Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2023 – 09:14 AM EDT

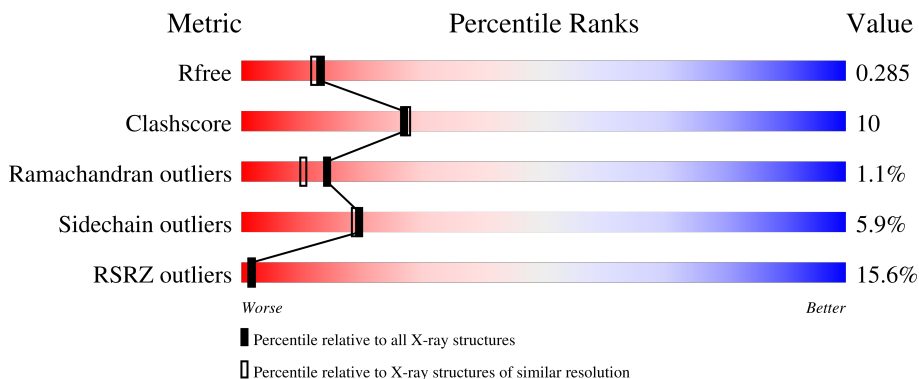|		
PDB ID	:	2OHP
Title	:	X-ray crystal structure of beta secretase complexed with compound 3
Authors	:	Patel, S.
Deposited on	:	2007-01-10
Resolution	:	2.25 Å(reported)

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	Percentile Ranks	Value
Rfree		0.285
Clashscore		10
Ramachandran outliers		1.1%
Sidechain outliers		5.9%
RSRZ outliers		15.6%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (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 <=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	15% / 75% / 16% / 6%

2 Entry composition ⓘ

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
1	A	377	Total 2966	C 1898	N 493	O 561	S 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	2	Total 2	I 2	0	0

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).
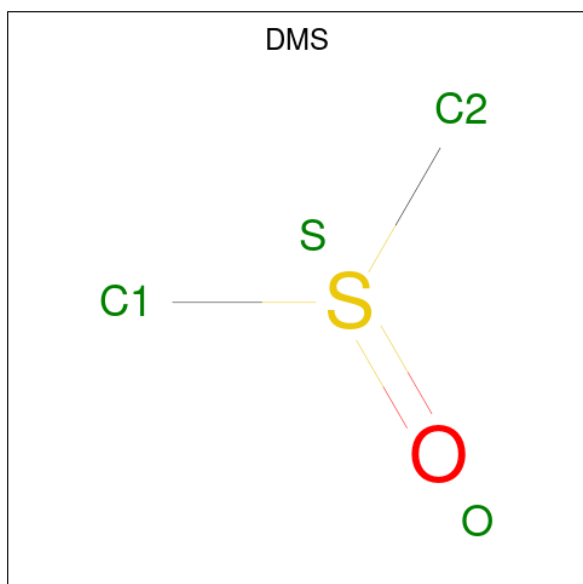
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 1	S 1	0	0

- Molecule 4 is 6-[2-(1H-INDOL-6-YL)ETHYL]PYRIDIN-2-AMINE (three-letter code: 6IP) (formula: $C_{15}H_{15}N_3$).
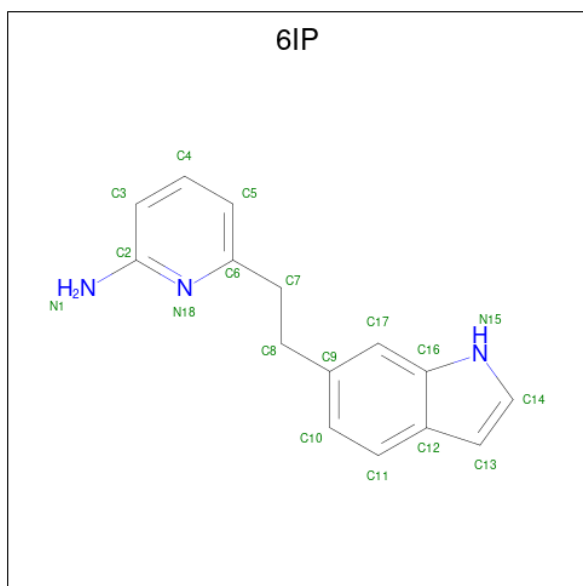
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 34	C 15	H 16	N 3	0	0

- Molecule 5 is water.

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

3 Residue-property plots ⓘ

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
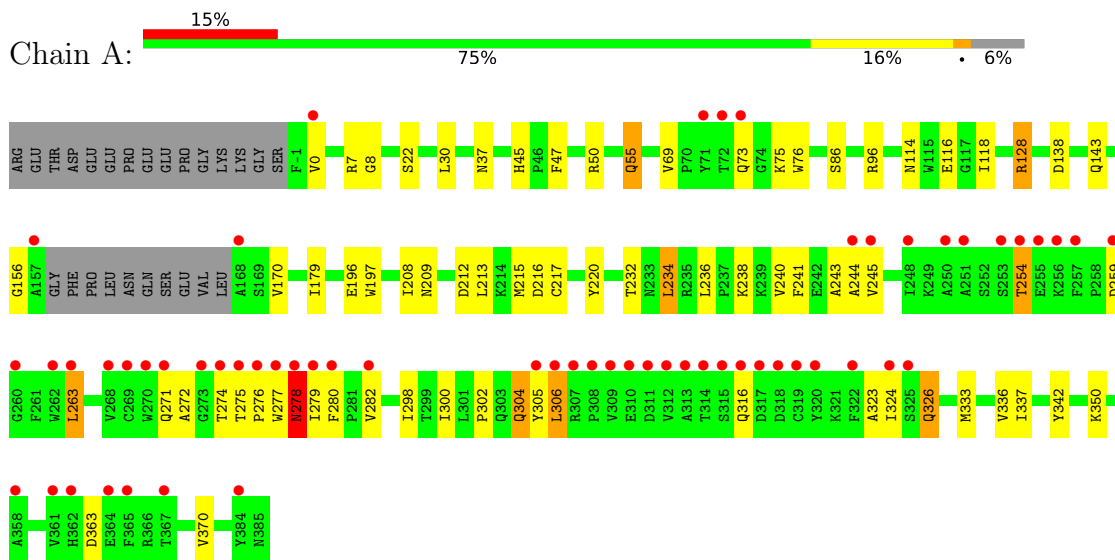
4 Data and refinement statistics (i)

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
$< I/\sigma(I) >$ [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 (5.10%)	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)	0.34 , 50.8	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	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.*

[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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, 6IP

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	0.63	0/3041	0.72	1/4132 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	238	LYS	CD-CE-NZ	5.33	123.97	111.70

There are no chirality outliers.

There are no planarity outliers.

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	59	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	60	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.

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All (60) 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	1.50	0.92
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:215:MET:CE	1:A:243:ALA:HB3	2.23	0.69
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: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:215:MET:CE	1:A:243:ALA:CB	2.84	0.54
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: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:259:ASP:O	1:A:263:LEU:HD22	2.11	0.50
1:A:213:LEU:HD23	1:A:215:MET:HE3	1.95	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:213:LEU:HB3	1:A:215:MET:HE3	1.95	0.48
1:A:69:VAL:HG21	1:A:76:TRP:CZ2	2.48	0.48
1:A:8:GLY:C	1:A:170:VAL:HG22	2.34	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:333:MET:HE3	1:A:337:ILE:HG21	1.95	0.47
1:A:50:ARG:HH22	1:A:114:ASN:ND2	2.14	0.46
1:A:73:GLN:HE21	1:A:73:GLN:HA	1.81	0.46
1:A:215:MET:HE1	1:A:243:ALA:CB	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:MET:O	1:A:216:ASP:C	2.53	0.46
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: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: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 ⓘ

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%)	18 (5%)	4 (1%)	14	10

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	277	TRP

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Mol	Chain	Res	Type
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%)	302 (94%)	19 (6%)	19	19

All (19) 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	75	LYS
1	A	86	SER
1	A	128	ARG
1	A	138	ASP
1	A	197	TRP
1	A	212	ASP
1	A	234	LEU
1	A	254	THR
1	A	263	LEU
1	A	275	THR
1	A	278	ASN
1	A	306	LEU
1	A	316	GLN
1	A	326	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) 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	114	ASN
1	A	143	GLN
1	A	209	ASN
1	A	233	ASN
1	A	278	ASN

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 monosaccharides 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	#$|Z| > 2$
4	6IP	A	389	-	18,20,20	0.81	0	24,27,27	1.39	4 (16%)
3	DMS	A	388	-	3,3,3	2.54	1 (33%)	3,3,3	0.45	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	6IP	A	389	-	-	0/5/5/5	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	388	DMS	O-S	4.26	1.79	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	389	6IP	C2-N18-C6	4.25	121.32	118.10
4	A	389	6IP	C5-C6-N18	-2.40	119.36	122.41
4	A	389	6IP	C9-C17-C16	-2.27	119.09	121.08
4	A	389	6IP	C7-C6-N18	2.25	119.30	115.95

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

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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%)	0.70	59 (15%)	2	1	18, 37, 90, 114	2 (0%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	313	ALA	11.0
1	A	310	GLU	8.8
1	A	319	CYS	8.4
1	A	279	ILE	7.9
1	A	271	GLN	7.5
1	A	314	THR	7.2
1	A	259	ASP	6.3
1	A	269	CYS	5.8
1	A	280	PHE	5.8
1	A	311	ASP	5.5
1	A	260	GLY	5.4
1	A	306	LEU	5.2
1	A	317	ASP	4.9
1	A	365	PHE	4.8
1	A	276	PRO	4.7
1	A	270	TRP	4.7
1	A	254	THR	4.7
1	A	277	TRP	4.6
1	A	157	ALA	4.6
1	A	309	VAL	4.2
1	A	253	SER	4.2
1	A	72	THR	4.1
1	A	273	GLY	3.8
1	A	362	HIS	3.8
1	A	71	TYR	3.7
1	A	168	ALA	3.6
1	A	274	THR	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	73	GLN	3.5
1	A	364	GLU	3.4
1	A	307	ARG	3.4
1	A	244	ALA	3.3
1	A	361	VAL	3.2
1	A	312	VAL	3.2
1	A	315	SER	3.1
1	A	263	LEU	3.0
1	A	305	TYR	3.0
1	A	278	ASN	2.9
1	A	255	GLU	2.8
1	A	268	VAL	2.8
1	A	250	ALA	2.8
1	A	318	ASP	2.7
1	A	257	PHE	2.7
1	A	282	VAL	2.7
1	A	367	THR	2.6
1	A	316	GLN	2.5
1	A	325	SER	2.4
1	A	245	VAL	2.4
1	A	256	LYS	2.3
1	A	0	VAL	2.3
1	A	320	TYR	2.2
1	A	384	TYR	2.2
1	A	324	ILE	2.2
1	A	322	PHE	2.2
1	A	308	PRO	2.1
1	A	358	ALA	2.1
1	A	248	ILE	2.1
1	A	262	TRP	2.1
1	A	275	THR	2.0
1	A	251	ALA	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 monosaccharides 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. 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	6IP	A	389	18/18	0.75	0.24	31,56,66,67	0
2	IOD	A	387	1/1	0.95	0.22	57,57,57,57	1
3	DMS	A	388	4/4	0.96	0.21	64,65,65,65	0
2	IOD	A	386	1/1	1.00	0.09	37,37,37,37	1

6.5 Other polymers ⓘ

There are no such residues in this entry.