



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:32 PM UTC

PDB ID : 2OHP / pdb_00002ohp
Title : X-ray crystal structure of beta secretase complexed with compound 3
Authors : Patel, S.
Deposited on : 2007-01-10
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

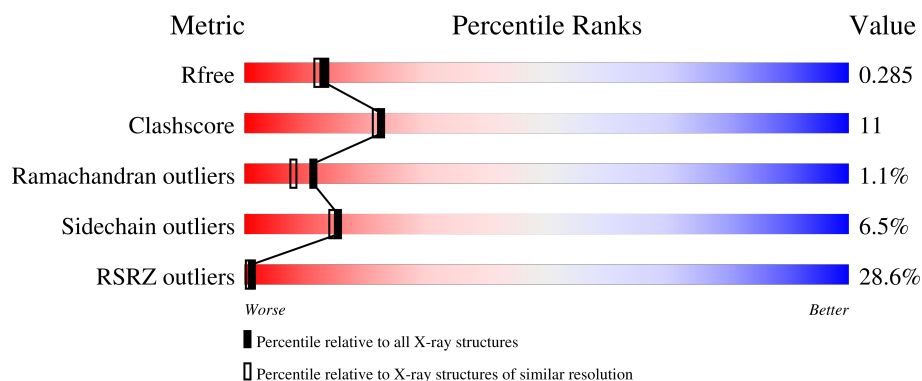
1 Overall quality at a glance

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	27% 74% 18% 6%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3129 atoms, of which 16 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

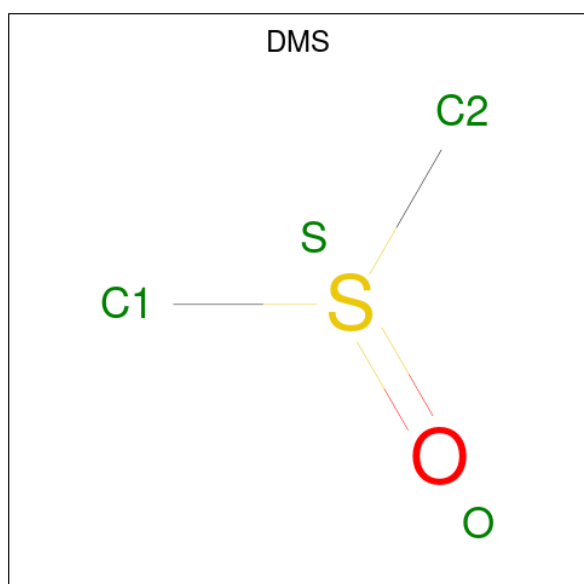
There are 2 discrepancies between the modelled and reference sequences:

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

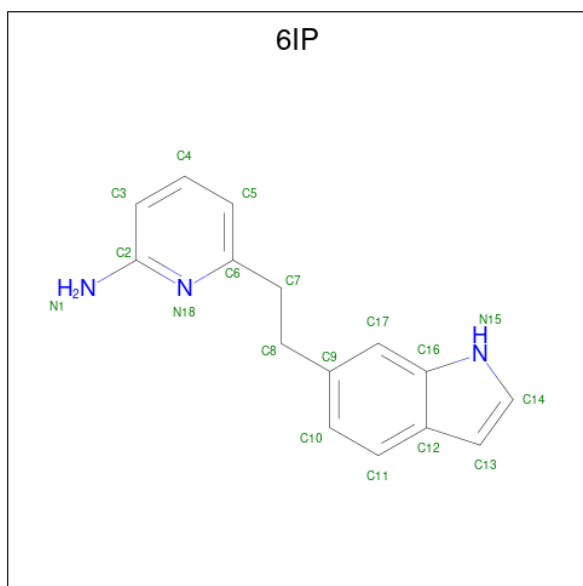
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total I 2 2	0	0

- 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 6-[2-(1H-INDOL-6-YL)ETHYL]PYRIDIN-2-AMINE (CCD ID: 6IP) (formula: C₁₅H₁₅N₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	N	0	0
			34	15	16	3		

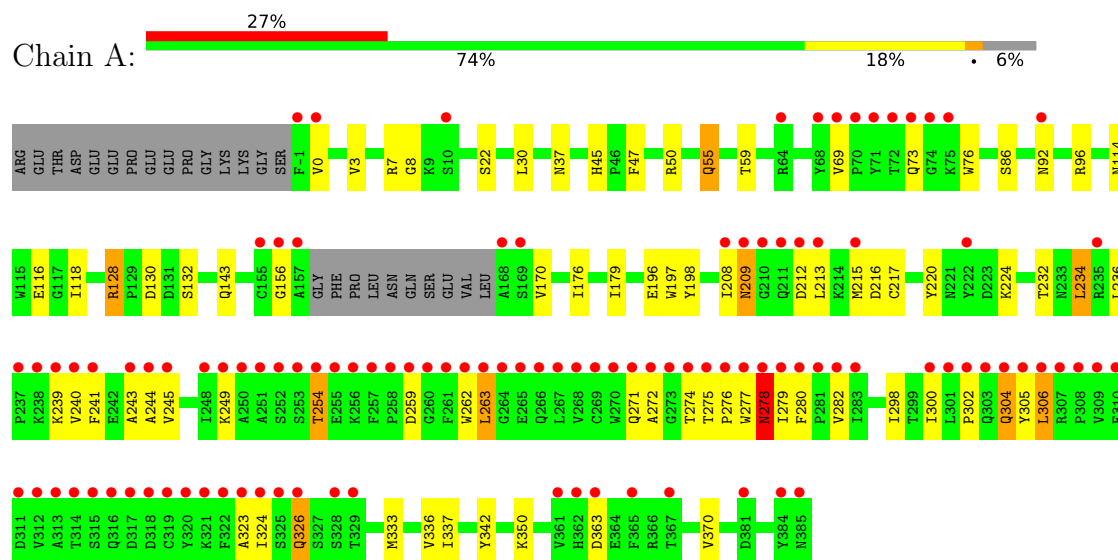
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	123	Total	O	0	0
			123	123		

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	102.54Å 102.54Å 169.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.58 – 2.25 47.58 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.58-2.25) 99.7 (47.58-2.25)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.26 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.2.0019g	Depositor
R, R_{free}	0.232 , 0.281 0.238 , 0.285	Depositor DCC
R_{free} test set	1304 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.1	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	0.92	EDS
Total number of atoms	3129	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 3.69% 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: DMS, 6IP, IOD

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	0.80	1/3041 (0.0%)	0.88	0/4132

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3	VAL	CA-CB	5.66	1.60	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	2966	0	2878	61	0
2	A	2	0	0	1	0
3	A	4	0	6	0	0
4	A	18	16	15	2	0
5	A	123	0	0	2	0
All	All	3113	16	2899	62	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 11.

All (62) 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:243:ALA:HB3	1.30	1.12
1:A:215:MET:HE1	1:A:243:ALA:CB	2.05	0.86
1:A:37:ASN:HD21	1:A:128:ARG:H	1.30	0.78
1:A:323:ALA:HB1	1:A:336:VAL:HG21	1.67	0.76
2:A:386:IOD:I	5:A:407:HOH:O	2.75	0.74
1:A:241:PHE:CE1	1:A:245:VAL:HG23	2.30	0.67
1:A:300:ILE:HD13	1:A:337:ILE:HD13	1.77	0.67
1:A:96:ARG:H	1:A:143:GLN:HE22	1.42	0.66
1:A:208:ILE:HD13	1:A:213:LEU:HD11	1.78	0.66
1:A:241:PHE:CZ	1:A:245:VAL:HG21	2.32	0.65
1:A:213:LEU:HD23	1:A:215:MET:HE3	1.78	0.64
1:A:241:PHE:CE1	1:A:245:VAL:CG2	2.81	0.63
1:A:271:GLN:HB2	1:A:274:THR:HG21	1.81	0.62
1:A:209:ASN:HA	1:A:282:VAL:HG22	1.83	0.61
1:A:323:ALA:CB	1:A:336:VAL:HG21	2.35	0.55
1:A:254:THR:CB	1:A:279:ILE:HD12	2.36	0.55
1:A:156:GLY:HA2	1:A:170:VAL:CB	2.38	0.54
1:A:254:THR:HB	1:A:279:ILE:HD12	1.90	0.53
1:A:305:TYR:HB2	1:A:324:ILE:HD11	1.91	0.53
1:A:118:ILE:HD12	4:A:389:6IP:H81	1.92	0.52
1:A:8:GLY:C	1:A:170:VAL:HG22	2.34	0.52
1:A:232:THR:O	1:A:336:VAL:HG23	2.09	0.51
1:A:156:GLY:HA2	1:A:170:VAL:HG12	1.93	0.51
1:A:272:ALA:O	1:A:274:THR:HG23	2.11	0.51
1:A:55:GLN:HE21	1:A:55:GLN:H	1.59	0.51
1:A:156:GLY:HA2	1:A:170:VAL:HB	1.92	0.51
1:A:333:MET:CE	1:A:337:ILE:HG21	2.41	0.51
1:A:179:ILE:HG23	1:A:342:TYR:HE2	1.76	0.51
1:A:215:MET:O	1:A:216:ASP:C	2.53	0.50
1:A:259:ASP:O	1:A:263:LEU:HD22	2.11	0.50
1:A:215:MET:CE	1:A:243:ALA:CB	2.84	0.49
1:A:234:LEU:O	1:A:324:ILE:HA	2.13	0.49
1:A:50:ARG:O	1:A:116:GLU:HG2	2.13	0.48
1:A:69:VAL:HG21	1:A:76:TRP:CZ2	2.48	0.48
1:A:279:ILE:HG22	1:A:279:ILE:O	2.13	0.47
1:A:220:TYR:HA	1:A:240:VAL:HG21	1.94	0.47
1:A:50:ARG:HH22	1:A:114:ASN:ND2	2.14	0.46
1:A:333:MET:HE3	1:A:337:ILE:HG21	1.96	0.46
1:A:249:LYS:HZ3	1:A:262:TRP:CD1	2.33	0.46
1:A:73:GLN:HE21	1:A:73:GLN:HA	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:ASP:OD2	1:A:132:SER:OG	2.29	0.45
1:A:280:PHE:HB2	1:A:302:PRO:HG2	1.98	0.45
1:A:323:ALA:HB1	1:A:336:VAL:CG2	2.43	0.45
1:A:304:GLN:O	1:A:336:VAL:HG13	2.17	0.44
1:A:236:LEU:O	1:A:326:GLN:HA	2.17	0.44
1:A:302:PRO:O	1:A:306:LEU:HB2	2.19	0.43
1:A:50:ARG:NH2	1:A:116:GLU:OE2	2.52	0.43
1:A:156:GLY:HA2	1:A:170:VAL:CG1	2.48	0.43
1:A:241:PHE:CE1	1:A:245:VAL:HG21	2.49	0.43
1:A:305:TYR:CB	1:A:324:ILE:HD11	2.48	0.43
1:A:197:TRP:CG	1:A:198:TYR:H	2.36	0.43
1:A:196:GLU:OE2	5:A:492:HOH:O	2.22	0.42
1:A:217:CYS:HA	1:A:220:TYR:CD1	2.54	0.42
1:A:279:ILE:O	1:A:279:ILE:CG2	2.68	0.42
1:A:254:THR:HG21	1:A:279:ILE:CD1	2.49	0.42
1:A:276:PRO:O	1:A:278:ASN:N	2.53	0.41
1:A:304:GLN:C	1:A:336:VAL:HG13	2.45	0.41
1:A:118:ILE:HD12	4:A:389:6IP:C8	2.49	0.41
1:A:298:ILE:HG22	1:A:370:VAL:HG22	2.02	0.41
1:A:45:HIS:CD2	1:A:47:PHE:H	2.39	0.41
1:A:240:VAL:O	1:A:244:ALA:HB2	2.20	0.41
1:A:350:LYS:HE2	1:A:350:LYS:HB3	1.92	0.40

There are no symmetry-related clashes.

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	373/402 (93%)	351 (94%)	18 (5%)	4 (1%)	11 8

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	277	TRP
1	A	278	ASN
1	A	304	GLN
1	A	363	ASP

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%)	300 (94%)	21 (6%)	15	14

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	VAL
1	A	7	ARG
1	A	22	SER
1	A	30	LEU
1	A	55	GLN
1	A	59	THR
1	A	86	SER
1	A	92	ASN
1	A	128	ARG
1	A	176	ILE
1	A	209	ASN
1	A	212	ASP
1	A	224	LYS
1	A	234	LEU
1	A	239	LYS
1	A	254	THR
1	A	263	LEU
1	A	275	THR
1	A	278	ASN
1	A	306	LEU
1	A	326	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	37	ASN
1	A	45	HIS
1	A	49	HIS
1	A	55	GLN
1	A	73	GLN
1	A	89	HIS
1	A	98	ASN
1	A	114	ASN
1	A	143	GLN
1	A	266	GLN
1	A	278	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 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	388	-	3,3,3	2.60	1 (33%)	3,3,3	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	6IP	A	389	-	20,20,20	0.84	1 (5%)	27,27,27	1.40	3 (11%)

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	6IP	A	389	-	-	0/5/5/5	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	388	DMS	O-S	4.37	1.79	1.50
4	A	389	6IP	C14-C13	2.13	1.40	1.36

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	389	6IP	C2-N18-C6	4.35	121.32	118.07
4	A	389	6IP	C5-C6-N18	-2.41	119.36	122.40
4	A	389	6IP	C7-C6-N18	2.14	119.30	116.06

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	389	6IP	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, 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%)	1.19	108 (28%) 1 1	18, 37, 90, 114	2 (0%)

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260	GLY	8.0
1	A	319	CYS	7.0
1	A	313	ALA	6.9
1	A	157	ALA	6.9
1	A	280	PHE	6.6
1	A	365	PHE	6.6
1	A	306	LEU	6.2
1	A	308	PRO	6.2
1	A	314	THR	5.9
1	A	309	VAL	5.7
1	A	254	THR	5.7
1	A	279	ILE	5.7
1	A	73	GLN	5.6
1	A	263	LEU	5.6
1	A	272	ALA	5.5
1	A	259	ASP	5.5
1	A	305	TYR	5.3
1	A	257	PHE	5.2
1	A	245	VAL	4.9
1	A	312	VAL	4.9
1	A	320	TYR	4.9
1	A	71	TYR	4.9
1	A	244	ALA	4.8
1	A	277	TRP	4.6
1	A	310	GLU	4.6
1	A	367	THR	4.5
1	A	282	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	268	VAL	4.5
1	A	275	THR	4.4
1	A	384	TYR	4.4
1	A	251	ALA	4.2
1	A	322	PHE	4.1
1	A	270	TRP	4.1
1	A	168	ALA	4.1
1	A	256	LYS	4.0
1	A	311	ASP	4.0
1	A	250	ALA	4.0
1	A	325	SER	4.0
1	A	307	ARG	3.9
1	A	269	CYS	3.9
1	A	262	TRP	3.9
1	A	258	PRO	3.8
1	A	326	GLN	3.8
1	A	276	PRO	3.8
1	A	281	PRO	3.8
1	A	324	ILE	3.8
1	A	278	ASN	3.7
1	A	328	SER	3.7
1	A	301	LEU	3.7
1	A	318	ASP	3.7
1	A	264	GLY	3.7
1	A	303	GLN	3.5
1	A	72	THR	3.4
1	A	215	MET	3.3
1	A	261	PHE	3.3
1	A	253	SER	3.3
1	A	248	ILE	3.3
1	A	209	ASN	3.3
1	A	74	GLY	3.2
1	A	267	LEU	3.2
1	A	304	GLN	3.2
1	A	316	GLN	3.2
1	A	315	SER	3.1
1	A	317	ASP	3.1
1	A	-1	PHE	3.1
1	A	0	VAL	3.1
1	A	222	TYR	3.0
1	A	266	GLN	3.0
1	A	302	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	213	LEU	3.0
1	A	156	GLY	3.0
1	A	241	PHE	2.9
1	A	361	VAL	2.9
1	A	70	PRO	2.9
1	A	362	HIS	2.9
1	A	323	ALA	2.9
1	A	208	ILE	2.8
1	A	271	GLN	2.8
1	A	68	TYR	2.8
1	A	238	LYS	2.8
1	A	240	VAL	2.8
1	A	273	GLY	2.8
1	A	212	ASP	2.7
1	A	210	GLY	2.7
1	A	329	THR	2.7
1	A	274	THR	2.6
1	A	243	ALA	2.6
1	A	321	LYS	2.6
1	A	10	SER	2.5
1	A	265	GLU	2.5
1	A	252	SER	2.5
1	A	300	ILE	2.4
1	A	237	PRO	2.4
1	A	211	GLN	2.4
1	A	363	ASP	2.3
1	A	69	VAL	2.3
1	A	255	GLU	2.3
1	A	169	SER	2.3
1	A	75	LYS	2.2
1	A	381	ASP	2.2
1	A	385	ASN	2.2
1	A	239	LYS	2.1
1	A	249	LYS	2.1
1	A	155	CYS	2.1
1	A	92	ASN	2.0
1	A	283	ILE	2.0
1	A	64	ARG	2.0
1	A	235	ARG	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($\text{\AA}^2$)	Q<0.9
4	6IP	A	389	18/18	0.80	0.19	31,56,66,67	0
3	DMS	A	388	4/4	0.86	0.24	64,65,65,65	0
2	IOD	A	387	1/1	0.96	0.08	57,57,57,57	1
2	IOD	A	386	1/1	1.00	0.04	37,37,37,37	1

6.5 Other polymers [i](#)

There are no such residues in this entry.