



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:23 AM UTC

PDB ID : 6GY7 / pdb_00006gy7
Title : Crystal structure of XaxB from Xenorhabdus nematophil
Authors : Schubert, E.; Raunser, S.; Vetter, I.R.; Prumbaum, D.; Penczek, P.A.
Deposited on : 2018-06-28
Resolution : 3.40 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

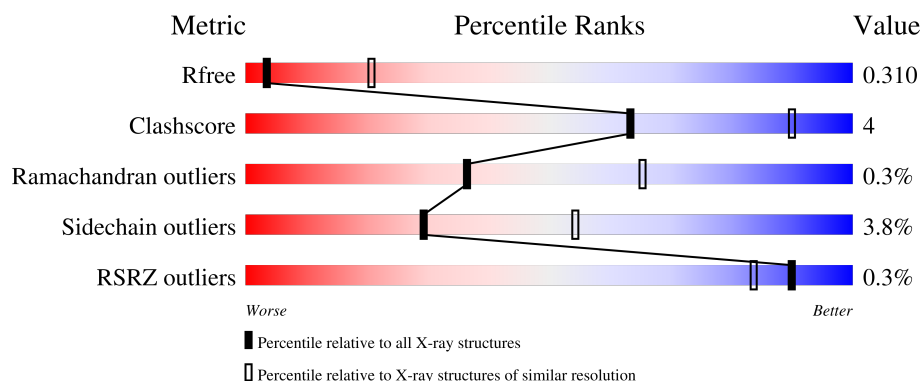
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	367	80% 11% • 8%
1	B	367	78% 13% • 8%
1	C	367	% 74% 11% • 14%
1	D	367	81% 10% • 8%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 21528 atoms, of which 10904 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 XaxB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	337	Total	C	H	N	O	S	0	0	0
			5451	1676	2761	466	541	7			
1	B	338	Total	C	H	N	O	S	0	0	0
			5472	1685	2770	467	543	7			
1	C	316	Total	C	H	N	O	S	0	0	0
			5134	1579	2604	440	504	7			
1	D	338	Total	C	H	N	O	S	0	0	0
			5471	1685	2769	467	543	7			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	HIS	-	expression tag	UNP D3VB23
A	-15	HIS	-	expression tag	UNP D3VB23
A	-14	HIS	-	expression tag	UNP D3VB23
A	-13	HIS	-	expression tag	UNP D3VB23
A	-12	HIS	-	expression tag	UNP D3VB23
A	-11	HIS	-	expression tag	UNP D3VB23
A	-10	SER	-	expression tag	UNP D3VB23
A	-9	SER	-	expression tag	UNP D3VB23
A	-8	GLY	-	expression tag	UNP D3VB23
A	-7	LEU	-	expression tag	UNP D3VB23
A	-6	GLU	-	expression tag	UNP D3VB23
A	-5	VAL	-	expression tag	UNP D3VB23
A	-4	LEU	-	expression tag	UNP D3VB23
A	-3	PHE	-	expression tag	UNP D3VB23
A	-2	GLN	-	expression tag	UNP D3VB23
A	-1	GLY	-	expression tag	UNP D3VB23
A	0	PRO	-	expression tag	UNP D3VB23
B	-16	HIS	-	expression tag	UNP D3VB23
B	-15	HIS	-	expression tag	UNP D3VB23
B	-14	HIS	-	expression tag	UNP D3VB23
B	-13	HIS	-	expression tag	UNP D3VB23

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP D3VB23
B	-11	HIS	-	expression tag	UNP D3VB23
B	-10	SER	-	expression tag	UNP D3VB23
B	-9	SER	-	expression tag	UNP D3VB23
B	-8	GLY	-	expression tag	UNP D3VB23
B	-7	LEU	-	expression tag	UNP D3VB23
B	-6	GLU	-	expression tag	UNP D3VB23
B	-5	VAL	-	expression tag	UNP D3VB23
B	-4	LEU	-	expression tag	UNP D3VB23
B	-3	PHE	-	expression tag	UNP D3VB23
B	-2	GLN	-	expression tag	UNP D3VB23
B	-1	GLY	-	expression tag	UNP D3VB23
B	0	PRO	-	expression tag	UNP D3VB23
C	-16	HIS	-	expression tag	UNP D3VB23
C	-15	HIS	-	expression tag	UNP D3VB23
C	-14	HIS	-	expression tag	UNP D3VB23
C	-13	HIS	-	expression tag	UNP D3VB23
C	-12	HIS	-	expression tag	UNP D3VB23
C	-11	HIS	-	expression tag	UNP D3VB23
C	-10	SER	-	expression tag	UNP D3VB23
C	-9	SER	-	expression tag	UNP D3VB23
C	-8	GLY	-	expression tag	UNP D3VB23
C	-7	LEU	-	expression tag	UNP D3VB23
C	-6	GLU	-	expression tag	UNP D3VB23
C	-5	VAL	-	expression tag	UNP D3VB23
C	-4	LEU	-	expression tag	UNP D3VB23
C	-3	PHE	-	expression tag	UNP D3VB23
C	-2	GLN	-	expression tag	UNP D3VB23
C	-1	GLY	-	expression tag	UNP D3VB23
C	0	PRO	-	expression tag	UNP D3VB23
D	-16	HIS	-	expression tag	UNP D3VB23
D	-15	HIS	-	expression tag	UNP D3VB23
D	-14	HIS	-	expression tag	UNP D3VB23
D	-13	HIS	-	expression tag	UNP D3VB23
D	-12	HIS	-	expression tag	UNP D3VB23
D	-11	HIS	-	expression tag	UNP D3VB23
D	-10	SER	-	expression tag	UNP D3VB23
D	-9	SER	-	expression tag	UNP D3VB23
D	-8	GLY	-	expression tag	UNP D3VB23
D	-7	LEU	-	expression tag	UNP D3VB23
D	-6	GLU	-	expression tag	UNP D3VB23
D	-5	VAL	-	expression tag	UNP D3VB23

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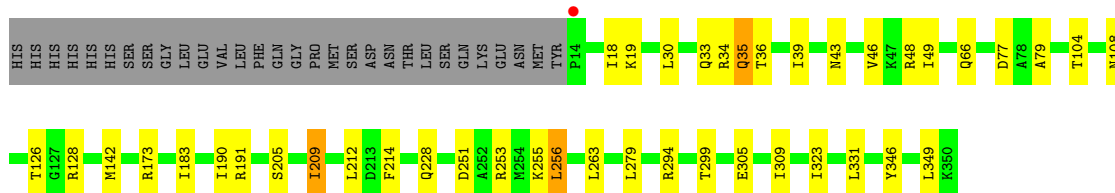
Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	LEU	-	expression tag	UNP D3VB23
D	-3	PHE	-	expression tag	UNP D3VB23
D	-2	GLN	-	expression tag	UNP D3VB23
D	-1	GLY	-	expression tag	UNP D3VB23
D	0	PRO	-	expression tag	UNP D3VB23

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.

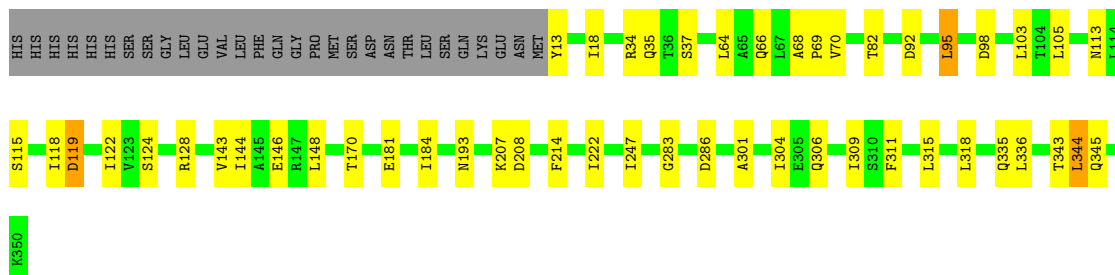
• Molecule 1: XaxB

Chain A: 



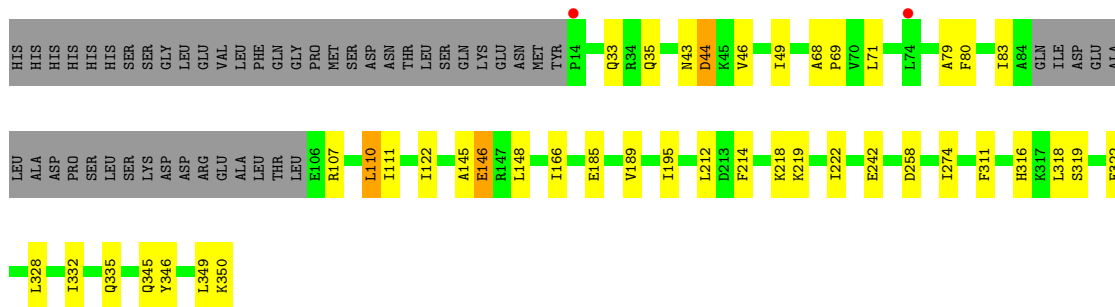
• Molecule 1: XaxB

Chain B: 



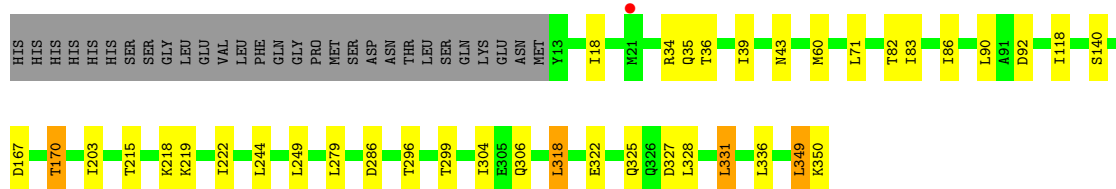
• Molecule 1: XaxB

Chain C: 



• Molecule 1: XaxB

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.70Å 99.41Å 194.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.54 – 3.40 48.54 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.54-3.40) 99.9 (48.54-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 3.40Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.264 , 0.304 0.267 , 0.310	Depositor DCC
R_{free} test set	1215 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	137.2	Xtriage
Anisotropy	0.356	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 91.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	21528	wwPDB-VP
Average B, all atoms (Å ²)	152.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% 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	0.17	0/2712	0.43	0/3651
1	B	0.19	0/2725	0.41	0/3670
1	C	0.19	0/2550	0.41	0/3429
1	D	0.18	0/2725	0.39	0/3670
All	All	0.18	0/10712	0.41	0/14420

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	A	2690	2761	2761	20	1
1	B	2702	2770	2769	26	0
1	C	2530	2604	2604	23	1
1	D	2702	2769	2769	20	0
All	All	10624	10904	10903	87	2

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 (87) 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:D:39:ILE:O	1:D:43:ASN:ND2	2.11	0.84
1:B:146:GLU:OE1	1:B:146:GLU:N	2.19	0.74
1:C:146:GLU:N	1:C:146:GLU:OE1	2.28	0.67
1:D:34:ARG:NH1	1:D:286:ASP:OD2	2.30	0.65
1:C:35:GLN:NE2	1:C:43:ASN:OD1	2.36	0.59
1:D:167:ASP:O	1:D:170:THR:OG1	2.21	0.59
1:B:34:ARG:NH1	1:B:286:ASP:OD2	2.36	0.58
1:D:39:ILE:H	1:D:39:ILE:HD12	1.70	0.57
1:A:305:GLU:OE1	1:D:306:GLN:NE2	2.36	0.56
1:C:80:PHE:HA	1:C:83:ILE:HG22	1.88	0.55
1:A:104:THR:O	1:A:108:ASN:ND2	2.40	0.54
1:C:44:ASP:C	1:C:44:ASP:OD1	2.50	0.54
1:A:251:ASP:O	1:A:255:LYS:HG2	2.07	0.54
1:C:145:ALA:HB3	1:C:148:LEU:HD13	1.90	0.53
1:B:207:LYS:NZ	1:B:208:ASP:OD1	2.42	0.53
1:A:36:THR:OG1	1:A:279:LEU:O	2.27	0.53
1:B:193:ASN:ND2	1:B:222:ILE:HD11	2.23	0.53
1:A:142:MET:O	1:A:294:ARG:NH1	2.36	0.52
1:A:183:ILE:HG21	1:A:253:ARG:HB2	1.91	0.51
1:B:34:ARG:O	1:B:34:ARG:CD	2.59	0.51
1:D:218:LYS:O	1:D:222:ILE:HG12	2.11	0.51
1:B:64:LEU:HD21	1:B:343:THR:OG1	2.12	0.50
1:D:349:LEU:O	1:D:350:LYS:C	2.54	0.50
1:A:77:ASP:OD1	1:A:79:ALA:N	2.44	0.50
1:B:315:LEU:HA	1:B:318:LEU:HD23	1.94	0.50
1:C:345:GLN:O	1:C:349:LEU:HG	2.12	0.49
1:A:48:ARG:HD3	1:A:142:MET:HE3	1.95	0.49
1:D:34:ARG:O	1:D:34:ARG:HG3	2.11	0.48
1:A:39:ILE:O	1:A:43:ASN:ND2	2.46	0.48
1:D:36:THR:HB	1:D:279:LEU:HG	1.94	0.48
1:D:35:GLN:O	1:D:35:GLN:HG3	2.11	0.48
1:A:46:VAL:HA	1:A:49:ILE:HG22	1.97	0.47
1:C:71:LEU:HD11	1:C:332:ILE:HG23	1.97	0.47
1:C:107:ARG:O	1:C:111:ILE:HG13	2.15	0.47
1:A:256:LEU:HD12	1:A:256:LEU:C	2.40	0.46
1:D:71:LEU:HB2	1:D:336:LEU:HD23	1.98	0.46
1:B:68:ALA:HB3	1:B:69:PRO:HD3	1.98	0.46
1:C:185:GLU:O	1:C:189:VAL:HG23	2.15	0.46
1:B:95:LEU:HA	1:B:98:ASP:OD1	2.16	0.46
1:B:301:ALA:O	1:B:304:ILE:HG13	2.16	0.46
1:B:306:GLN:O	1:B:309:ILE:HG13	2.16	0.45
1:C:318:LEU:O	1:C:322:GLU:N	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:ILE:HD12	1:D:244:LEU:HB3	1.98	0.45
1:A:49:ILE:HD11	1:A:294:ARG:HD3	1.97	0.45
1:B:344:LEU:HD12	1:B:344:LEU:C	2.41	0.45
1:A:205:SER:O	1:A:209:ILE:HG22	2.16	0.45
1:C:110:LEU:C	1:C:110:LEU:HD23	2.41	0.45
1:C:218:LYS:O	1:C:222:ILE:HG22	2.15	0.45
1:B:66:GLN:OE1	1:B:128:ARG:NE	2.50	0.45
1:C:349:LEU:O	1:C:350:LYS:C	2.59	0.45
1:C:189:VAL:HG12	1:C:222:ILE:HD13	1.99	0.45
1:D:82:THR:O	1:D:86:ILE:HG23	2.17	0.45
1:C:212:LEU:O	1:C:219:LYS:CE	2.65	0.44
1:D:215:THR:O	1:D:219:LYS:HG2	2.18	0.44
1:C:46:VAL:HA	1:C:49:ILE:HG22	2.00	0.44
1:C:68:ALA:HB3	1:C:69:PRO:HD3	2.00	0.43
1:B:336:LEU:O	1:B:336:LEU:HD23	2.18	0.43
1:B:34:ARG:O	1:B:34:ARG:HD2	2.18	0.43
1:D:318:LEU:O	1:D:322:GLU:N	2.40	0.43
1:D:60:MET:HE1	1:D:304:ILE:HG21	2.00	0.43
1:B:64:LEU:C	1:B:64:LEU:HD23	2.44	0.43
1:B:124:SER:O	1:B:128:ARG:HG2	2.17	0.43
1:D:296:THR:O	1:D:299:THR:OG1	2.30	0.43
1:A:35:GLN:O	1:A:35:GLN:NE2	2.52	0.42
1:A:66:GLN:HB3	1:A:128:ARG:NH2	2.33	0.42
1:C:166:ILE:HD12	1:C:274:ILE:HD12	2.02	0.42
1:B:66:GLN:O	1:B:70:VAL:HG23	2.19	0.42
1:B:311:PHE:CZ	1:B:335:GLN:HB2	2.55	0.42
1:A:19:LYS:HA	1:A:349:LEU:HD11	2.01	0.42
1:A:305:GLU:O	1:A:309:ILE:HG12	2.20	0.42
1:B:115:SER:HA	1:B:118:ILE:HG22	2.02	0.42
1:B:35:GLN:O	1:B:283:GLY:HA2	2.20	0.41
1:C:79:ALA:O	1:C:83:ILE:HG22	2.20	0.41
1:A:299:THR:HG21	1:D:140:SER:CB	2.51	0.41
1:B:247:ILE:HD12	1:B:247:ILE:H	1.86	0.41
1:C:311:PHE:CD2	1:C:335:GLN:HG3	2.54	0.41
1:B:119:ASP:O	1:B:122:ILE:HG22	2.20	0.41
1:A:30:LEU:O	1:A:34:ARG:HG2	2.20	0.41
1:B:122:ILE:HB	1:B:315:LEU:HD23	2.02	0.41
1:C:318:LEU:HB3	1:C:328:LEU:HD12	2.02	0.41
1:D:331:LEU:O	1:D:331:LEU:HD23	2.21	0.41
1:D:203:ILE:HD11	1:D:249:LEU:HD13	2.03	0.40
1:B:181:GLU:HA	1:B:184:ILE:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:316:HIS:O	1:C:319:SER:OG	2.31	0.40
1:B:18:ILE:CG2	1:B:345:GLN:HB3	2.52	0.40
1:C:35:GLN:CD	1:C:43:ASN:OD1	2.64	0.40
1:A:255:LYS:N	1:A:255:LYS:HD2	2.36	0.40

All (2) 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:C:33:GLN:NE2	1:C:258:ASP:OD2[4_556]	2.09	0.11
1:A:33:GLN:OE1	1:A:255:LYS:HZ3[4_456]	1.55	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	335/367 (91%)	328 (98%)	5 (2%)	2 (1%)	21	50
1	B	336/367 (92%)	324 (96%)	12 (4%)	0	100	100
1	C	312/367 (85%)	304 (97%)	6 (2%)	2 (1%)	21	50
1	D	336/367 (92%)	330 (98%)	6 (2%)	0	100	100
All	All	1319/1468 (90%)	1286 (98%)	29 (2%)	4 (0%)	36	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	PHE
1	C	214	PHE
1	A	323	ILE
1	C	242	GLU

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	305/333 (92%)	292 (96%)	13 (4%)	26	51
1	B	306/333 (92%)	291 (95%)	15 (5%)	22	49
1	C	287/333 (86%)	281 (98%)	6 (2%)	47	64
1	D	306/333 (92%)	294 (96%)	12 (4%)	28	53
All	All	1204/1332 (90%)	1158 (96%)	46 (4%)	29	54

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ILE
1	A	35	GLN
1	A	126	THR
1	A	173	ARG
1	A	190	ILE
1	A	191	ARG
1	A	209	ILE
1	A	212	LEU
1	A	228	GLN
1	A	256	LEU
1	A	263	LEU
1	A	331	LEU
1	A	346	TYR
1	B	13	TYR
1	B	37	SER
1	B	82	THR
1	B	92	ASP
1	B	95	LEU
1	B	103	LEU
1	B	105	LEU
1	B	113	ASN
1	B	119	ASP
1	B	143	VAL
1	B	144	ILE

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Mol	Chain	Res	Type
1	B	148	LEU
1	B	170	THR
1	B	214	PHE
1	B	344	LEU
1	C	44	ASP
1	C	110	LEU
1	C	122	ILE
1	C	146	GLU
1	C	195	ILE
1	C	346	TYR
1	D	18	ILE
1	D	83	ILE
1	D	90	LEU
1	D	92	ASP
1	D	118	ILE
1	D	170	THR
1	D	318	LEU
1	D	325	GLN
1	D	327	ASP
1	D	328	LEU
1	D	331	LEU
1	D	349	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	109	ASN
1	A	117	HIS
1	B	26	ASN
1	B	73	GLN
1	B	193	ASN
1	C	26	ASN
1	C	163	GLN
1	C	224	GLN
1	D	163	GLN
1	D	259	GLN

5.3.3 RNA ⓘ

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	337/367 (91%)	-0.31	1 (0%) 90 84	105, 148, 189, 211	0
1	B	338/367 (92%)	-0.30	0 100 100	108, 157, 213, 230	0
1	C	316/367 (86%)	-0.34	2 (0%) 85 75	115, 152, 193, 222	0
1	D	338/367 (92%)	-0.36	1 (0%) 90 84	95, 139, 190, 213	0
All	All	1329/1468 (90%)	-0.33	4 (0%) 90 84	95, 148, 197, 230	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	14	PRO	3.5
1	A	14	PRO	2.6
1	D	21	MET	2.3
1	C	74	LEU	2.2

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 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.