



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 05:47 AM UTC

PDB ID : 7UIE / pdb_00007uie
Title : Crystal structure of HcE-JLE-G6
Authors : Jin, R.; Lam, K.
Deposited on : 2022-03-29
Resolution : 3.23 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
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

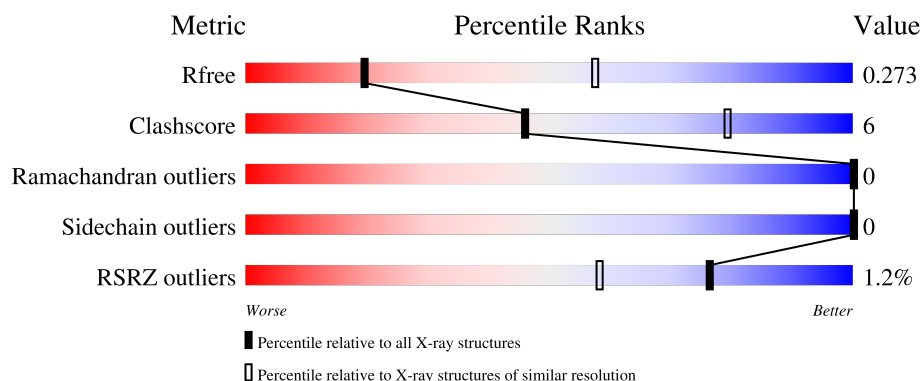
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.23 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	2153 (3.28-3.20)
Clashscore	190562	2275 (3.28-3.20)
Ramachandran outliers	187476	2233 (3.28-3.20)
Sidechain outliers	187428	2232 (3.28-3.20)
RSRZ outliers	180081	2153 (3.28-3.20)

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	B	138	9% 80% 12% 7%
1	C	138	78% 14% 8%
1	E	138	79% 14% 7%
1	G	138	80% 12% 9%
1	I	138	9% 75% 17% 8%

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Mol	Chain	Length	Quality of chain
2	A	423	81%15%•
2	D	423	83%12%•
2	F	423	81%14%•
2	H	423	81%14%5%
2	J	423	3% 81%15%•

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 21293 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 JLE-G6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	128	Total	C	N	O	S	0	0	0
			967	612	156	195	4			
1	C	127	Total	C	N	O	S	0	0	0
			970	614	156	196	4			
1	E	129	Total	C	N	O	S	0	0	0
			991	627	160	200	4			
1	I	127	Total	C	N	O	S	0	0	0
			961	607	155	195	4			
1	G	126	Total	C	N	O	S	0	0	0
			945	602	150	189	4			

- Molecule 2 is a protein called Botulinum neurotoxin E heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	406	Total	C	N	O	S	0	0	0
			3318	2097	571	641	9			
2	D	405	Total	C	N	O	S	0	1	0
			3312	2093	571	639	9			
2	F	405	Total	C	N	O	S	0	0	0
			3314	2094	571	640	9			
2	H	403	Total	C	N	O	S	0	0	0
			3283	2073	564	637	9			
2	J	404	Total	C	N	O	S	0	0	0
			3232	2048	551	624	9			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	830	HIS	-	expression tag	UNP A5H0J8
A	831	HIS	-	expression tag	UNP A5H0J8
A	832	HIS	-	expression tag	UNP A5H0J8
A	833	HIS	-	expression tag	UNP A5H0J8
A	834	HIS	-	expression tag	UNP A5H0J8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	835	HIS	-	expression tag	UNP A5H0J8
A	836	GLY	-	expression tag	UNP A5H0J8
A	837	SER	-	expression tag	UNP A5H0J8
A	838	LEU	-	expression tag	UNP A5H0J8
A	839	GLU	-	expression tag	UNP A5H0J8
A	840	VAL	-	expression tag	UNP A5H0J8
A	841	LEU	-	expression tag	UNP A5H0J8
A	842	PHE	-	expression tag	UNP A5H0J8
A	843	GLN	-	expression tag	UNP A5H0J8
A	844	GLY	-	expression tag	UNP A5H0J8
A	845	PRO	-	expression tag	UNP A5H0J8
D	830	HIS	-	expression tag	UNP A5H0J8
D	831	HIS	-	expression tag	UNP A5H0J8
D	832	HIS	-	expression tag	UNP A5H0J8
D	833	HIS	-	expression tag	UNP A5H0J8
D	834	HIS	-	expression tag	UNP A5H0J8
D	835	HIS	-	expression tag	UNP A5H0J8
D	836	GLY	-	expression tag	UNP A5H0J8
D	837	SER	-	expression tag	UNP A5H0J8
D	838	LEU	-	expression tag	UNP A5H0J8
D	839	GLU	-	expression tag	UNP A5H0J8
D	840	VAL	-	expression tag	UNP A5H0J8
D	841	LEU	-	expression tag	UNP A5H0J8
D	842	PHE	-	expression tag	UNP A5H0J8
D	843	GLN	-	expression tag	UNP A5H0J8
D	844	GLY	-	expression tag	UNP A5H0J8
D	845	PRO	-	expression tag	UNP A5H0J8
F	830	HIS	-	expression tag	UNP A5H0J8
F	831	HIS	-	expression tag	UNP A5H0J8
F	832	HIS	-	expression tag	UNP A5H0J8
F	833	HIS	-	expression tag	UNP A5H0J8
F	834	HIS	-	expression tag	UNP A5H0J8
F	835	HIS	-	expression tag	UNP A5H0J8
F	836	GLY	-	expression tag	UNP A5H0J8
F	837	SER	-	expression tag	UNP A5H0J8
F	838	LEU	-	expression tag	UNP A5H0J8
F	839	GLU	-	expression tag	UNP A5H0J8
F	840	VAL	-	expression tag	UNP A5H0J8
F	841	LEU	-	expression tag	UNP A5H0J8
F	842	PHE	-	expression tag	UNP A5H0J8
F	843	GLN	-	expression tag	UNP A5H0J8
F	844	GLY	-	expression tag	UNP A5H0J8

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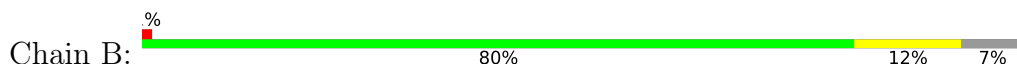
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Chain	Residue	Modelled	Actual	Comment	Reference
F	845	PRO	-	expression tag	UNP A5H0J8
H	830	HIS	-	expression tag	UNP A5H0J8
H	831	HIS	-	expression tag	UNP A5H0J8
H	832	HIS	-	expression tag	UNP A5H0J8
H	833	HIS	-	expression tag	UNP A5H0J8
H	834	HIS	-	expression tag	UNP A5H0J8
H	835	HIS	-	expression tag	UNP A5H0J8
H	836	GLY	-	expression tag	UNP A5H0J8
H	837	SER	-	expression tag	UNP A5H0J8
H	838	LEU	-	expression tag	UNP A5H0J8
H	839	GLU	-	expression tag	UNP A5H0J8
H	840	VAL	-	expression tag	UNP A5H0J8
H	841	LEU	-	expression tag	UNP A5H0J8
H	842	PHE	-	expression tag	UNP A5H0J8
H	843	GLN	-	expression tag	UNP A5H0J8
H	844	GLY	-	expression tag	UNP A5H0J8
H	845	PRO	-	expression tag	UNP A5H0J8
J	830	HIS	-	expression tag	UNP A5H0J8
J	831	HIS	-	expression tag	UNP A5H0J8
J	832	HIS	-	expression tag	UNP A5H0J8
J	833	HIS	-	expression tag	UNP A5H0J8
J	834	HIS	-	expression tag	UNP A5H0J8
J	835	HIS	-	expression tag	UNP A5H0J8
J	836	GLY	-	expression tag	UNP A5H0J8
J	837	SER	-	expression tag	UNP A5H0J8
J	838	LEU	-	expression tag	UNP A5H0J8
J	839	GLU	-	expression tag	UNP A5H0J8
J	840	VAL	-	expression tag	UNP A5H0J8
J	841	LEU	-	expression tag	UNP A5H0J8
J	842	PHE	-	expression tag	UNP A5H0J8
J	843	GLN	-	expression tag	UNP A5H0J8
J	844	GLY	-	expression tag	UNP A5H0J8
J	845	PRO	-	expression tag	UNP A5H0J8

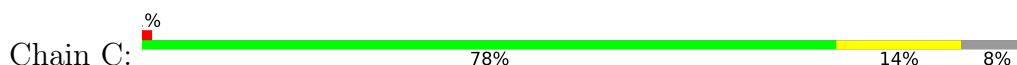
3 Residue-property plots [i](#)

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.

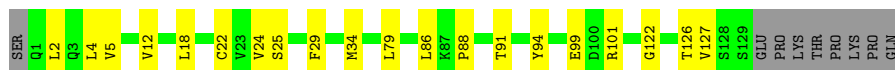
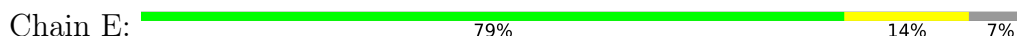
- Molecule 1: JLE-G6



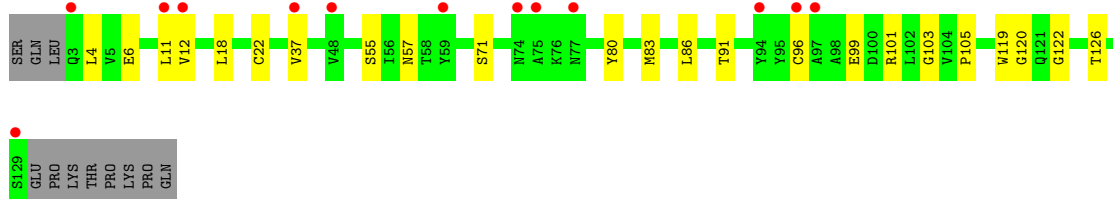
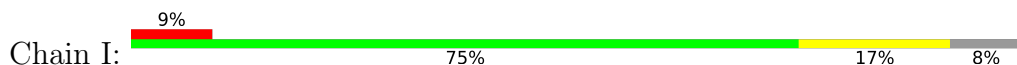
- Molecule 1: JLE-G6



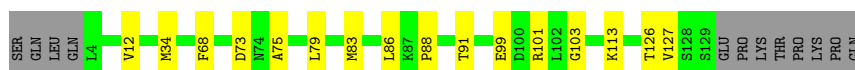
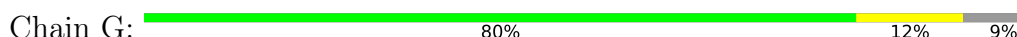
- Molecule 1: JLE-G6



- Molecule 1: JLE-G6



- Molecule 1: JLE-G6



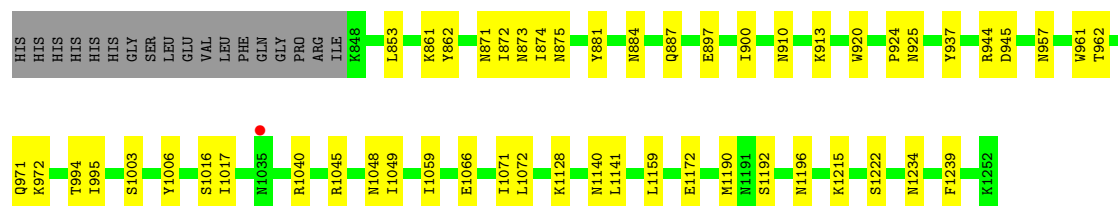
- Molecule 2: Botulinum neurotoxin E heavy chain

Chain A: 



- Molecule 2: Botulinum neurotoxin E heavy chain

Chain D: 



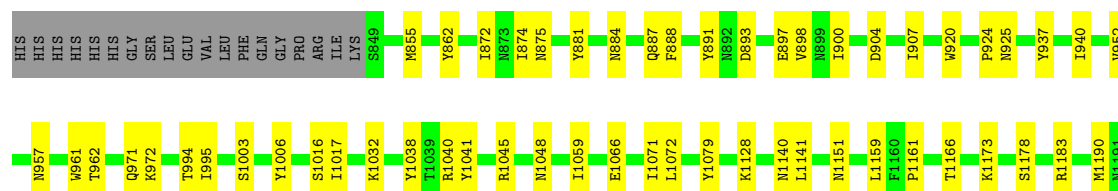
- Molecule 2: Botulinum neurotoxin E heavy chain

Chain F: 



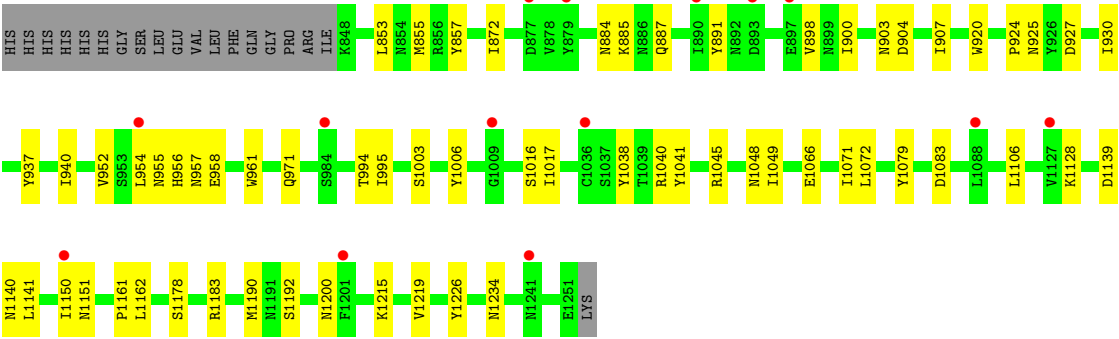
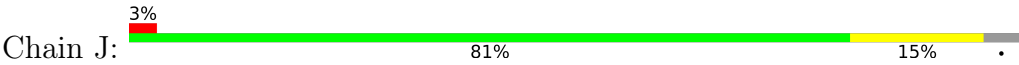
- Molecule 2: Botulinum neurotoxin E heavy chain

Chain H: 





● Molecule 2: Botulinum neurotoxin E heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	88.74Å 174.63Å 214.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	135.41 – 3.23 135.41 – 3.23	Depositor EDS
% Data completeness (in resolution range)	97.2 (135.41-3.23) 87.6 (135.41-3.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.74 (at 3.26Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.230 , 0.273 0.230 , 0.273	Depositor DCC
R_{free} test set	2618 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	65.7	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 55.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	21293	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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	B	0.09	0/992	0.29	0/1359
1	C	0.10	0/995	0.32	0/1361
1	E	0.19	0/1016	0.37	0/1389
1	G	0.10	0/970	0.30	0/1329
1	I	0.11	0/985	0.36	0/1348
2	A	0.09	0/3388	0.29	0/4598
2	D	0.08	0/3385	0.30	0/4594
2	F	0.08	0/3384	0.28	0/4591
2	H	0.08	0/3353	0.29	0/4557
2	J	0.09	0/3302	0.29	0/4497
All	All	0.10	0/21770	0.30	0/29623

There are no bond length outliers.

There are no bond angle outliers.

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	B	967	0	877	10	0
1	C	970	0	890	13	0
1	E	991	0	918	13	0
1	G	945	0	861	11	0
1	I	961	0	881	26	0
2	A	3318	0	3190	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3312	0	3183	33	0
2	F	3314	0	3190	36	0
2	H	3283	0	3131	37	0
2	J	3232	0	3039	43	0
All	All	21293	0	20160	241	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 6.

The worst 5 of 241 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:I:22:CYS:HB2	1:I:96:CYS:SG	2.06	0.95
1:I:22:CYS:CB	1:I:96:CYS:HG	1.87	0.85
1:I:22:CYS:CB	1:I:96:CYS:SG	2.69	0.80
2:F:924:PRO:O	2:F:1040:ARG:NH2	2.21	0.72
2:D:924:PRO:O	2:D:1040:ARG:NH2	2.22	0.72

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	B	126/138 (91%)	122 (97%)	4 (3%)	0	100	100
1	C	125/138 (91%)	121 (97%)	4 (3%)	0	100	100
1	E	127/138 (92%)	123 (97%)	4 (3%)	0	100	100
1	G	124/138 (90%)	120 (97%)	4 (3%)	0	100	100
1	I	125/138 (91%)	122 (98%)	3 (2%)	0	100	100
2	A	404/423 (96%)	382 (95%)	22 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	404/423 (96%)	383 (95%)	21 (5%)	0	100	100
2	F	403/423 (95%)	380 (94%)	23 (6%)	0	100	100
2	H	401/423 (95%)	379 (94%)	22 (6%)	0	100	100
2	J	402/423 (95%)	381 (95%)	21 (5%)	0	100	100
All	All	2641/2805 (94%)	2513 (95%)	128 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	B	101/120 (84%)	101 (100%)	0	100	100
1	C	103/120 (86%)	103 (100%)	0	100	100
1	E	106/120 (88%)	106 (100%)	0	100	100
1	G	98/120 (82%)	98 (100%)	0	100	100
1	I	101/120 (84%)	101 (100%)	0	100	100
2	A	373/392 (95%)	373 (100%)	0	100	100
2	D	372/392 (95%)	372 (100%)	0	100	100
2	F	373/392 (95%)	373 (100%)	0	100	100
2	H	368/392 (94%)	368 (100%)	0	100	100
2	J	353/392 (90%)	353 (100%)	0	100	100
All	All	2348/2560 (92%)	2348 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	902	GLN

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Mol	Chain	Res	Type
2	J	1158	HIS
2	F	935	ASN
2	J	1228	HIS
2	J	902	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	B	128/138 (92%)	0.15	1 (0%) 82 67	61, 96, 143, 191	0
1	C	127/138 (92%)	-0.01	1 (0%) 82 67	55, 78, 101, 125	0
1	E	129/138 (93%)	0.05	0 100 100	56, 81, 117, 145	0
1	G	126/138 (91%)	0.24	0 100 100	74, 119, 165, 191	0
1	I	127/138 (92%)	0.96	13 (10%) 12 8	118, 162, 201, 239	0
2	A	406/423 (95%)	-0.13	1 (0%) 91 85	42, 63, 96, 183	0
2	D	405/423 (95%)	-0.06	1 (0%) 91 85	48, 74, 111, 201	1 (0%)
2	F	405/423 (95%)	0.02	0 100 100	56, 81, 122, 197	0
2	H	403/423 (95%)	-0.03	0 100 100	50, 76, 119, 203	0
2	J	404/423 (95%)	0.60	14 (3%) 47 30	70, 126, 174, 241	0
All	All	2660/2805 (94%)	0.13	31 (1%) 76 58	42, 84, 162, 241	1 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	877	ASP	3.7
1	I	37	VAL	3.0
2	A	847	ILE	3.0
2	J	1241	ASN	2.9
1	I	96	CYS	2.9

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.