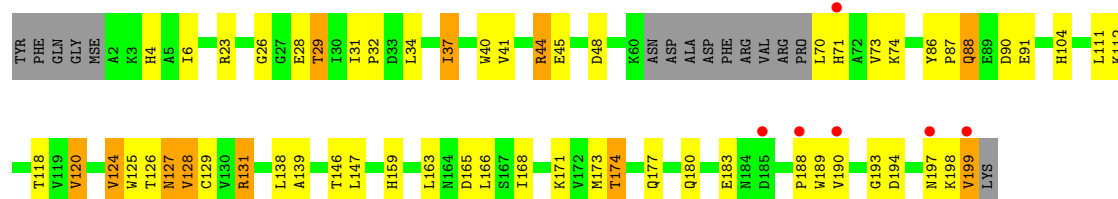


#### • Molecule 1: Isochorismatase hydrolase

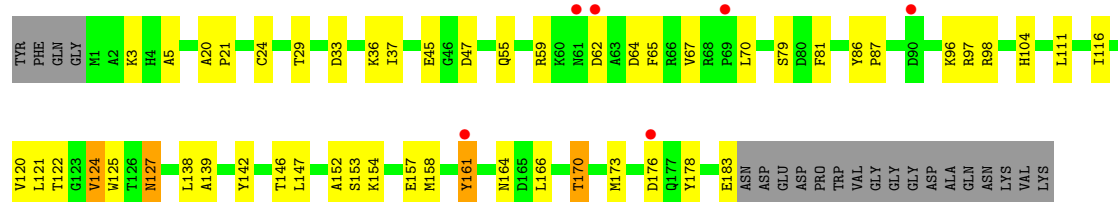




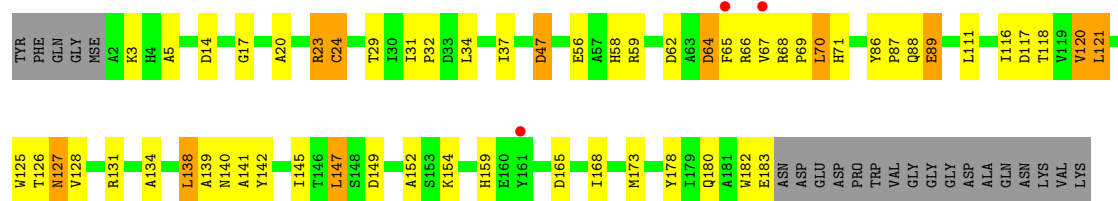
- Molecule 1: Isochorismatase hydrolase



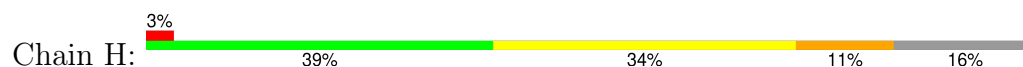
- Molecule 1: Isochorismatase hydrolase



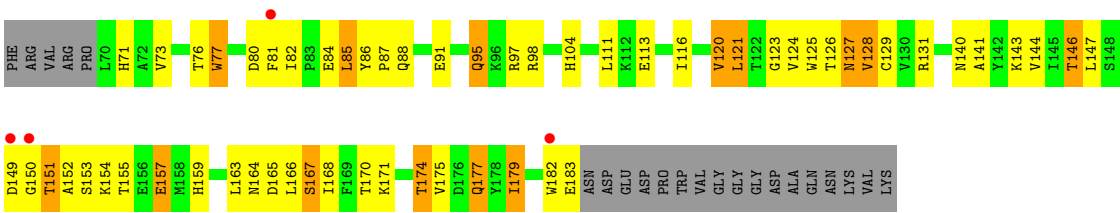
- Molecule 1: Isochorismatase hydrolase



- Molecule 1: Isochorismatase hydrolase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.65Å 105.42Å 106.27Å 90.00° 103.90° 90.00°	Depositor
Resolution (Å)	46.32 – 2.30 46.32 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.32-2.30) 99.5 (46.32-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.01 (at 2.29Å)	Xtriage
Refinement program	REFMAC refmac_5.5.0054	Depositor
R, $R_{free}$	0.196 , 0.238 0.230 , 0.270	Depositor DCC
$R_{free}$ test set	4054 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.1	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 33.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11682	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NH4, NA

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	1.56	4/1515 (0.3%)	0.78	0/2057
1	B	1.58	3/1451 (0.2%)	0.81	2/1965 (0.1%)
1	C	1.45	3/1424 (0.2%)	0.73	0/1934
1	D	1.45	2/1425 (0.1%)	0.70	0/1932
1	E	1.33	0/1504	0.70	0/2042
1	F	1.49	2/1467 (0.1%)	0.72	0/1992
1	G	1.44	2/1453 (0.1%)	0.72	0/1974
1	H	1.23	1/1334 (0.1%)	0.75	0/1813
All	All	1.45	17/11573 (0.1%)	0.74	2/15709 (0.0%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	9[A]	ILE	N-CA	-12.13	1.22	1.46
1	B	9[B]	ILE	N-CA	-12.13	1.22	1.46
1	A	9[A]	ILE	N-CA	-10.13	1.26	1.46
1	A	9[B]	ILE	N-CA	-10.13	1.26	1.46
1	C	24	CYS	CB-SG	-7.41	1.69	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	9[A]	ILE	CA-C-O	5.75	132.18	120.10
1	B	9[B]	ILE	CA-C-O	5.75	132.18	120.10

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	1478	0	1424	41	0
1	B	1419	0	1377	38	0
1	C	1396	0	1341	58	0
1	D	1398	0	1352	57	0
1	E	1474	0	1409	61	0
1	F	1437	0	1385	32	1
1	G	1423	0	1367	46	0
1	H	1309	0	1242	115	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
4	A	69	0	0	0	0
4	B	67	0	0	1	0
4	C	52	0	0	3	0
4	D	38	0	0	2	0
4	E	19	0	0	0	0
4	F	44	0	0	2	0
4	G	35	0	0	0	0
4	H	13	0	0	2	0
All	All	11682	0	10897	417	1

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

The worst 5 of 417 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:H:13:ASN:ND2	1:H:77:TRP:CE3	1.68	1.55
1:E:174:THR:CG2	1:E:177:GLN:HG3	1.34	1.53
1:H:82:ILE:HD11	1:H:85:LEU:CD1	1.53	1.35
1:H:146:THR:OG1	1:H:170:THR:HG21	1.26	1.32
1:H:13:ASN:ND2	1:H:77:TRP:CZ3	1.95	1.31

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:ARG:NH2	1:H:113:GLU:OE1[1_655]	2.15	0.05

## 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	188/204 (92%)	185 (98%)	3 (2%)	0	100	100
1	B	176/204 (86%)	172 (98%)	4 (2%)	0	100	100
1	C	174/204 (85%)	170 (98%)	3 (2%)	1 (1%)	22	27
1	D	175/204 (86%)	171 (98%)	4 (2%)	0	100	100
1	E	185/204 (91%)	179 (97%)	5 (3%)	1 (0%)	25	32
1	F	181/204 (89%)	178 (98%)	3 (2%)	0	100	100
1	G	180/204 (88%)	176 (98%)	2 (1%)	2 (1%)	12	13
1	H	165/204 (81%)	160 (97%)	4 (2%)	1 (1%)	22	27
All	All	1424/1632 (87%)	1391 (98%)	28 (2%)	5 (0%)	30	39

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	89	GLU

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Mol	Chain	Res	Type
1	E	128	VAL
1	H	128	VAL
1	C	128	VAL
1	G	128	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	153/170 (90%)	136 (89%)	17 (11%)	5	6
1	B	150/170 (88%)	135 (90%)	15 (10%)	6	8
1	C	147/170 (86%)	130 (88%)	17 (12%)	4	5
1	D	146/170 (86%)	135 (92%)	11 (8%)	11	15
1	E	154/170 (91%)	134 (87%)	20 (13%)	3	3
1	F	151/170 (89%)	133 (88%)	18 (12%)	4	5
1	G	149/170 (88%)	135 (91%)	14 (9%)	7	9
1	H	133/170 (78%)	103 (77%)	30 (23%)	1	0
All	All	1183/1360 (87%)	1041 (88%)	142 (12%)	4	4

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	28	GLU
1	H	37	ILE
1	H	120	VAL
1	B	138	LEU
1	B	131	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	53	HIS

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Mol	Chain	Res	Type
1	H	55	GLN
1	H	159	HIS
1	D	55	GLN
1	B	159	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](#)

Of 11 ligands modelled in this entry, 6 are modelled with single atom and 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, 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	184/204 (90%)	-0.06	4 (2%) 62 63	8, 21, 30, 56	2 (1%)
1	B	175/204 (85%)	0.04	7 (4%) 43 44	8, 23, 32, 64	1 (0%)
1	C	175/204 (85%)	-0.04	2 (1%) 77 78	14, 24, 30, 36	0
1	D	175/204 (85%)	0.01	3 (1%) 69 69	15, 24, 31, 55	0
1	E	186/204 (91%)	0.26	6 (3%) 50 52	19, 28, 49, 66	0
1	F	179/204 (87%)	0.10	6 (3%) 48 50	14, 23, 29, 38	0
1	G	179/204 (87%)	0.07	3 (1%) 69 69	11, 24, 39, 62	0
1	H	168/204 (82%)	0.63	6 (3%) 46 48	17, 30, 38, 40	0
All	All	1421/1632 (87%)	0.12	37 (2%) 57 58	8, 24, 36, 66	3 (0%)

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	199	VAL	3.3
1	F	62	ASP	3.3
1	B	69	PRO	3.2
1	B	-2	PHE	3.2
1	H	47	ASP	3.2

### 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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	NH4	D	201	1/1	0.87	0.40	25,25,25,25	0
2	NH4	E	201	1/1	0.87	0.28	30,30,30,30	0
2	NH4	C	201	1/1	0.89	0.43	28,28,28,28	0
3	NA	G	201	1/1	0.91	0.26	49,49,49,49	0
2	NH4	H	201	1/1	0.93	0.25	27,27,27,27	0
2	NH4	A	201	1/1	0.94	0.26	20,20,20,20	0
3	NA	E	202	1/1	0.95	0.29	41,41,41,41	0
3	NA	F	201	1/1	0.96	0.32	29,29,29,29	0
3	NA	B	202	1/1	0.97	0.29	31,31,31,31	0
2	NH4	B	201	1/1	0.97	0.37	26,26,26,26	0
3	NA	A	202	1/1	0.98	0.24	27,27,27,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.