



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:02 AM GMT

PDB ID : 3NSH
Title : BACE-1 in complex with ELN475957
Authors : Probst, G.D.; Bowers, S.; Sealy, J.M.; Brecht, E.; Yao, N.
Deposited on : 2010-07-01
Resolution : 2.20 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

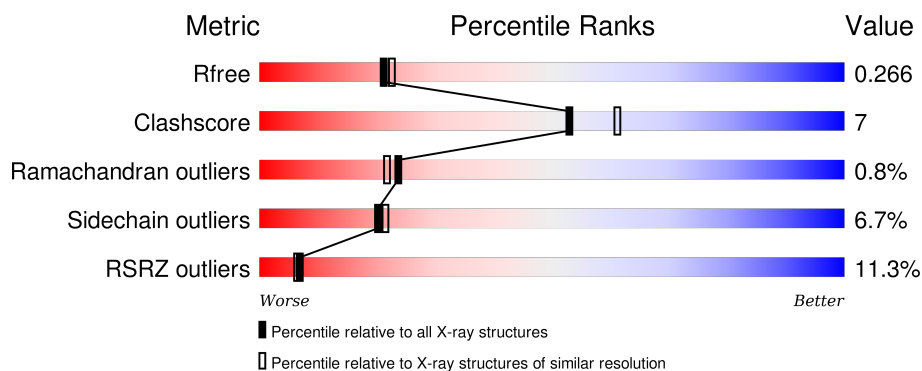
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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 ≥ 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	406	<div> <div>9%</div> <div> <div></div> <div>75%</div> <div>13%</div> <div>• • 8%</div> </div> </div>
1	B	406	<div> <div>12%</div> <div> <div></div> <div>71%</div> <div>18%</div> <div>• 7%</div> </div> </div>
1	C	406	<div> <div>11%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>• 7%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9293 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	372	Total	C	N	O	S	0	0	0
			2928	1876	487	551	14			
1	B	376	Total	C	N	O	S	0	0	0
			2958	1900	491	553	14			
1	C	376	Total	C	N	O	S	0	0	0
			2958	1898	492	554	14			

There are 27 discrepancies between the modelled and reference sequences:

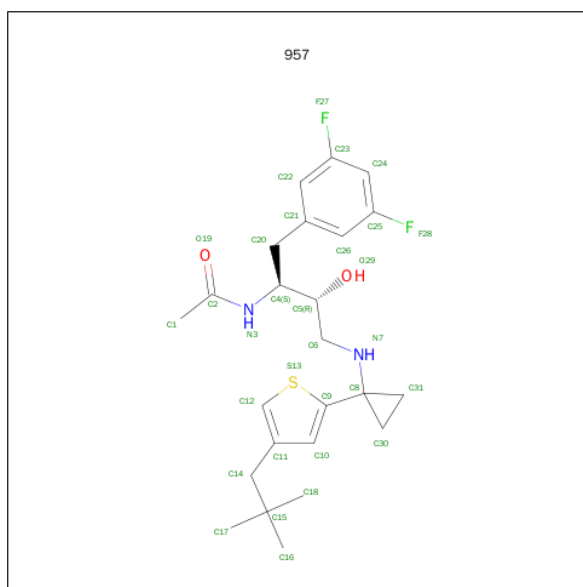
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP P56817
A	399	ARG	-	EXPRESSION TAG	UNP P56817
A	400	SER	-	EXPRESSION TAG	UNP P56817
A	401	HIS	-	EXPRESSION TAG	UNP P56817
A	402	HIS	-	EXPRESSION TAG	UNP P56817
A	403	HIS	-	EXPRESSION TAG	UNP P56817
A	404	HIS	-	EXPRESSION TAG	UNP P56817
A	405	HIS	-	EXPRESSION TAG	UNP P56817
A	406	HIS	-	EXPRESSION TAG	UNP P56817
B	1	MET	-	INITIATING METHIONINE	UNP P56817
B	399	ARG	-	EXPRESSION TAG	UNP P56817
B	400	SER	-	EXPRESSION TAG	UNP P56817
B	401	HIS	-	EXPRESSION TAG	UNP P56817
B	402	HIS	-	EXPRESSION TAG	UNP P56817
B	403	HIS	-	EXPRESSION TAG	UNP P56817
B	404	HIS	-	EXPRESSION TAG	UNP P56817
B	405	HIS	-	EXPRESSION TAG	UNP P56817
B	406	HIS	-	EXPRESSION TAG	UNP P56817
C	1	MET	-	INITIATING METHIONINE	UNP P56817
C	399	ARG	-	EXPRESSION TAG	UNP P56817
C	400	SER	-	EXPRESSION TAG	UNP P56817
C	401	HIS	-	EXPRESSION TAG	UNP P56817
C	402	HIS	-	EXPRESSION TAG	UNP P56817

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Chain	Residue	Modelled	Actual	Comment	Reference
C	403	HIS	-	EXPRESSION TAG	UNP P56817
C	404	HIS	-	EXPRESSION TAG	UNP P56817
C	405	HIS	-	EXPRESSION TAG	UNP P56817
C	406	HIS	-	EXPRESSION TAG	UNP P56817

- Molecule 2 is N-[(1S,2R)-1-(3,5-DIFLUOROBENZYL)-3-({1-[4-(2,2-DIMETHYLPROPYL)THIOPHEN-2-YL]CYCLOPROPYL}AMINO)-2-HYDROXYPROPYL]ACETAMIDE (three-letter code: 957) (formula: C₂₄H₃₂F₂N₂O₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			31	24	2	2	2	1		
2	B	1	Total	C	F	N	O	S	0	0
			31	24	2	2	2	1		
2	C	1	Total	C	F	N	O	S	0	0
			31	24	2	2	2	1		

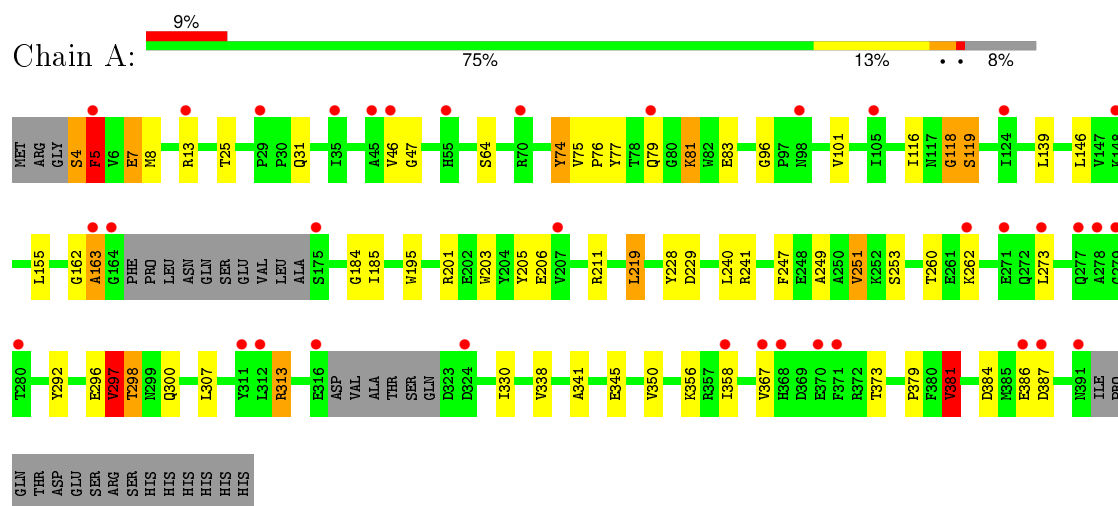
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	121	Total	O	0	0
			121	121		
3	B	108	Total	O	0	0
			108	108		
3	C	127	Total	O	0	0
			127	127		

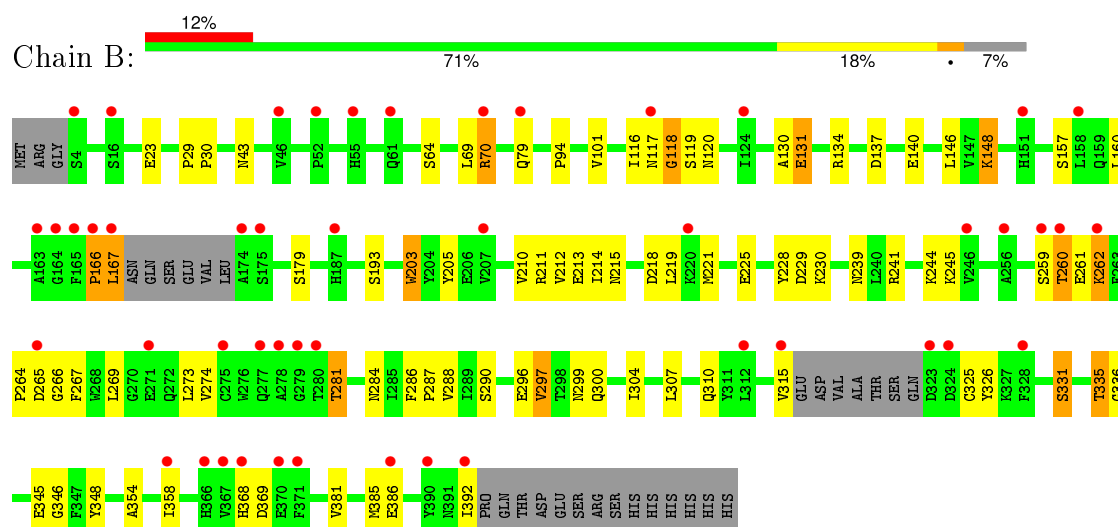
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

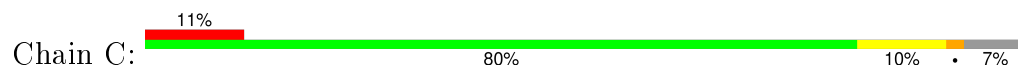
• Molecule 1: Beta-secretase 1

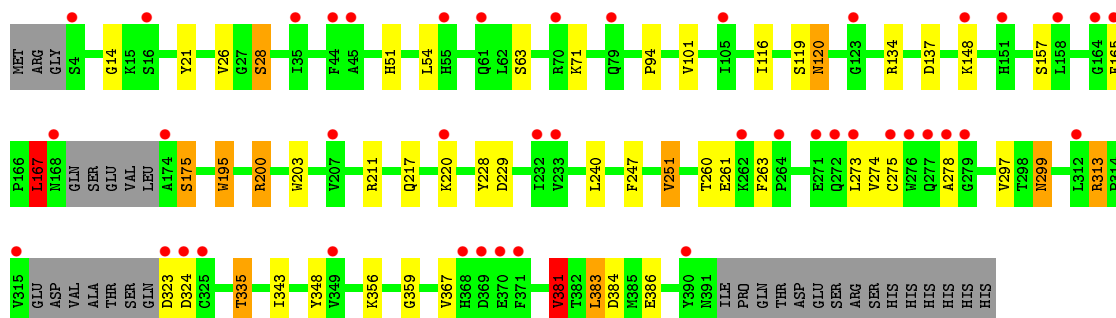


• Molecule 1: Beta-secretase 1



• Molecule 1: Beta-secretase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.16Å 104.59Å 100.16Å 90.00° 104.50° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 19.90 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.5 (20.00-2.20) 96.5 (19.90-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.231 , 0.279 0.220 , 0.266	Depositor DCC
R_{free} test set	4011 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	57.3	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Outliers	1 of 80228 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9293	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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, 0.375 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:
957

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	1.08	5/3002 (0.2%)	0.98	5/4077 (0.1%)
1	B	1.09	3/3034 (0.1%)	0.97	2/4122 (0.0%)
1	C	1.05	1/3034 (0.0%)	0.99	12/4122 (0.3%)
All	All	1.07	9/9070 (0.1%)	0.98	19/12321 (0.2%)

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
1	B	0	3
All	All	0	5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	195	TRP	CE3-CZ3	6.64	1.49	1.38
1	B	386	GLU	CG-CD	6.45	1.61	1.51
1	B	354	ALA	CA-CB	5.87	1.64	1.52
1	A	201	ARG	CG-CD	5.84	1.66	1.51
1	A	297	VAL	CB-CG1	-5.67	1.41	1.52
1	A	206	GLU	CG-CD	5.62	1.60	1.51
1	A	74	TYR	CD2-CE2	5.60	1.47	1.39
1	B	386	GLU	CB-CG	5.41	1.62	1.52
1	A	249	ALA	CA-CB	5.27	1.63	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	200	ARG	NE-CZ-NH2	-9.29	115.66	120.30
1	C	167	LEU	CA-CB-CG	8.53	134.92	115.30
1	A	381	VAL	CB-CA-C	-6.94	98.21	111.40
1	C	381	VAL	CB-CA-C	-6.73	98.61	111.40
1	C	200	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	C	175	SER	N-CA-C	6.59	128.79	111.00
1	C	211	ARG	NE-CZ-NH2	-6.53	117.03	120.30
1	B	118	GLY	N-CA-C	-5.84	98.49	113.10
1	C	211	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	313	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	C	381	VAL	CG1-CB-CG2	5.54	119.77	110.90
1	A	201	ARG	NE-CZ-NH2	5.47	123.04	120.30
1	C	134	ARG	NE-CZ-NH1	-5.34	117.63	120.30
1	C	137	ASP	CB-CG-OD1	5.33	123.09	118.30
1	A	201	ARG	NE-CZ-NH1	-5.32	117.64	120.30
1	B	137	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	119	SER	N-CA-C	5.27	125.22	111.00
1	C	313	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	C	313	ARG	NE-CZ-NH1	5.06	122.83	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	GLY	Peptide
1	A	4	SER	Peptide
1	B	117	ASN	Peptide
1	B	203	TRP	Peptide
1	B	346	GLY	Peptide

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	2928	0	2839	43	0
1	B	2958	0	2876	56	0
1	C	2958	0	2871	23	0
2	A	31	0	32	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	31	0	32	1	0
2	C	31	0	32	0	0
3	A	121	0	0	5	0
3	B	108	0	0	9	1
3	C	127	0	0	2	1
All	All	9293	0	8682	117	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 7.

All (117) 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:5:PHE:HB3	3:A:502:HOH:O	1.48	1.10
1:B:215:ASN:HA	3:B:411:HOH:O	1.58	1.01
1:B:166:PRO:O	1:B:167:LEU:HB2	1.70	0.91
1:C:335:THR:HG23	3:C:511:HOH:O	1.69	0.91
1:A:381:VAL:HG22	1:C:381:VAL:HG22	1.56	0.88
1:B:118:GLY:CA	3:B:439:HOH:O	2.21	0.88
1:B:119:SER:HA	3:B:439:HOH:O	1.78	0.84
1:A:155:LEU:HD22	1:A:184:GLY:HA2	1.61	0.83
1:B:214:ILE:HD12	1:B:219:LEU:HD13	1.62	0.79
1:B:43:ASN:HD21	1:B:134:ARG:H	1.33	0.75
1:B:118:GLY:HA3	3:B:439:HOH:O	1.85	0.70
1:A:296:GLU:H	1:A:300:GLN:HE22	1.39	0.70
1:B:119:SER:CA	3:B:439:HOH:O	2.39	0.69
1:B:23:GLU:HG2	1:B:94:PRO:HG2	1.74	0.69
1:C:260:THR:O	1:C:261:GLU:HG3	1.92	0.67
1:A:4:SER:O	1:A:4:SER:OG	2.01	0.67
1:A:155:LEU:CD2	1:A:184:GLY:HA2	2.24	0.67
1:A:247:PHE:O	1:A:251:VAL:CG1	2.45	0.65
1:B:213:GLU:OE1	3:B:434:HOH:O	2.13	0.64
1:C:275:CYS:HA	1:C:324:ASP:O	1.99	0.62
1:B:214:ILE:HD12	1:B:219:LEU:CD1	2.30	0.62
1:A:116:ILE:O	1:A:119:SER:HB2	1.98	0.62
1:B:166:PRO:O	1:B:167:LEU:CB	2.46	0.61
1:A:8:MET:HG2	1:A:96:GLY:HA2	1.83	0.61
1:A:247:PHE:O	1:A:251:VAL:HG13	2.01	0.59
1:B:211:ARG:NH1	1:C:384:ASP:OD1	2.35	0.59
1:A:162:GLY:O	1:A:163:ALA:HB3	2.04	0.58
1:A:356:LYS:HD3	3:A:473:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:VAL:O	1:B:325:CYS:HB2	2.04	0.57
1:A:7:GLU:HB2	3:A:502:HOH:O	2.04	0.56
1:C:119:SER:O	1:C:120:ASN:HB2	2.06	0.56
1:C:247:PHE:O	1:C:251:VAL:HG13	2.06	0.56
1:B:335:THR:HG23	3:B:486:HOH:O	2.05	0.56
1:C:157:SER:HB2	1:C:348:TYR:CE1	2.40	0.56
1:B:296:GLU:H	1:B:300:GLN:HE22	1.53	0.55
1:B:335:THR:CG2	3:B:486:HOH:O	2.55	0.54
1:B:281:THR:HG21	1:B:326:TYR:CE1	2.41	0.54
1:B:239:ASN:HD22	1:B:331:SER:HB3	1.72	0.54
1:A:5:PHE:CB	3:A:502:HOH:O	2.27	0.54
1:C:299:ASN:HB3	1:C:381:VAL:HG13	1.89	0.54
1:B:116:ILE:O	1:B:119:SER:HB3	2.08	0.52
1:C:299:ASN:HA	1:C:381:VAL:HA	1.91	0.52
1:B:210:VAL:HG11	1:B:385:MET:HG2	1.92	0.52
1:B:221:MET:HE2	1:B:225:GLU:CB	2.40	0.52
1:B:140:GLU:OE1	1:B:148:LYS:HE3	2.09	0.52
1:C:28:SER:O	1:C:63:SER:HA	2.09	0.52
1:A:241:ARG:HB2	1:A:338:VAL:HB	1.92	0.52
1:A:195:TRP:CZ3	1:B:297:VAL:HG13	2.45	0.52
1:A:247:PHE:O	1:A:251:VAL:HG12	2.11	0.51
1:A:25:THR:HA	1:A:31:GLN:O	2.11	0.51
1:A:240:LEU:O	1:A:330:ILE:HA	2.12	0.50
1:A:162:GLY:O	1:A:163:ALA:CB	2.59	0.50
1:A:101:VAL:HG11	1:A:146:LEU:HA	1.93	0.50
2:B:407:957:C10	2:B:407:957:H18A	2.42	0.50
1:B:211:ARG:HG2	1:B:212:VAL:N	2.26	0.50
1:A:4:SER:N	1:A:185:ILE:O	2.45	0.49
1:A:5:PHE:HD1	3:A:502:HOH:O	1.96	0.49
1:B:211:ARG:NH2	1:B:218:ASP:HB2	2.27	0.49
1:B:160:LEU:O	1:B:345:GLU:HA	2.13	0.49
1:B:288:VAL:HG12	1:B:307:LEU:HD23	1.94	0.48
1:A:155:LEU:CD2	1:A:184:GLY:CA	2.91	0.48
1:C:165:PHE:O	1:C:167:LEU:HD22	2.13	0.47
1:C:14:GLY:HA2	1:C:21:TYR:CE2	2.49	0.47
1:C:195:TRP:O	1:C:359:GLY:HA2	2.16	0.46
1:A:384:ASP:HB3	1:A:387:ASP:OD1	2.14	0.46
1:A:298:THR:HG23	3:B:464:HOH:O	2.15	0.46
1:B:221:MET:HE2	1:B:225:GLU:HB2	1.98	0.46
1:B:281:THR:CG2	1:B:326:TYR:CE1	2.98	0.46
1:C:116:ILE:HB	1:C:119:SER:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:392:ILE:HD12	1:B:392:ILE:H	1.80	0.46
1:A:298:THR:HG21	1:B:193:SER:HB3	1.98	0.46
1:B:267:PHE:CD1	1:B:274:VAL:HG23	2.51	0.46
1:B:221:MET:CE	1:B:225:GLU:HG3	2.46	0.45
1:A:77:TYR:CG	2:A:407:957:H26	2.52	0.45
1:A:46:VAL:O	1:A:47:GLY:C	2.52	0.45
1:A:297:VAL:H	1:A:300:GLN:NE2	2.13	0.45
1:B:264:PRO:C	1:B:266:GLY:H	2.20	0.45
1:B:262:LYS:HD2	1:B:262:LYS:N	2.31	0.45
1:B:273:LEU:HD12	1:B:273:LEU:H	1.81	0.45
1:C:299:ASN:CB	1:C:381:VAL:HG13	2.47	0.45
1:B:307:LEU:N	1:B:310:GLN:OE1	2.49	0.44
1:C:228:TYR:HA	1:C:229:ASP:HA	1.73	0.44
1:B:335:THR:HG23	1:B:335:THR:O	2.18	0.43
1:A:76:PRO:HA	1:A:81:LYS:HB3	2.00	0.43
1:A:211:ARG:HB3	1:A:292:TYR:HB2	2.00	0.43
1:A:219:LEU:HA	1:A:219:LEU:HD12	1.60	0.43
1:B:273:LEU:N	1:B:273:LEU:HD12	2.33	0.43
1:B:230:LYS:O	1:B:336:GLY:HA3	2.19	0.43
1:B:259:SER:O	1:B:261:GLU:N	2.51	0.43
1:A:74:TYR:HA	1:A:83:GLU:HA	2.01	0.43
1:C:299:ASN:HD22	1:C:299:ASN:C	2.22	0.43
1:B:241:ARG:HA	1:B:331:SER:O	2.19	0.43
1:B:381:VAL:CG2	1:C:383:LEU:HD13	2.49	0.43
1:B:286:PHE:HA	1:B:287:PRO:HD3	1.89	0.42
1:B:101:VAL:HG11	1:B:146:LEU:HA	2.01	0.42
1:B:299:ASN:O	1:B:381:VAL:HA	2.19	0.42
1:B:157:SER:HB2	1:B:348:TYR:CE1	2.54	0.42
1:A:139:LEU:HA	1:A:139:LEU:HD12	1.91	0.42
1:B:205:TYR:HB3	1:B:358:ILE:HD11	2.00	0.42
1:A:379:PRO:HG2	1:B:381:VAL:HG12	2.00	0.42
1:B:221:MET:HE2	1:B:225:GLU:HG3	2.01	0.42
1:B:228:TYR:HA	1:B:229:ASP:HA	1.77	0.42
1:A:228:TYR:HA	1:A:229:ASP:HA	1.74	0.42
1:B:130:ALA:O	1:B:131:GLU:C	2.57	0.42
1:A:296:GLU:N	1:A:300:GLN:HE22	2.12	0.41
1:B:290:SER:HA	1:B:304:ILE:O	2.20	0.41
1:A:205:TYR:HB3	1:A:358:ILE:HD11	2.02	0.41
1:C:263:PHE:CD2	1:C:274:VAL:HG21	2.56	0.41
1:A:75:VAL:HA	1:A:76:PRO:HD3	1.78	0.41
1:C:51:HIS:HB3	1:C:54:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:335:THR:CG2	3:C:511:HOH:O	2.46	0.41
1:A:350:VAL:O	1:A:358:ILE:HA	2.21	0.40
1:A:341:ALA:O	1:A:345:GLU:HG3	2.21	0.40
1:A:307:LEU:HD12	1:A:367:VAL:HG23	2.02	0.40
1:B:29:PRO:HA	1:B:30:PRO:HD3	1.96	0.40
1:C:240:LEU:HB2	1:C:343:ILE:HD11	2.02	0.40
1:B:69:LEU:HA	1:B:69:LEU:HD23	1.84	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)
3:B:478:HOH:O	3:C:463:HOH:O[1_455]	2.04	0.16

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	366/406 (90%)	347 (95%)	16 (4%)	3 (1%)	24	22
1	B	370/406 (91%)	349 (94%)	16 (4%)	5 (1%)	14	10
1	C	370/406 (91%)	343 (93%)	26 (7%)	1 (0%)	46	50
All	All	1106/1218 (91%)	1039 (94%)	58 (5%)	9 (1%)	24	22

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	166	PRO
1	A	118	GLY
1	B	260	THR
1	B	265	ASP
1	C	278	ALA

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Mol	Chain	Res	Type
1	A	163	ALA
1	A	5	PHE
1	B	70	ARG
1	B	369	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	317/348 (91%)	298 (94%)	19 (6%)	24	26
1	B	320/348 (92%)	300 (94%)	20 (6%)	22	24
1	C	320/348 (92%)	295 (92%)	25 (8%)	16	15
All	All	957/1044 (92%)	893 (93%)	64 (7%)	20	21

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	PHE
1	A	7	GLU
1	A	13	ARG
1	A	64	SER
1	A	79	GLN
1	A	81	LYS
1	A	203	TRP
1	A	219	LEU
1	A	251	VAL
1	A	253	SER
1	A	260	THR
1	A	262	LYS
1	A	273	LEU
1	A	297	VAL
1	A	298	THR
1	A	313	ARG
1	A	373	THR
1	A	381	VAL

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Mol	Chain	Res	Type
1	A	386	GLU
1	B	64	SER
1	B	70	ARG
1	B	79	GLN
1	B	120	ASN
1	B	131	GLU
1	B	148	LYS
1	B	167	LEU
1	B	179	SER
1	B	203	TRP
1	B	244	LYS
1	B	245	LYS
1	B	260	THR
1	B	262	LYS
1	B	269	LEU
1	B	281	THR
1	B	284	ASN
1	B	297	VAL
1	B	331	SER
1	B	335	THR
1	B	368	HIS
1	C	26	VAL
1	C	28	SER
1	C	71	LYS
1	C	94	PRO
1	C	101	VAL
1	C	120	ASN
1	C	148	LYS
1	C	167	LEU
1	C	175	SER
1	C	200	ARG
1	C	203	TRP
1	C	217	GLN
1	C	220	LYS
1	C	251	VAL
1	C	273	LEU
1	C	297	VAL
1	C	299	ASN
1	C	313	ARG
1	C	323	ASP
1	C	335	THR
1	C	356	LYS

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Mol	Chain	Res	Type
1	C	367	VAL
1	C	381	VAL
1	C	383	LEU
1	C	386	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	ASN
1	A	284	ASN
1	A	300	GLN
1	B	43	ASN
1	B	104	ASN
1	B	300	GLN
1	B	366	HIS
1	C	104	ASN
1	C	117	ASN
1	C	217	GLN
1	C	299	ASN
1	C	300	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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	$\# Z > 2$
2	957	A	407	-	31,33,33	1.94	6 (19%)	41,49,49	2.19	11 (26%)
2	957	B	407	-	31,33,33	2.46	7 (22%)	41,49,49	2.51	11 (26%)
2	957	C	407	-	31,33,33	2.30	10 (32%)	41,49,49	2.25	12 (29%)

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
2	957	A	407	-	-	0/19/33/33	0/2/3/3
2	957	B	407	-	-	0/19/33/33	0/2/3/3
2	957	C	407	-	-	0/19/33/33	0/2/3/3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	407	957	C8-C9	-4.38	1.49	1.53
2	A	407	957	C8-C9	-3.90	1.50	1.53
2	C	407	957	C8-C9	-2.60	1.51	1.53
2	A	407	957	C5-C4	-2.08	1.50	1.54
2	A	407	957	C26-C25	2.02	1.41	1.37
2	B	407	957	C22-C23	2.03	1.41	1.37
2	C	407	957	C14-C11	2.15	1.55	1.51
2	C	407	957	C30-C8	2.24	1.54	1.51
2	C	407	957	C22-C23	2.39	1.41	1.37
2	C	407	957	C31-C30	2.48	1.56	1.50
2	B	407	957	C10-C11	2.71	1.44	1.40
2	B	407	957	C31-C8	2.76	1.55	1.51
2	C	407	957	C26-C25	3.08	1.43	1.37
2	C	407	957	C12-S13	3.28	1.75	1.70
2	A	407	957	C12-C11	3.74	1.39	1.37
2	A	407	957	F27-C23	3.90	1.45	1.36
2	C	407	957	F27-C23	5.08	1.48	1.36
2	C	407	957	F28-C25	5.63	1.49	1.36
2	B	407	957	F27-C23	5.67	1.49	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	407	957	F28-C25	5.81	1.49	1.36
2	A	407	957	F28-C25	6.03	1.50	1.36
2	C	407	957	C12-C11	6.43	1.41	1.37
2	B	407	957	C12-C11	8.12	1.42	1.37

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	407	957	C14-C11-C12	-9.40	118.35	128.09
2	C	407	957	C30-C8-N7	-5.50	111.62	117.36
2	B	407	957	C21-C20-C4	-5.29	105.06	113.48
2	A	407	957	C21-C20-C4	-4.88	105.72	113.48
2	C	407	957	C14-C11-C12	-4.55	123.38	128.09
2	A	407	957	C14-C11-C12	-4.33	123.60	128.09
2	C	407	957	C20-C4-N3	-3.81	105.97	110.14
2	B	407	957	C11-C12-S13	-3.79	107.96	112.09
2	C	407	957	C6-N7-C8	-3.58	110.21	116.86
2	A	407	957	C26-C25-C24	-3.02	119.53	123.52
2	C	407	957	C21-C20-C4	-2.80	109.03	113.48
2	A	407	957	C14-C11-C10	-2.62	122.57	127.47
2	B	407	957	C24-C23-C22	-2.60	120.08	123.52
2	B	407	957	C26-C25-C24	-2.51	120.21	123.52
2	C	407	957	C14-C11-C10	-2.46	122.87	127.47
2	C	407	957	C11-C12-S13	-2.31	109.57	112.09
2	B	407	957	C15-C14-C11	-2.26	113.70	116.84
2	C	407	957	C26-C25-C24	-2.13	120.71	123.52
2	B	407	957	O19-C2-C1	-2.13	118.15	122.06
2	A	407	957	C20-C4-N3	-2.13	107.81	110.14
2	A	407	957	C24-C23-C22	-2.05	120.82	123.52
2	B	407	957	F28-C25-C26	2.22	121.18	118.22
2	C	407	957	F27-C23-C22	2.38	121.39	118.22
2	C	407	957	F28-C25-C26	2.46	121.49	118.22
2	A	407	957	C25-C24-C23	2.59	120.03	116.07
2	B	407	957	C25-C24-C23	2.96	120.59	116.07
2	B	407	957	F27-C23-C22	3.22	122.50	118.22
2	A	407	957	F27-C23-C22	3.61	123.02	118.22
2	A	407	957	C31-C8-N7	4.22	121.75	117.36
2	A	407	957	F28-C25-C26	4.86	124.70	118.22
2	C	407	957	C31-C8-N7	4.99	122.56	117.36
2	C	407	957	C10-C11-C12	5.77	113.62	104.49
2	A	407	957	C10-C11-C12	5.87	113.79	104.49
2	B	407	957	C10-C11-C12	7.26	115.99	104.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	407	957	1	0
2	B	407	957	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	372/406 (91%)	0.44	36 (9%) 10 9	34, 51, 81, 89	0
1	B	376/406 (92%)	0.57	48 (12%) 5 4	33, 52, 84, 93	0
1	C	376/406 (92%)	0.44	43 (11%) 7 6	36, 50, 81, 90	0
All	All	1124/1218 (92%)	0.48	127 (11%) 7 6	33, 51, 82, 93	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	174	ALA	7.3
1	C	368	HIS	6.1
1	A	164	GLY	5.9
1	C	371	PHE	5.6
1	B	392	ILE	5.4
1	C	278	ALA	5.3
1	A	279	GLY	5.3
1	C	325	CYS	5.2
1	B	260	THR	5.0
1	B	165	PHE	4.9
1	A	371	PHE	4.8
1	B	166	PRO	4.7
1	B	371	PHE	4.7
1	B	279	GLY	4.7
1	B	278	ALA	4.3
1	B	164	GLY	4.3
1	A	368	HIS	4.2
1	C	370	GLU	4.2
1	A	370	GLU	4.2
1	C	4	SER	3.8
1	B	262	LYS	3.8
1	C	151	HIS	3.7
1	B	4	SER	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	315	VAL	3.6
1	C	262	LYS	3.5
1	C	315	VAL	3.5
1	B	151	HIS	3.4
1	B	368	HIS	3.4
1	B	323	ASP	3.3
1	B	277	GLN	3.3
1	A	386	GLU	3.3
1	A	70	ARG	3.3
1	A	316	GLU	3.2
1	C	174	ALA	3.2
1	C	70	ARG	3.2
1	C	271	GLU	3.2
1	C	164	GLY	3.1
1	B	52	PRO	3.1
1	B	271	GLU	3.1
1	B	370	GLU	3.0
1	A	277	GLN	3.0
1	C	272	GLN	3.0
1	C	279	GLY	3.0
1	C	16	SER	3.0
1	B	366	HIS	3.0
1	A	5	PHE	3.0
1	B	367	VAL	2.9
1	B	16	SER	2.9
1	C	349	VAL	2.9
1	B	324	ASP	2.9
1	A	262	LYS	2.9
1	A	98	ASN	2.9
1	B	124	ILE	2.8
1	B	167	LEU	2.8
1	B	175	SER	2.8
1	A	367	VAL	2.8
1	B	312	LEU	2.7
1	A	387	ASP	2.7
1	A	124	ILE	2.7
1	B	259	SER	2.6
1	A	105	ILE	2.6
1	C	79	GLN	2.6
1	C	55	HIS	2.6
1	C	312	LEU	2.6
1	C	323	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	220	LYS	2.6
1	B	207	VAL	2.6
1	B	280	THR	2.6
1	B	328	PHE	2.5
1	A	55	HIS	2.5
1	B	79	GLN	2.5
1	C	168	ASN	2.5
1	A	175	SER	2.5
1	A	391	ASN	2.5
1	A	280	THR	2.5
1	B	46	VAL	2.5
1	B	55	HIS	2.5
1	A	278	ALA	2.5
1	B	265	ASP	2.5
1	B	70	ARG	2.5
1	C	207	VAL	2.5
1	C	105	ILE	2.5
1	A	358	ILE	2.4
1	B	61	GLN	2.4
1	A	312	LEU	2.4
1	A	13	ARG	2.4
1	C	369	ASP	2.4
1	B	158	LEU	2.4
1	B	390	TYR	2.4
1	A	324	ASP	2.4
1	B	256	ALA	2.3
1	A	163	ALA	2.3
1	C	35	ILE	2.3
1	C	277	GLN	2.3
1	B	246	VAL	2.3
1	B	163	ALA	2.3
1	A	46	VAL	2.3
1	B	358	ILE	2.3
1	C	324	ASP	2.2
1	C	158	LEU	2.2
1	C	273	LEU	2.2
1	C	148	LYS	2.2
1	C	45	ALA	2.2
1	A	311	TYR	2.2
1	A	79	GLN	2.2
1	C	232	ILE	2.2
1	A	35	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	276	TRP	2.2
1	C	61	GLN	2.2
1	B	117	ASN	2.1
1	A	273	LEU	2.1
1	B	275	CYS	2.1
1	C	44	PHE	2.1
1	A	271	GLU	2.1
1	C	220	LYS	2.1
1	C	123	GLY	2.1
1	B	386	GLU	2.1
1	A	45	ALA	2.1
1	B	187	HIS	2.1
1	C	233	VAL	2.1
1	C	165	PHE	2.0
1	C	275	CYS	2.0
1	C	264	PRO	2.0
1	A	29	PRO	2.0
1	A	148	LYS	2.0
1	A	207	VAL	2.0
1	C	390	TYR	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 carbohydrates 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. 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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	957	B	407	31/31	0.96	0.11	-0.55	35,43,47,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	957	A	407	31/31	0.96	0.11	-0.58	32,42,46,50	0
2	957	C	407	31/31	0.96	0.11	-0.71	32,37,41,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.