



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:38 PM GMT

PDB ID : 4J0Z  
Title : CRYSTAL STRUCTURE OF BACE-1 IN COMPLEX WITH 5-Cyano-pyridine-2-carboxylic acid [3-((4S,5R)-2-amino-5-fluoro-4-fluoromethyl-5,6-dihydro-4H-[1,3]oxazin-4-yl)-4-fluoro-phenyl]-amide  
Authors : Kuglstatter, A.; Stihle, M.  
Deposited on : 2013-01-31  
Resolution : 2.13 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

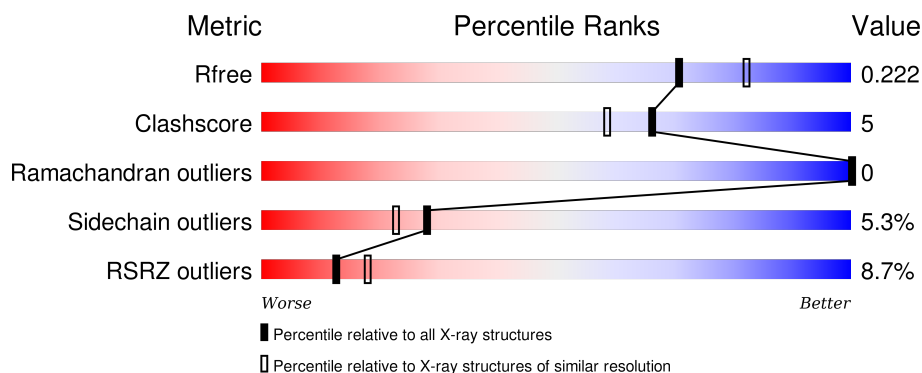
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.13 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))
$R_{free}$	91344	1693 (2.16-2.12)
Clashscore	102246	1824 (2.16-2.12)
Ramachandran outliers	100387	1798 (2.16-2.12)
Sidechain outliers	100360	1798 (2.16-2.12)
RSRZ outliers	91569	1699 (2.16-2.12)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	409	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DMS	A	503	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3242 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 Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	381	Total	C	N	O	S	0	0	0
			2983	1907	499	563	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	307	ALA	LYS	ENGINEERED MUTATION	UNP P56817

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

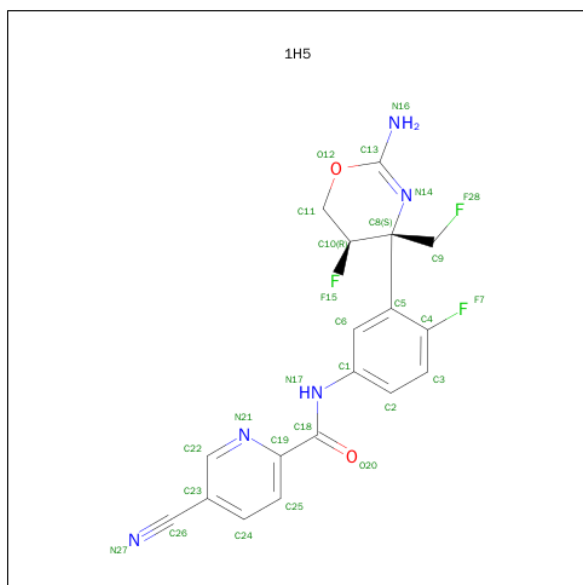
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Na	0	0
			2	2		

- 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 N-{3-[(4S,5R)-2-AMINO-5-FLUORO-4-(FLUOROMETHYL)-5,6-DIHYDRO-4H-1,3-OXAZIN-4-YL]-4-FLUOROPHENYL}-5-CYANOPYRIDINE-2-CARBOXAMIDE (three-letter code: 1H5) (formula: C<sub>18</sub>H<sub>14</sub>F<sub>3</sub>N<sub>5</sub>O<sub>2</sub>).



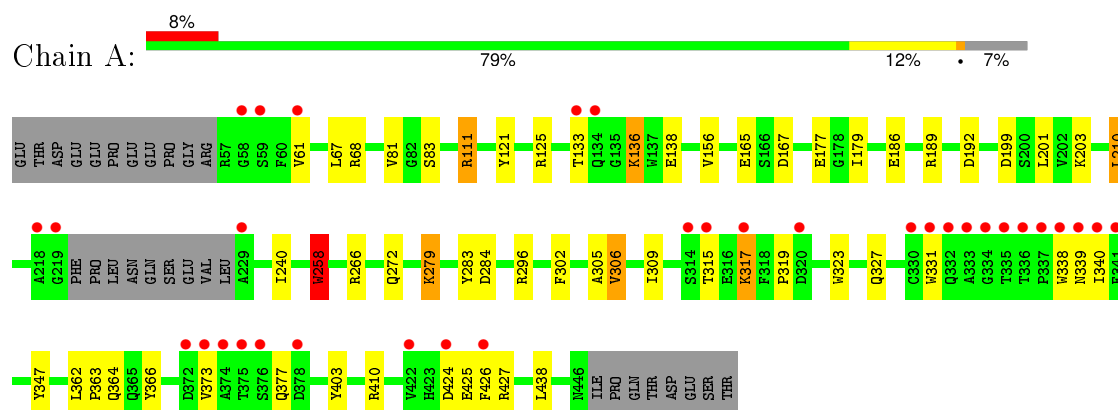
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			28	18	3	5	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	225	Total	O	0	0
			225	225		



- 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, $\alpha$ , $\beta$ , $\gamma$	102.76 Å   102.76 Å   170.75 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	47.95 – 2.13 47.95 – 2.13	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.95-2.13) 100.0 (47.95-2.13)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.41 (at 2.14 Å)	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
R, $R_{free}$	0.179   ,   0.223 0.178   ,   0.222	Depositor DCC
$R_{free}$ test set	1541 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.1	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 41.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 30518 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3242	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, DMS, 1H5

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	1.02	6/3058 (0.2%)	1.09	12/4156 (0.3%)

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	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	258	TRP	CD2-CE2	6.00	1.48	1.41
1	A	323	TRP	CD2-CE2	5.69	1.48	1.41
1	A	121	TYR	CG-CD2	5.54	1.46	1.39
1	A	331	TRP	CD2-CE2	5.39	1.47	1.41
1	A	111	ARG	CZ-NH1	5.28	1.40	1.33
1	A	338	TRP	CD2-CE2	5.01	1.47	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	ARG	NE-CZ-NH1	16.88	128.74	120.30
1	A	111	ARG	NE-CZ-NH2	-15.60	112.50	120.30
1	A	210	LEU	CB-CG-CD2	-6.63	99.73	111.00
1	A	199	ASP	CB-CG-OD2	6.62	124.25	118.30
1	A	189	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	A	427	ARG	NE-CZ-NH1	5.71	123.16	120.30
1	A	192	ASP	CB-CG-OD1	5.63	123.37	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	410	ARG	CG-CD-NE	-5.61	100.02	111.80
1	A	410	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	A	424	ASP	CB-CG-OD1	5.52	123.27	118.30
1	A	189	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	A	81	VAL	CG1-CB-CG2	-5.29	102.43	110.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	258	TRP	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	2983	0	2889	27	0
2	A	2	0	0	0	0
3	A	4	0	6	0	0
4	A	28	0	14	2	0
5	A	225	0	0	7	1
All	All	3242	0	2909	29	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 5.

All (29) 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:296:ARG:HD3	5:A:1087:HOH:O	1.61	1.01
1:A:179:ILE:HB	5:A:1202:HOH:O	0.76	0.93
1:A:305:ALA:O	1:A:309:ILE:HG13	1.73	0.88
1:A:136:LYS:NZ	1:A:165:GLU:OE1	2.15	0.80
1:A:339:ASN:HB2	5:A:1143:HOH:O	1.91	0.70
1:A:111:ARG:O	1:A:177:GLU:HG2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:ILE:HG23	1:A:403:TYR:HE2	1.63	0.63
4:A:504:1H5:H5	4:A:504:1H5:F7	1.89	0.61
1:A:302:PHE:O	1:A:306:VAL:HG12	2.06	0.56
1:A:319:PRO:HB2	1:A:327:GLN:NE2	2.22	0.54
1:A:339:ASN:HB3	5:A:1193:HOH:O	2.07	0.54
1:A:362:LEU:HB3	1:A:363:PRO:HD2	1.94	0.49
1:A:279:LYS:HE2	5:A:1100:HOH:O	2.13	0.49
1:A:340:ILE:HG23	5:A:1193:HOH:O	2.13	0.48
1:A:317:LYS:HA	1:A:317:LYS:HE3	1.95	0.48
1:A:156:VAL:HG11	1:A:201:LEU:HA	1.96	0.47
1:A:425:GLU:HG3	1:A:426:PHE:CE1	2.49	0.47
4:A:504:1H5:O20	4:A:504:1H5:H1	2.14	0.47
1:A:266:ARG:HB3	1:A:347:TYR:HB2	1.98	0.45
1:A:240:ILE:HG23	1:A:403:TYR:CE2	2.49	0.44
1:A:363:PRO:HA	1:A:366:TYR:CE2	2.53	0.44
1:A:179:ILE:HD13	1:A:179:ILE:HG21	1.66	0.44
1:A:68:ARG:HD3	1:A:68:ARG:HA	1.76	0.44
1:A:373:VAL:HG12	1:A:373:VAL:O	2.18	0.44
1:A:67:LEU:O	1:A:68:ARG:NH1	2.45	0.43
1:A:186:GLU:HG3	1:A:186:GLU:O	2.19	0.43
1:A:283:TYR:HA	1:A:284:ASP:HA	1.89	0.42
1:A:364:GLN:NE2	5:A:1198:HOH:O	2.52	0.41
1:A:186:GLU:HG2	1:A:258:TRP:HB3	2.03	0.40

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)
5:A:1123:HOH:O	5:A:1123:HOH:O[10_664]	1.62	0.58

## 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	377/409 (92%)	364 (97%)	13 (3%)	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	A	321/349 (92%)	304 (95%)	17 (5%)	28	23

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

Mol	Chain	Res	Type
1	A	61	VAL
1	A	83	SER
1	A	125	ARG
1	A	133	THR
1	A	136	LYS
1	A	138	GLU
1	A	167	ASP
1	A	203	LYS
1	A	210	LEU
1	A	258	TRP
1	A	272	GLN
1	A	279	LYS
1	A	306	VAL
1	A	315	THR
1	A	317	LYS
1	A	377	GLN
1	A	438	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	327	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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 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	503	-	3,3,3	0.32	0	3,3,3	0.77	0
4	1H5	A	504	-	27,30,30	1.24	3 (11%)	25,43,43	2.18	7 (28%)

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
3	DMS	A	503	-	-	0/0/0/0	0/0/0/0
4	1H5	A	504	-	-	0/13/35/35	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	504	1H5	C1-N17	-2.29	1.37	1.41
4	A	504	1H5	C8-C10	2.13	1.57	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	504	1H5	C24-C23	2.80	1.45	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	504	1H5	F15-C10-C11	-7.22	102.19	108.27
4	A	504	1H5	C23-C22-N21	-3.95	117.85	123.70
4	A	504	1H5	C3-C4-C5	-3.46	121.14	124.00
4	A	504	1H5	C3-C2-C1	-2.28	117.73	120.28
4	A	504	1H5	C2-C1-C6	2.12	122.22	119.69
4	A	504	1H5	C22-N21-C19	2.64	122.46	117.43
4	A	504	1H5	C24-C23-C22	2.86	120.91	117.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504	1H5	2	0

## 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, 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	381/409 (93%)	0.13	33 (8%) 13 18	19, 33, 81, 125	37 (9%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	GLY	7.4
1	A	372	ASP	6.6
1	A	332	GLN	6.2
1	A	219	GLY	5.6
1	A	134	GLN	5.4
1	A	335	THR	4.8
1	A	336	THR	4.6
1	A	333	ALA	4.5
1	A	331	TRP	4.2
1	A	330	CYS	3.7
1	A	133	THR	3.6
1	A	314	SER	3.4
1	A	340	ILE	3.4
1	A	426	PHE	3.4
1	A	378	ASP	3.3
1	A	218	ALA	3.3
1	A	58	GLY	3.2
1	A	229	ALA	3.2
1	A	375	THR	3.1
1	A	376	SER	3.1
1	A	339	ASN	2.9
1	A	374	ALA	2.8
1	A	337	PRO	2.7
1	A	373	VAL	2.7
1	A	317	LYS	2.7
1	A	59	SER	2.6
1	A	61	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	341	PHE	2.4
1	A	422	VAL	2.3
1	A	338	TRP	2.3
1	A	320	ASP	2.2
1	A	424	ASP	2.1
1	A	315	THR	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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	DMS	A	503	4/4	0.98	0.11	3.36	62,64,65,66	0
2	NA	A	502	1/1	0.96	0.16	1.23	55,55,55,55	0
4	1H5	A	504	28/28	0.98	0.16	0.53	27,30,34,34	0
2	NA	A	501	1/1	0.92	0.17	-	56,56,56,56	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.