



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:01 PM GMT

PDB ID : 4K8S
Title : Hydroxyethylamine-based inhibitors of BACE1: P1-P3 macrocyclization can improve potency, selectivity, and cell activity
Authors : Jordan, S.R.
Deposited on : 2013-04-18
Resolution : 2.39 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

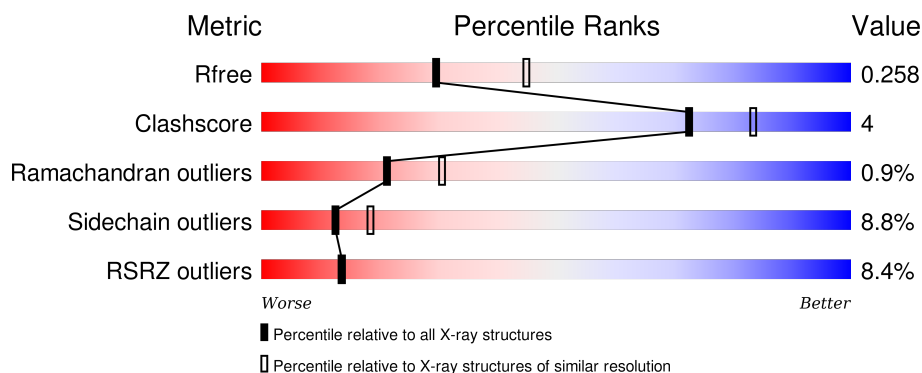
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	388	<div> <div>8%</div> <div>80%12% . .</div> </div>
1	B	388	<div> <div>6%</div> <div>80%15% . .</div> </div>
1	C	388	<div> <div>10%</div> <div>78%15% . .</div> </div>

2 Entry composition [i](#)

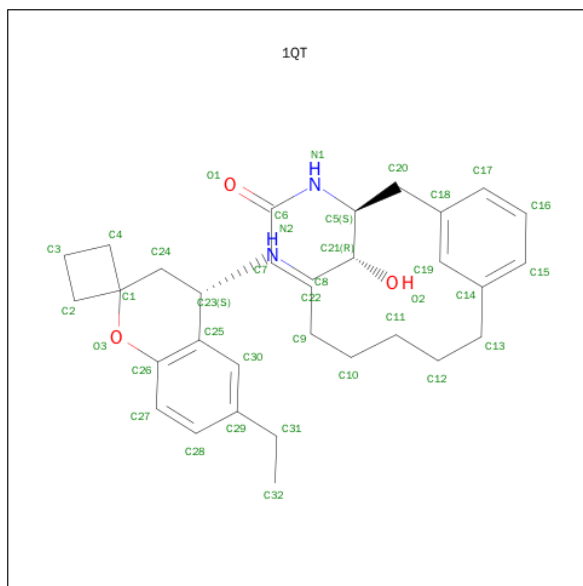
There are 2 unique types of molecules in this entry. The entry contains 8883 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	371	Total	C	N	O	S	0	0	0
			2924	1874	487	549	14			
1	B	371	Total	C	N	O	S	0	0	0
			2924	1874	486	550	14			
1	C	371	Total	C	N	O	S	0	0	0
			2924	1874	486	550	14			

- Molecule 2 is (3S)-3-[(1R)-2-{[(4S)-6-ETHYL-3,4-DIHYDROSPIRO[CHROMENE-2,1'-CYCLOBUTAN]-4-YL]AMINO}-1-HYDROXYETHYL]-4-AZABICYCLO[11.3.1]HEPTADEC A-1(17),13,15-TRIEN-5-ONE (three-letter code: 1QT) (formula: C₃₂H₄₄N₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			37	32	2	3		
2	B	1	Total	C	N	O	0	0
			37	32	2	3		

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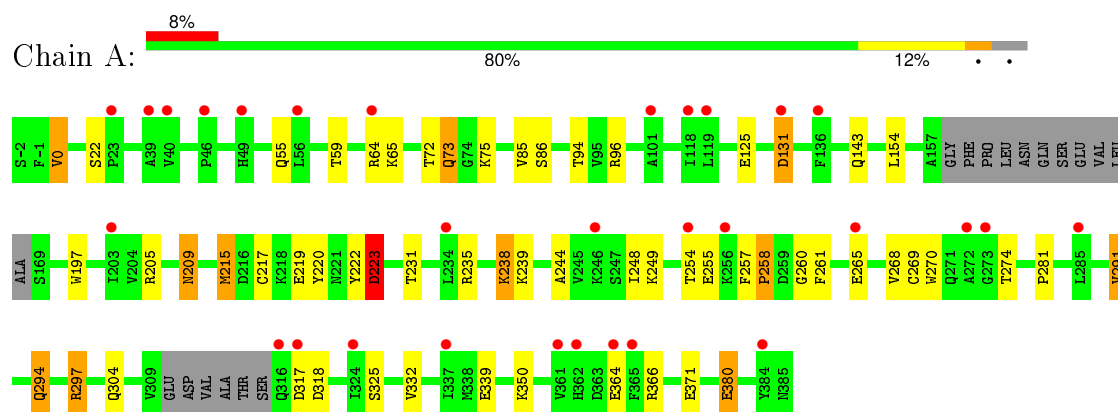
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			37	32	2	3		

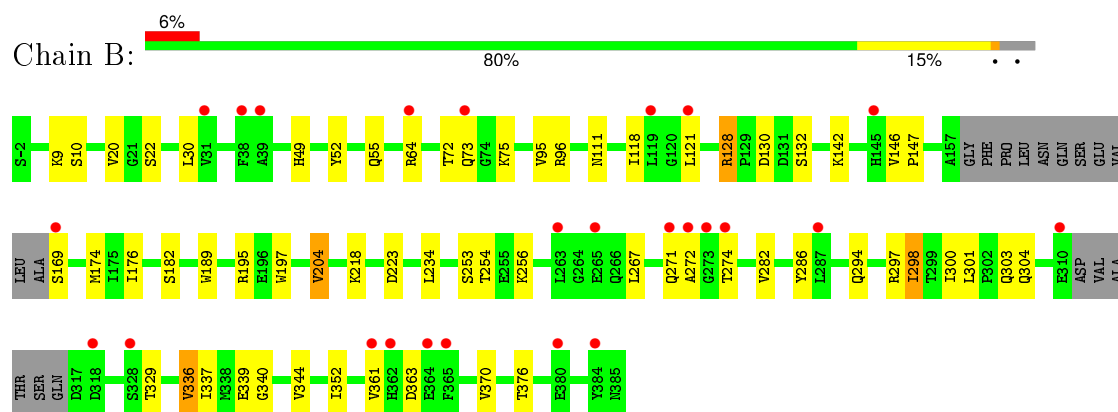
3 Residue-property plots

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.

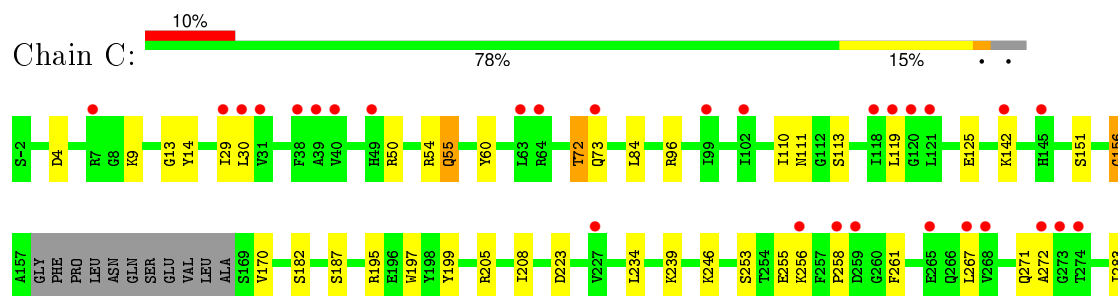
• Molecule 1: Beta-secretase 1

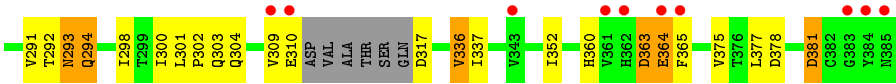


• Molecule 1: Beta-secretase 1



• 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	81.84Å 102.56Å 101.32Å 90.00° 105.24° 90.00°	Depositor
Resolution (Å)	25.00 – 2.39 26.12 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.1 (25.00-2.39) 99.2 (26.12-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.210 , 0.260 0.214 , 0.258	Depositor DCC
R_{free} test set	3232 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 32.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 63216 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8883	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% 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: 1QT

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	0.82	0/2998	0.95	5/4072 (0.1%)
1	B	0.86	0/2998	0.92	2/4072 (0.0%)
1	C	0.81	1/2998 (0.0%)	0.91	1/4072 (0.0%)
All	All	0.83	1/8994 (0.0%)	0.92	8/12216 (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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	293	ASN	N-CA	5.21	1.56	1.46

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	64	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	B	128	ARG	NE-CZ-NH1	5.69	123.15	120.30
1	A	0	VAL	CB-CA-C	-5.66	100.65	111.40
1	A	297	ARG	NE-CZ-NH2	-5.47	117.57	120.30
1	C	205	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	B	96	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	A	131	ASP	CB-CG-OD1	5.18	122.96	118.30
1	A	73	GLN	N-CA-C	-5.04	97.40	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	340	GLY	Peptide

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	2924	0	2841	22	0
1	B	2924	0	2839	24	0
1	C	2924	0	2839	26	0
2	A	37	0	44	0	0
2	B	37	0	44	2	0
2	C	37	0	44	2	0
All	All	8883	0	8651	73	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 4.

All (73) 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:C:363:ASP:O	1:C:365:PHE:N	2.19	0.75
1:A:96:ARG:H	1:A:143:GLN:HE22	1.33	0.73
1:C:156:GLY:HA2	1:C:170:VAL:HG22	1.74	0.70
1:C:363:ASP:OD1	1:C:363:ASP:O	2.09	0.69
1:C:304:GLN:O	1:C:336:VAL:HG22	1.92	0.69
1:B:204:VAL:HG13	1:B:376:THR:HG21	1.78	0.66
1:A:257:PHE:O	1:A:258:PRO:O	2.14	0.65
1:C:72:THR:HB	2:C:401:1QT:O1	1.97	0.65
1:A:297:ARG:NH2	1:A:371:GLU:OE2	2.31	0.64
1:A:380:GLU:H	1:A:380:GLU:CD	2.01	0.64
1:C:55:GLN:H	1:C:55:GLN:HE21	1.48	0.62
1:C:156:GLY:CA	1:C:170:VAL:HG22	2.30	0.61
1:B:72:THR:HB	2:B:401:1QT:O1	2.03	0.58
1:B:304:GLN:O	1:B:336:VAL:HG22	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:VAL:HG12	1:A:294:GLN:HB3	1.84	0.57
1:B:20:VAL:CG1	1:B:52:TYR:CE1	2.89	0.56
1:A:209:ASN:ND2	1:A:281:PRO:HB3	2.21	0.55
1:B:234:LEU:HB2	1:B:337:ILE:CD1	2.38	0.53
1:A:215:MET:HE2	1:A:219:GLU:HB2	1.92	0.52
1:C:301:LEU:HB3	1:C:302:PRO:HD2	1.91	0.52
1:C:309:VAL:O	1:C:310:GLU:C	2.49	0.52
1:C:291:VAL:HG23	1:C:294:GLN:HB2	1.92	0.51
1:B:303:GLN:NE2	1:B:363:ASP:HB3	2.27	0.50
1:B:344:VAL:O	1:B:352:ILE:HA	2.12	0.50
1:C:13:GLY:HA3	1:C:30:LEU:HD11	1.94	0.49
1:C:208:ILE:HG12	1:C:283:ILE:HD12	1.94	0.49
1:B:174:MET:HE2	1:B:176:ILE:CD1	2.42	0.49
1:A:238:LYS:HD2	1:A:239:LYS:H	1.77	0.49
1:C:110:ILE:HB	1:C:113:SER:HB3	1.94	0.49
1:A:154:LEU:O	1:A:339:GLU:HA	2.13	0.49
1:B:304:GLN:HG3	1:B:361:VAL:HG21	1.95	0.49
2:C:401:1QT:H40	2:C:401:1QT:H34	1.55	0.48
1:C:303:GLN:NE2	1:C:363:ASP:HB3	2.27	0.48
1:C:199:TYR:HB3	1:C:352:ILE:HD11	1.95	0.48
1:B:9:LYS:O	1:B:10:SER:HB3	2.14	0.47
1:B:121:LEU:HD11	1:B:174:MET:HE3	1.96	0.47
1:C:14:TYR:CE2	1:C:170:VAL:CG1	2.97	0.47
1:C:84:LEU:HD23	1:C:96:ARG:HB2	1.97	0.47
2:B:401:1QT:H34	2:B:401:1QT:H40	1.58	0.46
1:B:271:GLN:HG2	1:B:274:THR:OG1	2.15	0.46
1:A:238:LYS:N	1:A:238:LYS:HD2	2.31	0.46
1:A:231:THR:HG21	1:A:332:VAL:HG11	1.98	0.45
1:C:258:PRO:O	1:C:261:PHE:HB3	2.17	0.45
1:B:234:LEU:HB2	1:B:337:ILE:HD13	1.99	0.45
1:A:72:THR:HG21	1:A:235:ARG:HH22	1.81	0.44
1:A:217:CYS:HA	1:A:220:TYR:CD2	2.52	0.44
1:B:234:LEU:HB2	1:B:337:ILE:HD11	2.00	0.44
1:B:130:ASP:OD1	1:B:132:SER:OG	2.29	0.44
1:C:271:GLN:OE1	1:C:271:GLN:N	2.51	0.44
1:B:174:MET:HE2	1:B:176:ILE:HD13	2.00	0.44
1:B:121:LEU:CD1	1:B:174:MET:HE3	2.48	0.44
1:B:30:LEU:HD23	1:B:118:ILE:HD12	2.00	0.44
1:A:291:VAL:HG12	1:A:294:GLN:CB	2.48	0.43
1:A:269:CYS:HA	1:A:318:ASP:O	2.17	0.43
1:C:304:GLN:O	1:C:336:VAL:CG2	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:TRP:HB3	1:A:274:THR:OG1	2.18	0.43
1:A:244:ALA:O	1:A:248:ILE:HG13	2.19	0.43
1:B:286:TYR:CZ	1:B:297:ARG:HD3	2.54	0.43
1:A:222:TYR:O	1:A:223:ASP:HB2	2.19	0.43
1:A:291:VAL:HG13	1:B:189:TRP:CZ3	2.54	0.42
1:B:282:VAL:HG12	1:B:301:LEU:HD23	2.01	0.42
1:C:234:LEU:HD13	1:C:337:ILE:HG13	2.01	0.42
1:C:54:ARG:HD2	1:C:60:TYR:CZ	2.55	0.42
1:A:260:GLY:O	1:A:265:GLU:N	2.52	0.41
1:B:174:MET:CE	1:B:176:ILE:HD11	2.50	0.41
1:A:85:VAL:HG12	1:A:86:SER:N	2.36	0.41
1:B:298:ILE:HG22	1:B:370:VAL:HG13	2.03	0.41
1:C:303:GLN:NE2	1:C:363:ASP:CB	2.83	0.41
1:A:261:PHE:CD1	1:A:268:VAL:HG23	2.55	0.41
1:B:146:VAL:HA	1:B:147:PRO:HD3	1.94	0.41
1:C:378:ASP:OD1	1:C:381:ASP:OD2	2.39	0.40
1:C:29:ILE:HG21	1:C:119:LEU:HB2	2.02	0.40
1:C:291:VAL:C	1:C:292:THR:O	2.54	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	365/388 (94%)	341 (93%)	21 (6%)	3 (1%)	24	35
1	B	365/388 (94%)	342 (94%)	20 (6%)	3 (1%)	24	35
1	C	365/388 (94%)	343 (94%)	18 (5%)	4 (1%)	17	25
All	All	1095/1164 (94%)	1026 (94%)	59 (5%)	10 (1%)	21	30

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	ASP
1	A	258	PRO
1	C	364	GLU
1	C	156	GLY
1	C	223	ASP
1	B	223	ASP
1	B	253	SER
1	A	209	ASN
1	B	272	ALA
1	C	272	ALA

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	317/331 (96%)	290 (92%)	27 (8%)	13	20
1	B	317/331 (96%)	292 (92%)	25 (8%)	15	23
1	C	317/331 (96%)	285 (90%)	32 (10%)	9	13
All	All	951/993 (96%)	867 (91%)	84 (9%)	12	18

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	VAL
1	A	22	SER
1	A	55	GLN
1	A	59	THR
1	A	65	LYS
1	A	73	GLN
1	A	75	LYS
1	A	94	THR
1	A	125	GLU
1	A	131	ASP
1	A	197	TRP
1	A	205	ARG
1	A	215	MET

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Mol	Chain	Res	Type
1	A	223	ASP
1	A	238	LYS
1	A	249	LYS
1	A	254	THR
1	A	255	GLU
1	A	291	VAL
1	A	294	GLN
1	A	304	GLN
1	A	317	ASP
1	A	325	SER
1	A	350	LYS
1	A	364	GLU
1	A	366	ARG
1	A	380	GLU
1	B	22	SER
1	B	49	HIS
1	B	55	GLN
1	B	64	ARG
1	B	73	GLN
1	B	75	LYS
1	B	95	VAL
1	B	111	ASN
1	B	128	ARG
1	B	142	LYS
1	B	169	SER
1	B	182	SER
1	B	195	ARG
1	B	197	TRP
1	B	204	VAL
1	B	218	LYS
1	B	254	THR
1	B	256	LYS
1	B	267	LEU
1	B	294	GLN
1	B	298	ILE
1	B	300	ILE
1	B	329	THR
1	B	336	VAL
1	B	339	GLU
1	C	4	ASP
1	C	9	LYS
1	C	50	ARG

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Mol	Chain	Res	Type
1	C	55	GLN
1	C	72	THR
1	C	73	GLN
1	C	111	ASN
1	C	125	GLU
1	C	142	LYS
1	C	151	SER
1	C	182	SER
1	C	187	SER
1	C	195	ARG
1	C	197	TRP
1	C	239	LYS
1	C	246	LYS
1	C	253	SER
1	C	255	GLU
1	C	256	LYS
1	C	267	LEU
1	C	293	ASN
1	C	294	GLN
1	C	298	ILE
1	C	300	ILE
1	C	317	ASP
1	C	336	VAL
1	C	360	HIS
1	C	363	ASP
1	C	364	GLU
1	C	375	VAL
1	C	377	LEU
1	C	381	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	111	ASN
1	A	143	GLN
1	B	28	ASN
1	B	73	GLN
1	B	111	ASN
1	B	271	GLN
1	B	278	ASN
1	B	293	ASN

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Mol	Chain	Res	Type
1	C	25	GLN
1	C	53	GLN
1	C	55	GLN
1	C	92	ASN
1	C	98	ASN
1	C	111	ASN
1	C	114	ASN
1	C	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 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	1QT	A	401	-	38,41,41	1.27	4 (10%)	45,57,57	1.15	4 (8%)
2	1QT	B	401	-	38,41,41	1.45	2 (5%)	45,57,57	1.00	1 (2%)
2	1QT	C	401	-	38,41,41	1.52	4 (10%)	45,57,57	1.25	2 (4%)

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	1QT	A	401	-	-	0/29/51/51	0/3/5/5
2	1QT	B	401	-	-	0/29/51/51	0/3/5/5
2	1QT	C	401	-	-	0/29/51/51	0/3/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	1QT	O3-C1	-6.98	1.38	1.47
2	C	401	1QT	O3-C1	-5.95	1.39	1.47
2	A	401	1QT	O3-C1	-4.16	1.42	1.47
2	A	401	1QT	O3-C26	-2.57	1.33	1.37
2	B	401	1QT	C25-C23	2.35	1.54	1.52
2	A	401	1QT	C23-N2	2.52	1.51	1.47
2	C	401	1QT	C21-C5	2.58	1.58	1.54
2	A	401	1QT	C24-C23	3.41	1.58	1.53
2	C	401	1QT	C23-N2	3.67	1.53	1.47
2	C	401	1QT	C25-C23	3.91	1.55	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	1QT	O2-C21-C22	-3.10	102.95	110.27
2	A	401	1QT	C25-C30-C29	-2.65	119.44	122.00
2	B	401	1QT	C18-C20-C5	-2.62	109.31	113.48
2	A	401	1QT	C21-C5-N1	2.16	113.20	109.73
2	A	401	1QT	C28-C29-C30	2.19	121.79	118.55
2	A	401	1QT	C22-C21-C5	2.34	116.23	111.97
2	C	401	1QT	C22-C21-C5	2.62	116.75	111.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	1QT	2	0
2	C	401	1QT	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.

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	371/388 (95%)	0.41	30 (8%) 15 14	28, 47, 78, 128	0
1	B	371/388 (95%)	0.28	25 (6%) 21 21	27, 43, 82, 126	0
1	C	371/388 (95%)	0.46	39 (10%) 8 8	30, 46, 85, 129	0
All	All	1113/1164 (95%)	0.39	94 (8%) 14 13	27, 45, 84, 129	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	316	GLN	7.0
1	C	272	ALA	6.0
1	C	384	TYR	6.0
1	A	365	PHE	5.7
1	C	273	GLY	5.6
1	A	364	GLU	5.5
1	C	385	ASN	5.1
1	C	362	HIS	5.1
1	A	272	ALA	5.0
1	B	310	GLU	4.7
1	B	365	PHE	4.5
1	B	364	GLU	4.5
1	C	38	PHE	4.2
1	A	49	HIS	3.8
1	C	310	GLU	3.7
1	A	362	HIS	3.7
1	C	145	HIS	3.7
1	B	119	LEU	3.7
1	C	64	ARG	3.7
1	C	39	ALA	3.5
1	B	273	GLY	3.5
1	B	272	ALA	3.3
1	A	273	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	265	GLU	3.2
1	B	64	ARG	3.2
1	C	365	PHE	3.1
1	B	169	SER	3.1
1	A	119	LEU	3.1
1	C	256	LYS	3.1
1	A	118	ILE	3.0
1	C	119	LEU	3.0
1	C	274	THR	3.0
1	C	364	GLU	3.0
1	B	73	GLN	2.9
1	C	383	GLY	2.9
1	C	121	LEU	2.8
1	A	256	LYS	2.8
1	C	73	GLN	2.7
1	A	203	ILE	2.7
1	C	29	ILE	2.7
1	C	40	VAL	2.7
1	A	40	VAL	2.7
1	A	324	ILE	2.6
1	C	99	ILE	2.6
1	C	227	VAL	2.6
1	A	254	THR	2.6
1	C	142	LYS	2.6
1	B	145	HIS	2.5
1	C	120	GLY	2.5
1	A	39	ALA	2.5
1	B	328	SER	2.5
1	C	309	VAL	2.5
1	C	102	ILE	2.5
1	A	317	ASP	2.5
1	C	118	ILE	2.5
1	B	384	TYR	2.4
1	B	318	ASP	2.4
1	B	31	VAL	2.4
1	A	384	TYR	2.4
1	A	337	ILE	2.4
1	B	38	PHE	2.4
1	A	46	PRO	2.4
1	B	380	GLU	2.4
1	A	136	PHE	2.4
1	B	39	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	343	VAL	2.3
1	C	258	PRO	2.3
1	C	265	GLU	2.3
1	A	361	VAL	2.3
1	B	361	VAL	2.3
1	B	287	LEU	2.3
1	C	361	VAL	2.2
1	B	121	LEU	2.2
1	A	246	LYS	2.2
1	A	23	PRO	2.2
1	C	259	ASP	2.2
1	C	30	LEU	2.2
1	B	274	THR	2.2
1	A	265	GLU	2.1
1	B	263	LEU	2.1
1	C	267	LEU	2.1
1	C	31	VAL	2.1
1	C	7	ARG	2.1
1	A	131	ASP	2.1
1	B	271	GLN	2.1
1	C	49	HIS	2.1
1	C	268	VAL	2.1
1	A	285	LEU	2.0
1	A	64	ARG	2.0
1	A	56	LEU	2.0
1	A	101	ALA	2.0
1	B	362	HIS	2.0
1	A	234	LEU	2.0
1	C	63	LEU	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 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	1QT	C	401	37/37	0.95	0.12	-0.53	32,37,45,47	0
2	1QT	B	401	37/37	0.95	0.12	-0.54	33,38,54,58	0
2	1QT	A	401	37/37	0.96	0.11	-0.89	33,40,51,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.