



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 07:01 PM EDT

PDB ID : 3K5F / pdb_00003k5f
Title : Human BACE-1 COMPLEX WITH AYH011
Authors : Rondeau, J.-M.
Deposited on : 2009-10-07
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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

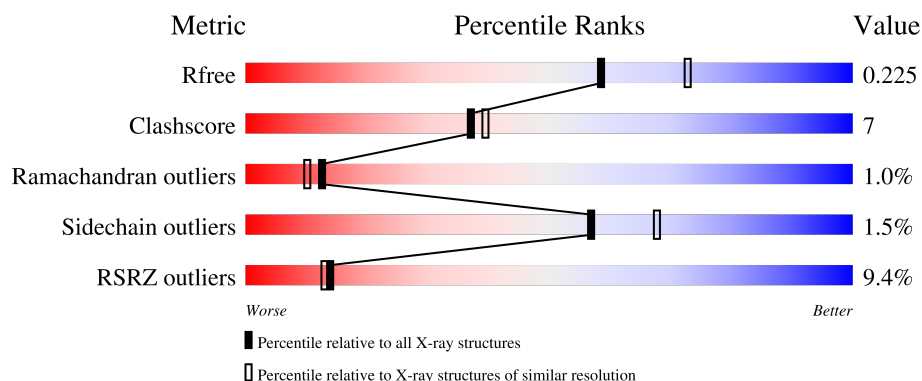
1 Overall quality at a glance

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	
1	B	402	
1	C	402	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9464 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	373	Total	C	N	O	S	0	0	0
			2928	1874	487	553	14			
1	B	377	Total	C	N	O	S	0	0	0
			2966	1898	493	561	14			
1	C	377	Total	C	N	O	S	0	0	0
			2966	1898	493	561	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33P	GLY	-	expression tag	UNP P56817
A	34P	PRO	-	expression tag	UNP P56817
B	33P	GLY	-	expression tag	UNP P56817
B	34P	PRO	-	expression tag	UNP P56817
C	33P	GLY	-	expression tag	UNP P56817
C	34P	PRO	-	expression tag	UNP P56817

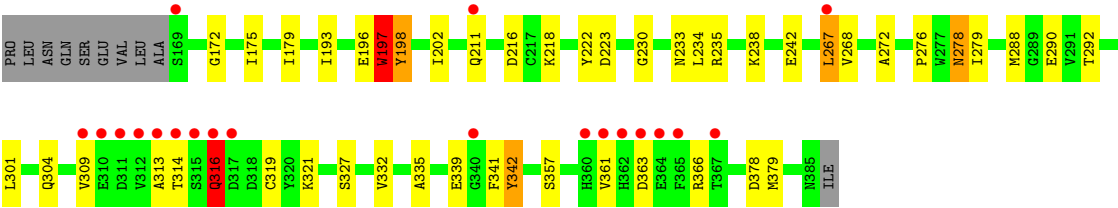
- Molecule 2 is (1R,3S)-3-[1-(acetylamino)-1-methylethyl]-N-[(1S,2S,4R)-1-benzyl-5-(butylamino)-2-hydroxy-4-methyl-5-oxopentyl]cyclohexanecarboxamide (CCD ID: AYH) (formula: C₂₉H₄₇N₃O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 36	C 29	N 3	O 4	0	0
2	B	1	Total 36	C 29	N 3	O 4	0	0
2	C	1	Total 36	C 29	N 3	O 4	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	176	Total O 176 176	0	0
3	B	170	Total O 170 170	0	0
3	C	150	Total O 150 150	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.65Å 103.71Å 101.82Å 90.00° 102.53° 90.00°	Depositor
Resolution (Å)	43.62 – 2.25 43.62 – 2.25	Depositor EDS
% Data completeness (in resolution range)	91.6 (43.62-2.25) 91.7 (43.62-2.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.54 (at 2.24Å)	Xtriage
Refinement program	CNS, CNX	Depositor
R, R_{free}	0.209 , 0.232 0.201 , 0.225	Depositor DCC
R_{free} test set	3718 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	42.7	Xtriage
Anisotropy	0.300	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.3	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	0.95	EDS
Total number of atoms	9464	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 4.04% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AYH

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	0.39	0/3000	0.91	9/4076 (0.2%)
1	B	0.39	0/3041	0.90	10/4133 (0.2%)
1	C	0.38	0/3041	0.90	8/4133 (0.2%)
All	All	0.39	0/9082	0.90	27/12342 (0.2%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	359	CYS	N-CA-C	8.80	122.32	108.67
1	B	198	TYR	N-CA-C	-8.21	98.69	110.59
1	C	198	TYR	N-CA-C	-7.79	99.30	110.59
1	A	198	TYR	N-CA-C	-7.67	99.47	110.59
1	A	342	TYR	N-CA-C	-7.28	96.87	108.73
1	C	233	ASN	N-CA-C	6.70	119.17	110.53
1	B	342	TYR	N-CA-C	-6.26	98.52	108.73
1	B	193	ILE	N-CA-C	-6.21	99.35	108.54
1	B	123	TYR	N-CA-C	6.17	118.88	110.55
1	A	193	ILE	N-CA-C	-6.15	99.43	108.54
1	C	193	ILE	N-CA-C	-6.09	99.53	108.54
1	C	123	TYR	N-CA-C	5.69	118.24	110.55
1	C	290	GLU	N-CA-C	-5.67	105.19	111.71
1	B	234	LEU	N-CA-C	-5.67	99.94	108.96
1	A	197	TRP	N-CA-C	-5.64	98.78	110.80
1	A	233	ASN	N-CA-C	5.55	117.69	110.53
1	A	123	TYR	N-CA-C	5.53	118.02	110.55
1	C	342	TYR	N-CA-C	-5.52	99.52	108.52
1	C	234	LEU	N-CA-C	-5.50	100.21	108.96
1	B	23	PRO	CA-C-N	5.49	125.76	119.83
1	B	23	PRO	C-N-CA	5.49	125.76	119.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	197	TRP	N-CA-C	-5.38	99.34	110.80
1	B	359	CYS	N-CA-C	-5.32	106.56	112.57
1	B	233	ASN	N-CA-C	5.29	117.36	110.53
1	A	29	ILE	N-CA-C	5.29	115.47	107.75
1	A	341	PHE	N-CA-C	5.18	117.28	109.41
1	B	197	TRP	N-CA-C	-5.02	100.12	110.80

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	2928	0	2848	44	0
1	B	2966	0	2875	35	0
1	C	2966	0	2875	50	0
2	A	36	0	47	0	0
2	B	36	0	47	0	0
2	C	36	0	47	0	0
3	A	176	0	0	4	0
3	B	170	0	0	1	0
3	C	150	0	0	6	0
All	All	9464	0	8739	125	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 (125) 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:288:MET:HE1	1:C:379:MET:HE3	1.53	0.87
1:C:202:ILE:CD1	1:C:379:MET:HG3	2.11	0.78
1:A:196:GLU:HG3	3:A:531:HOH:O	1.84	0.78
1:C:267:LEU:HD23	1:C:267:LEU:H	1.49	0.76
1:B:363:ASP:HB3	1:B:366:ARG:O	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:335:ALA:O	1:C:339:GLU:HG3	1.93	0.68
1:C:196:GLU:HG3	3:C:535:HOH:O	1.95	0.66
1:A:106:ASP:OD1	1:C:1:GLU:HG2	1.97	0.64
1:A:276:PRO:O	1:A:279:ILE:HG12	1.98	0.64
1:C:363:ASP:HB3	1:C:366:ARG:O	1.98	0.63
1:A:2:MET:HG2	1:A:90:GLY:HA2	1.82	0.62
1:C:304:GLN:HG3	1:C:361:VAL:HG11	1.81	0.62
1:B:260:GLY:HA3	1:B:266:GLN:HE21	1.65	0.60
1:C:276:PRO:O	1:C:279:ILE:HG12	2.02	0.60
1:B:335:ALA:O	1:B:339:GLU:HG3	2.01	0.60
1:A:205:ARG:HD3	1:A:212:ASP:OD2	2.02	0.59
1:C:267:LEU:HD23	1:C:267:LEU:N	2.17	0.59
1:C:197:TRP:CG	1:C:198:TYR:H	2.20	0.59
1:C:235:ARG:HB2	1:C:332:VAL:HB	1.85	0.58
1:B:196:GLU:HG3	3:B:490:HOH:O	2.02	0.58
1:B:197:TRP:CG	1:B:198:TYR:H	2.22	0.58
1:C:2:MET:HG2	1:C:90:GLY:HA2	1.84	0.58
1:C:20:VAL:HG12	1:C:85:VAL:HG22	1.86	0.57
1:A:104:GLU:OE1	1:C:46(P):SER:HA	2.04	0.57
1:A:197:TRP:CG	1:A:198:TYR:H	2.23	0.57
1:A:260:GLY:HA3	1:A:266:GLN:HE21	1.70	0.56
1:B:20:VAL:HG12	1:B:85:VAL:HG22	1.88	0.56
1:A:20:VAL:HG12	1:A:85:VAL:HG22	1.88	0.55
1:A:123:TYR:CZ	1:A:196:GLU:HG2	2.42	0.55
1:B:365:PHE:CD1	1:B:366:ARG:HG3	2.41	0.55
1:C:202:ILE:HD12	1:C:379:MET:HE2	1.89	0.55
1:B:2:MET:HG2	1:B:90:GLY:HA2	1.88	0.55
1:B:235:ARG:HB2	1:B:332:VAL:HB	1.90	0.54
1:C:202:ILE:HD13	1:C:379:MET:HG3	1.89	0.54
1:A:325:SER:HB3	3:A:537:HOH:O	2.08	0.53
1:B:271:GLN:HA	1:B:317:ASP:OD1	2.08	0.53
1:A:280:PHE:HB3	1:A:302:PRO:HB3	1.92	0.52
1:C:309:VAL:HG11	1:C:321:LYS:HG3	1.92	0.52
1:B:301:LEU:HD11	1:B:367:THR:HA	1.92	0.52
1:C:202:ILE:HD11	1:C:379:MET:HG3	1.88	0.51
1:A:314:THR:HB	1:A:316:GLN:NE2	2.26	0.51
1:C:216:ASP:HA	3:C:536:HOH:O	2.10	0.51
1:C:238:LYS:O	1:C:242:GLU:HG3	2.12	0.50
1:A:235:ARG:HB2	1:A:332:VAL:HB	1.94	0.50
1:B:110:ILE:HB	1:B:113:SER:HB3	1.93	0.49
1:C:202:ILE:CD1	1:C:379:MET:HE2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:GLU:HG2	1:C:48(P):VAL:HB	1.94	0.49
1:C:123:TYR:CZ	1:C:196:GLU:HG2	2.48	0.49
1:C:110:ILE:HB	1:C:113:SER:HB3	1.94	0.49
1:B:238:LYS:O	1:B:242:GLU:HG3	2.12	0.49
1:B:267:LEU:H	1:B:267:LEU:HD23	1.78	0.49
1:B:276:PRO:O	1:B:279:ILE:HG12	2.13	0.48
1:A:269:CYS:HA	1:A:319:CYS:HA	1.95	0.48
1:A:378:ASP:HB3	1:A:381:ASP:OD2	2.14	0.48
1:B:260:GLY:HA3	1:B:266:GLN:HG3	1.93	0.48
1:A:314:THR:HB	1:A:316:GLN:HE22	1.78	0.48
1:B:8:GLY:O	1:B:170:VAL:HG22	2.13	0.48
1:C:278:ASN:H	1:C:278:ASN:HD22	1.60	0.48
1:B:123:TYR:CZ	1:B:196:GLU:HG2	2.48	0.47
1:A:113:SER:N	3:A:420:HOH:O	2.48	0.47
1:A:238:LYS:O	1:A:242:GLU:HG3	2.15	0.47
1:B:197:TRP:CD1	1:B:198:TYR:H	2.32	0.47
1:B:179:ILE:HG23	1:B:342:TYR:HE2	1.78	0.47
1:B:265:GLU:O	1:B:321:LYS:HE2	2.14	0.47
1:B:272:ALA:HB2	1:B:316:GLN:O	2.14	0.47
1:A:65:LYS:HE2	1:A:129:PRO:HG3	1.97	0.47
1:A:235:ARG:HB3	1:A:327:SER:HB2	1.96	0.47
1:A:110:ILE:HB	1:A:113:SER:HB3	1.95	0.46
1:A:298:ILE:HB	1:A:341:PHE:CZ	2.50	0.46
1:C:32:ASP:OD1	1:C:230:GLY:HA3	2.16	0.46
1:C:63:LEU:HG	1:C:81:GLY:HA2	1.98	0.46
1:C:288:MET:HE1	1:C:379:MET:CE	2.36	0.46
1:C:197:TRP:CD1	1:C:198:TYR:H	2.34	0.45
1:B:235:ARG:HB3	1:B:327:SER:HB2	1.99	0.45
1:B:303:GLN:HB2	1:B:361:VAL:HG11	1.98	0.45
1:A:314:THR:HG22	1:A:315:SER:N	2.32	0.45
1:C:211:GLN:HB2	3:C:526:HOH:O	2.17	0.45
1:A:113:SER:O	1:A:114:ASN:CB	2.65	0.45
1:C:235:ARG:HB3	1:C:327:SER:HB2	1.98	0.45
1:A:267:LEU:N	1:A:267:LEU:HD23	2.31	0.45
1:A:288:MET:HE1	1:A:380:GLU:HA	1.99	0.45
1:B:63:LEU:HG	1:B:81:GLY:HA2	1.98	0.45
1:A:1:GLU:HG2	1:B:106:ASP:OD1	2.17	0.44
1:A:197:TRP:CD1	1:A:198:TYR:H	2.35	0.44
1:B:113:SER:O	1:B:114:ASN:CB	2.65	0.44
1:A:259:ASP:O	1:A:263:LEU:HG	2.17	0.44
1:C:278:ASN:HD22	1:C:278:ASN:N	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:378:ASP:HB2	3:C:487:HOH:O	2.15	0.44
1:A:63:LEU:HG	1:A:81:GLY:HA2	1.99	0.44
1:C:23:PRO:HA	1:C:24:PRO:HD3	1.87	0.44
1:C:179:ILE:HG23	1:C:342:TYR:HE2	1.83	0.44
1:A:222:TYR:HA	1:A:223:ASP:HA	1.69	0.44
1:B:19:THR:HA	1:B:25:GLN:O	2.18	0.44
1:A:265:GLU:O	1:A:321:LYS:HE2	2.17	0.44
1:A:271:GLN:HB3	1:A:274:THR:HG21	1.99	0.44
1:C:272:ALA:HB2	1:C:316:GLN:O	2.17	0.44
1:B:301:LEU:HD11	1:B:367:THR:CA	2.48	0.44
1:C:44:PRO:HA	3:C:440:HOH:O	2.18	0.43
1:A:23:PRO:HA	1:A:24:PRO:HD3	1.88	0.43
1:B:65:LYS:HE2	1:B:129:PRO:HG3	2.00	0.43
1:C:151:SER:OG	1:C:175:ILE:HB	2.18	0.43
1:A:32:ASP:OD1	1:A:230:GLY:HA3	2.18	0.43
1:C:222:TYR:HA	1:C:223:ASP:HA	1.67	0.43
1:B:22:SER:HA	1:B:23:PRO:C	2.43	0.43
1:C:341:PHE:C	1:C:357:SER:HB2	2.44	0.43
1:A:184:TYR:HB2	1:A:356:VAL:O	2.19	0.42
1:B:45:HIS:HA	1:B:46:PRO:HD3	1.91	0.42
1:C:197:TRP:CG	1:C:198:TYR:N	2.86	0.42
1:A:271:GLN:HB3	1:A:274:THR:CG2	2.50	0.42
1:C:113:SER:O	1:C:114:ASN:CB	2.68	0.41
1:B:344:VAL:O	1:B:352:ILE:HA	2.21	0.41
1:C:292:THR:HG21	1:C:378:ASP:HB3	2.02	0.41
1:A:197:TRP:CG	1:A:198:TYR:N	2.88	0.41
1:C:4:ASP:HA	1:C:172:GLY:O	2.21	0.41
1:A:181:HIS:HB3	3:A:540:HOH:O	2.19	0.41
1:C:268:VAL:O	1:C:319:CYS:HA	2.21	0.41
1:A:114:ASN:HD22	1:A:114:ASN:HA	1.67	0.41
1:B:8:GLY:C	1:B:170:VAL:HG22	2.46	0.41
1:C:75:LYS:HE2	3:C:400:HOH:O	2.20	0.41
1:C:216:ASP:OD1	1:C:218:LYS:HB2	2.21	0.41
1:B:134:GLU:HA	1:B:135:PRO:HD3	1.93	0.40
1:A:45:HIS:HA	1:A:46:PRO:HD3	1.92	0.40
1:A:126:ILE:HG23	1:A:197:TRP:HB2	2.03	0.40
1:C:301:LEU:HD12	1:C:361:VAL:HG23	2.04	0.40
1:C:314:THR:HB	1:C:316:GLN:OE1	2.21	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	367/402 (91%)	350 (95%)	12 (3%)	5 (1%)	9	5
1	B	373/402 (93%)	354 (95%)	16 (4%)	3 (1%)	16	14
1	C	373/402 (93%)	357 (96%)	13 (4%)	3 (1%)	16	14
All	All	1113/1206 (92%)	1061 (95%)	41 (4%)	11 (1%)	12	10

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	360	HIS
1	C	313	ALA
1	A	316	GLN
1	B	272	ALA
1	C	316	GLN
1	A	315	SER
1	A	272	ALA
1	A	313	ALA
1	A	70	PRO
1	C	70	PRO
1	B	70	PRO

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	318/342 (93%)	313 (98%)	5 (2%)	55	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	322/342 (94%)	318 (99%)	4 (1%)	63	74
1	C	322/342 (94%)	317 (98%)	5 (2%)	55	66
All	All	962/1026 (94%)	948 (98%)	14 (2%)	57	68

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
1	A	197	TRP
1	A	205	ARG
1	A	316	GLN
1	A	360	HIS
1	B	114	ASN
1	B	197	TRP
1	B	254	THR
1	B	373	PRO
1	C	114	ASN
1	C	197	TRP
1	C	267	LEU
1	C	278	ASN
1	C	316	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	73	GLN
1	A	89	HIS
1	A	114	ASN
1	A	211	GLN
1	A	266	GLN
1	A	271	GLN
1	A	316	GLN
1	A	326	GLN
1	A	385	ASN
1	B	53	GLN
1	B	73	GLN
1	B	89	HIS
1	B	114	ASN
1	B	153	GLN

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Mol	Chain	Res	Type
1	B	211	GLN
1	B	266	GLN
1	B	271	GLN
1	B	278	ASN
1	B	316	GLN
1	B	326	GLN
1	C	53	GLN
1	C	73	GLN
1	C	89	HIS
1	C	98	ASN
1	C	114	ASN
1	C	211	GLN
1	C	271	GLN
1	C	278	ASN
1	C	294	GLN
1	C	316	GLN
1	C	326	GLN
1	C	360	HIS

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](#)

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	AYH	B	387	-	35,37,37	1.12	1 (2%)	43,50,50	1.14	5 (11%)
2	AYH	C	387	-	35,37,37	1.16	4 (11%)	43,50,50	1.09	3 (6%)
2	AYH	A	387	-	35,37,37	1.01	1 (2%)	43,50,50	1.10	4 (9%)

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	AYH	B	387	-	-	0/40/50/50	0/2/2/2
2	AYH	C	387	-	-	0/40/50/50	0/2/2/2
2	AYH	A	387	-	-	0/40/50/50	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	387	AYH	C76-C67	3.07	1.56	1.53
2	B	387	AYH	C80-C67	2.81	1.55	1.53
2	C	387	AYH	C80-C67	2.04	1.55	1.53
2	A	387	AYH	C80-C67	2.03	1.55	1.53
2	C	387	AYH	C41-C39	2.03	1.42	1.38
2	C	387	AYH	C58-C56	2.01	1.57	1.53

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	387	AYH	C3-N1-C49	-3.48	117.19	123.25
2	A	387	AYH	C3-N1-C49	-3.02	117.99	123.25
2	B	387	AYH	C3-N1-C49	-2.96	118.09	123.25
2	B	387	AYH	C5-C3-N1	2.75	115.13	109.97
2	A	387	AYH	C5-C3-N1	2.43	114.52	109.97
2	C	387	AYH	C5-C3-N1	2.36	114.39	109.97
2	B	387	AYH	C80-C67-N68	2.27	111.77	107.37
2	B	387	AYH	C14-C12-C18	-2.13	105.72	109.64
2	C	387	AYH	C80-C67-N68	2.12	111.48	107.37
2	A	387	AYH	C80-C67-N68	2.06	111.37	107.37
2	A	387	AYH	C22-N20-C18	-2.05	118.86	122.55
2	B	387	AYH	C22-N20-C18	-2.05	118.87	122.55

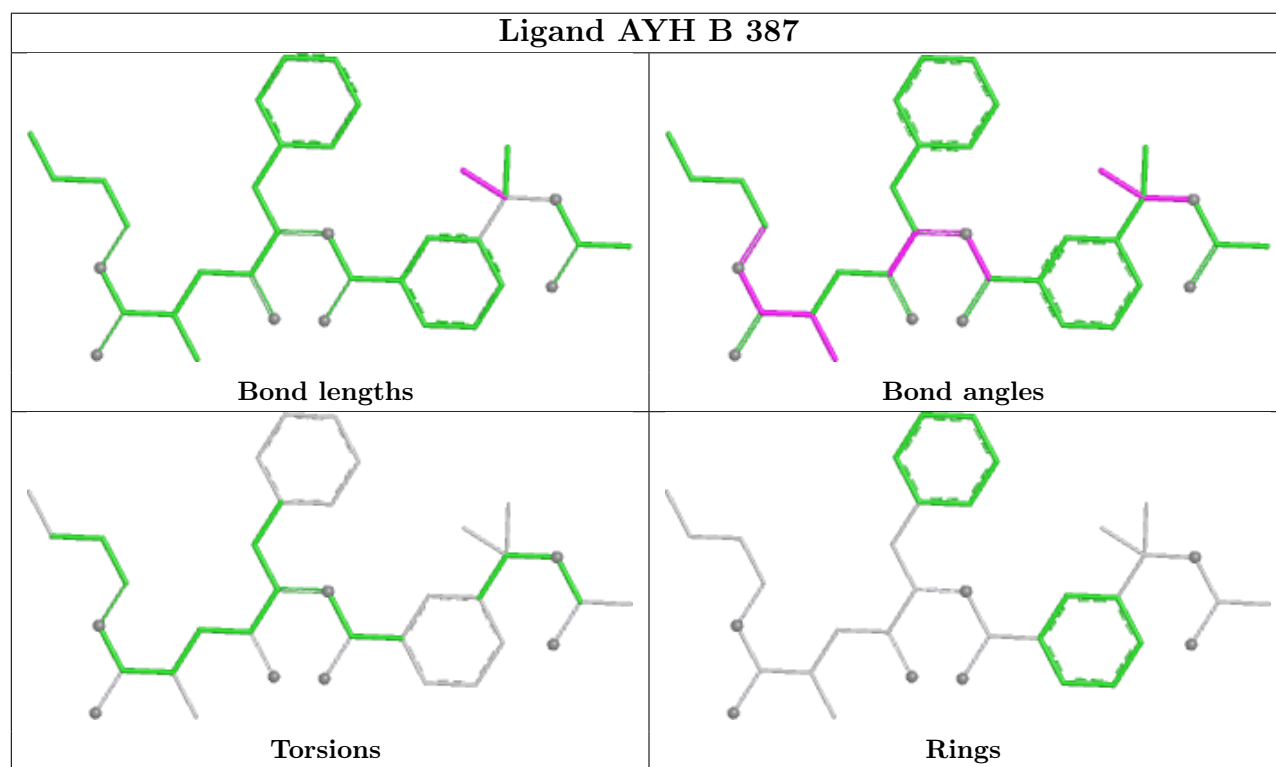
There are no chirality outliers.

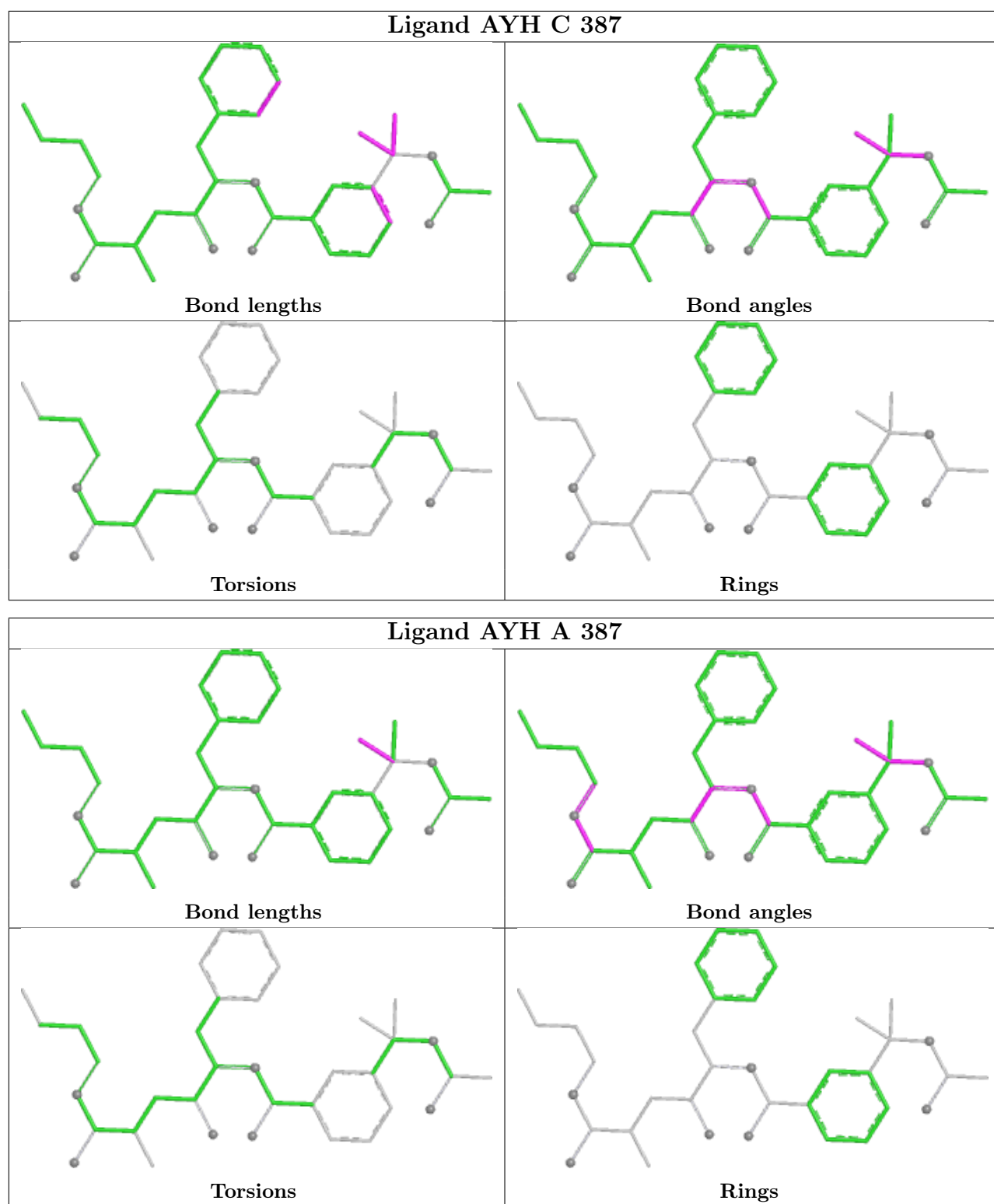
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [\(i\)](#)

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	373/402 (92%)	0.51	45 (12%) 8 8	25, 42, 82, 112	0
1	B	377/402 (93%)	0.51	35 (9%) 14 13	26, 43, 77, 112	0
1	C	377/402 (93%)	0.46	26 (6%) 23 21	27, 44, 72, 107	0
All	All	1127/1206 (93%)	0.49	106 (9%) 14 13	25, 43, 78, 112	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	365	PHE	7.2
1	B	361	VAL	6.7
1	A	361	VAL	5.9
1	C	362	HIS	5.7
1	B	312	VAL	5.6
1	C	365	PHE	5.6
1	A	360	HIS	5.2
1	C	313	ALA	5.1
1	C	312	VAL	4.9
1	A	312	VAL	4.7
1	B	367	THR	4.7
1	A	314	THR	4.5
1	B	314	THR	4.4
1	A	157	ALA	4.3
1	B	362	HIS	4.1
1	A	169	SER	4.0
1	B	360	HIS	4.0
1	A	313	ALA	4.0
1	C	314	THR	3.9
1	B	315	SER	3.8
1	B	313	ALA	3.7
1	C	367	THR	3.7
1	A	267	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	169	SER	3.5
1	A	315	SER	3.4
1	A	311	ASP	3.4
1	B	46(P)	SER	3.4
1	C	46(P)	SER	3.4
1	C	361	VAL	3.4
1	A	46(P)	SER	3.3
1	A	367	THR	3.3
1	B	272	ALA	3.2
1	B	363	ASP	3.2
1	C	267	LEU	3.2
1	C	310	GLU	3.1
1	C	169	SER	3.1
1	C	157	ALA	3.1
1	B	254	THR	3.0
1	C	317	ASP	3.0
1	C	316	GLN	3.0
1	B	256	LYS	3.0
1	A	273	GLY	3.0
1	A	368	ALA	2.9
1	A	309	VAL	2.9
1	A	254	THR	2.9
1	B	114	ASN	2.9
1	A	268	VAL	2.9
1	C	311	ASP	2.9
1	A	112	GLY	2.8
1	C	47	PHE	2.8
1	B	112	GLY	2.8
1	A	258	PRO	2.8
1	A	310	GLU	2.7
1	B	364	GLU	2.7
1	C	364	GLU	2.7
1	A	317	ASP	2.7
1	C	49	HIS	2.7
1	A	110	ILE	2.6
1	B	113	SER	2.6
1	C	315	SER	2.6
1	B	267	LEU	2.6
1	B	268	VAL	2.6
1	A	92	ASN	2.5
1	C	363	ASP	2.5
1	B	368	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	360	HIS	2.5
1	A	95	VAL	2.4
1	B	340	GLY	2.4
1	A	209	ASN	2.4
1	A	359	CYS	2.4
1	B	258	PRO	2.3
1	B	47	PHE	2.3
1	A	64	ARG	2.3
1	B	366	ARG	2.3
1	B	259	ASP	2.3
1	C	340	GLY	2.3
1	B	110	ILE	2.3
1	C	112	GLY	2.3
1	A	214	LYS	2.3
1	C	309	VAL	2.3
1	B	49	HIS	2.2
1	B	22	SER	2.2
1	B	316	GLN	2.2
1	A	366	ARG	2.2
1	A	211	GLN	2.2
1	A	114	ASN	2.2
1	A	142	LYS	2.2
1	B	359	CYS	2.2
1	A	253	SER	2.2
1	B	157	ALA	2.2
1	B	271	GLN	2.1
1	A	272	ALA	2.1
1	A	65	LYS	2.1
1	A	270	TRP	2.1
1	A	319	CYS	2.1
1	A	279	ILE	2.1
1	C	211	GLN	2.1
1	A	256	LYS	2.0
1	A	250	ALA	2.0
1	A	251	ALA	2.0
1	A	113	SER	2.0
1	A	49	HIS	2.0
1	A	301	LEU	2.0
1	A	50	ARG	2.0
1	C	50	ARG	2.0
1	B	214	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](#)

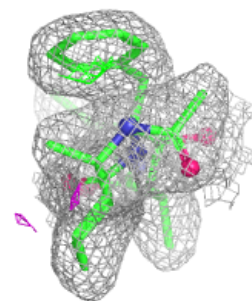
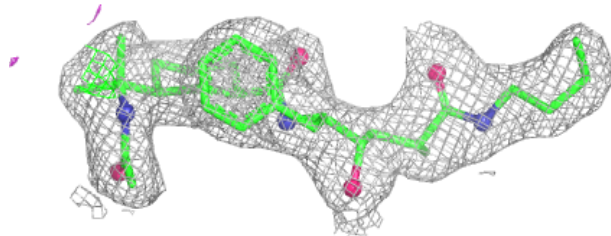
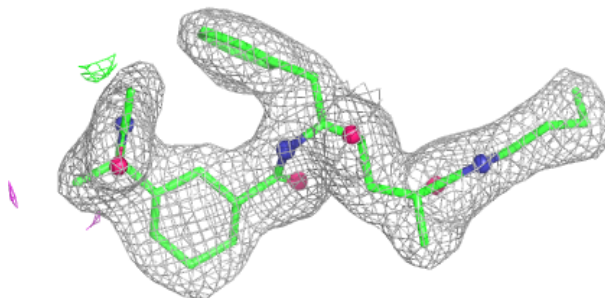
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	AYH	A	387	36/36	0.96	0.07	26,34,39,41	0
2	AYH	B	387	36/36	0.96	0.08	27,33,38,40	0
2	AYH	C	387	36/36	0.96	0.08	27,32,38,45	0

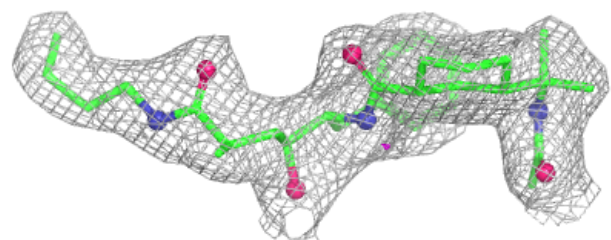
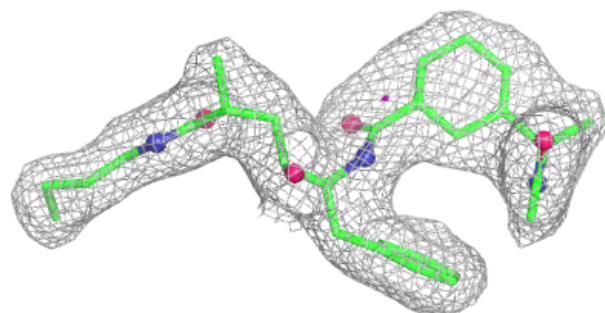
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around AYH A 387:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

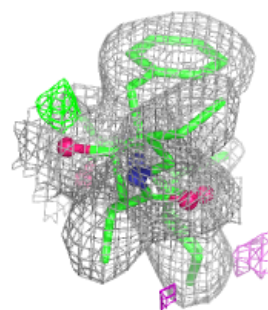
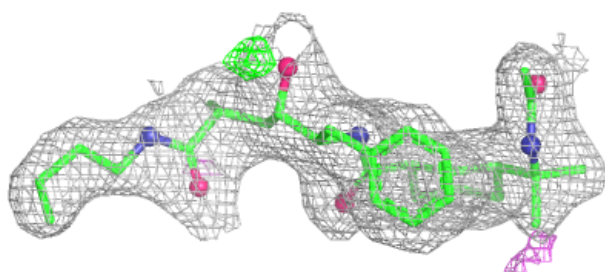
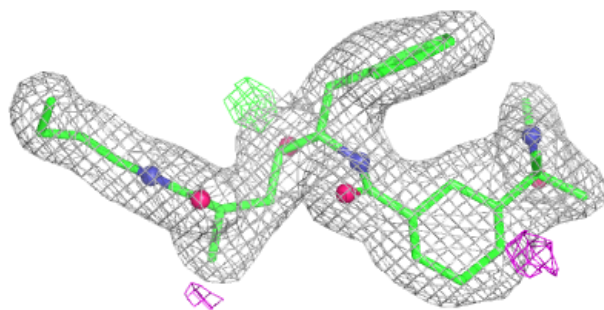
**Electron density around AYH B 387:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around AYH C 387:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.