



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 08:07 PM UTC

PDB ID : 3HT4 / pdb_00003ht4
Title : Crystal Structure of the Q81A77_BACCR Protein from Bacillus cereus.
Northeast Structural Genomics Consortium Target BeR213
Authors : Vorobiev, S.; Lew, S.; Seetharaman, J.; Wang, H.; Foote, E.; Ciccocanti, C.;
Janjua, H.; Xiao, R.; Mao, L.; Acton, T.B.; Montelione, G.T.; Hunt, J.F.;
Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2009-06-11
Resolution : 2.90 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

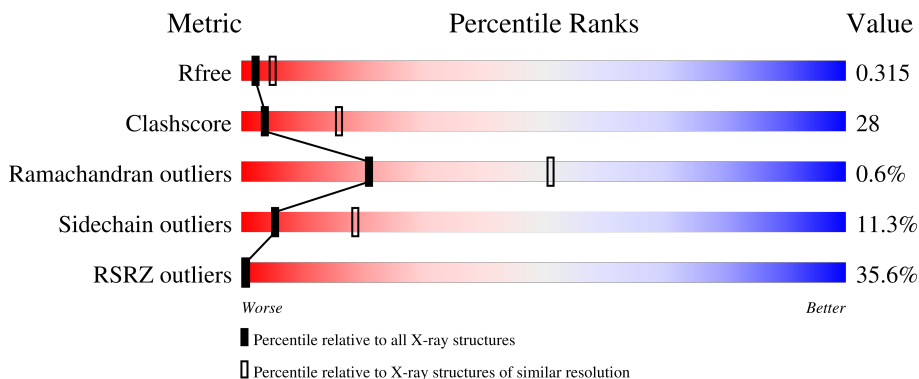
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	431	
1	B	431	
1	C	431	
1	D	431	

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Mol	Chain	Length	Quality of chain
1	E	431	 <p>31% 49% 40% 5% 5%</p>
1	F	431	 <p>29% 48% 41% 6% 5%</p>
1	G	431	 <p>39% 52% 38% 5% 5%</p>
1	H	431	 <p>43% 46% 43% 5% 6%</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 25070 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 Aluminum resistance protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	416	Total 3151	C 2015	N 517	O 605	S 5	Se 9	0	0	0
1	B	407	Total 3112	C 1994	N 509	O 596	S 5	Se 8	0	0	0
1	C	411	Total 3123	C 2001	N 513	O 596	S 5	Se 8	0	0	0
1	D	408	Total 3117	C 1997	N 510	O 597	S 5	Se 8	0	0	0
1	E	409	Total 3117	C 1997	N 511	O 596	S 5	Se 8	0	0	0
1	F	410	Total 3118	C 1998	N 512	O 595	S 5	Se 8	0	0	0
1	G	408	Total 3102	C 1986	N 510	O 593	S 5	Se 8	0	0	0
1	H	407	Total 3104	C 1989	N 508	O 594	S 5	Se 8	0	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	424	LEU	-	expression tag	UNP Q81A77
A	425	GLU	-	expression tag	UNP Q81A77
A	426	HIS	-	expression tag	UNP Q81A77
A	427	HIS	-	expression tag	UNP Q81A77
A	428	HIS	-	expression tag	UNP Q81A77
A	429	HIS	-	expression tag	UNP Q81A77
A	430	HIS	-	expression tag	UNP Q81A77
A	431	HIS	-	expression tag	UNP Q81A77
B	424	LEU	-	expression tag	UNP Q81A77
B	425	GLU	-	expression tag	UNP Q81A77
B	426	HIS	-	expression tag	UNP Q81A77
B	427	HIS	-	expression tag	UNP Q81A77
B	428	HIS	-	expression tag	UNP Q81A77

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Chain	Residue	Modelled	Actual	Comment	Reference
B	429	HIS	-	expression tag	UNP Q81A77
B	430	HIS	-	expression tag	UNP Q81A77
B	431	HIS	-	expression tag	UNP Q81A77
C	424	LEU	-	expression tag	UNP Q81A77
C	425	GLU	-	expression tag	UNP Q81A77
C	426	HIS	-	expression tag	UNP Q81A77
C	427	HIS	-	expression tag	UNP Q81A77
C	428	HIS	-	expression tag	UNP Q81A77
C	429	HIS	-	expression tag	UNP Q81A77
C	430	HIS	-	expression tag	UNP Q81A77
C	431	HIS	-	expression tag	UNP Q81A77
D	424	LEU	-	expression tag	UNP Q81A77
D	425	GLU	-	expression tag	UNP Q81A77
D	426	HIS	-	expression tag	UNP Q81A77
D	427	HIS	-	expression tag	UNP Q81A77
D	428	HIS	-	expression tag	UNP Q81A77
D	429	HIS	-	expression tag	UNP Q81A77
D	430	HIS	-	expression tag	UNP Q81A77
D	431	HIS	-	expression tag	UNP Q81A77
E	424	LEU	-	expression tag	UNP Q81A77
E	425	GLU	-	expression tag	UNP Q81A77
E	426	HIS	-	expression tag	UNP Q81A77
E	427	HIS	-	expression tag	UNP Q81A77
E	428	HIS	-	expression tag	UNP Q81A77
E	429	HIS	-	expression tag	UNP Q81A77
E	430	HIS	-	expression tag	UNP Q81A77
E	431	HIS	-	expression tag	UNP Q81A77
F	424	LEU	-	expression tag	UNP Q81A77
F	425	GLU	-	expression tag	UNP Q81A77
F	426	HIS	-	expression tag	UNP Q81A77
F	427	HIS	-	expression tag	UNP Q81A77
F	428	HIS	-	expression tag	UNP Q81A77
F	429	HIS	-	expression tag	UNP Q81A77
F	430	HIS	-	expression tag	UNP Q81A77
F	431	HIS	-	expression tag	UNP Q81A77
G	424	LEU	-	expression tag	UNP Q81A77
G	425	GLU	-	expression tag	UNP Q81A77
G	426	HIS	-	expression tag	UNP Q81A77
G	427	HIS	-	expression tag	UNP Q81A77
G	428	HIS	-	expression tag	UNP Q81A77
G	429	HIS	-	expression tag	UNP Q81A77
G	430	HIS	-	expression tag	UNP Q81A77

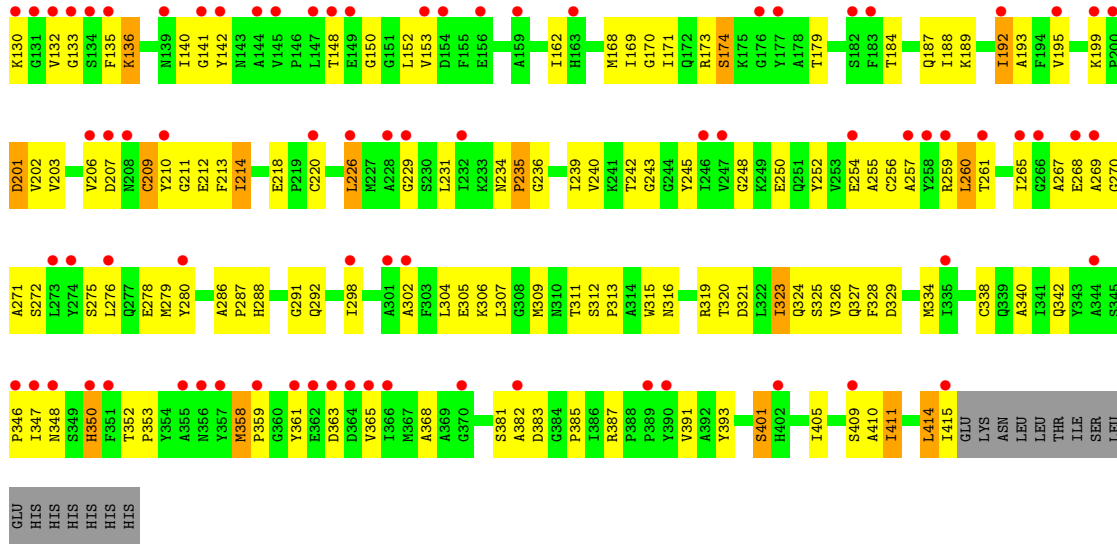
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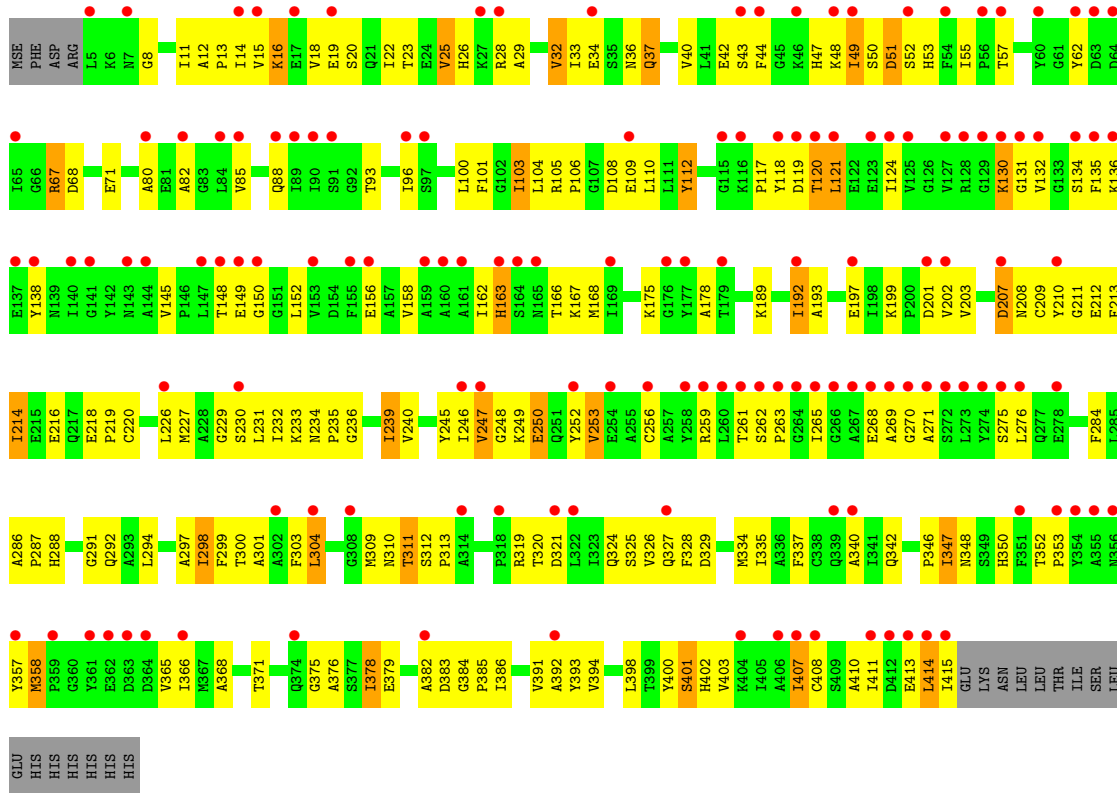
Chain	Residue	Modelled	Actual	Comment	Reference
G	431	HIS	-	expression tag	UNP Q81A77
H	424	LEU	-	expression tag	UNP Q81A77
H	425	GLU	-	expression tag	UNP Q81A77
H	426	HIS	-	expression tag	UNP Q81A77
H	427	HIS	-	expression tag	UNP Q81A77
H	428	HIS	-	expression tag	UNP Q81A77
H	429	HIS	-	expression tag	UNP Q81A77
H	430	HIS	-	expression tag	UNP Q81A77
H	431	HIS	-	expression tag	UNP Q81A77

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	19	Total O 19 19	0	0
2	B	16	Total O 16 16	0	0
2	C	12	Total O 12 12	0	0
2	D	24	Total O 24 24	0	0
2	E	18	Total O 18 18	0	0
2	F	18	Total O 18 18	0	0
2	G	10	Total O 10 10	0	0
2	H	9	Total O 9 9	0	0



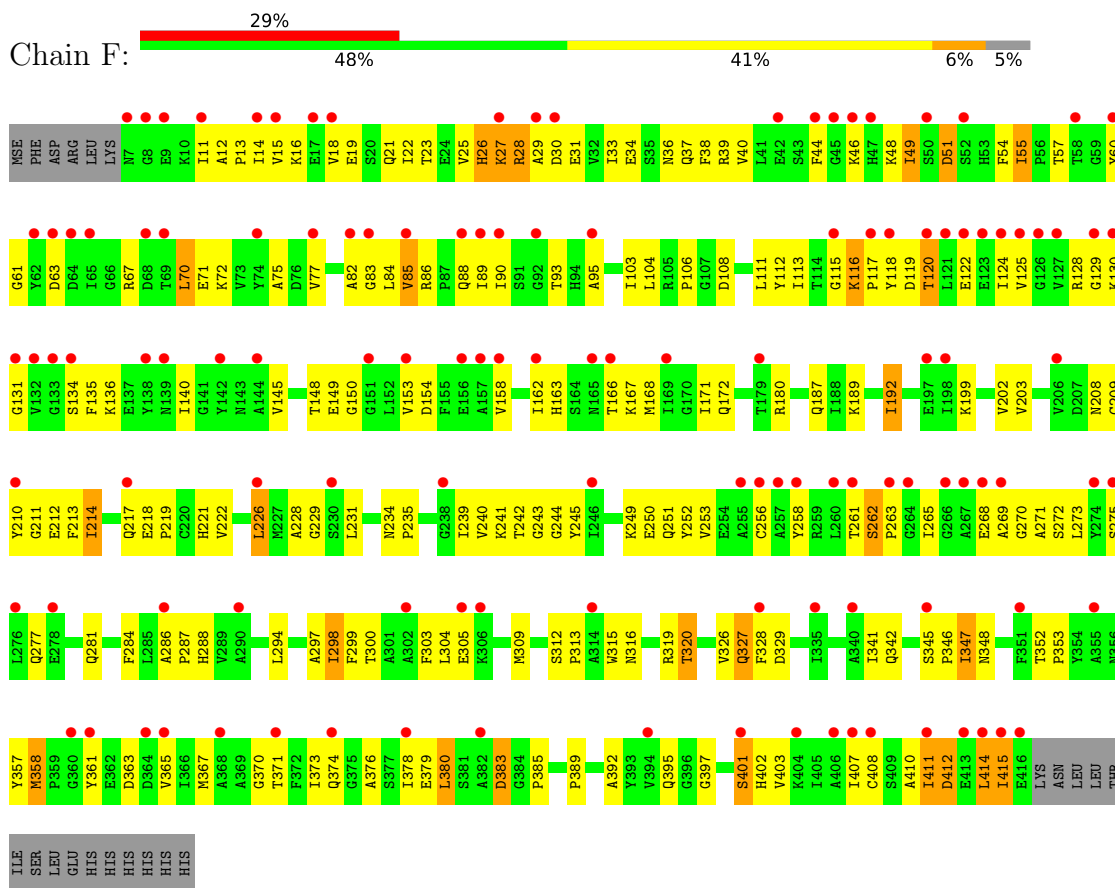
• Molecule 1: Aluminum resistance protein



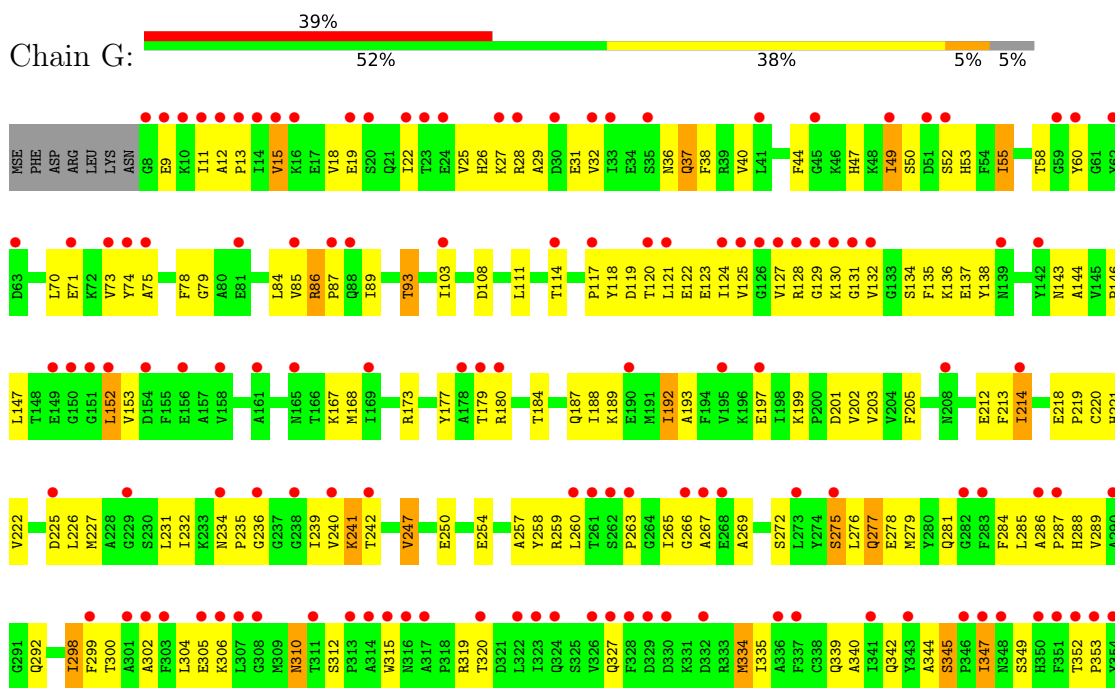
• Molecule 1: Aluminum resistance protein

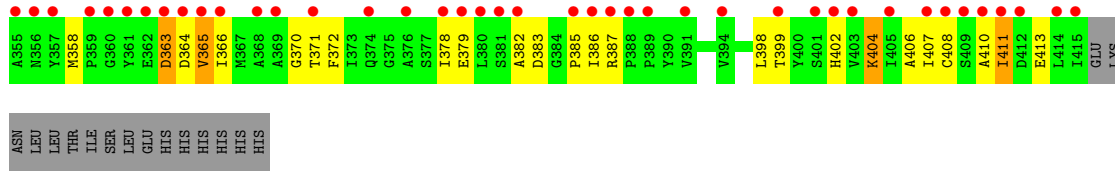


• Molecule 1: Aluminum resistance protein

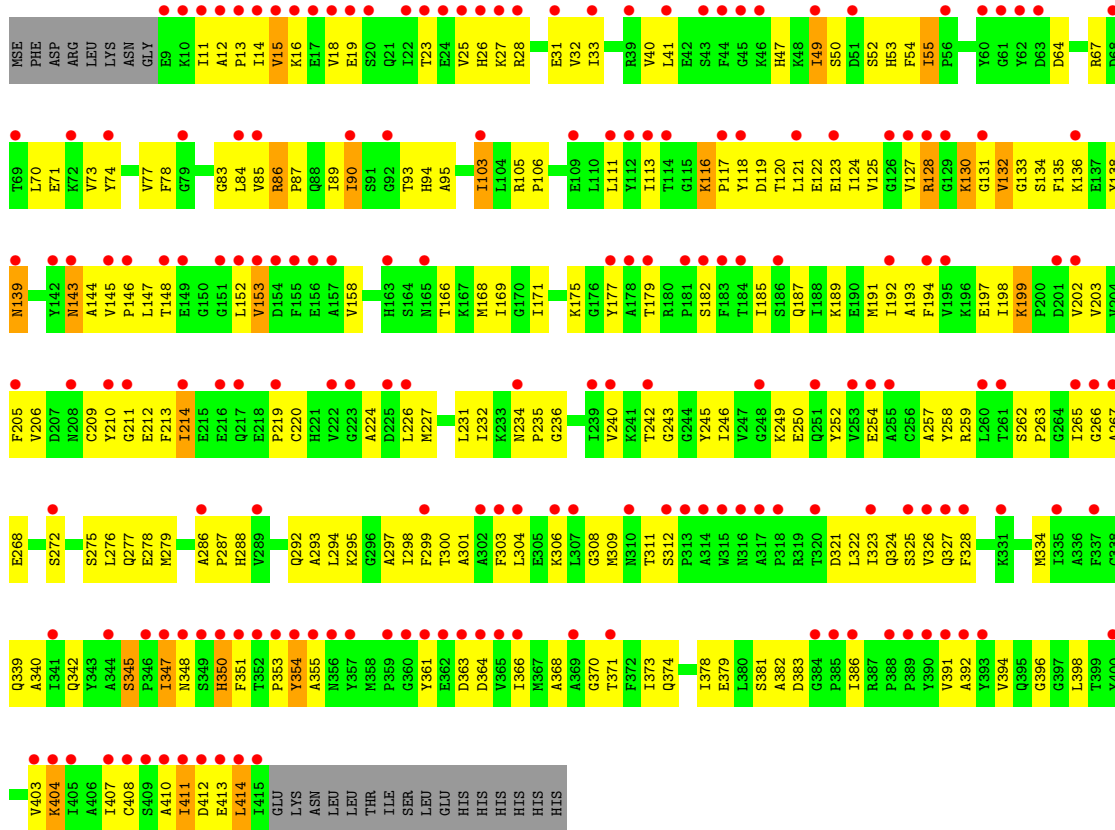


• Molecule 1: Aluminum resistance protein





● Molecule 1: Aluminum resistance protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.41Å 144.99Å 131.97Å 90.00° 106.24° 90.00°	Depositor
Resolution (Å)	46.19 – 2.90 46.19 – 2.90	Depositor EDS
% Data completeness (in resolution range)	75.0 (46.19-2.90) 87.2 (46.19-2.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.86 (at 2.91Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.274 , 0.299 0.287 , 0.315	Depositor DCC
R_{free} test set	6339 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	34.2	Xtrriage
Anisotropy	0.207	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	25070	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.75 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.7445e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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	0.29	0/3213	0.66	1/4346 (0.0%)
1	B	0.29	0/3174	0.65	0/4291
1	C	0.28	0/3185	0.68	0/4307
1	D	0.30	0/3179	0.67	1/4298 (0.0%)
1	E	0.29	0/3179	0.66	0/4298
1	F	0.29	0/3180	0.67	2/4300 (0.0%)
1	G	0.28	0/3164	0.68	2/4278 (0.0%)
1	H	0.27	0/3166	0.67	3/4282 (0.1%)
All	All	0.29	0/25440	0.67	9/34400 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	415	ILE	N-CA-C	-12.47	101.80	111.90
1	H	138	TYR	CB-CA-C	6.43	119.16	109.13
1	H	272	SER	N-CA-C	-5.75	104.39	111.40
1	F	272	SER	N-CA-C	-5.48	105.21	111.07
1	H	86	ARG	N-CA-C	5.39	113.07	108.22

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	3151	0	3073	210	0
1	B	3112	0	3066	181	0
1	C	3123	0	3067	178	0
1	D	3117	0	3068	165	0
1	E	3117	0	3067	187	0
1	F	3118	0	3065	185	0
1	G	3102	0	3043	184	0
1	H	3104	0	3051	196	0
2	A	19	0	0	1	0
2	B	16	0	0	0	0
2	C	12	0	0	2	0
2	D	24	0	0	4	0
2	E	18	0	0	3	0
2	F	18	0	0	4	0
2	G	10	0	0	1	0
2	H	9	0	0	1	0
All	All	25070	0	24500	1408	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 28.

The worst 5 of 1408 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:327:GLN:HG2	1:H:391:VAL:HG22	1.33	1.10
1:E:414:LEU:O	1:E:415:ILE:HG13	1.51	1.09
1:E:8:GLY:HA2	1:E:11:ILE:HG22	1.36	1.04
1:E:184:THR:H	1:E:187:GLN:HE21	1.03	1.02
1:B:49:ILE:HD11	1:C:346:PRO:O	1.60	1.01

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	414/431 (96%)	356 (86%)	53 (13%)	5 (1%)	10	34
1	B	405/431 (94%)	347 (86%)	56 (14%)	2 (0%)	24	54
1	C	409/431 (95%)	361 (88%)	45 (11%)	3 (1%)	18	48
1	D	406/431 (94%)	350 (86%)	55 (14%)	1 (0%)	43	72
1	E	407/431 (94%)	361 (89%)	45 (11%)	1 (0%)	43	72
1	F	408/431 (95%)	356 (87%)	51 (12%)	1 (0%)	43	72
1	G	406/431 (94%)	344 (85%)	60 (15%)	2 (0%)	24	54
1	H	405/431 (94%)	335 (83%)	65 (16%)	5 (1%)	10	34
All	All	3260/3448 (94%)	2810 (86%)	430 (13%)	20 (1%)	21	51

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	265	ILE
1	A	166	THR
1	A	351	PHE
1	B	89	ILE
1	C	67	ARG

5.3.2 Protein sidechains [i](#)

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	325/340 (96%)	290 (89%)	35 (11%)	6	21
1	B	326/340 (96%)	287 (88%)	39 (12%)	5	16
1	C	324/340 (95%)	285 (88%)	39 (12%)	5	16
1	D	326/340 (96%)	290 (89%)	36 (11%)	6	20
1	E	325/340 (96%)	289 (89%)	36 (11%)	6	20
1	F	324/340 (95%)	279 (86%)	45 (14%)	3	11
1	G	322/340 (95%)	292 (91%)	30 (9%)	8	27
1	H	324/340 (95%)	290 (90%)	34 (10%)	6	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2596/2720 (95%)	2302 (89%)	294 (11%)	5 19

5 of 294 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	49	ILE
1	H	350	HIS
1	G	153	VAL
1	H	15	VAL
1	C	247	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	356	ASN
1	F	277	GLN
1	H	217	GLN
1	E	21	GLN
1	F	21	GLN

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 [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	407/431 (94%)	1.78	145 (35%)	1 0	15, 33, 51, 62	0
1	B	399/431 (92%)	1.66	120 (30%)	1 1	14, 30, 50, 66	0
1	C	403/431 (93%)	1.70	142 (35%)	1 1	15, 32, 55, 69	0
1	D	400/431 (92%)	1.63	123 (30%)	1 1	10, 28, 57, 71	0
1	E	401/431 (93%)	1.68	133 (33%)	1 1	8, 29, 56, 67	0
1	F	402/431 (93%)	1.65	124 (30%)	1 1	14, 30, 53, 64	0
1	G	400/431 (92%)	1.98	169 (42%)	0 0	17, 36, 71, 84	0
1	H	399/431 (92%)	2.06	186 (46%)	0 0	20, 37, 67, 81	0
All	All	3211/3448 (93%)	1.77	1142 (35%)	1 0	8, 32, 60, 84	0

The worst 5 of 1142 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	360	GLY	11.1
1	D	359	PRO	7.8
1	F	267	ALA	7.2
1	E	359	PRO	7.1
1	F	15	VAL	6.8

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.