



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 12:11 AM UTC

PDB ID : 3G76 / pdb_00003g76
Title : Crystal structure of XIAP-BIR3 in complex with a bivalent compound
Authors : Cossu, F.; Milani, M.; Mastrangelo, E.; Bolognesi, M.
Deposited on : 2009-02-09
Resolution : 3.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

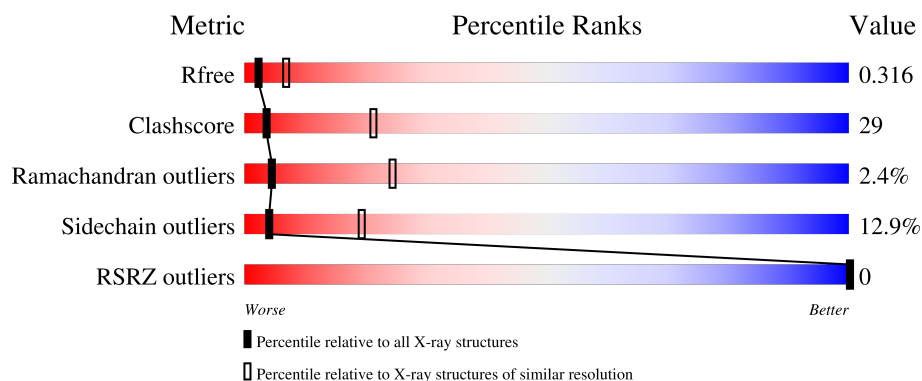
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	122	43% 24% 10% • 20%
1	B	122	40% 37% 7% • 14%
1	C	122	43% 30% • • 21%
1	D	122	39% 38% 6% • 14%
1	E	122	45% 29% • • 22%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	122	 42% 37% 7% 15%
1	G	122	 48% 25% 5% 22%
1	H	122	 43% 30% 11% • 14%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7590 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 Baculoviral IAP repeat-containing protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	97	Total	C	N	O	S	0	0	0
			789	505	135	145	4			
1	B	105	Total	C	N	O	S	0	0	0
			855	545	147	158	5			
1	C	96	Total	C	N	O	S	0	0	0
			781	501	133	143	4			
1	D	105	Total	C	N	O	S	0	0	0
			855	545	147	158	5			
1	E	95	Total	C	N	O	S	0	0	0
			773	495	132	142	4			
1	F	104	Total	C	N	O	S	0	0	0
			852	544	148	155	5			
1	G	95	Total	C	N	O	S	0	0	0
			773	495	132	142	4			
1	H	105	Total	C	N	O	S	0	0	0
			855	545	147	158	5			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	357	HIS	-	expression tag	UNP P98170
A	358	HIS	-	expression tag	UNP P98170
A	359	HIS	-	expression tag	UNP P98170
A	360	HIS	-	expression tag	UNP P98170
A	361	HIS	-	expression tag	UNP P98170
A	362	HIS	-	expression tag	UNP P98170
B	357	HIS	-	expression tag	UNP P98170
B	358	HIS	-	expression tag	UNP P98170
B	359	HIS	-	expression tag	UNP P98170
B	360	HIS	-	expression tag	UNP P98170
B	361	HIS	-	expression tag	UNP P98170
B	362	HIS	-	expression tag	UNP P98170
C	357	HIS	-	expression tag	UNP P98170

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	358	HIS	-	expression tag	UNP P98170
C	359	HIS	-	expression tag	UNP P98170
C	360	HIS	-	expression tag	UNP P98170
C	361	HIS	-	expression tag	UNP P98170
C	362	HIS	-	expression tag	UNP P98170
D	357	HIS	-	expression tag	UNP P98170
D	358	HIS	-	expression tag	UNP P98170
D	359	HIS	-	expression tag	UNP P98170
D	360	HIS	-	expression tag	UNP P98170
D	361	HIS	-	expression tag	UNP P98170
D	362	HIS	-	expression tag	UNP P98170
E	357	HIS	-	expression tag	UNP P98170
E	358	HIS	-	expression tag	UNP P98170
E	359	HIS	-	expression tag	UNP P98170
E	360	HIS	-	expression tag	UNP P98170
E	361	HIS	-	expression tag	UNP P98170
E	362	HIS	-	expression tag	UNP P98170
F	357	HIS	-	expression tag	UNP P98170
F	358	HIS	-	expression tag	UNP P98170
F	359	HIS	-	expression tag	UNP P98170
F	360	HIS	-	expression tag	UNP P98170
F	361	HIS	-	expression tag	UNP P98170
F	362	HIS	-	expression tag	UNP P98170
G	357	HIS	-	expression tag	UNP P98170
G	358	HIS	-	expression tag	UNP P98170
G	359	HIS	-	expression tag	UNP P98170
G	360	HIS	-	expression tag	UNP P98170
G	361	HIS	-	expression tag	UNP P98170
G	362	HIS	-	expression tag	UNP P98170
H	357	HIS	-	expression tag	UNP P98170
H	358	HIS	-	expression tag	UNP P98170
H	359	HIS	-	expression tag	UNP P98170
H	360	HIS	-	expression tag	UNP P98170
H	361	HIS	-	expression tag	UNP P98170
H	362	HIS	-	expression tag	UNP P98170

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

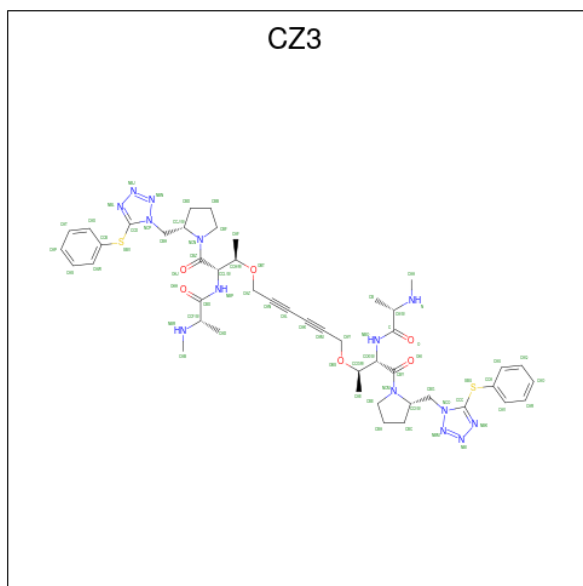
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		
2	G	1	Total	Zn	0	0
			1	1		
2	H	1	Total	Zn	0	0
			1	1		

- Molecule 3 is 1,1'-{hexa-2,4-diyne-1,6-diylbis[oxy{(2S,3R)-2-[(N-methyl-L-alanyl)amino]-1-oxobutane-3,1-diyl}(2S)pyrrolidine-1,2-diylmethanediyl]}bis[5-(phenylsulfanyl)-1H-tetrazole] (CCD ID: CZ3) (formula: C₄₆H₆₀N₁₄O₆S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	1
			68	46	14	6	2		
3	B	1	Total	C	N	O	S	0	1
			68	46	14	6	2		
3	C	1	Total	C	N	O	S	0	1
			68	46	14	6	2		
3	D	1	Total	C	N	O	S	0	1
			68	46	14	6	2		

Continued on next page...

Continued from previous page...

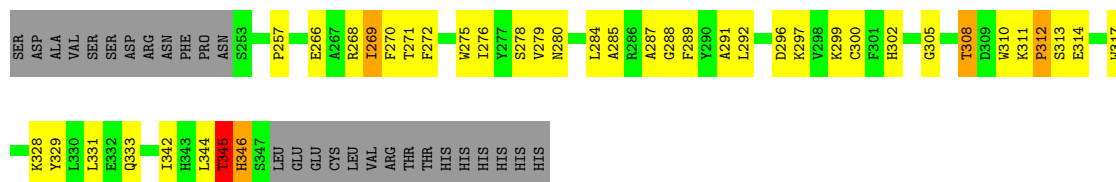
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	E	1	Total	C	N	O	S	0	1
			68	46	14	6	2		
3	F	1	Total	C	N	O	S	0	1
			68	46	14	6	2		
3	G	1	Total	C	N	O	S	0	1
			68	46	14	6	2		
3	H	1	Total	C	N	O	S	0	1
			68	46	14	6	2		

- Molecule 4 is water.

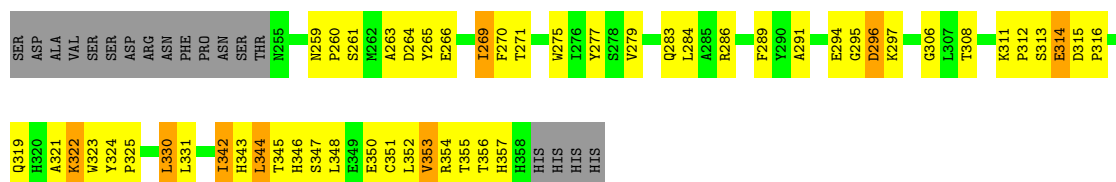
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total	O	0	0
			32	32		
4	B	34	Total	O	0	0
			34	34		
4	C	20	Total	O	0	0
			20	20		
4	D	48	Total	O	0	0
			48	48		
4	E	275	Total	O	0	0
			275	275		
4	F	23	Total	O	0	0
			23	23		
4	G	54	Total	O	0	0
			54	54		
4	H	19	Total	O	0	0
			19	19		



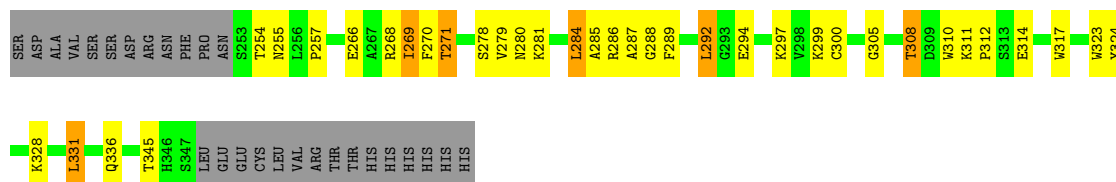
- Molecule 1: Baculoviral IAP repeat-containing protein 4



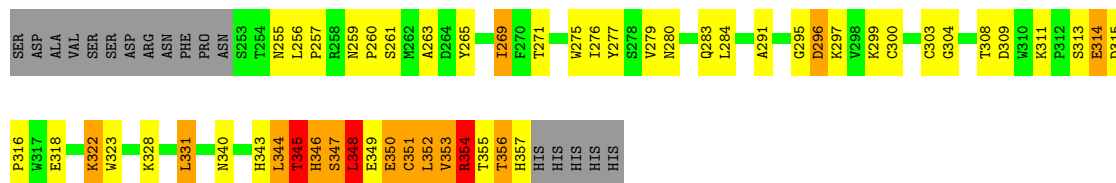
- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	119.08Å 119.08Å 105.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 3.00 40.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-3.00) 99.8 (40.00-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.231 , 0.311 0.243 , 0.316	Depositor DCC
R_{free} test set	1688 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	70.0	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 142.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.458 for -h,-k,l 0.309 for h,-h-k,-l 0.310 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7590	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.52% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CZ3

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	1.15	7/815 (0.9%)	1.76	21/1105 (1.9%)
1	B	0.58	0/882	1.38	7/1196 (0.6%)
1	C	0.52	1/807 (0.1%)	1.33	9/1094 (0.8%)
1	D	0.55	0/882	1.09	7/1196 (0.6%)
1	E	0.49	1/799 (0.1%)	1.25	5/1083 (0.5%)
1	F	0.44	0/880	0.87	1/1193 (0.1%)
1	G	0.45	0/799	0.79	0/1083
1	H	0.49	0/882	1.13	7/1196 (0.6%)
All	All	0.62	9/6746 (0.1%)	1.23	57/9146 (0.6%)

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	A	0	4
1	C	0	1
1	D	0	1
1	E	0	1
All	All	0	7

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	261	SER	C-N	20.22	1.62	1.33
1	A	256	LEU	C-N	-11.23	1.22	1.33
1	A	258	ARG	C-N	-10.65	1.21	1.33
1	A	260	PRO	N-CD	-8.99	1.35	1.47
1	A	260	PRO	C-N	8.88	1.46	1.33

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	346	HIS	N-CA-C	21.58	137.99	111.02
1	C	347	SER	N-CA-C	18.16	149.49	110.80
1	B	347	SER	N-CA-C	18.16	137.15	110.10
1	A	347	SER	O-C-N	-17.93	101.54	123.06
1	A	258	ARG	O-C-N	-17.42	99.43	122.59

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	257	PRO	Peptide,Mainchain
1	A	347	SER	Peptide,Mainchain
1	C	347	SER	Mainchain
1	D	346	HIS	Mainchain
1	E	346	HIS	Mainchain

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	789	0	734	37	0
1	B	855	0	801	57	0
1	C	781	0	729	44	0
1	D	855	0	801	42	0
1	E	773	0	719	30	0
1	F	852	0	797	71	1
1	G	773	0	719	31	0
1	H	855	0	803	60	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	68	0	32	3	0
3	B	68	0	16	1	0
3	C	68	0	32	2	0
3	D	68	0	19	4	0
3	E	68	0	32	3	0
3	F	68	0	23	7	0
3	G	68	0	32	7	0
3	H	68	0	23	6	0
4	A	32	0	0	3	0
4	B	34	0	0	3	0
4	C	20	0	0	1	0
4	D	48	0	0	5	1
4	E	275	0	0	8	0
4	F	23	0	0	4	0
4	G	54	0	0	2	0
4	H	19	0	0	2	0
All	All	7590	0	6312	393	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 29.

The worst 5 of 393 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:F:348:LEU:CD1	1:F:352:LEU:HD11	1.11	1.57
1:H:346:HIS:CB	1:H:347:SER:HB2	1.35	1.56
1:F:348:LEU:CD1	1:F:352:LEU:CD1	1.92	1.47
1:B:323:TRP:HA	1:B:348:LEU:CD2	1.59	1.32
1:H:346:HIS:HB3	1:H:347:SER:CB	1.65	1.26

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)
1:F:344:LEU:O	4:D:17:HOH:O[1_556]	2.09	0.11

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	95/122 (78%)	83 (87%)	11 (12%)	1 (1%)	11	43
1	B	103/122 (84%)	91 (88%)	9 (9%)	3 (3%)	3	20
1	C	94/122 (77%)	79 (84%)	13 (14%)	2 (2%)	5	27
1	D	103/122 (84%)	88 (85%)	11 (11%)	4 (4%)	2	14
1	E	93/122 (76%)	81 (87%)	11 (12%)	1 (1%)	11	43
1	F	102/122 (84%)	91 (89%)	9 (9%)	2 (2%)	6	28
1	G	93/122 (76%)	81 (87%)	11 (12%)	1 (1%)	11	43
1	H	103/122 (84%)	86 (84%)	12 (12%)	5 (5%)	1	10
All	All	786/976 (80%)	680 (86%)	87 (11%)	19 (2%)	4	24

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	353	VAL
1	A	258	ARG
1	B	348	LEU
1	C	255	ASN
1	D	295	GLY

5.3.2 Protein sidechains [i](#)

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	82/106 (77%)	70 (85%)	12 (15%)	3	15

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	90/106 (85%)	77 (86%)	13 (14%)	3	15
1	C	81/106 (76%)	74 (91%)	7 (9%)	10	36
1	D	90/106 (85%)	76 (84%)	14 (16%)	2	13
1	E	80/106 (76%)	73 (91%)	7 (9%)	9	35
1	F	89/106 (84%)	76 (85%)	13 (15%)	3	15
1	G	80/106 (76%)	71 (89%)	9 (11%)	5	24
1	H	90/106 (85%)	77 (86%)	13 (14%)	3	15
All	All	682/848 (80%)	594 (87%)	88 (13%)	4	19

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	296	ASP
1	G	292	LEU
1	F	330	LEU
1	F	353	VAL
1	H	269	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	357	HIS
1	G	343	HIS
1	H	283	GLN
1	H	255	ASN
1	C	283	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](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	261:SER	C	262:MET	N	1.62

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	97/122 (79%)	-1.09	0 100 100	34, 56, 96, 128	1 (1%)
1	B	105/122 (86%)	-1.11	0 100 100	34, 54, 92, 134	1 (0%)
1	C	96/122 (78%)	-1.06	0 100 100	34, 57, 99, 128	1 (1%)
1	D	105/122 (86%)	-1.14	0 100 100	33, 53, 85, 117	1 (0%)
1	E	95/122 (77%)	-0.89	0 100 100	52, 81, 121, 141	1 (1%)
1	F	104/122 (85%)	-0.78	0 100 100	54, 95, 118, 140	1 (0%)
1	G	95/122 (77%)	-0.85	0 100 100	60, 83, 118, 150	1 (1%)
1	H	105/122 (86%)	-0.68	0 100 100	45, 92, 121, 149	1 (0%)
All	All	802/976 (82%)	-0.95	0 100 100	33, 75, 114, 150	8 (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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CZ3	A	600[B]	68/68	0.97	0.10	21,57,83,133	36
3	CZ3	E	600[B]	68/68	0.97	0.10	31,73,105,114	36
3	CZ3	G	600[B]	68/68	0.97	0.12	40,73,113,125	36
3	CZ3	F	600[A]	68/68	0.98	0.08	14,61,102,123	36
3	CZ3	C	600[B]	68/68	0.98	0.10	15,57,94,172	36
3	CZ3	H	600[B]	68/68	0.98	0.09	10,65,100,116	36
3	CZ3	B	600[A]	68/68	0.99	0.06	7,34,57,88	36
3	CZ3	D	600[B]	68/68	0.99	0.07	4,32,69,124	36
2	ZN	A	502	1/1	1.00	0.01	41,41,41,41	0
2	ZN	B	502	1/1	1.00	0.01	44,44,44,44	0
2	ZN	C	502	1/1	1.00	0.01	46,46,46,46	0
2	ZN	D	502	1/1	1.00	0.01	41,41,41,41	0
2	ZN	E	502	1/1	1.00	0.01	75,75,75,75	0
2	ZN	F	502	1/1	1.00	0.02	92,92,92,92	0
2	ZN	G	502	1/1	1.00	0.02	80,80,80,80	0
2	ZN	H	502	1/1	1.00	0.02	108,108,108,108	0

6.5 Other polymers ⓘ

There are no such residues in this entry.