



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:14 AM UTC

PDB ID : 5XP1 / pdb_00005xp1
Title : Structure of monomeric mutant of REI immunoglobulin light chain variable domain crystallized at pH 6
Authors : Mine, S.; Nakamura, T.; Uegaki, K.; Hamada, D.
Deposited on : 2017-05-31
Resolution : 2.88 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

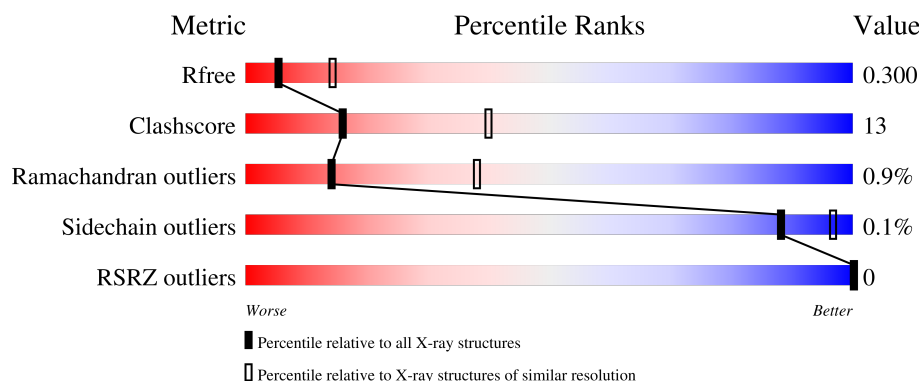
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.88 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	3557 (2.90-2.86)
Clashscore	190562	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)
RSRZ outliers	180081	3558 (2.90-2.86)

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	109	 76% 23% .
1	B	109	 73% 25% .
1	C	109	 87% 12% .
1	D	109	 75% 24% .
1	E	109	 74% 25% .

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Mol	Chain	Length	Quality of chain
1	F	109	 77%21%•
1	G	109	 62%34%••
1	H	109	 70%29%•

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6669 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 Immunoglobulin kappa variable 1D-33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	109	Total	C	N	O	S	0	0	0
			834	524	136	171	3			
1	B	109	Total	C	N	O	S	0	0	0
			834	524	136	171	3			
1	C	109	Total	C	N	O	S	0	0	0
			840	527	139	171	3			
1	D	109	Total	C	N	O	S	0	0	0
			840	527	139	171	3			
1	E	109	Total	C	N	O	S	0	0	0
			834	524	136	171	3			
1	F	109	Total	C	N	O	S	0	0	0
			840	527	139	171	3			
1	G	107	Total	C	N	O	S	0	0	0
			808	505	134	166	3			
1	H	109	Total	C	N	O	S	0	0	0
			827	515	139	170	3			

There are 184 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	CYS	see sequence details	UNP P01593
A	30	ILE	SER	see sequence details	UNP P01593
A	31	LYS	ASN	see sequence details	UNP P01593
A	39	THR	LYS	see sequence details	UNP P01593
A	50	GLU	ASP	see sequence details	UNP P01593
A	55	GLN	GLU	see sequence details	UNP P01593
A	56	ALA	THR	see sequence details	UNP P01593
A	71	TYR	PHE	see sequence details	UNP P01593
A	92	GLN	ASP	see sequence details	UNP P01593
A	93	SER	ASN	see sequence details	UNP P01593
A	96	LYS	-	expression tag	UNP P01593
A	97	THR	-	expression tag	UNP P01593
A	98	PHE	-	expression tag	UNP P01593

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Chain	Residue	Modelled	Actual	Comment	Reference
A	99	GLY	-	expression tag	UNP P01593
A	100	GLN	-	expression tag	UNP P01593
A	101	GLY	-	expression tag	UNP P01593
A	102	THR	-	expression tag	UNP P01593
A	103	LYS	-	expression tag	UNP P01593
A	104	LEU	-	expression tag	UNP P01593
A	105	GLN	-	expression tag	UNP P01593
A	106	ILE	-	expression tag	UNP P01593
A	107	THR	-	expression tag	UNP P01593
A	108	ARG	-	expression tag	UNP P01593
B	0	ALA	CYS	see sequence details	UNP P01593
B	30	ILE	SER	see sequence details	UNP P01593
B	31	LYS	ASN	see sequence details	UNP P01593
B	39	THR	LYS	see sequence details	UNP P01593
B	50	GLU	ASP	see sequence details	UNP P01593
B	55	GLN	GLU	see sequence details	UNP P01593
B	56	ALA	THR	see sequence details	UNP P01593
B	71	TYR	PHE	see sequence details	UNP P01593
B	92	GLN	ASP	see sequence details	UNP P01593
B	93	SER	ASN	see sequence details	UNP P01593
B	96	LYS	-	expression tag	UNP P01593
B	97	THR	-	expression tag	UNP P01593
B	98	PHE	-	expression tag	UNP P01593
B	99	GLY	-	expression tag	UNP P01593
B	100	GLN	-	expression tag	UNP P01593
B	101	GLY	-	expression tag	UNP P01593
B	102	THR	-	expression tag	UNP P01593
B	103	LYS	-	expression tag	UNP P01593
B	104	LEU	-	expression tag	UNP P01593
B	105	GLN	-	expression tag	UNP P01593
B	106	ILE	-	expression tag	UNP P01593
B	107	THR	-	expression tag	UNP P01593
B	108	ARG	-	expression tag	UNP P01593
C	0	ALA	CYS	see sequence details	UNP P01593
C	30	ILE	SER	see sequence details	UNP P01593
C	31	LYS	ASN	see sequence details	UNP P01593
C	39	THR	LYS	see sequence details	UNP P01593
C	50	GLU	ASP	see sequence details	UNP P01593
C	55	GLN	GLU	see sequence details	UNP P01593
C	56	ALA	THR	see sequence details	UNP P01593
C	71	TYR	PHE	see sequence details	UNP P01593
C	92	GLN	ASP	see sequence details	UNP P01593

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Chain	Residue	Modelled	Actual	Comment	Reference
C	93	SER	ASN	see sequence details	UNP P01593
C	96	LYS	-	expression tag	UNP P01593
C	97	THR	-	expression tag	UNP P01593
C	98	PHE	-	expression tag	UNP P01593
C	99	GLY	-	expression tag	UNP P01593
C	100	GLN	-	expression tag	UNP P01593
C	101	GLY	-	expression tag	UNP P01593
C	102	THR	-	expression tag	UNP P01593
C	103	LYS	-	expression tag	UNP P01593
C	104	LEU	-	expression tag	UNP P01593
C	105	GLN	-	expression tag	UNP P01593
C	106	ILE	-	expression tag	UNP P01593
C	107	THR	-	expression tag	UNP P01593
C	108	ARG	-	expression tag	UNP P01593
D	0	ALA	CYS	see sequence details	UNP P01593
D	30	ILE	SER	see sequence details	UNP P01593
D	31	LYS	ASN	see sequence details	UNP P01593
D	39	THR	LYS	see sequence details	UNP P01593
D	50	GLU	ASP	see sequence details	UNP P01593
D	55	GLN	GLU	see sequence details	UNP P01593
D	56	ALA	THR	see sequence details	UNP P01593
D	71	TYR	PHE	see sequence details	UNP P01593
D	92	GLN	ASP	see sequence details	UNP P01593
D	93	SER	ASN	see sequence details	UNP P01593
D	96	LYS	-	expression tag	UNP P01593
D	97	THR	-	expression tag	UNP P01593
D	98	PHE	-	expression tag	UNP P01593
D	99	GLY	-	expression tag	UNP P01593
D	100	GLN	-	expression tag	UNP P01593
D	101	GLY	-	expression tag	UNP P01593
D	102	THR	-	expression tag	UNP P01593
D	103	LYS	-	expression tag	UNP P01593
D	104	LEU	-	expression tag	UNP P01593
D	105	GLN	-	expression tag	UNP P01593
D	106	ILE	-	expression tag	UNP P01593
D	107	THR	-	expression tag	UNP P01593
D	108	ARG	-	expression tag	UNP P01593
E	0	ALA	CYS	see sequence details	UNP P01593
E	30	ILE	SER	see sequence details	UNP P01593
E	31	LYS	ASN	see sequence details	UNP P01593
E	39	THR	LYS	see sequence details	UNP P01593
E	50	GLU	ASP	see sequence details	UNP P01593

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Chain	Residue	Modelled	Actual	Comment	Reference
E	55	GLN	GLU	see sequence details	UNP P01593
E	56	ALA	THR	see sequence details	UNP P01593
E	71	TYR	PHE	see sequence details	UNP P01593
E	92	GLN	ASP	see sequence details	UNP P01593
E	93	SER	ASN	see sequence details	UNP P01593
E	96	LYS	-	expression tag	UNP P01593
E	97	THR	-	expression tag	UNP P01593
E	98	PHE	-	expression tag	UNP P01593
E	99	GLY	-	expression tag	UNP P01593
E	100	GLN	-	expression tag	UNP P01593
E	101	GLY	-	expression tag	UNP P01593
E	102	THR	-	expression tag	UNP P01593
E	103	LYS	-	expression tag	UNP P01593
E	104	LEU	-	expression tag	UNP P01593
E	105	GLN	-	expression tag	UNP P01593
E	106	ILE	-	expression tag	UNP P01593
E	107	THR	-	expression tag	UNP P01593
E	108	ARG	-	expression tag	UNP P01593
F	0	ALA	CYS	see sequence details	UNP P01593
F	30	ILE	SER	see sequence details	UNP P01593
F	31	LYS	ASN	see sequence details	UNP P01593
F	39	THR	LYS	see sequence details	UNP P01593
F	50	GLU	ASP	see sequence details	UNP P01593
F	55	GLN	GLU	see sequence details	UNP P01593
F	56	ALA	THR	see sequence details	UNP P01593
F	71	TYR	PHE	see sequence details	UNP P01593
F	92	GLN	ASP	see sequence details	UNP P01593
F	93	SER	ASN	see sequence details	UNP P01593
F	96	LYS	-	expression tag	UNP P01593
F	97	THR	-	expression tag	UNP P01593
F	98	PHE	-	expression tag	UNP P01593
F	99	GLY	-	expression tag	UNP P01593
F	100	GLN	-	expression tag	UNP P01593
F	101	GLY	-	expression tag	UNP P01593
F	102	THR	-	expression tag	UNP P01593
F	103	LYS	-	expression tag	UNP P01593
F	104	LEU	-	expression tag	UNP P01593
F	105	GLN	-	expression tag	UNP P01593
F	106	ILE	-	expression tag	UNP P01593
F	107	THR	-	expression tag	UNP P01593
F	108	ARG	-	expression tag	UNP P01593
G	0	ALA	CYS	see sequence details	UNP P01593

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Chain	Residue	Modelled	Actual	Comment	Reference
G	30	ILE	SER	see sequence details	UNP P01593
G	31	LYS	ASN	see sequence details	UNP P01593
G	39	THR	LYS	see sequence details	UNP P01593
G	50	GLU	ASP	see sequence details	UNP P01593
G	55	GLN	GLU	see sequence details	UNP P01593
G	56	ALA	THR	see sequence details	UNP P01593
G	71	TYR	PHE	see sequence details	UNP P01593
G	92	GLN	ASP	see sequence details	UNP P01593
G	93	SER	ASN	see sequence details	UNP P01593
G	96	LYS	-	expression tag	UNP P01593
G	97	THR	-	expression tag	UNP P01593
G	98	PHE	-	expression tag	UNP P01593
G	99	GLY	-	expression tag	UNP P01593
G	100	GLN	-	expression tag	UNP P01593
G	101	GLY	-	expression tag	UNP P01593
G	102	THR	-	expression tag	UNP P01593
G	103	LYS	-	expression tag	UNP P01593
G	104	LEU	-	expression tag	UNP P01593
G	105	GLN	-	expression tag	UNP P01593
G	106	ILE	-	expression tag	UNP P01593
G	107	THR	-	expression tag	UNP P01593
G	108	ARG	-	expression tag	UNP P01593
H	0	ALA	CYS	see sequence details	UNP P01593
H	30	ILE	SER	see sequence details	UNP P01593
H	31	LYS	ASN	see sequence details	UNP P01593
H	39	THR	LYS	see sequence details	UNP P01593
H	50	GLU	ASP	see sequence details	UNP P01593
H	55	GLN	GLU	see sequence details	UNP P01593
H	56	ALA	THR	see sequence details	UNP P01593
H	71	TYR	PHE	see sequence details	UNP P01593
H	92	GLN	ASP	see sequence details	UNP P01593
H	93	SER	ASN	see sequence details	UNP P01593
H	96	LYS	-	expression tag	UNP P01593
H	97	THR	-	expression tag	UNP P01593
H	98	PHE	-	expression tag	UNP P01593
H	99	GLY	-	expression tag	UNP P01593
H	100	GLN	-	expression tag	UNP P01593
H	101	GLY	-	expression tag	UNP P01593
H	102	THR	-	expression tag	UNP P01593
H	103	LYS	-	expression tag	UNP P01593
H	104	LEU	-	expression tag	UNP P01593
H	105	GLN	-	expression tag	UNP P01593

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Chain	Residue	Modelled	Actual	Comment	Reference
H	106	ILE	-	expression tag	UNP P01593
H	107	THR	-	expression tag	UNP P01593
H	108	ARG	-	expression tag	UNP P01593

- Molecule 2 is water.

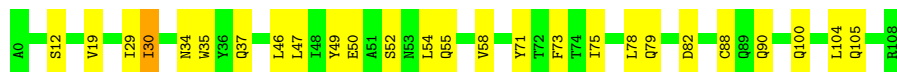
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	6	Total O 6 6	0	0
2	B	2	Total O 2 2	0	0
2	C	2	Total O 2 2	0	0
2	E	1	Total O 1 1	0	0
2	F	1	Total O 1 1	0	0

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: Immunoglobulin kappa variable 1D-33

Chain A:  76% 23% .



- Molecule 1: Immunoglobulin kappa variable 1D-33

Chain B:  73% 25% .



- Molecule 1: Immunoglobulin kappa variable 1D-33

Chain C:  87% 12% .



- Molecule 1: Immunoglobulin kappa variable 1D-33

Chain D:  75% 24% .



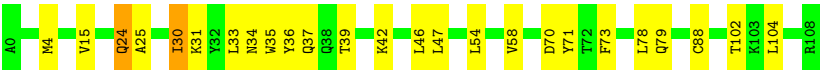
- Molecule 1: Immunoglobulin kappa variable 1D-33

Chain E:  74% 25% .



- Molecule 1: Immunoglobulin kappa variable 1D-33

Chain F:  77% 21% .

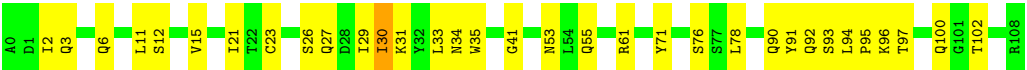


• Molecule 1: Immunoglobulin kappa variable 1D-33



THR
ARG

• Molecule 1: Immunoglobulin kappa variable 1D-33



4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	130.76Å 130.76Å 92.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.96 – 2.88 17.96 – 2.88	Depositor EDS
% Data completeness (in resolution range)	99.9 (17.96-2.88) 99.9 (17.96-2.88)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.02 (at 2.87Å)	Xtriage
Refinement program	PHENIX (1.11 _ 2567: ???)	Depositor
R, R_{free}	0.257 , 0.297 0.258 , 0.300	Depositor DCC
R_{free} test set	1763 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	67.8	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 24.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.488 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6669	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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](#)

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	0.14	0/851	0.39	0/1156
1	B	0.17	0/851	0.51	1/1156 (0.1%)
1	C	0.14	0/857	0.41	0/1163
1	D	0.14	0/857	0.39	0/1163
1	E	0.12	0/851	0.37	0/1156
1	F	0.20	0/857	0.49	1/1163 (0.1%)
1	G	0.35	0/823	0.73	1/1119 (0.1%)
1	H	0.25	0/842	0.62	0/1143
All	All	0.20	0/6789	0.50	3/9219 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	24	GLN	CA-CB-CG	-9.61	94.87	114.10
1	B	103	LYS	CB-CG-CD	8.49	130.84	111.30
1	F	24	GLN	CA-CB-CG	5.34	124.79	114.10

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	834	0	811	20	0
1	B	834	0	811	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	840	0	822	7	0
1	D	840	0	822	19	0
1	E	834	0	811	18	0
1	F	840	0	822	17	0
1	G	808	0	788	45	0
1	H	827	0	808	34	0
2	A	6	0	0	1	0
2	B	2	0	0	1	0
2	C	2	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
All	All	6669	0	6495	174	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 13.

All (174) 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:89:GLN:OE1	1:G:90:GLN:O	1.80	1.00
1:G:80:PRO:O	1:G:83:ILE:CD1	2.12	0.97
1:G:80:PRO:O	1:G:83:ILE:HD12	1.69	0.93
1:G:24:GLN:HG3	1:G:25:ALA:N	1.92	0.85
1:H:2:ILE:HG23	1:H:27:GLN:HE21	1.38	0.85
1:G:94:LEU:HD22	1:G:95:PRO:HA	1.58	0.84
1:G:89:GLN:OE1	1:G:90:GLN:C	2.22	0.83
1:G:6:GLN:OE1	1:G:102:THR:OG1	1.98	0.81
1:F:24:GLN:NE2	1:F:70:ASP:OD1	2.14	0.81
1:G:30:ILE:O	1:G:71:TYR:OH	1.99	0.81
1:E:78:LEU:HD11	1:E:104:LEU:HD21	1.65	0.78
1:C:83:ILE:HD11	1:C:106:ILE:HG12	1.65	0.78
1:G:30:ILE:HG13	1:G:31:LYS:H	1.50	0.77
1:G:90:GLN:HE21	1:G:97:THR:HG22	1.50	0.76
1:B:85:THR:OG1	1:B:103:LYS:HG3	1.88	0.74
1:H:90:GLN:OE1	1:H:92:GLN:HB3	1.89	0.73
1:H:21:ILE:HD11	1:H:35:TRP:HZ3	1.54	0.72
1:G:90:GLN:O	1:G:90:GLN:HG3	1.88	0.72
1:F:30:ILE:O	1:F:71:TYR:OH	2.08	0.71
1:E:30:ILE:O	1:E:71:TYR:OH	2.09	0.71
1:D:6:GLN:HB2	1:D:23:CYS:SG	2.31	0.71
1:B:55:GLN:HA	1:G:55:GLN:HE22	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:11:LEU:HD11	1:E:19:VAL:HG23	1.75	0.69
1:F:78:LEU:HD11	1:F:104:LEU:HD21	1.73	0.69
1:D:19:VAL:HG11	1:D:104:LEU:HD21	1.77	0.67
1:G:90:GLN:HG2	1:G:97:THR:HG22	1.77	0.66
1:C:30:ILE:O	1:C:71:TYR:OH	2.08	0.66
1:H:30:ILE:O	1:H:71:TYR:OH	2.13	0.66
1:H:90:GLN:OE1	1:H:92:GLN:N	2.29	0.66
1:E:34:ASN:HB3	1:E:46:LEU:HD21	1.79	0.64
1:H:30:ILE:HG23	1:H:31:LYS:H	1.61	0.64
1:A:30:ILE:O	1:A:71:TYR:OH	2.14	0.64
1:B:37:GLN:NE2	2:B:201:HOH:O	2.07	0.63
1:C:6:GLN:HB2	1:C:23:CYS:SG	2.41	0.60
1:E:8:PRO:O	1:E:102:THR:HG22	2.00	0.60
1:G:36:TYR:CZ	1:G:46:LEU:HB2	2.37	0.60
1:A:78:LEU:HD11	1:A:104:LEU:HD21	1.85	0.59
1:G:41:GLY:HA3	1:H:41:GLY:HA3	1.83	0.59
1:D:34:ASN:HD22	1:D:89:GLN:NE2	1.99	0.59
1:H:33:LEU:HD23	1:H:34:ASN:N	2.17	0.59
1:A:55:GLN:HA	1:H:55:GLN:HE22	1.68	0.58
1:D:34:ASN:HD22	1:D:89:GLN:HE21	1.52	0.57
1:H:21:ILE:HD11	1:H:35:TRP:CZ3	2.38	0.57
1:A:37:GLN:NE2	2:A:201:HOH:O	2.37	0.57
1:H:26:SER:OG	1:H:27:GLN:OE1	2.15	0.57
1:C:69:THR:HG23	1:C:70:ASP:OD1	2.06	0.56
1:G:25:ALA:HB1	1:G:27:GLN:OE1	2.06	0.56
1:G:30:ILE:HG13	1:G:31:LYS:N	2.21	0.55
1:E:83:ILE:HD11	1:E:106:ILE:HG23	1.89	0.55
1:H:90:GLN:O	1:H:96:LYS:HB3	2.07	0.55
1:G:33:LEU:HD23	1:G:34:ASN:N	2.22	0.54
1:G:29:ILE:N	1:G:29:ILE:HD12	2.23	0.54
1:A:29:ILE:HG21	1:A:90:GLN:HG3	1.90	0.53
1:G:20:THR:HG22	1:G:74:THR:HG23	1.90	0.53
1:G:27:GLN:OE1	1:G:27:GLN:N	2.42	0.52
1:H:90:GLN:OE1	1:H:93:SER:N	2.39	0.52
1:G:25:ALA:CB	1:G:29:ILE:HD11	2.38	0.52
1:G:2:ILE:HB	1:G:90:GLN:NE2	2.25	0.52
1:D:82:ASP:O	1:D:86:TYR:OH	2.22	0.52
1:D:33:LEU:HD11	1:D:88:CYS:HB2	1.92	0.52
1:F:36:TYR:CZ	1:F:46:LEU:HD23	2.45	0.52
1:G:80:PRO:O	1:G:83:ILE:HD13	2.06	0.51
1:G:34:ASN:HB3	1:G:46:LEU:HD13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:4:MET:HE1	1:F:25:ALA:HB2	1.91	0.51
1:B:11:LEU:HD11	1:B:104:LEU:HD13	1.93	0.50
1:G:2:ILE:HA	1:G:27:GLN:NE2	2.26	0.50
1:H:94:LEU:HD12	1:H:95:PRO:HA	1.92	0.50
1:D:83:ILE:HD12	1:D:83:ILE:O	2.12	0.50
1:F:39:THR:HG23	1:F:42:LYS:HB2	1.94	0.50
1:E:37:GLN:HB2	1:E:47:LEU:HD11	1.94	0.50
1:H:29:ILE:HG21	1:H:90:GLN:HG2	1.94	0.50
1:H:90:GLN:OE1	1:H:92:GLN:CB	2.59	0.49
1:F:15:VAL:HG13	1:F:79:GLN:HA	1.95	0.49
1:C:50:GLU:HG2	1:C:91:TYR:OH	2.12	0.49
1:H:2:ILE:HG23	1:H:27:GLN:NE2	2.17	0.49
1:H:29:ILE:HG22	1:H:29:ILE:O	2.12	0.49
1:D:30:ILE:O	1:D:71:TYR:OH	2.17	0.49
1:B:35:TRP:CE2	1:B:73:PHE:HB2	2.48	0.49
1:G:4:MET:HE3	1:G:90:GLN:HB3	1.95	0.49
1:E:36:TYR:CZ	1:E:46:LEU:HD23	2.48	0.49
1:H:6:GLN:HB2	1:H:23:CYS:SG	2.52	0.48
1:H:2:ILE:O	1:H:97:THR:HG21	2.13	0.48
1:G:89:GLN:CD	1:G:96:LYS:HE2	2.39	0.48
1:A:35:TRP:CD2	1:A:73:PHE:HB2	2.49	0.48
1:A:35:TRP:CE2	1:A:73:PHE:HB2	2.49	0.48
1:C:89:GLN:NE2	1:C:96:LYS:HD2	2.29	0.48
1:G:35:TRP:O	1:G:46:LEU:HD12	2.14	0.48
1:F:33:LEU:HD21	1:F:88:CYS:HB2	1.96	0.47
1:D:36:TYR:CZ	1:D:46:LEU:HD23	2.49	0.47
1:A:35:TRP:CZ3	1:A:88:CYS:HB3	2.49	0.47
1:G:90:GLN:NE2	1:G:95:PRO:O	2.48	0.47
1:A:37:GLN:HB3	1:A:47:LEU:HD11	1.97	0.47
1:G:3:GLN:O	1:G:25:ALA:HA	2.13	0.47
1:H:90:GLN:OE1	1:H:92:GLN:CA	2.62	0.47
1:G:2:ILE:HB	1:G:90:GLN:HE22	1.80	0.47
1:D:68:GLY:O	1:D:71:TYR:OH	2.32	0.47
1:H:15:VAL:HA	1:H:78:LEU:HD11	1.96	0.47
1:C:36:TYR:CZ	1:C:46:LEU:HD23	2.50	0.47
1:B:35:TRP:CZ3	1:B:88:CYS:HB3	2.50	0.46
1:F:54:LEU:HD11	1:F:58:VAL:HB	1.97	0.46
1:B:30:ILE:O	1:B:71:TYR:OH	2.28	0.46
1:G:4:MET:SD	1:G:25:ALA:HB2	2.56	0.46
1:D:49:TYR:O	1:D:53:ASN:HB2	2.16	0.46
1:F:35:TRP:CE2	1:F:73:PHE:HB2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:61:ARG:NH1	1:E:82:ASP:OD2	2.44	0.46
1:B:30:ILE:HD12	1:B:92:GLN:HG3	1.97	0.45
1:G:90:GLN:NE2	1:G:97:THR:HG22	2.25	0.45
1:F:35:TRP:CZ3	1:F:88:CYS:HB3	2.51	0.45
1:A:34:ASN:HB3	1:A:46:LEU:HD21	1.98	0.45
1:H:33:LEU:HD13	1:H:71:TYR:CG	2.52	0.45
1:D:29:ILE:HD11	1:D:71:TYR:HE2	1.81	0.45
1:B:35:TRP:CD2	1:B:73:PHE:HB2	2.52	0.45
1:D:35:TRP:CE2	1:D:73:PHE:HB2	2.51	0.45
1:H:26:SER:HG	1:H:27:GLN:CD	2.16	0.45
1:F:35:TRP:CD2	1:F:73:PHE:HB2	2.52	0.45
1:A:19:VAL:CG1	1:A:75:ILE:HB	2.47	0.44
1:A:54:LEU:H	1:H:53:ASN:HB3	1.81	0.44
1:G:90:GLN:HG2	1:G:97:THR:H	1.82	0.44
1:A:54:LEU:N	1:H:53:ASN:HB3	2.32	0.44
1:F:30:ILE:HG22	1:F:31:LYS:N	2.32	0.44
1:B:35:TRP:HB2	1:B:48:ILE:HB	1.99	0.44
1:H:3:GLN:HA	1:H:97:THR:HG21	1.99	0.44
1:H:61:ARG:HB2	1:H:76:SER:OG	2.18	0.44
1:H:11:LEU:HD23	1:H:12:SER:N	2.32	0.44
1:A:79:GLN:N	1:A:82:ASP:OD1	2.37	0.44
1:B:56:ALA:HA	1:G:49:TYR:CE2	2.53	0.44
1:E:80:PRO:O	1:E:83:ILE:HG12	2.18	0.44
1:H:6:GLN:N	1:H:100:GLN:OE1	2.33	0.44
1:E:30:ILE:HG22	1:E:31:LYS:N	2.33	0.43
1:G:47:LEU:HA	1:G:58:VAL:HG21	2.01	0.43
1:B:86:TYR:CE2	1:B:104:LEU:HD23	2.53	0.43
1:F:34:ASN:HB3	1:F:46:LEU:HD21	2.01	0.43
1:H:91:TYR:CB	1:H:96:LYS:HD2	2.48	0.43
1:E:12:SER:HA	1:E:105:GLN:O	2.19	0.43
1:A:55:GLN:O	1:A:58:VAL:HG22	2.19	0.43
1:G:36:TYR:CE2	1:G:46:LEU:HB2	2.53	0.43
1:G:4:MET:HE1	1:G:29:ILE:HG12	2.01	0.43
1:D:62:PHE:HD2	1:D:73:PHE:CZ	2.36	0.43
1:D:89:GLN:HB2	1:D:98:PHE:CD1	2.54	0.43
1:E:29:ILE:HA	1:E:92:GLN:HG3	2.01	0.43
1:H:6:GLN:NE2	1:H:102:THR:OG1	2.51	0.43
1:A:50:GLU:O	1:A:52:SER:N	2.47	0.42
1:F:36:TYR:CE1	1:F:46:LEU:HD23	2.53	0.42
1:A:12:SER:HA	1:A:105:GLN:O	2.19	0.42
1:B:68:GLY:O	1:B:71:TYR:OH	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:GLN:O	1:B:58:VAL:HG22	2.20	0.42
1:G:26:SER:N	1:G:27:GLN:OE1	2.52	0.42
1:H:27:GLN:HG2	1:H:29:ILE:HD11	2.01	0.42
1:G:32:TYR:HD1	1:G:91:TYR:CE2	2.37	0.42
1:G:2:ILE:HA	1:G:27:GLN:HE22	1.85	0.42
1:B:53:ASN:HB3	1:G:54:LEU:H	1.85	0.41
1:B:12:SER:HA	1:B:105:GLN:O	2.20	0.41
1:B:90:GLN:HE21	1:B:97:THR:H	1.68	0.41
1:D:33:LEU:HD22	1:D:71:TYR:CD2	2.55	0.41
1:D:35:TRP:CD2	1:D:73:PHE:HB2	2.55	0.41
1:B:9:SER:O	1:B:102:THR:HA	2.20	0.41
1:A:46:LEU:HD13	1:A:55:GLN:HG3	2.02	0.41
1:B:12:SER:HB3	1:B:107:THR:HG22	2.03	0.41
1:B:78:LEU:CD1	1:B:104:LEU:HD21	2.50	0.41
1:F:102:THR:O	1:F:102:THR:OG1	2.38	0.41
1:D:7:SER:HA	1:D:8:PRO:HA	1.94	0.41
1:F:37:GLN:HB2	1:F:47:LEU:HD11	2.03	0.41
1:B:54:LEU:N	1:G:53:ASN:HB3	2.35	0.41
1:E:24:GLN:HG3	1:E:70:ASP:OD1	2.21	0.41
1:E:35:TRP:CE2	1:E:73:PHE:HB2	2.56	0.41
1:B:50:GLU:O	1:B:52:SER:N	2.47	0.41
1:D:50:GLU:HG2	1:D:91:TYR:OH	2.21	0.41
1:E:35:TRP:CD2	1:E:73:PHE:HB2	2.56	0.41
1:E:36:TYR:CE1	1:E:46:LEU:HD23	2.55	0.41
1:H:29:ILE:HD12	1:H:29:ILE:N	2.36	0.41
1:G:12:SER:CB	1:G:105:GLN:HG3	2.50	0.40
1:A:34:ASN:OD1	1:A:49:TYR:HA	2.22	0.40
1:A:90:GLN:HE21	1:A:90:GLN:HB3	1.72	0.40
1:E:35:TRP:CZ3	1:E:88:CYS:HB3	2.56	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	107/109 (98%)	101 (94%)	5 (5%)	1 (1%)	14	38
1	B	107/109 (98%)	102 (95%)	4 (4%)	1 (1%)	14	38
1	C	107/109 (98%)	96 (90%)	10 (9%)	1 (1%)	14	38
1	D	107/109 (98%)	99 (92%)	7 (6%)	1 (1%)	14	38
1	E	107/109 (98%)	103 (96%)	3 (3%)	1 (1%)	14	38
1	F	107/109 (98%)	103 (96%)	3 (3%)	1 (1%)	14	38
1	G	105/109 (96%)	94 (90%)	10 (10%)	1 (1%)	12	35
1	H	107/109 (98%)	98 (92%)	8 (8%)	1 (1%)	14	38
All	All	854/872 (98%)	796 (93%)	50 (6%)	8 (1%)	14	38

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	30	ILE
1	A	30	ILE
1	B	30	ILE
1	C	30	ILE
1	D	30	ILE
1	E	30	ILE
1	F	30	ILE
1	G	30	ILE

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	93/94 (99%)	92 (99%)	1 (1%)	65	86
1	B	93/94 (99%)	93 (100%)	0	100	100
1	C	94/94 (100%)	94 (100%)	0	100	100
1	D	94/94 (100%)	94 (100%)	0	100	100
1	E	93/94 (99%)	93 (100%)	0	100	100
1	F	94/94 (100%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	90/94 (96%)	90 (100%)	0	100	100
1	H	92/94 (98%)	92 (100%)	0	100	100
All	All	743/752 (99%)	742 (100%)	1 (0%)	88	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	B	79	GLN
1	D	6	GLN
1	D	79	GLN
1	D	89	GLN
1	D	100	GLN
1	D	105	GLN
1	E	79	GLN
1	E	89	GLN
1	F	24	GLN
1	F	55	GLN
1	F	79	GLN
1	G	53	ASN
1	G	55	GLN
1	G	90	GLN
1	H	3	GLN
1	H	6	GLN
1	H	37	GLN
1	H	55	GLN

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](#)

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	109/109 (100%)	-1.69	0 100 100	40, 54, 84, 109	0
1	B	109/109 (100%)	-1.71	0 100 100	39, 55, 85, 106	0
1	C	109/109 (100%)	-1.59	0 100 100	47, 68, 88, 108	0
1	D	109/109 (100%)	-1.61	0 100 100	48, 67, 90, 105	0
1	E	109/109 (100%)	-1.64	0 100 100	47, 62, 81, 96	0
1	F	109/109 (100%)	-1.68	0 100 100	46, 62, 82, 102	0
1	G	107/109 (98%)	-1.12	0 100 100	56, 99, 127, 137	0
1	H	109/109 (100%)	-1.15	0 100 100	54, 98, 128, 142	0
All	All	870/872 (99%)	-1.52	0 100 100	39, 67, 116, 142	0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.