



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:00 PM UTC

PDB ID : 2OF0 / pdb_00002of0
Title : X-ray crystal structure of beta secretase complexed with compound 5
Authors : Patel, S.
Deposited on : 2007-01-02
Resolution : 2.25 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
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

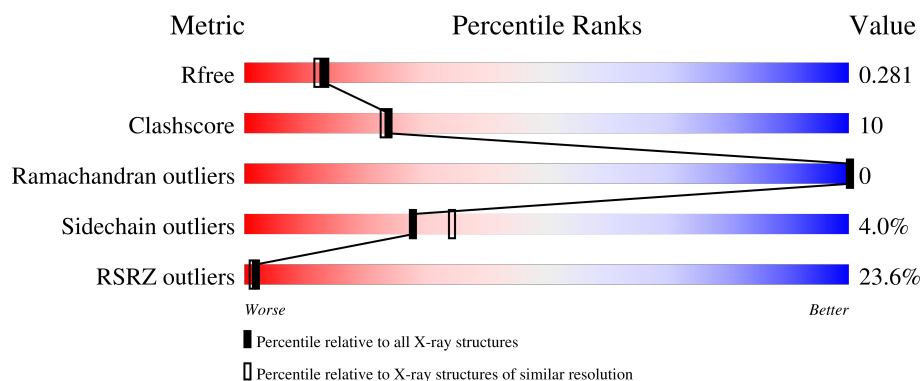
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	402	22% 76% 16% 6%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3171 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
			Total	C	N	O	S			
1	A	377	2966	1898	493	561	14	15	0	0

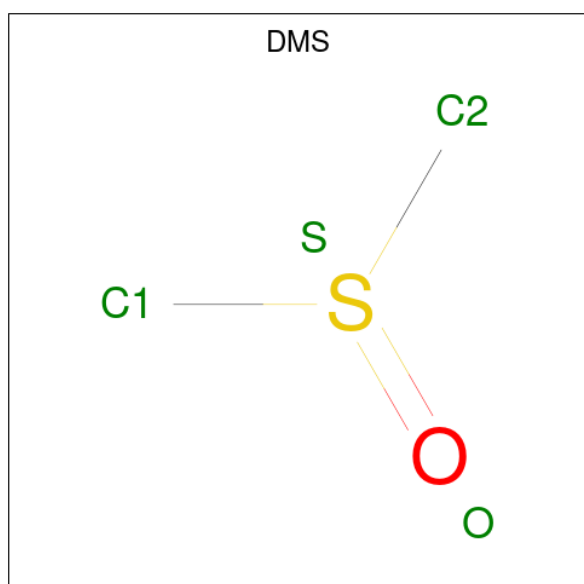
There are 2 discrepancies between the modelled and reference sequences:

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 (CCD ID: IOD) (formula: I).

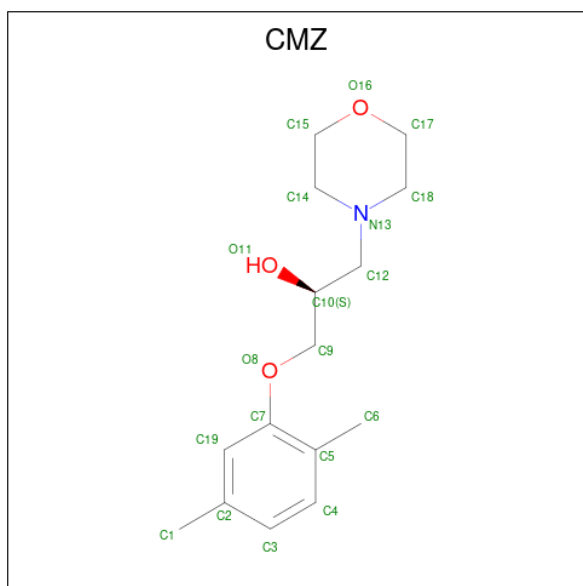
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	I	0	0
			3	3		

- Molecule 3 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



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

- Molecule 4 is (2S)-1-(2,5-dimethylphenoxy)-3-morpholin-4-ylpropan-2-ol (CCD ID: CMZ) (formula: C₁₅H₂₃NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			19	15	1	3		

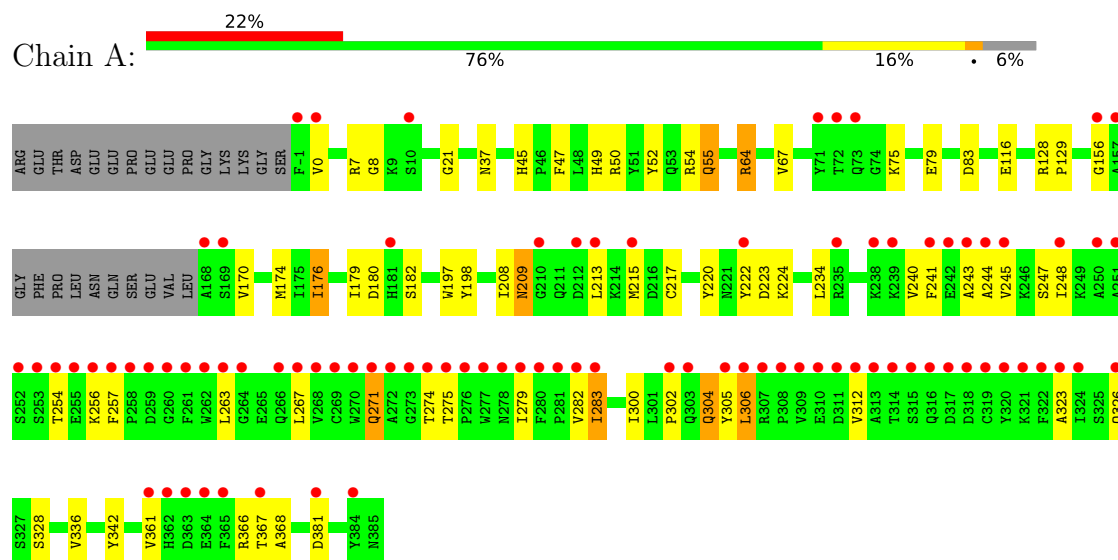
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	179	Total	O	0	0
			179	179		

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, α , β , γ	102.41Å 102.41Å 169.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.19 – 2.25 38.19 – 2.25	Depositor EDS
% Data completeness (in resolution range)	97.3 (38.19-2.25) 97.3 (38.19-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.2.0019c	Depositor
R, R_{free}	0.220 , 0.280 0.226 , 0.281	Depositor DCC
R_{free} test set	1278 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3171	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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: IOD, DMS, CMZ

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	0.84	1/3041 (0.0%)	0.89	4/4132 (0.1%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	64	ARG	CD-NE	-18.76	1.20	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	64	ARG	CG-CD-NE	8.42	130.52	112.00
1	A	271	GLN	CA-CB-CG	6.99	128.08	114.10
1	A	381	ASP	CA-CB-CG	6.61	119.21	112.60
1	A	64	ARG	CD-NE-CZ	6.01	132.82	124.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	64	ARG	Sidechain
1	A	7	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	2966	0	2878	58	0
2	A	3	0	0	1	0
3	A	4	0	6	0	0
4	A	19	0	23	0	0
5	A	179	0	0	3	0
All	All	3171	0	2907	59	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 (59) 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:A:388:IOD:I	5:A:550:HOH:O	2.26	1.20
1:A:215:MET:HE1	1:A:243:ALA:HB3	1.39	1.04
1:A:215:MET:CE	1:A:243:ALA:HB3	1.95	0.96
1:A:37:ASN:HD21	1:A:128:ARG:H	1.29	0.80
1:A:208:ILE:HD12	1:A:213:LEU:HD11	1.67	0.77
1:A:241:PHE:CE1	1:A:245:VAL:HG21	2.24	0.72
1:A:241:PHE:CZ	1:A:245:VAL:HG21	2.26	0.70
1:A:241:PHE:CD2	1:A:326:GLN:HG2	2.30	0.67
1:A:271:GLN:HB2	1:A:274:THR:HG21	1.77	0.65
1:A:209:ASN:ND2	5:A:509:HOH:O	2.31	0.62
1:A:215:MET:CE	1:A:243:ALA:CB	2.75	0.62
1:A:156:GLY:HA2	1:A:170:VAL:HB	1.83	0.61
1:A:241:PHE:CE1	1:A:245:VAL:CG2	2.84	0.61
1:A:215:MET:HE2	1:A:243:ALA:HB3	1.82	0.59
1:A:208:ILE:CD1	1:A:213:LEU:HD11	2.34	0.57
1:A:283:ILE:HG23	1:A:300:ILE:CG1	2.34	0.57
1:A:215:MET:HE2	1:A:243:ALA:CB	2.35	0.57
1:A:208:ILE:HD13	1:A:247:SER:HB3	1.89	0.54
1:A:282:VAL:HG13	1:A:366:ARG:NH1	2.21	0.54
1:A:283:ILE:HG23	1:A:300:ILE:HG12	1.89	0.54
1:A:21:GLY:HA2	1:A:83:ASP:OD1	2.08	0.54
1:A:213:LEU:HD23	1:A:215:MET:HE3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:THR:CB	1:A:279:ILE:HD12	2.38	0.54
1:A:52:TYR:OH	1:A:83:ASP:OD2	2.24	0.52
1:A:361:VAL:O	1:A:361:VAL:HG23	2.10	0.52
1:A:282:VAL:HG13	1:A:366:ARG:HH11	1.75	0.51
1:A:156:GLY:HA2	1:A:170:VAL:CB	2.40	0.51
1:A:254:THR:HB	1:A:279:ILE:HD12	1.92	0.51
1:A:217:CYS:HA	1:A:220:TYR:CD1	2.47	0.50
1:A:323:ALA:HB1	1:A:336:VAL:HG21	1.93	0.50
1:A:55:GLN:HE21	1:A:55:GLN:H	1.60	0.49
1:A:49:HIS:HD2	5:A:559:HOH:O	1.96	0.48
1:A:279:ILE:HG22	1:A:279:ILE:O	2.14	0.47
1:A:367:THR:HG22	1:A:368:ALA:N	2.30	0.46
1:A:197:TRP:CG	1:A:198:TYR:H	2.34	0.45
1:A:174:MET:HE3	1:A:176:ILE:HD11	1.98	0.45
1:A:222:TYR:HA	1:A:223:ASP:HA	1.81	0.45
1:A:271:GLN:HB2	1:A:274:THR:CG2	2.45	0.45
1:A:8:GLY:C	1:A:170:VAL:HG22	2.41	0.44
1:A:213:LEU:N	1:A:213:LEU:CD1	2.81	0.44
1:A:220:TYR:HA	1:A:240:VAL:HG21	1.99	0.43
1:A:302:PRO:O	1:A:306:LEU:HB2	2.19	0.43
1:A:305:TYR:HA	1:A:323:ALA:HB3	2.00	0.43
1:A:209:ASN:HD22	1:A:209:ASN:HA	1.71	0.43
1:A:156:GLY:HA2	1:A:170:VAL:CG1	2.48	0.43
1:A:156:GLY:HA2	1:A:170:VAL:HG12	2.00	0.43
1:A:179:ILE:HG23	1:A:342:TYR:HE2	1.83	0.43
1:A:275:THR:O	1:A:275:THR:HG23	2.19	0.42
1:A:67:VAL:CG1	1:A:129:PRO:HD3	2.49	0.42
1:A:302:PRO:HB2	1:A:306:LEU:HD22	2.01	0.42
1:A:54:ARG:NH1	1:A:79:GLU:OE2	2.49	0.42
1:A:256:LYS:O	1:A:257:PHE:CD2	2.73	0.41
1:A:45:HIS:CD2	1:A:47:PHE:H	2.39	0.41
1:A:244:ALA:O	1:A:248:ILE:HG13	2.20	0.41
1:A:180:ASP:OD1	1:A:182:SER:OG	2.37	0.41
1:A:312:VAL:O	1:A:312:VAL:HG23	2.21	0.41
1:A:50:ARG:O	1:A:116:GLU:HG2	2.21	0.40
1:A:283:ILE:HG23	1:A:300:ILE:HG13	2.03	0.40
1:A:304:GLN:HE21	1:A:304:GLN:CA	2.34	0.40

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%)	360 (96%)	13 (4%)	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	321/343 (94%)	308 (96%)	13 (4%)	28	34

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	VAL
1	A	55	GLN
1	A	75	LYS
1	A	176	ILE
1	A	209	ASN
1	A	224	LYS
1	A	234	LEU
1	A	263	LEU
1	A	267	LEU
1	A	283	ILE
1	A	304	GLN
1	A	306	LEU
1	A	328	SER

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	37	ASN
1	A	49	HIS
1	A	55	GLN
1	A	89	HIS
1	A	114	ASN
1	A	211	GLN
1	A	233	ASN
1	A	266	GLN
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 oligosaccharides 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	389	-	3,3,3	2.70	1 (33%)	3,3,3	0.69	0
4	CMZ	A	390	-	20,20,20	0.56	0	26,26,26	0.98	0

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	CMZ	A	390	-	-	0/9/17/17	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	389	DMS	O-S	4.54	1.80	1.50

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](#)

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	377/402 (93%)	0.90	89 (23%) 2 1	20, 38, 92, 116	7 (1%)

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	277	TRP	8.2
1	A	313	ALA	7.5
1	A	319	CYS	6.6
1	A	312	VAL	6.4
1	A	314	THR	6.4
1	A	309	VAL	6.3
1	A	157	ALA	6.1
1	A	280	PHE	6.1
1	A	276	PRO	6.0
1	A	260	GLY	5.8
1	A	365	PHE	5.7
1	A	320	TYR	5.7
1	A	275	THR	5.6
1	A	306	LEU	5.4
1	A	272	ALA	5.3
1	A	267	LEU	5.1
1	A	279	ILE	4.8
1	A	270	TRP	4.8
1	A	254	THR	4.7
1	A	308	PRO	4.7
1	A	268	VAL	4.6
1	A	310	GLU	4.5
1	A	245	VAL	4.4
1	A	244	ALA	4.2
1	A	273	GLY	4.0
1	A	271	GLN	4.0
1	A	307	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	264	GLY	3.8
1	A	367	THR	3.7
1	A	305	TYR	3.7
1	A	263	LEU	3.6
1	A	384	TYR	3.6
1	A	317	ASP	3.6
1	A	274	THR	3.6
1	A	257	PHE	3.5
1	A	73	GLN	3.4
1	A	261	PHE	3.4
1	A	278	ASN	3.3
1	A	242	GLU	3.3
1	A	71	TYR	3.3
1	A	256	LYS	3.2
1	A	262	TRP	3.2
1	A	250	ALA	3.1
1	A	251	ALA	3.1
1	A	269	CYS	3.1
1	A	259	ASP	3.1
1	A	311	ASP	3.1
1	A	281	PRO	3.0
1	A	318	ASP	3.0
1	A	315	SER	3.0
1	A	215	MET	2.9
1	A	362	HIS	2.9
1	A	241	PHE	2.9
1	A	169	SER	2.9
1	A	302	PRO	2.8
1	A	322	PHE	2.8
1	A	222	TYR	2.8
1	A	303	GLN	2.7
1	A	363	ASP	2.7
1	A	248	ILE	2.7
1	A	283	ILE	2.6
1	A	168	ALA	2.6
1	A	252	SER	2.6
1	A	266	GLN	2.6
1	A	316	GLN	2.6
1	A	326	GLN	2.6
1	A	181	HIS	2.6
1	A	243	ALA	2.5
1	A	364	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	10	SER	2.5
1	A	324	ILE	2.5
1	A	323	ALA	2.4
1	A	255	GLU	2.4
1	A	253	SER	2.4
1	A	156	GLY	2.3
1	A	210	GLY	2.3
1	A	-1	PHE	2.2
1	A	0	VAL	2.2
1	A	361	VAL	2.2
1	A	212	ASP	2.2
1	A	213	LEU	2.2
1	A	282	VAL	2.2
1	A	235	ARG	2.2
1	A	258	PRO	2.2
1	A	381	ASP	2.1
1	A	321	LYS	2.1
1	A	238	LYS	2.0
1	A	72	THR	2.0
1	A	239	LYS	2.0

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(Å ²)	Q<0.9
4	CMZ	A	390	19/19	0.83	0.19	51,59,69,70	0
3	DMS	A	389	4/4	0.94	0.16	55,57,61,61	0
2	IOD	A	388	1/1	0.95	0.14	47,47,47,47	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IOD	A	387	1/1	0.97	0.06	53,53,53,53	1
2	IOD	A	386	1/1	1.00	0.01	29,29,29,29	1

6.5 Other polymers [i](#)

There are no such residues in this entry.