



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:22 PM UTC

PDB ID : 4XZG / pdb_00004xzg
Title : Crystal structure of HIRAN domain of human HLTF
Authors : Ikegaya, Y.; Hara, K.; Hashimoto, H.
Deposited on : 2015-02-04
Resolution : 2.40 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

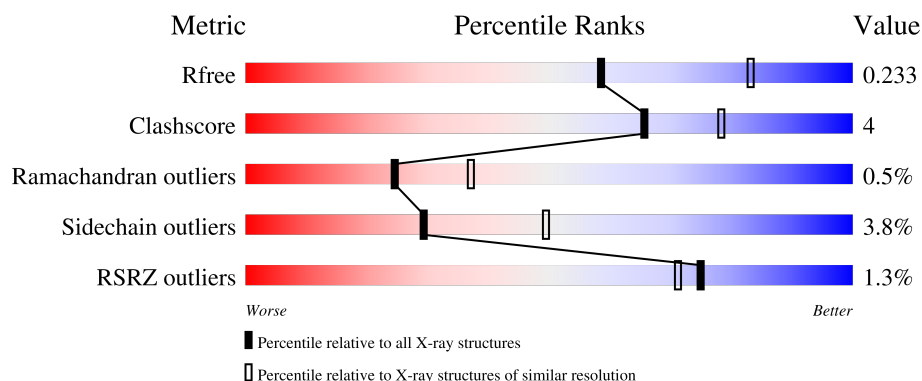
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	138	 77% 11% 12%
1	B	138	 78% 9% 12%
1	C	138	 77% 9% 13%
1	D	138	 81% 6% 12%
1	E	138	 76% 12% 12%

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Mol	Chain	Length	Quality of chain
1	F	138	 75% 12% • 12%
1	G	138	 78% 9% • 11%
1	H	138	 78% 9% • 12%
1	I	138	 71% 15% • 12%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8853 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 Helicase-like transcription factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	121	Total	C	N	O	S	0	0	0
			939	596	171	168	4			
1	B	121	Total	C	N	O	S	0	0	0
			939	596	171	168	4			
1	C	120	Total	C	N	O	S	0	0	0
			928	587	170	167	4			
1	D	121	Total	C	N	O	S	0	0	0
			939	596	171	168	4			
1	E	121	Total	C	N	O	S	0	0	0
			939	596	171	168	4			
1	F	122	Total	C	N	O	S	0	0	0
			951	605	172	170	4			
1	G	123	Total	C	N	O	S	0	0	0
			959	611	173	171	4			
1	H	122	Total	C	N	O	S	0	0	0
			944	599	172	169	4			
1	I	122	Total	C	N	O	S	0	0	0
			951	605	172	170	4			

There are 180 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	37	MET	-	expression tag	UNP Q14527
A	38	ARG	-	expression tag	UNP Q14527
A	39	GLY	-	expression tag	UNP Q14527
A	40	SER	-	expression tag	UNP Q14527
A	41	HIS	-	expression tag	UNP Q14527
A	42	HIS	-	expression tag	UNP Q14527
A	43	HIS	-	expression tag	UNP Q14527
A	44	HIS	-	expression tag	UNP Q14527
A	45	HIS	-	expression tag	UNP Q14527
A	46	HIS	-	expression tag	UNP Q14527
A	47	GLY	-	expression tag	UNP Q14527

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Chain	Residue	Modelled	Actual	Comment	Reference
A	48	SER	-	expression tag	UNP Q14527
A	49	GLU	-	expression tag	UNP Q14527
A	50	ASN	-	expression tag	UNP Q14527
A	51	LEU	-	expression tag	UNP Q14527
A	52	TYR	-	expression tag	UNP Q14527
A	53	PHE	-	expression tag	UNP Q14527
A	54	GLN	-	expression tag	UNP Q14527
A	55	GLY	-	expression tag	UNP Q14527
A	56	GLY	-	expression tag	UNP Q14527
B	37	MET	-	expression tag	UNP Q14527
B	38	ARG	-	expression tag	UNP Q14527
B	39	GLY	-	expression tag	UNP Q14527
B	40	SER	-	expression tag	UNP Q14527
B	41	HIS	-	expression tag	UNP Q14527
B	42	HIS	-	expression tag	UNP Q14527
B	43	HIS	-	expression tag	UNP Q14527
B	44	HIS	-	expression tag	UNP Q14527
B	45	HIS	-	expression tag	UNP Q14527
B	46	HIS	-	expression tag	UNP Q14527
B	47	GLY	-	expression tag	UNP Q14527
B	48	SER	-	expression tag	UNP Q14527
B	49	GLU	-	expression tag	UNP Q14527
B	50	ASN	-	expression tag	UNP Q14527
B	51	LEU	-	expression tag	UNP Q14527
B	52	TYR	-	expression tag	UNP Q14527
B	53	PHE	-	expression tag	UNP Q14527
B	54	GLN	-	expression tag	UNP Q14527
B	55	GLY	-	expression tag	UNP Q14527
B	56	GLY	-	expression tag	UNP Q14527
C	37	MET	-	expression tag	UNP Q14527
C	38	ARG	-	expression tag	UNP Q14527
C	39	GLY	-	expression tag	UNP Q14527
C	40	SER	-	expression tag	UNP Q14527
C	41	HIS	-	expression tag	UNP Q14527
C	42	HIS	-	expression tag	UNP Q14527
C	43	HIS	-	expression tag	UNP Q14527
C	44	HIS	-	expression tag	UNP Q14527
C	45	HIS	-	expression tag	UNP Q14527
C	46	HIS	-	expression tag	UNP Q14527
C	47	GLY	-	expression tag	UNP Q14527
C	48	SER	-	expression tag	UNP Q14527
C	49	GLU	-	expression tag	UNP Q14527

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Chain	Residue	Modelled	Actual	Comment	Reference
C	50	ASN	-	expression tag	UNP Q14527
C	51	LEU	-	expression tag	UNP Q14527
C	52	TYR	-	expression tag	UNP Q14527
C	53	PHE	-	expression tag	UNP Q14527
C	54	GLN	-	expression tag	UNP Q14527
C	55	GLY	-	expression tag	UNP Q14527
C	56	GLY	-	expression tag	UNP Q14527
D	37	MET	-	expression tag	UNP Q14527
D	38	ARG	-	expression tag	UNP Q14527
D	39	GLY	-	expression tag	UNP Q14527
D	40	SER	-	expression tag	UNP Q14527
D	41	HIS	-	expression tag	UNP Q14527
D	42	HIS	-	expression tag	UNP Q14527
D	43	HIS	-	expression tag	UNP Q14527
D	44	HIS	-	expression tag	UNP Q14527
D	45	HIS	-	expression tag	UNP Q14527
D	46	HIS	-	expression tag	UNP Q14527
D	47	GLY	-	expression tag	UNP Q14527
D	48	SER	-	expression tag	UNP Q14527
D	49	GLU	-	expression tag	UNP Q14527
D	50	ASN	-	expression tag	UNP Q14527
D	51	LEU	-	expression tag	UNP Q14527
D	52	TYR	-	expression tag	UNP Q14527
D	53	PHE	-	expression tag	UNP Q14527
D	54	GLN	-	expression tag	UNP Q14527
D	55	GLY	-	expression tag	UNP Q14527
D	56	GLY	-	expression tag	UNP Q14527
E	37	MET	-	expression tag	UNP Q14527
E	38	ARG	-	expression tag	UNP Q14527
E	39	GLY	-	expression tag	UNP Q14527
E	40	SER	-	expression tag	UNP Q14527
E	41	HIS	-	expression tag	UNP Q14527
E	42	HIS	-	expression tag	UNP Q14527
E	43	HIS	-	expression tag	UNP Q14527
E	44	HIS	-	expression tag	UNP Q14527
E	45	HIS	-	expression tag	UNP Q14527
E	46	HIS	-	expression tag	UNP Q14527
E	47	GLY	-	expression tag	UNP Q14527
E	48	SER	-	expression tag	UNP Q14527
E	49	GLU	-	expression tag	UNP Q14527
E	50	ASN	-	expression tag	UNP Q14527
E	51	LEU	-	expression tag	UNP Q14527

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Chain	Residue	Modelled	Actual	Comment	Reference
E	52	TYR	-	expression tag	UNP Q14527
E	53	PHE	-	expression tag	UNP Q14527
E	54	GLN	-	expression tag	UNP Q14527
E	55	GLY	-	expression tag	UNP Q14527
E	56	GLY	-	expression tag	UNP Q14527
F	37	MET	-	expression tag	UNP Q14527
F	38	ARG	-	expression tag	UNP Q14527
F	39	GLY	-	expression tag	UNP Q14527
F	40	SER	-	expression tag	UNP Q14527
F	41	HIS	-	expression tag	UNP Q14527
F	42	HIS	-	expression tag	UNP Q14527
F	43	HIS	-	expression tag	UNP Q14527
F	44	HIS	-	expression tag	UNP Q14527
F	45	HIS	-	expression tag	UNP Q14527
F	46	HIS	-	expression tag	UNP Q14527
F	47	GLY	-	expression tag	UNP Q14527
F	48	SER	-	expression tag	UNP Q14527
F	49	GLU	-	expression tag	UNP Q14527
F	50	ASN	-	expression tag	UNP Q14527
F	51	LEU	-	expression tag	UNP Q14527
F	52	TYR	-	expression tag	UNP Q14527
F	53	PHE	-	expression tag	UNP Q14527
F	54	GLN	-	expression tag	UNP Q14527
F	55	GLY	-	expression tag	UNP Q14527
F	56	GLY	-	expression tag	UNP Q14527
G	37	MET	-	expression tag	UNP Q14527
G	38	ARG	-	expression tag	UNP Q14527
G	39	GLY	-	expression tag	UNP Q14527
G	40	SER	-	expression tag	UNP Q14527
G	41	HIS	-	expression tag	UNP Q14527
G	42	HIS	-	expression tag	UNP Q14527
G	43	HIS	-	expression tag	UNP Q14527
G	44	HIS	-	expression tag	UNP Q14527
G	45	HIS	-	expression tag	UNP Q14527
G	46	HIS	-	expression tag	UNP Q14527
G	47	GLY	-	expression tag	UNP Q14527
G	48	SER	-	expression tag	UNP Q14527
G	49	GLU	-	expression tag	UNP Q14527
G	50	ASN	-	expression tag	UNP Q14527
G	51	LEU	-	expression tag	UNP Q14527
G	52	TYR	-	expression tag	UNP Q14527
G	53	PHE	-	expression tag	UNP Q14527

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Chain	Residue	Modelled	Actual	Comment	Reference
G	54	GLN	-	expression tag	UNP Q14527
G	55	GLY	-	expression tag	UNP Q14527
G	56	GLY	-	expression tag	UNP Q14527
H	37	MET	-	expression tag	UNP Q14527
H	38	ARG	-	expression tag	UNP Q14527
H	39	GLY	-	expression tag	UNP Q14527
H	40	SER	-	expression tag	UNP Q14527
H	41	HIS	-	expression tag	UNP Q14527
H	42	HIS	-	expression tag	UNP Q14527
H	43	HIS	-	expression tag	UNP Q14527
H	44	HIS	-	expression tag	UNP Q14527
H	45	HIS	-	expression tag	UNP Q14527
H	46	HIS	-	expression tag	UNP Q14527
H	47	GLY	-	expression tag	UNP Q14527
H	48	SER	-	expression tag	UNP Q14527
H	49	GLU	-	expression tag	UNP Q14527
H	50	ASN	-	expression tag	UNP Q14527
H	51	LEU	-	expression tag	UNP Q14527
H	52	TYR	-	expression tag	UNP Q14527
H	53	PHE	-	expression tag	UNP Q14527
H	54	GLN	-	expression tag	UNP Q14527
H	55	GLY	-	expression tag	UNP Q14527
H	56	GLY	-	expression tag	UNP Q14527
I	37	MET	-	expression tag	UNP Q14527
I	38	ARG	-	expression tag	UNP Q14527
I	39	GLY	-	expression tag	UNP Q14527
I	40	SER	-	expression tag	UNP Q14527
I	41	HIS	-	expression tag	UNP Q14527
I	42	HIS	-	expression tag	UNP Q14527
I	43	HIS	-	expression tag	UNP Q14527
I	44	HIS	-	expression tag	UNP Q14527
I	45	HIS	-	expression tag	UNP Q14527
I	46	HIS	-	expression tag	UNP Q14527
I	47	GLY	-	expression tag	UNP Q14527
I	48	SER	-	expression tag	UNP Q14527
I	49	GLU	-	expression tag	UNP Q14527
I	50	ASN	-	expression tag	UNP Q14527
I	51	LEU	-	expression tag	UNP Q14527
I	52	TYR	-	expression tag	UNP Q14527
I	53	PHE	-	expression tag	UNP Q14527
I	54	GLN	-	expression tag	UNP Q14527
I	55	GLY	-	expression tag	UNP Q14527

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Chain	Residue	Modelled	Actual	Comment	Reference
I	56	GLY	-	expression tag	UNP Q14527

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	48	Total O 48 48	0	0
2	B	58	Total O 58 58	0	0
2	C	45	Total O 45 45	0	0
2	D	30	Total O 30 30	0	0
2	E	27	Total O 27 27	0	0
2	F	47	Total O 47 47	0	0
2	G	45	Total O 45 45	0	0
2	H	49	Total O 49 49	0	0
2	I	15	Total O 15 15	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: Helicase-like transcription factor

Chain A: 



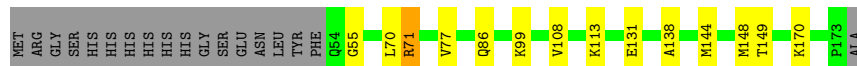
- Molecule 1: Helicase-like transcription factor

Chain B: 



- Molecule 1: Helicase-like transcription factor

Chain C: 



- Molecule 1: Helicase-like transcription factor

Chain D: 

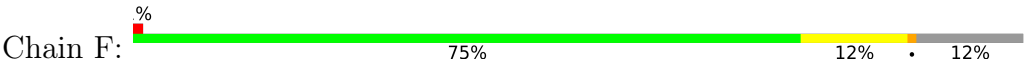


- Molecule 1: Helicase-like transcription factor

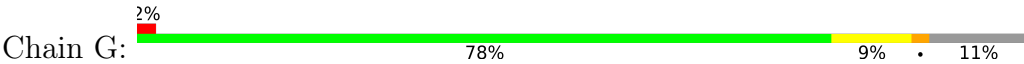
Chain E: 



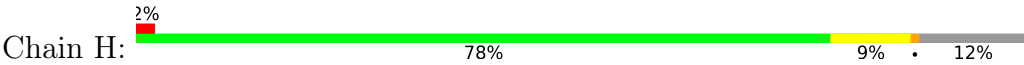
- Molecule 1: Helicase-like transcription factor



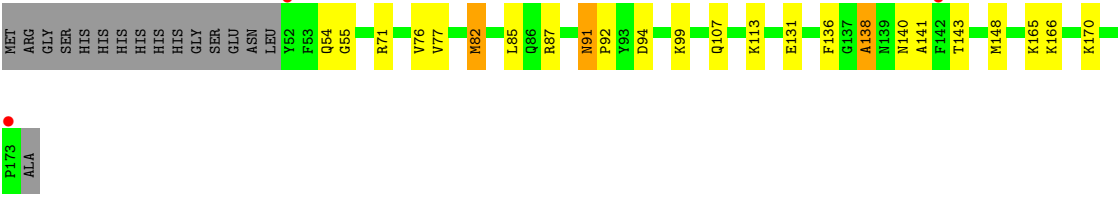
• Molecule 1: Helicase-like transcription factor



• Molecule 1: Helicase-like transcription factor



• Molecule 1: Helicase-like transcription factor



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	129.44Å 129.44Å 143.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 20.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.5 (20.00-2.40) 99.5 (20.00-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.79 (at 2.41Å)	Xtrriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.214 , 0.231 0.215 , 0.233	Depositor DCC
R_{free} test set	2430 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	42.1	Xtrriage
Anisotropy	0.155	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8853	wwPDB-VP
Average B, all atoms (Å ²)	48.0	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 34.50 % 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 6.7538e-04. 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

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	1.00	1/959 (0.1%)	1.11	2/1293 (0.2%)
1	B	0.99	1/959 (0.1%)	1.08	3/1293 (0.2%)
1	C	0.93	0/947	1.12	3/1277 (0.2%)
1	D	0.92	0/959	1.08	0/1293
1	E	0.90	0/959	1.04	1/1293 (0.1%)
1	F	0.92	0/972	1.00	0/1311
1	G	0.85	0/980	1.06	1/1322 (0.1%)
1	H	0.97	0/964	1.01	1/1300 (0.1%)
1	I	0.86	0/972	1.05	2/1311 (0.2%)
All	All	0.93	2/8671 (0.0%)	1.06	13/11693 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	165	LYS	N-CA	-5.59	1.39	1.46
1	B	77	VAL	N-CA	-5.46	1.39	1.46

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	144	MET	CA-C-N	-6.70	113.74	120.31
1	C	144	MET	C-N-CA	-6.70	113.74	120.31
1	G	129	GLN	N-CA-C	-6.58	99.57	110.17
1	H	54	GLN	N-CA-C	6.53	118.06	111.07
1	C	55	GLY	N-CA-C	-5.47	108.09	115.21
1	B	129	GLN	CA-C-N	-5.47	115.98	123.14
1	B	129	GLN	C-N-CA	-5.47	115.98	123.14
1	I	91	ASN	CA-C-N	5.39	125.03	119.05
1	I	91	ASN	C-N-CA	5.39	125.03	119.05
1	E	113	LYS	N-CA-C	5.30	117.81	111.71
1	B	54	GLN	N-CA-C	5.28	117.44	111.11
1	A	54	GLN	N-CA-C	5.22	121.93	110.80
1	A	133	VAL	CB-CA-C	-5.06	102.71	110.50

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	939	0	935	7	0
1	B	939	0	935	7	0
1	C	928	0	926	7	0
1	D	939	0	935	5	0
1	E	939	0	935	5	0
1	F	951	0	944	7	0
1	G	959	0	955	13	0
1	H	944	0	940	7	0
1	I	951	0	944	12	0
2	A	48	0	0	0	0
2	B	58	0	0	2	0
2	C	45	0	0	1	0
2	D	30	0	0	1	0
2	E	27	0	0	0	0
2	F	47	0	0	1	0
2	G	45	0	0	3	0
2	H	49	0	0	0	0
2	I	15	0	0	0	0
All	All	8853	0	8449	64	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 4.

All (64) 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:G:64:ARG:HG2	1:G:64:ARG:HH11	1.42	0.83
1:B:77:VAL:HG13	1:B:138:ALA:HB1	1.66	0.77
1:C:71:ARG:NH1	1:H:80:ASN:HD22	1.83	0.77
1:A:91:ASN:HA	1:G:72:TYR:OH	1.86	0.74
1:E:78:ASN:O	1:E:81:GLU:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:VAL:HG12	1:D:143:THR:HG22	1.69	0.72
1:F:64:ARG:HD3	1:F:147:HIS:CE1	2.25	0.72
1:C:71:ARG:HH12	1:H:80:ASN:HD22	1.38	0.67
1:I:77:VAL:HG13	1:I:138:ALA:HB1	1.75	0.66
1:G:77:VAL:O	1:G:138:ALA:HB1	1.96	0.65
1:A:170:LYS:NZ	1:E:131:GLU:OE2	2.31	0.64
1:B:92:PRO:HG2	1:B:93:TYR:CE2	2.32	0.64
1:A:92:PRO:HD3	1:G:72:TYR:CE2	2.32	0.63
1:B:71:ARG:HG2	2:B:232:HOH:O	1.99	0.62
1:F:155:GLU:HG3	2:F:245:HOH:O	1.99	0.62
1:H:136:PHE:CE1	1:H:145:PRO:HG3	2.35	0.61
1:C:86:GLN:OE1	1:C:99:LYS:HD2	2.02	0.59
1:I:91:ASN:HB3	1:I:94:ASP:O	2.02	0.59
1:D:149:THR:HG23	2:D:222:HOH:O	2.02	0.59
1:A:136:PHE:CE2	1:A:145:PRO:HG3	2.38	0.58
1:G:91:ASN:HB3	1:G:94:ASP:O	2.04	0.57
1:G:64:ARG:HH11	1:G:64:ARG:CG	2.17	0.55
1:D:53:PHE:N	1:D:53:PHE:CD1	2.75	0.54
1:G:129:GLN:HG2	1:G:151:TRP:HB2	1.92	0.51
1:A:68:VAL:HG12	1:A:143:THR:HG22	1.93	0.50
1:F:82:MET:HG3	1:F:132:GLY:O	2.12	0.50
1:B:122:ILE:HG13	1:B:163:GLN:HG2	1.94	0.49
1:C:77:VAL:O	1:C:138:ALA:HB1	2.15	0.47
1:B:92:PRO:HD3	1:H:72:TYR:HE2	1.79	0.47
1:G:165:LYS:HD2	2:G:242:HOH:O	2.15	0.47
1:H:77:VAL:O	1:H:138:ALA:HB1	2.15	0.47
1:A:115:LEU:HD21	1:A:148:MET:HE1	1.97	0.46
1:C:77:VAL:CG2	1:C:108:VAL:HG21	2.46	0.46
1:I:131:GLU:O	1:I:148:MET:HA	2.15	0.46
1:F:77:VAL:CG2	1:F:108:VAL:HG21	2.45	0.46
1:B:155:GLU:HG3	2:B:207:HOH:O	2.16	0.45
1:I:165:LYS:O	1:I:166:LYS:C	2.58	0.45
1:F:98:ILE:HD13	1:F:123:MET:SD	2.57	0.45
1:E:71:ARG:HD3	1:E:142:PHE:CE2	2.52	0.45
1:I:54:GLN:CG	1:I:55:GLY:H	2.30	0.45
1:C:149:THR:HG23	2:C:236:HOH:O	2.17	0.44
1:D:91:ASN:HB3	1:D:94:ASP:O	2.17	0.44
1:I:82:MET:C	1:I:82:MET:SD	3.00	0.44
1:I:91:ASN:HA	1:I:92:PRO:HD2	1.72	0.44
1:G:140:ASN:HB3	2:G:232:HOH:O	2.16	0.44
1:I:136:PHE:C	1:I:138:ALA:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:153:LYS:HB3	1:F:155:GLU:OE2	2.18	0.43
1:I:140:ASN:OD1	1:I:141:ALA:N	2.51	0.43
1:D:131:GLU:O	1:D:148:MET:HA	2.18	0.43
1:I:99:LYS:HG2	1:I:107:GLN:NE2	2.34	0.43
1:G:110:HIS:HB3	2:G:229:HOH:O	2.18	0.42
1:G:166:LYS:HG2	1:G:167:HIS:CD2	2.54	0.42
1:H:135:PRO:HG3	1:H:147:HIS:CD2	2.54	0.42
1:I:76:VAL:HG12	1:I:77:VAL:N	2.34	0.42
1:F:88:ASP:HB2	1:F:99:LYS:HG3	2.02	0.41
1:G:64:ARG:HG2	1:G:64:ARG:NH1	2.22	0.41
1:B:53:PHE:HB3	1:B:153:LYS:HE2	2.03	0.41
1:C:131:GLU:O	1:C:148:MET:HA	2.21	0.41
1:G:114:GLU:H	1:G:114:GLU:CD	2.29	0.41
1:E:63:LEU:HD12	1:E:63:LEU:HA	1.82	0.41
1:E:99:LYS:HB2	1:E:99:LYS:HE3	1.97	0.41
1:I:87:ARG:HD2	1:I:87:ARG:HA	1.87	0.41
1:H:115:LEU:HD21	1:H:148:MET:HE1	2.03	0.40
1:A:98:ILE:HD13	1:A:123:MET:SD	2.62	0.40

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	119/138 (86%)	114 (96%)	5 (4%)	0	100	100
1	B	119/138 (86%)	115 (97%)	3 (2%)	1 (1%)	16	25
1	C	118/138 (86%)	116 (98%)	2 (2%)	0	100	100
1	D	119/138 (86%)	116 (98%)	3 (2%)	0	100	100
1	E	119/138 (86%)	111 (93%)	6 (5%)	2 (2%)	7	10
1	F	120/138 (87%)	116 (97%)	3 (2%)	1 (1%)	16	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	121/138 (88%)	118 (98%)	3 (2%)	0	100	100
1	H	120/138 (87%)	118 (98%)	2 (2%)	0	100	100
1	I	120/138 (87%)	111 (92%)	8 (7%)	1 (1%)	16	25
All	All	1075/1242 (87%)	1035 (96%)	35 (3%)	5 (0%)	24	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	138	ALA
1	I	138	ALA
1	E	72	TYR
1	B	135	PRO
1	F	53	PHE

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	98/112 (88%)	97 (99%)	1 (1%)	68	84
1	B	98/112 (88%)	97 (99%)	1 (1%)	68	84
1	C	97/112 (87%)	93 (96%)	4 (4%)	27	46
1	D	98/112 (88%)	96 (98%)	2 (2%)	48	70
1	E	98/112 (88%)	92 (94%)	6 (6%)	17	30
1	F	99/112 (88%)	93 (94%)	6 (6%)	17	30
1	G	100/112 (89%)	96 (96%)	4 (4%)	28	47
1	H	98/112 (88%)	94 (96%)	4 (4%)	27	46
1	I	99/112 (88%)	93 (94%)	6 (6%)	17	30
All	All	885/1008 (88%)	851 (96%)	34 (4%)	29	49

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	LEU
1	B	82	MET
1	C	70	LEU
1	C	71	ARG
1	C	113	LYS
1	C	170	LYS
1	D	53	PHE
1	D	113	LYS
1	E	82	MET
1	E	85	LEU
1	E	129	GLN
1	E	140	ASN
1	E	155	GLU
1	E	166	LYS
1	F	54	GLN
1	F	70	LEU
1	F	71	ARG
1	F	95	LYS
1	F	129	GLN
1	F	155	GLU
1	G	51	LEU
1	G	58	VAL
1	G	64	ARG
1	G	166	LYS
1	H	54	GLN
1	H	58	VAL
1	H	103	VAL
1	H	166	LYS
1	I	71	ARG
1	I	82	MET
1	I	85	LEU
1	I	113	LYS
1	I	143	THR
1	I	170	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	HIS
1	B	66	HIS
1	B	104	ASN
1	B	125	ASN
1	B	147	HIS

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Mol	Chain	Res	Type
1	C	91	ASN
1	C	129	GLN
1	C	147	HIS
1	D	106	ASN
1	D	110	HIS
1	E	86	GLN
1	E	90	ASN
1	E	104	ASN
1	E	106	ASN
1	E	167	HIS
1	F	104	ASN
1	F	125	ASN
1	F	129	GLN
1	F	139	ASN
1	F	147	HIS
1	G	125	ASN
1	H	78	ASN
1	H	80	ASN
1	H	167	HIS
1	I	104	ASN
1	I	106	ASN
1	I	107	GLN
1	I	167	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 ⓘ

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, 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	121/138 (87%)	-0.47	0 100 100	24, 39, 71, 102	0
1	B	121/138 (87%)	-0.38	1 (0%) 82 80	26, 39, 74, 128	0
1	C	120/138 (86%)	-0.45	0 100 100	26, 40, 64, 85	0
1	D	121/138 (87%)	-0.23	2 (1%) 69 65	27, 47, 83, 143	0
1	E	121/138 (87%)	-0.06	0 100 100	29, 51, 90, 106	0
1	F	122/138 (88%)	-0.42	2 (1%) 70 66	22, 41, 77, 98	0
1	G	123/138 (89%)	-0.29	3 (2%) 59 55	29, 46, 73, 98	0
1	H	122/138 (88%)	-0.40	3 (2%) 58 54	24, 40, 69, 94	0
1	I	122/138 (88%)	0.00	3 (2%) 58 54	27, 54, 98, 117	0
All	All	1093/1242 (88%)	-0.30	14 (1%) 75 71	22, 44, 83, 143	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	93	TYR	5.4
1	H	93	TYR	3.9
1	B	53	PHE	3.7
1	G	51	LEU	2.9
1	H	174	ALA	2.7
1	D	53	PHE	2.7
1	G	93	TYR	2.6
1	F	136	PHE	2.5
1	I	52	TYR	2.4
1	I	173	PRO	2.3
1	G	54	GLN	2.2
1	F	52	TYR	2.1
1	H	142	PHE	2.0
1	I	142	PHE	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.