



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:34 PM UTC

PDB ID : 9PZI / pdb_00009pzi
Title : Crystal Structure of synthetic antibody COP-2 in complex with the C-terminal domain of Clostridium perfringens enterotoxin
Authors : Vecchio, A.J.; Ogbu, C.P.; Kapoor, S.
Deposited on : 2025-08-11
Resolution : 2.50 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

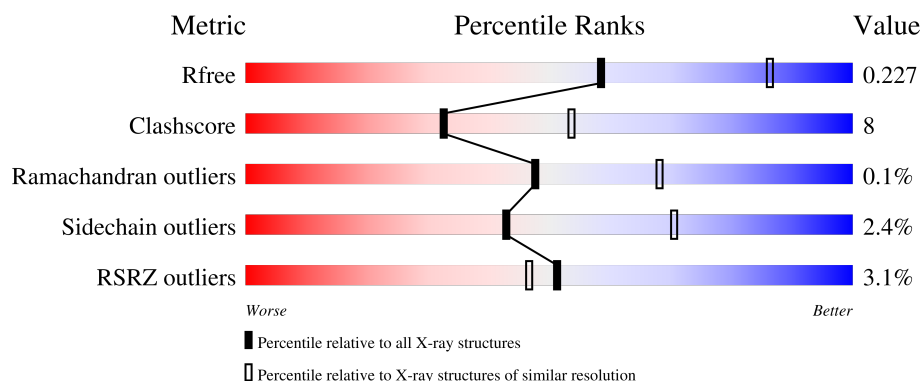
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	239	
1	C	239	
1	E	239	
2	B	260	
2	D	260	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	260	7% 73% 11% • 15%
3	G	134	% 82% 9% • 9%
3	H	134	2% 85% 8% • 6%
3	I	134	% 86% 6% • 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25529 atoms, of which 12397 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 COP-2 Light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	212	Total	C	H	N	O	S	0	0	0
			3210	1019	1583	273	330	5			
1	A	213	Total	C	H	N	O	S	0	0	0
			3220	1022	1588	274	331	5			
1	E	213	Total	C	H	N	O	S	0	0	0
			3220	1022	1588	274	331	5			

- Molecule 2 is a protein called COP-2 Heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	D	221	Total	C	H	N	O	S	0	0	0
			3257	1054	1595	274	329	5			
2	B	220	Total	C	H	N	O	S	0	0	0
			3246	1051	1590	273	327	5			
2	F	221	Total	C	H	N	O	S	0	0	0
			3209	1044	1561	272	327	5			

- Molecule 3 is a protein called Heat-labile enterotoxin B chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	G	122	Total	C	H	N	O	S	0	0	0
			1913	618	945	162	187	1			
3	I	123	Total	C	H	N	O	S	0	0	0
			1935	625	958	163	188	1			
3	H	126	Total	C	H	N	O	S	0	1	0
			1996	644	989	168	194	1			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	191	MET	-	initiating methionine	UNP P01558
G	320	GLY	-	expression tag	UNP P01558

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	321	LEU	-	expression tag	UNP P01558
G	322	VAL	-	expression tag	UNP P01558
G	323	PRO	-	expression tag	UNP P01558
G	324	ARG	-	expression tag	UNP P01558
I	191	MET	-	initiating methionine	UNP P01558
I	320	GLY	-	expression tag	UNP P01558
I	321	LEU	-	expression tag	UNP P01558
I	322	VAL	-	expression tag	UNP P01558
I	323	PRO	-	expression tag	UNP P01558
I	324	ARG	-	expression tag	UNP P01558
H	191	MET	-	initiating methionine	UNP P01558
H	320	GLY	-	expression tag	UNP P01558
H	321	LEU	-	expression tag	UNP P01558
H	322	VAL	-	expression tag	UNP P01558
H	323	PRO	-	expression tag	UNP P01558
H	324	ARG	-	expression tag	UNP P01558

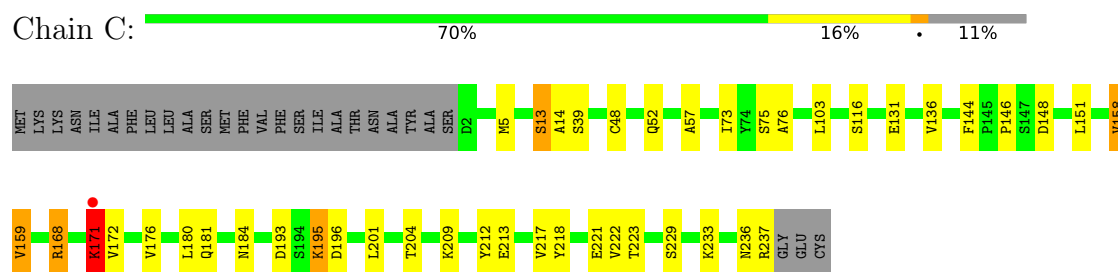
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	41	Total O 41 41	0	0
4	D	41	Total O 41 41	0	0
4	A	49	Total O 49 49	0	0
4	B	18	Total O 18 18	0	0
4	E	39	Total O 39 39	0	0
4	F	32	Total O 32 32	0	0
4	G	41	Total O 41 41	0	0
4	I	23	Total O 23 23	0	0
4	H	39	Total O 39 39	0	0

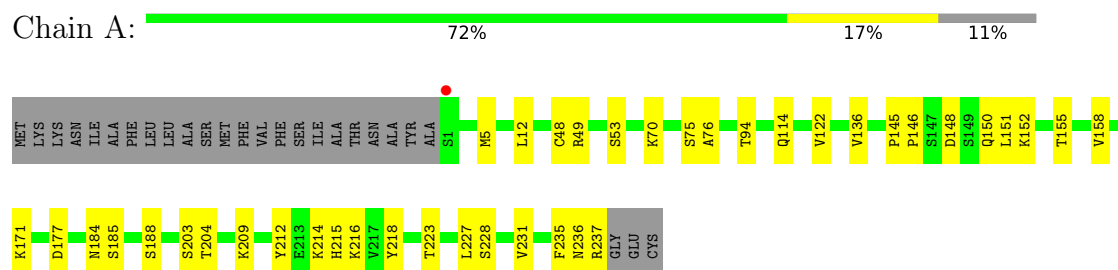
3 Residue-property plots [i](#)

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.

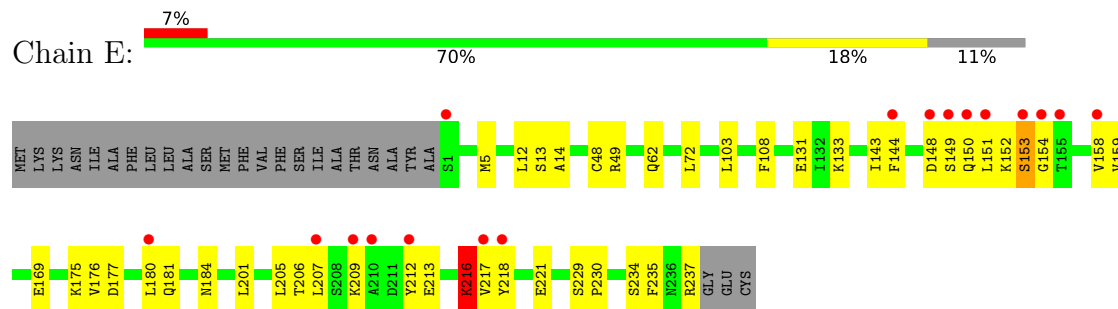
- Molecule 1: COP-2 Light chain



- Molecule 1: COP-2 Light chain



- Molecule 1: COP-2 Light chain



LYS
SER
CYS
ASP
LYS
THR
HIS
THR

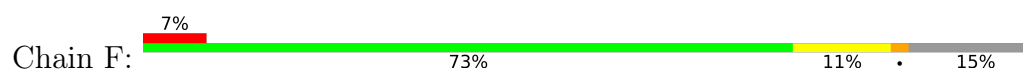
• Molecule 2: COP-2 Heavy chain



MET LYS LYS ASN ILE ALA PHE LEU LEU ALA SER MET SER PHE VAL PHE SER SER ILE ALA THR ASN ALA TYR ALA ALA GLU ILE SER E4 V5 Q6 L7 S10 L14 L46 S47 C48 S51 G68 K69 I77 T84 S97 M109 N110 S111 L112 R113 D116 Y141

V148 T149 S152 K156 G157 P158 S166 SER LYS SER THR SER GLY G173 K182 P188 L198 Q210 G213 L214 L217 V221 S226 Q231 T232 K240 P241 T244 K248 K249 P252 LYS SER CYS ASP LYS THR HIS THR

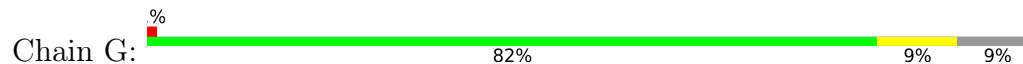
• Molecule 2: COP-2 Heavy chain



MET LYS LYS ASN ILE ALA PHE LEU LEU ALA SER MET SER PHE VAL PHE SER SER ILE ALA THR ASN ALA TYR ALA ALA GLU ILE SER E4 V5 Q6 V38 Q39 P40 S43 S51 M109 L112 V115 V148 S152 K156 S159 V160 F161 P162 L163 A164 P165 S166 S167 LYS

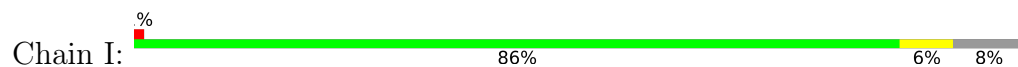
SER THR SER ASP GLY G173 L177 G178 K182 D183 Y184 V189 S192 L198 T199 S200 L214 Y215 S216 L217 V221 S227 L228 G229 T230 Q231 T232 C235 N236 D247 K248 K249 V250 E251 P252 LYS SER CYS ASP LYS THR HIS THR

• Molecule 3: Heat-labile enterotoxin B chain



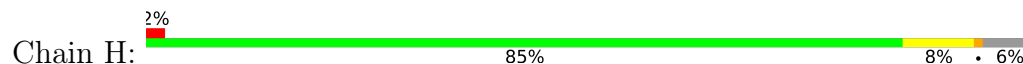
MET SER THR ASP ILE ILE ILE LYS GLU LEU D201 R208 L209 L223 L242 I258 I263 Y264 S265 N269 N270 L271 L274 E275 V322 PRO ARG

• Molecule 3: Heat-labile enterotoxin B chain



MET SER THR ASP ILE ILE ILE LYS GLU L199 L202 S229 H230 S231 K237 L242 K283 M300 N309 L321 VAL PRO ARG

• Molecule 3: Heat-labile enterotoxin B chain



MET SER THR ASP ILE ILE ILE LYS GLU K197 E198 I199 L200 T206 L215 P219 A220 G221 K237 N267 F268 N269 V322 PRO ARG

4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	111.47Å 198.52Å 115.80Å 90.00° 109.72° 90.00°	Depositor
Resolution (Å)	29.74 – 2.50 29.74 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.74-2.50) 99.1 (29.74-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.178 , 0.225 0.181 , 0.227	Depositor DCC
R_{free} test set	3984 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.008 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	25529	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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	0.56	0/1668	0.75	2/2267 (0.1%)
1	C	0.88	6/1663 (0.4%)	0.95	10/2260 (0.4%)
1	E	0.64	1/1668 (0.1%)	0.76	0/2267
2	B	0.66	3/1701 (0.2%)	0.88	10/2323 (0.4%)
2	D	0.57	0/1707	0.74	2/2331 (0.1%)
2	F	0.59	0/1693	0.88	7/2315 (0.3%)
3	G	0.61	0/989	0.74	0/1345
3	H	0.58	0/1031	0.77	0/1401
3	I	0.59	0/998	0.71	0/1357
All	All	0.65	10/13118 (0.1%)	0.81	31/17866 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	171	LYS	CE-NZ	12.57	1.87	1.49
1	C	171	LYS	CD-CE	12.54	1.90	1.52
2	B	232	THR	CB-CG2	10.64	1.87	1.52
1	C	195	LYS	CD-CE	10.08	1.82	1.52
1	C	195	LYS	CE-NZ	8.99	1.76	1.49

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	39	GLN	N-CA-CB	11.54	125.71	109.78
1	C	195	LYS	CD-CE-NZ	-10.70	77.67	111.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	232	THR	OG1-CB-CG2	-9.46	90.39	109.30
2	B	69	LYS	CA-CB-CG	9.28	132.66	114.10
1	C	171	LYS	CD-CE-NZ	-9.12	82.71	111.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	168	ARG	Sidechain

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	1632	1588	1588	24	0
1	C	1627	1583	1583	41	0
1	E	1632	1588	1588	41	0
2	B	1656	1590	1589	39	0
2	D	1662	1595	1594	8	0
2	F	1648	1561	1561	31	0
3	G	968	945	945	10	0
3	H	1007	989	992	9	0
3	I	977	958	958	3	0
4	A	49	0	0	3	0
4	B	18	0	0	1	0
4	C	41	0	0	3	0
4	D	41	0	0	1	0
4	E	39	0	0	2	0
4	F	32	0	0	0	0
4	G	41	0	0	0	0
4	H	39	0	0	0	1
4	I	23	0	0	0	0
All	All	13132	12397	12398	198	1

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 8.

The worst 5 of 198 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)
2:B:69:LYS:CD	2:B:69:LYS:CE	1.76	1.57
1:C:171:LYS:CG	1:C:171:LYS:CD	1.79	1.54
1:C:195:LYS:CD	1:C:195:LYS:CE	1.82	1.52
2:B:232:THR:CB	2:B:232:THR:CG2	1.87	1.50
1:C:171:LYS:CD	1:C:171:LYS:CE	1.90	1.49

All (1) 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)
4:H:437:HOH:O	4:H:437:HOH:O[2_553]	1.87	0.33

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	211/239 (88%)	207 (98%)	4 (2%)	0	100	100
1	C	210/239 (88%)	205 (98%)	5 (2%)	0	100	100
1	E	211/239 (88%)	201 (95%)	9 (4%)	1 (0%)	24	43
2	B	216/260 (83%)	209 (97%)	7 (3%)	0	100	100
2	D	217/260 (84%)	211 (97%)	6 (3%)	0	100	100
2	F	217/260 (84%)	205 (94%)	12 (6%)	0	100	100
3	G	120/134 (90%)	120 (100%)	0	0	100	100
3	H	125/134 (93%)	120 (96%)	5 (4%)	0	100	100
3	I	121/134 (90%)	121 (100%)	0	0	100	100
All	All	1648/1899 (87%)	1599 (97%)	48 (3%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	153	SER

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	187/208 (90%)	186 (100%)	1 (0%)	81	92
1	C	187/208 (90%)	181 (97%)	6 (3%)	34	62
1	E	187/208 (90%)	181 (97%)	6 (3%)	34	62
2	B	184/218 (84%)	177 (96%)	7 (4%)	29	56
2	D	185/218 (85%)	182 (98%)	3 (2%)	55	79
2	F	181/218 (83%)	177 (98%)	4 (2%)	45	73
3	G	106/118 (90%)	105 (99%)	1 (1%)	70	87
3	H	111/118 (94%)	109 (98%)	2 (2%)	51	77
3	I	107/118 (91%)	103 (96%)	4 (4%)	30	57
All	All	1435/1632 (88%)	1401 (98%)	34 (2%)	43	70

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	229	SER
3	I	237	LYS
3	H	206	THR
2	B	111	SER
2	B	69	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	103	ASN
2	F	203	HIS
2	F	144	GLN
3	G	269	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	192	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 ⓘ

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	213/239 (89%)	-0.35	1 (0%) 87 85	34, 52, 95, 121	0
1	C	212/239 (88%)	-0.28	1 (0%) 87 85	33, 52, 98, 108	0
1	E	213/239 (89%)	0.12	17 (7%) 18 16	33, 52, 128, 142	0
2	B	220/260 (84%)	-0.05	4 (1%) 67 64	35, 67, 106, 121	0
2	D	221/260 (85%)	-0.11	5 (2%) 61 57	33, 55, 110, 134	0
2	F	221/260 (85%)	0.13	17 (7%) 19 17	32, 58, 125, 145	0
3	G	122/134 (91%)	-0.54	1 (0%) 82 80	33, 46, 66, 81	0
3	H	126/134 (94%)	-0.38	3 (2%) 59 55	27, 49, 77, 115	1 (0%)
3	I	123/134 (91%)	-0.42	2 (1%) 70 67	38, 49, 73, 98	0
All	All	1671/1899 (87%)	-0.17	51 (3%) 51 47	27, 53, 111, 145	1 (0%)

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	210	ALA	5.2
1	E	1	SER	4.8
1	E	153	SER	4.3
2	F	252	PRO	4.2
1	E	218	TYR	3.7

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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.