



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:40 AM UTC

PDB ID : 3WB4 / pdb_00003wb4
Title : Crystal Structure of beta secetase in complex with 2-amino-3,6-dimethyl-6-(2-phenylethyl)-3,4,5,6-tetrahydropyrimidin-4-one
Authors : Yonezawa, S.; Fujiwara, K.; Yamamoto, T.; Hattori, K.; Yamakawa, H.; Muto, C.; Hosono, M.; Tanaka, Y.; Nakano, T.; Takemoto, H.; Arisawa, M.; Shuto, S.
Deposited on : 2013-05-13
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

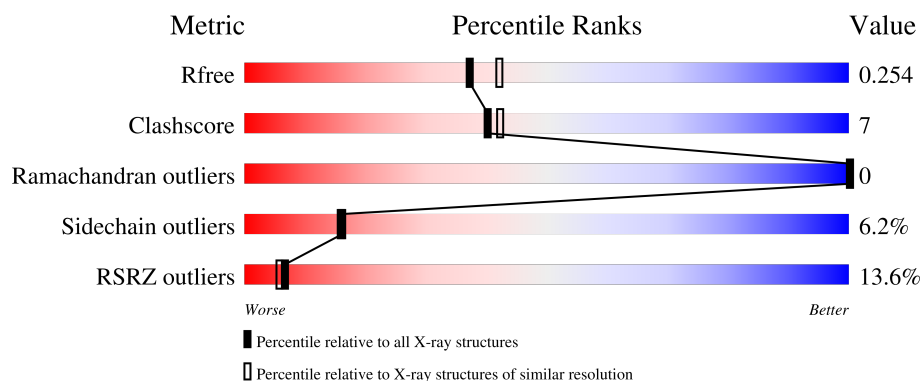
1 Overall quality at a glance

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	416	12% 71% 14% • 13%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2854 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.

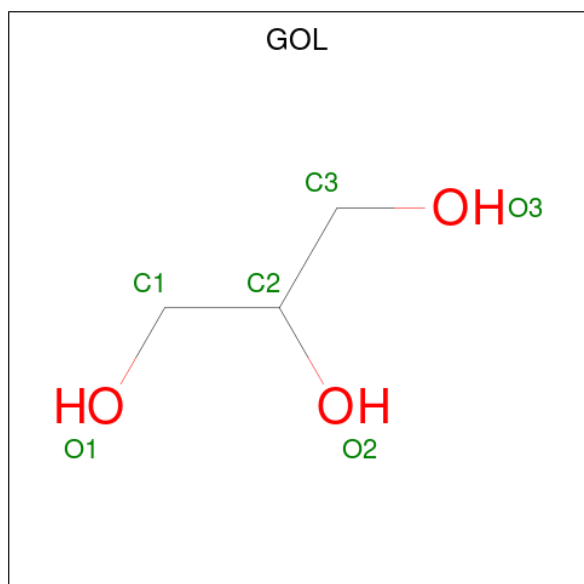
- Molecule 1 is a protein called Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	360	Total	C	N	O	S	0	0	0
			2709	1738	448	509	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	GLY	-	expression tag	UNP P56817
A	-21	SER	-	expression tag	UNP P56817
A	-20	HIS	-	expression tag	UNP P56817
A	-19	MET	-	expression tag	UNP P56817

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

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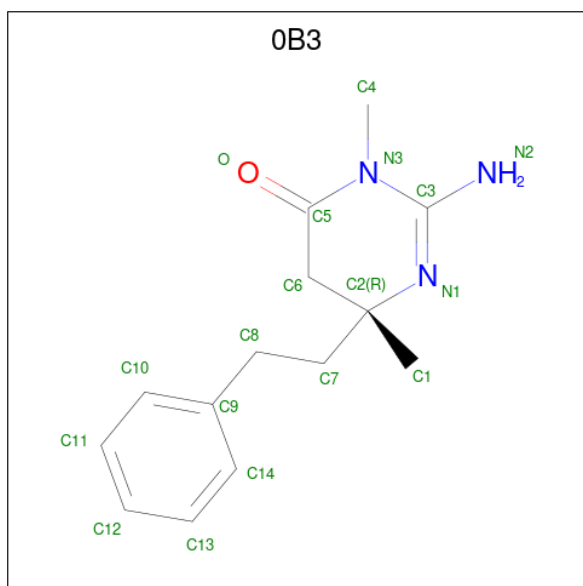
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is IODIDE ION (CCD ID: IOD) (formula: I).

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

- Molecule 4 is (6R)-2-amino-3,6-dimethyl-6-(2-phenylethyl)-5,6-dihydropyrimidin-4(3H)-one (CCD ID: 0B3) (formula: C₁₄H₁₉N₃O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			18	14	3	1		

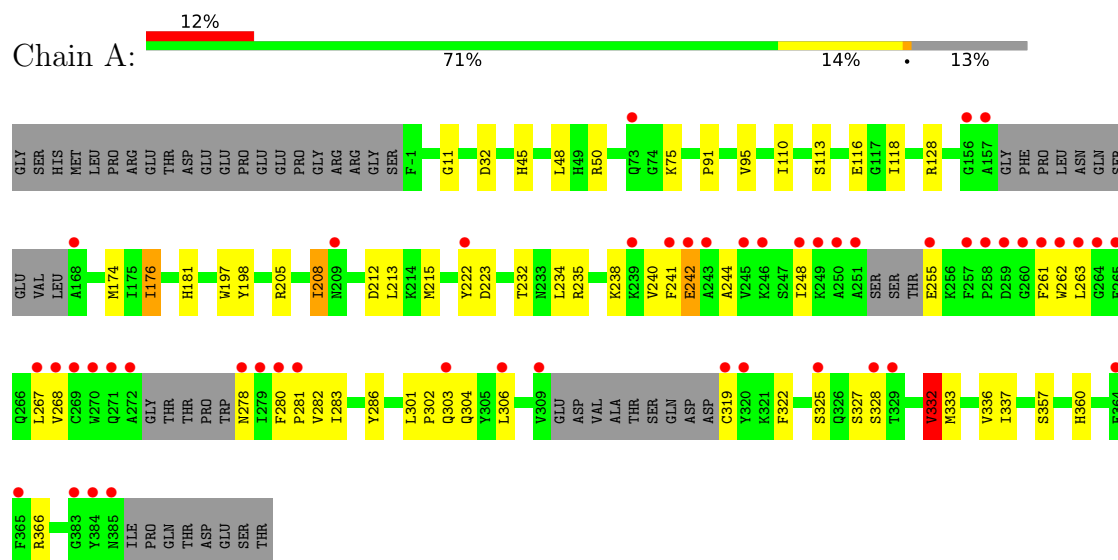
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	101	Total	O	0	0
			101	101		

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	102.21Å 102.21Å 169.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.45 – 2.25 33.45 – 2.25	Depositor EDS
% Data completeness (in resolution range)	95.1 (33.45-2.25) 95.1 (33.45-2.25)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.77 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.211 , 0.254 0.213 , 0.254	Depositor DCC
R_{free} test set	1253 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2854	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, IOD, 0B3

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	0.64	1/2772 (0.0%)	0.92	0/3773

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	332	VAL	CA-CB	5.69	1.61	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2709	0	2534	35	0
2	A	24	0	32	4	0
3	A	2	0	0	1	0
4	A	18	0	19	1	0
5	A	101	0	0	0	0
All	All	2854	0	2585	35	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 7.

All (35) 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:215:MET:HE1	1:A:240:VAL:HA	1.59	0.85
1:A:174:MET:HE3	1:A:176:ILE:HD11	1.67	0.76
1:A:235:ARG:HB2	1:A:332:VAL:HG13	1.70	0.73
1:A:181:HIS:HB3	2:A:504:GOL:H11	1.74	0.69
1:A:75:LYS:HE2	3:A:506:IOD:I	2.63	0.68
1:A:11:GLY:H	2:A:501:GOL:H2	1.62	0.64
1:A:302:PRO:O	1:A:306:LEU:HG	1.99	0.62
1:A:248:ILE:HD11	1:A:283:ILE:HD11	1.83	0.61
1:A:205:ARG:HB3	1:A:286:TYR:HB2	1.88	0.56
1:A:50:ARG:HH22	2:A:502:GOL:H2	1.70	0.56
1:A:261:PHE:CZ	1:A:322:PHE:HB2	2.47	0.50
1:A:304:GLN:OE1	1:A:304:GLN:N	2.45	0.49
1:A:110:ILE:HB	1:A:113:SER:HB3	1.95	0.49
1:A:32:ASP:OD2	1:A:118:ILE:HD11	2.14	0.48
1:A:238:LYS:O	1:A:242:GLU:HG2	2.12	0.48
1:A:50:ARG:O	1:A:116:GLU:HG2	2.14	0.47
1:A:222:TYR:HA	1:A:223:ASP:HA	1.57	0.47
1:A:261:PHE:CE1	1:A:322:PHE:HB2	2.49	0.47
1:A:333:MET:HE2	1:A:337:ILE:HG21	1.97	0.45
1:A:110:ILE:HD11	4:A:507:OB3:H17	1.97	0.45
1:A:197:TRP:CG	1:A:198:TYR:H	2.34	0.45
1:A:248:ILE:HG23	1:A:281:PRO:HD2	1.99	0.45
1:A:208:ILE:HD13	1:A:244:ALA:HA	2.00	0.43
1:A:50:ARG:NH1	2:A:502:GOL:O1	2.49	0.43
1:A:282:VAL:HG12	1:A:301:LEU:HD23	2.00	0.42
1:A:241:PHE:CZ	1:A:262:TRP:O	2.72	0.42
1:A:241:PHE:HZ	1:A:262:TRP:O	2.02	0.42
1:A:232:THR:O	1:A:336:VAL:HG23	2.19	0.42
1:A:268:VAL:O	1:A:319:CYS:HA	2.19	0.42
1:A:357:SER:HB3	1:A:360:HIS:HB3	2.01	0.41
1:A:45:HIS:HB3	1:A:48:LEU:HG	2.03	0.41
1:A:91:PRO:HD3	1:A:176:ILE:HB	2.02	0.41
1:A:278:ASN:C	1:A:280:PHE:H	2.28	0.41
1:A:242:GLU:HG2	1:A:242:GLU:H	1.66	0.40
1:A:333:MET:CE	1:A:337:ILE:HG21	2.52	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	350/416 (84%)	338 (97%)	12 (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	272/356 (76%)	255 (94%)	17 (6%)	16	16

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

Mol	Chain	Res	Type
1	A	95	VAL
1	A	128	ARG
1	A	176	ILE
1	A	208	ILE
1	A	212	ASP
1	A	213	LEU
1	A	234	LEU
1	A	242	GLU
1	A	255	GLU
1	A	263	LEU
1	A	267	LEU
1	A	303	GLN
1	A	325	SER

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Mol	Chain	Res	Type
1	A	327	SER
1	A	328	SER
1	A	332	VAL
1	A	366	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	HIS
1	A	98	ASN
1	A	233	ASN

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 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	$\# Z > 2$
4	0B3	A	507	-	18,19,19	0.82	1 (5%)	21,27,27	1.48	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	502	-	5,5,5	0.37	0	5,5,5	0.20	0
2	GOL	A	503	-	5,5,5	0.34	0	5,5,5	0.55	0
2	GOL	A	504	-	5,5,5	0.32	0	5,5,5	0.40	0
2	GOL	A	501	-	5,5,5	0.41	0	5,5,5	0.61	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	0B3	A	507	-	-	0/6/24/24	0/2/2/2
2	GOL	A	502	-	-	4/4/4/4	-
2	GOL	A	503	-	-	0/4/4/4	-
2	GOL	A	504	-	-	0/4/4/4	-
2	GOL	A	501	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	507	0B3	C5-N3	-2.41	1.35	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	507	0B3	C5-N3-C3	-5.42	118.27	124.20
4	A	507	0B3	C4-N3-C3	2.65	123.45	120.70

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-O2
2	A	502	GOL	O1-C1-C2-C3
2	A	502	GOL	C1-C2-C3-O3
2	A	501	GOL	O1-C1-C2-C3
2	A	502	GOL	O1-C1-C2-O2
2	A	502	GOL	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	507	0B3	1	0
2	A	502	GOL	2	0
2	A	504	GOL	1	0
2	A	501	GOL	1	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, 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	360/416 (86%)	0.48	49 (13%) 7 6	21, 41, 88, 125	1 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260	GLY	7.2
1	A	157	ALA	6.2
1	A	270	TRP	6.1
1	A	280	PHE	6.1
1	A	272	ALA	6.0
1	A	271	GLN	5.1
1	A	319	CYS	5.0
1	A	259	ASP	4.9
1	A	263	LEU	4.6
1	A	262	TRP	4.6
1	A	385	ASN	4.5
1	A	306	LEU	4.3
1	A	279	ILE	4.2
1	A	261	PHE	4.2
1	A	320	TYR	4.0
1	A	268	VAL	4.0
1	A	264	GLY	3.9
1	A	258	PRO	3.9
1	A	250	ALA	3.9
1	A	309	VAL	3.8
1	A	168	ALA	3.8
1	A	249	LYS	3.7
1	A	257	PHE	3.6
1	A	267	LEU	3.5
1	A	269	CYS	3.4
1	A	248	ILE	3.4
1	A	365	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	222	TYR	3.1
1	A	383	GLY	3.0
1	A	251	ALA	2.9
1	A	384	TYR	2.6
1	A	243	ALA	2.6
1	A	278	ASN	2.6
1	A	246	LYS	2.4
1	A	241	PHE	2.4
1	A	73	GLN	2.4
1	A	245	VAL	2.3
1	A	255	GLU	2.3
1	A	329	THR	2.3
1	A	242	GLU	2.2
1	A	265	GLU	2.2
1	A	209	ASN	2.2
1	A	303	GLN	2.2
1	A	156	GLY	2.2
1	A	364	GLU	2.1
1	A	328	SER	2.1
1	A	325	SER	2.1
1	A	281	PRO	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
3	IOD	A	506	1/1	0.77	0.22	194,194,194,194	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GOL	A	501	6/6	0.81	0.17	51,54,56,56	0
2	GOL	A	503	6/6	0.87	0.16	53,61,68,73	0
2	GOL	A	502	6/6	0.87	0.13	63,66,67,68	0
2	GOL	A	504	6/6	0.91	0.12	55,59,66,67	0
3	IOD	A	505	1/1	0.92	0.21	129,129,129,129	0
4	0B3	A	507	18/18	0.92	0.11	29,40,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.