



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 07:56 PM EDT

PDB ID : 2OHN  
Title : X-ray crystal structure of beta secretase complexed with 4-(4-fluorobenzyl)pi  
peridine  
Authors : Patel, S.  
Deposited on : 2007-01-10  
Resolution : 2.15 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

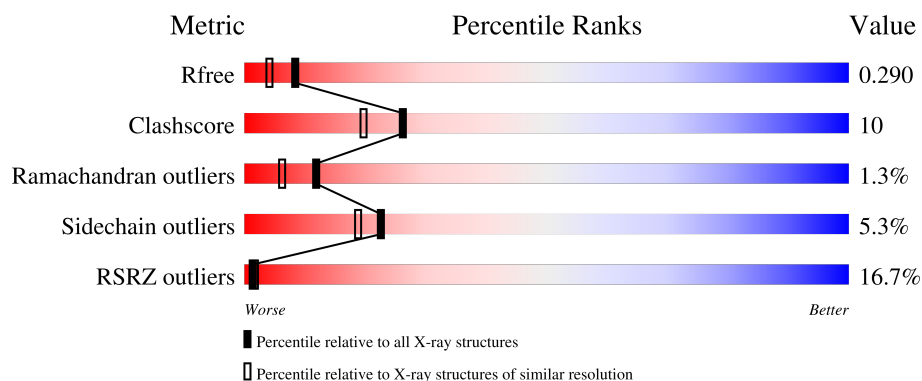
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
$R_{free}$	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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  $\geq 3$ , 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	402	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3240 atoms, of which 17 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 Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	377	2966	1898	493	561	14	0	0	0

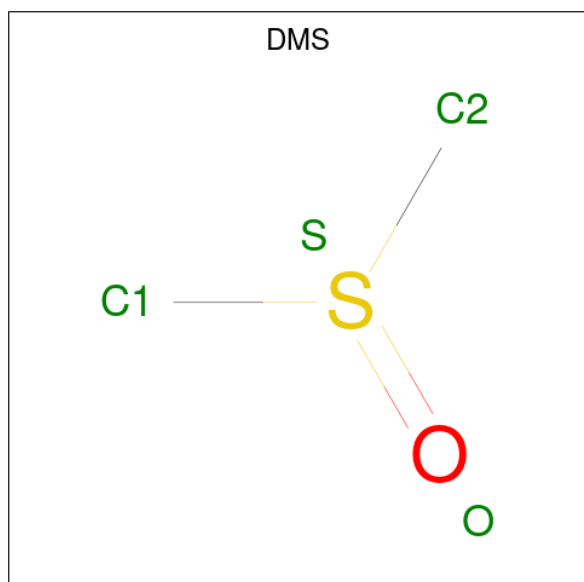
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	LYS	ARG	engineered mutation	UNP P56817
A	-4	LYS	ARG	engineered mutation	UNP P56817

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

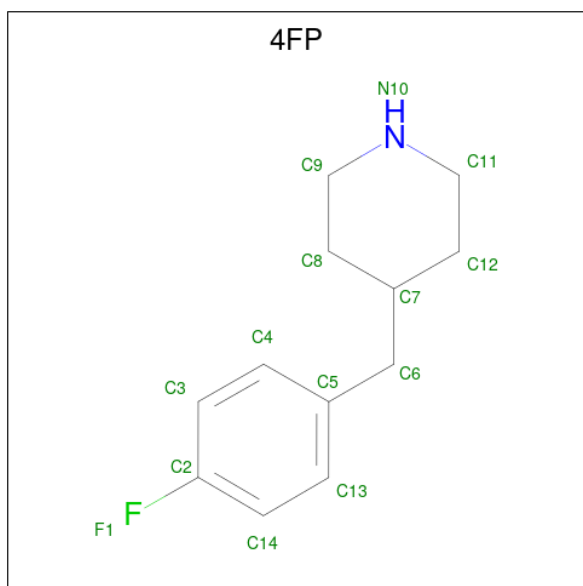
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	I	0	0
			3	3		

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 4 is 4-(4-FLUOROBENZYL)PIPERIDINE (three-letter code: 4FP) (formula: C<sub>12</sub>H<sub>16</sub>FN).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	H	N	0	0
			31	12	1	17	1		

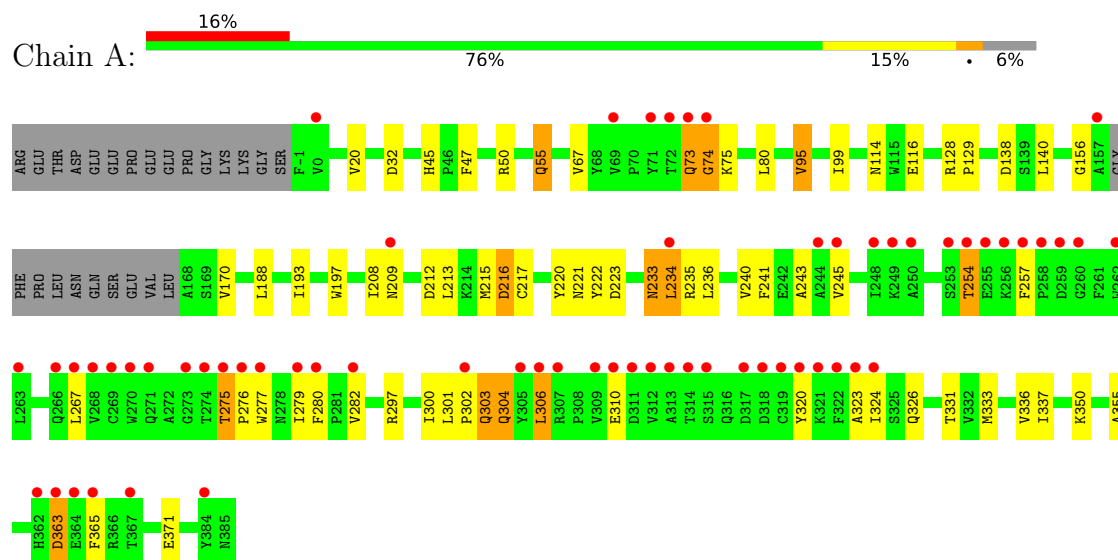
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	236	Total	O	0	0
			236	236		

### 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: Beta-secretase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.39Å 102.39Å 170.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.79 – 2.15 47.80 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.79-2.15) 99.4 (47.80-2.15)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019g	Depositor
R, $R_{free}$	0.228 , 0.285 0.236 , 0.290	Depositor DCC
$R_{free}$ test set	1487 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.4	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 61.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3240	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: DMS, IOD, 4FP

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	0.58	0/3041	0.70	0/4132

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	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	233	ASN	Peptide
1	A	74	GLY	Peptide

### 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	2966	0	2878	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	3	0	0	0	0
3	A	4	0	6	0	0
4	A	14	17	16	1	0
5	A	236	0	0	5	0
All	All	3223	17	2900	61	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 10.

All (61) 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:A:304:GLN:HE21	1:A:304:GLN:N	1.69	0.90
1:A:300:ILE:O	1:A:301:LEU:HD23	1.75	0.85
1:A:320:TYR:HB3	5:A:622:HOH:O	1.85	0.75
1:A:241:PHE:CD2	1:A:326:GLN:HG2	2.24	0.72
1:A:209:ASN:HA	1:A:282:VAL:HG22	1.74	0.70
1:A:212:ASP:OD2	5:A:608:HOH:O	2.10	0.69
1:A:221:ASN:O	5:A:606:HOH:O	2.12	0.66
1:A:215:MET:HE1	1:A:243:ALA:HB3	1.79	0.64
1:A:254:THR:HG21	1:A:279:ILE:HD12	1.82	0.62
1:A:300:ILE:HG21	1:A:337:ILE:HD13	1.81	0.62
1:A:208:ILE:HD12	1:A:213:LEU:HD11	1.82	0.62
1:A:241:PHE:CZ	1:A:245:VAL:HG21	2.35	0.61
1:A:156:GLY:HA2	1:A:170:VAL:HG12	1.83	0.60
1:A:302:PRO:O	1:A:306:LEU:N	2.29	0.60
1:A:254:THR:CB	1:A:279:ILE:HD12	2.32	0.59
1:A:67:VAL:HG12	1:A:129:PRO:HD3	1.86	0.58
1:A:302:PRO:O	1:A:306:LEU:HB2	2.04	0.57
1:A:45:HIS:HD2	1:A:47:PHE:H	1.52	0.56
1:A:20:VAL:HG11	1:A:99:ILE:HD13	1.87	0.56
1:A:234:LEU:O	1:A:324:ILE:HA	2.05	0.55
1:A:323:ALA:HB1	1:A:336:VAL:HG21	1.87	0.55
1:A:235:ARG:O	1:A:331:THR:HA	2.07	0.55
1:A:156:GLY:HA2	1:A:170:VAL:CG1	2.38	0.54
1:A:156:GLY:HA2	1:A:170:VAL:CB	2.38	0.54
1:A:236:LEU:O	1:A:326:GLN:HA	2.08	0.53
1:A:254:THR:OG1	1:A:279:ILE:HG23	2.08	0.53
1:A:275:THR:HG22	1:A:276:PRO:HD2	1.90	0.53
1:A:156:GLY:HA2	1:A:170:VAL:HB	1.91	0.53
1:A:215:MET:CE	1:A:243:ALA:HB3	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:TYR:HA	1:A:240:VAL:HG21	1.92	0.52
1:A:279:ILE:HG22	1:A:279:ILE:O	2.10	0.52
1:A:254:THR:HG21	1:A:279:ILE:CD1	2.40	0.51
1:A:363:ASP:OD2	1:A:365:PHE:N	2.40	0.48
1:A:254:THR:CG2	1:A:279:ILE:HD12	2.42	0.48
1:A:304:GLN:HE21	1:A:304:GLN:CA	2.26	0.48
1:A:32:ASP:OD2	4:A:405:4FP:H81	2.14	0.47
1:A:50:ARG:O	1:A:116:GLU:HG2	2.15	0.46
1:A:300:ILE:HD13	1:A:337:ILE:HD13	1.99	0.45
1:A:280:PHE:HB2	1:A:302:PRO:HG2	1.98	0.45
1:A:306:LEU:HA	5:A:622:HOH:O	2.16	0.45
1:A:241:PHE:CE1	1:A:245:VAL:CG2	3.00	0.44
1:A:20:VAL:HG11	1:A:99:ILE:CD1	2.47	0.44
1:A:215:MET:O	1:A:216:ASP:C	2.56	0.44
1:A:67:VAL:CG1	1:A:129:PRO:HD3	2.48	0.43
1:A:193:ILE:HD12	1:A:350:LYS:HA	2.00	0.43
1:A:50:ARG:HH22	1:A:114:ASN:ND2	2.17	0.42
1:A:55:GLN:NE2	5:A:549:HOH:O	2.46	0.42
1:A:95:VAL:HG11	1:A:140:LEU:HD13	2.01	0.42
1:A:67:VAL:CG1	1:A:80:LEU:HD11	2.50	0.42
1:A:301:LEU:HB2	1:A:303:GLN:HG2	2.01	0.42
1:A:45:HIS:CD2	1:A:47:PHE:H	2.34	0.42
1:A:241:PHE:CE1	1:A:245:VAL:HG23	2.54	0.42
1:A:217:CYS:HA	1:A:220:TYR:CD1	2.55	0.42
1:A:188:LEU:HD23	1:A:355:ALA:HB2	2.02	0.41
1:A:300:ILE:HD13	1:A:337:ILE:CD1	2.50	0.41
1:A:297:ARG:NH2	1:A:371:GLU:OE2	2.49	0.41
1:A:304:GLN:C	1:A:336:VAL:HG13	2.41	0.41
1:A:300:ILE:HG13	1:A:301:LEU:N	2.36	0.41
1:A:333:MET:HE2	1:A:337:ILE:HG21	2.03	0.41
1:A:55:GLN:HE21	1:A:55:GLN:H	1.67	0.41
1:A:222:TYR:HA	1:A:223:ASP:HA	1.79	0.41

There are no symmetry-related clashes.

## 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	373/402 (93%)	351 (94%)	17 (5%)	5 (1%)	12 6

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	310	GLU
1	A	363	ASP
1	A	216	ASP
1	A	74	GLY

### 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	321/343 (94%)	304 (95%)	17 (5%)	22 19

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	73	GLN
1	A	75	LYS
1	A	95	VAL
1	A	128	ARG
1	A	138	ASP
1	A	197	TRP
1	A	233	ASN
1	A	234	LEU
1	A	254	THR
1	A	257	PHE
1	A	267	LEU

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Mol	Chain	Res	Type
1	A	275	THR
1	A	277	TRP
1	A	303	GLN
1	A	304	GLN
1	A	306	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	45	HIS
1	A	55	GLN
1	A	114	ASN
1	A	211	GLN
1	A	266	GLN
1	A	271	GLN
1	A	278	ASN
1	A	304	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	DMS	A	404	-	3,3,3	2.78	1 (33%)	3,3,3	0.74	0
4	4FP	A	405	-	15,15,15	0.53	0	19,19,19	0.87	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	4FP	A	405	-	-	1/4/12/12	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	404	DMS	O-S	4.64	1.81	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	405	4FP	C14-C2-C3	-2.18	119.93	122.83

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	405	4FP	C5-C6-C7-C12

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	405	4FP	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	377/402 (93%)	0.76	63 (16%) ⓘ ⓘ	20, 37, 89, 117	2 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	313	ALA	14.5
1	A	314	THR	8.7
1	A	271	GLN	6.8
1	A	276	PRO	6.8
1	A	277	TRP	6.6
1	A	72	THR	6.6
1	A	279	ILE	6.6
1	A	365	PHE	6.5
1	A	270	TRP	6.1
1	A	273	GLY	6.1
1	A	280	PHE	5.9
1	A	312	VAL	5.8
1	A	311	ASP	5.8
1	A	310	GLU	5.7
1	A	319	CYS	5.3
1	A	274	THR	4.9
1	A	305	TYR	4.8
1	A	259	ASP	4.7
1	A	254	THR	4.7
1	A	253	SER	4.6
1	A	306	LEU	4.3
1	A	317	ASP	4.3
1	A	262	TRP	4.3
1	A	315	SER	4.2
1	A	73	GLN	4.1
1	A	263	LEU	3.8
1	A	256	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	74	GLY	3.7
1	A	309	VAL	3.5
1	A	364	GLU	3.5
1	A	157	ALA	3.4
1	A	71	TYR	3.4
1	A	269	CYS	3.3
1	A	322	PHE	3.2
1	A	267	LEU	3.2
1	A	318	ASP	3.1
1	A	268	VAL	3.1
1	A	320	TYR	2.9
1	A	245	VAL	2.9
1	A	250	ALA	2.8
1	A	257	PHE	2.8
1	A	384	TYR	2.6
1	A	209	ASN	2.6
1	A	275	THR	2.6
1	A	255	GLU	2.6
1	A	258	PRO	2.5
1	A	307	ARG	2.5
1	A	282	VAL	2.5
1	A	0	VAL	2.4
1	A	69	VAL	2.4
1	A	248	ILE	2.4
1	A	367	THR	2.3
1	A	323	ALA	2.3
1	A	244	ALA	2.3
1	A	260	GLY	2.3
1	A	302	PRO	2.2
1	A	362	HIS	2.2
1	A	324	ILE	2.1
1	A	249	LYS	2.1
1	A	266	GLN	2.1
1	A	321	LYS	2.1
1	A	363	ASP	2.0
1	A	234	LEU	2.0

## 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 [i](#)

There are no monosaccharides 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, 95<sup>th</sup> 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
4	4FP	A	405	14/14	0.79	0.17	38,48,58,61	0
2	IOD	A	402	1/1	0.92	0.35	59,59,59,59	1
3	DMS	A	404	4/4	0.93	0.18	63,65,66,69	0
2	IOD	A	403	1/1	0.95	0.35	33,33,33,33	1
2	IOD	A	401	1/1	1.00	0.18	25,25,25,25	1

### 6.5 Other polymers [i](#)

There are no such residues in this entry.