



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:53 PM UTC

PDB ID : 3FBR / pdb_00003fbr
Title : structure of HipA-amppnp-peptide
Authors : Schumacher, M.A.
Deposited on : 2008-11-19
Resolution : 3.50 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

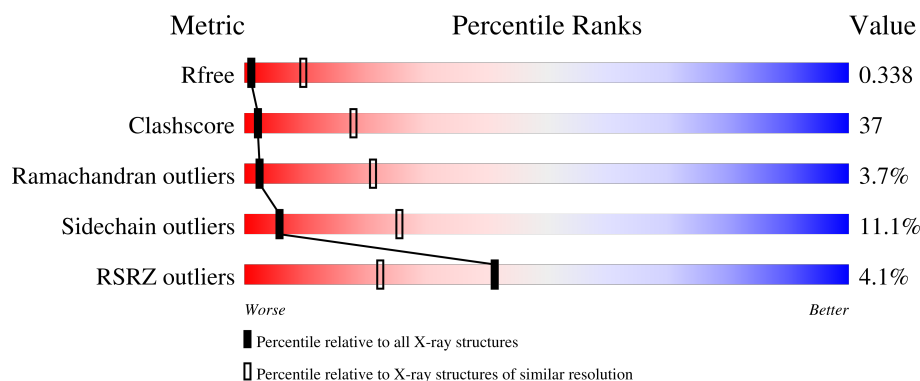
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	437	4% 39% 51% 9%
2	B	9	67% 33%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3521 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 Serine/threonine-protein kinase toxin HipA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	436	Total	C	N	O	S	0	0	0
			3446	2204	601	628	13			

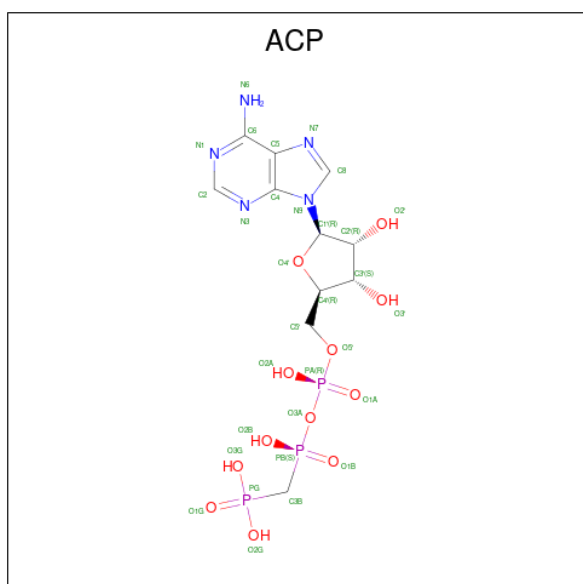
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	309	GLN	ASP	engineered mutation	UNP P23874

- Molecule 2 is a protein called peptide of EF-Tu.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	9	Total	C	N	O	0	0	0
			42	24	9	9			

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		

4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	128.40Å 128.40Å 203.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.90 – 3.50 33.90 – 3.50	Depositor EDS
% Data completeness (in resolution range)	89.7 (33.90-3.50) 89.6 (33.90-3.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 3.47Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.282 , 0.336 0.278 , 0.338	Depositor DCC
R_{free} test set	881 reflections (8.84%)	wwPDB-VP
Wilson B-factor (Å ²)	84.2	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	3521	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 3.10% 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: ACP

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	0.67	0/3523	1.07	16/4777 (0.3%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	VAL	N-CA-C	9.27	121.12	108.89
1	A	194	LEU	N-CA-C	8.79	123.93	109.24
1	A	196	LEU	N-CA-C	7.91	119.97	108.34
1	A	55	ASP	N-CA-C	-7.15	103.66	112.38
1	A	111	THR	N-CA-C	-6.63	96.38	108.65
1	A	185	GLY	N-CA-C	6.26	119.73	110.60
1	A	192	ALA	N-CA-C	6.23	119.29	108.76
1	A	73	ASP	N-CA-C	-5.86	105.02	111.82
1	A	15	GLU	N-CA-C	5.76	117.82	108.26
1	A	414	PHE	CA-C-N	5.63	126.88	119.84
1	A	414	PHE	C-N-CA	5.63	126.88	119.84
1	A	44	SER	N-CA-C	-5.45	106.00	113.30
1	A	333	ILE	N-CA-C	5.40	115.77	107.77
1	A	318	PHE	N-CA-C	-5.13	103.27	110.50
1	A	188	ARG	N-CA-C	5.08	121.62	110.80
1	A	110	VAL	CB-CA-C	-5.01	104.63	111.15

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	3446	0	3487	255	6
2	B	42	0	10	1	6
3	A	31	0	14	4	0
4	A	2	0	0	2	0
All	All	3521	0	3511	257	6

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 37.

All (257) 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:187:ILE:HB	1:A:194:LEU:HB2	1.35	1.04
1:A:363:LYS:HE2	1:A:368:LYS:HB3	1.49	0.94
1:A:78:ARG:NH2	1:A:142:ARG:HA	1.82	0.94
1:A:370:TYR:H	1:A:373:HIS:CD2	1.84	0.94
1:A:370:TYR:H	1:A:373:HIS:HD2	0.94	0.92
1:A:196:LEU:HB3	1:A:339:VAL:HG22	1.50	0.91
1:A:340:LEU:HD21	1:A:350:LEU:HD11	1.55	0.88
1:A:4:LEU:HD22	1:A:103:LEU:HB3	1.56	0.88
1:A:196:LEU:HB3	1:A:339:VAL:CG2	2.05	0.87
1:A:3:LYS:HB2	1:A:106:GLU:HG3	1.57	0.85
1:A:78:ARG:HH22	1:A:142:ARG:HA	1.39	0.83
3:A:500:ACP:H3B2	4:A:439:HOH:O	1.77	0.83
1:A:156:GLU:HG2	1:A:184:ILE:HD11	1.60	0.83
1:A:63:ASN:HB2	1:A:257:GLN:HE21	1.41	0.83
1:A:273:PRO:O	1:A:354:MET:HE2	1.82	0.78
1:A:180:ILE:HD12	1:A:180:ILE:H	1.47	0.78
1:A:105:PRO:HB2	1:A:108:GLU:HG2	1.66	0.77
1:A:304:LEU:HD13	1:A:399:ILE:HD11	1.68	0.76
1:A:156:GLU:HB3	1:A:184:ILE:HG13	1.68	0.76
1:A:24:HIS:NE2	1:A:87:PHE:HB2	2.01	0.76
1:A:370:TYR:N	1:A:373:HIS:HD2	1.79	0.76
1:A:75:ILE:HA	1:A:137:PRO:HG3	1.68	0.76
1:A:96:ASP:OD2	1:A:175:PRO:HA	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:ILE:HG22	1:A:188:ARG:H	1.55	0.71
1:A:124:ARG:HG2	1:A:124:ARG:HH11	1.56	0.70
1:A:93:ILE:HG21	1:A:140:MET:HE1	1.73	0.69
1:A:361:GLY:C	1:A:362:LYS:HD2	2.16	0.69
1:A:188:ARG:HD2	1:A:267:TYR:CE2	2.28	0.68
1:A:372:ARG:HH11	1:A:372:ARG:HB3	1.58	0.67
1:A:187:ILE:HD13	1:A:196:LEU:HD21	1.75	0.67
1:A:332:ASP:OD2	4:A:439:HOH:O	2.13	0.66
1:A:144:GLU:HG2	1:A:146:ASP:OD1	1.94	0.66
1:A:115:MET:HE3	1:A:117:TRP:HZ3	1.59	0.65
1:A:244:ARG:HD2	1:A:244:ARG:N	2.11	0.65
1:A:362:LYS:HD2	1:A:362:LYS:N	2.12	0.65
1:A:203:GLU:HB2	1:A:334:ILE:HD11	1.79	0.65
1:A:93:ILE:HB	1:A:149:ILE:O	1.97	0.64
1:A:141:ILE:O	1:A:141:ILE:HG13	1.96	0.64
1:A:302:GLN:HG2	1:A:307:ALA:HB3	1.80	0.64
1:A:358:ALA:HB2	1:A:363:LYS:HB2	1.79	0.64
1:A:206:CYS:HB3	1:A:333:ILE:HG22	1.80	0.64
1:A:4:LEU:CD2	1:A:103:LEU:HB3	2.27	0.64
1:A:95:ARG:HD3	1:A:95:ARG:N	2.12	0.64
1:A:140:MET:HA	1:A:147:PHE:CD1	2.34	0.63
1:A:6:THR:HG23	1:A:103:LEU:HD23	1.81	0.63
1:A:376:ALA:O	1:A:380:VAL:HG23	1.97	0.63
1:A:296:MET:HB3	1:A:388:MET:HE3	1.79	0.63
1:A:308:THR:HG22	1:A:351:LYS:O	1.99	0.63
1:A:74:ARG:HG2	1:A:135:ASP:OD2	1.98	0.62
1:A:93:ILE:H	1:A:93:ILE:CD1	2.12	0.62
1:A:180:ILE:HD12	1:A:180:ILE:N	2.14	0.62
1:A:217:VAL:HB	1:A:218:PRO:HD2	1.82	0.62
1:A:65:LEU:HD13	1:A:89:LEU:HD12	1.81	0.62
1:A:115:MET:HG3	1:A:174:THR:HG23	1.81	0.62
1:A:253:GLU:HG2	1:A:319:ILE:HD11	1.83	0.61
1:A:210:ALA:HA	1:A:215:LEU:HD12	1.82	0.61
2:B:21:UNK:O	2:B:23:UNK:N	2.34	0.61
1:A:371:PRO:HD2	1:A:372:ARG:NH2	2.16	0.60
1:A:258:THR:HG23	1:A:259:PHE:CD2	2.35	0.60
1:A:254:ASP:HA	1:A:316:SER:HA	1.83	0.60
1:A:65:LEU:HD11	1:A:86:PRO:HA	1.83	0.60
1:A:304:LEU:HD13	1:A:399:ILE:CD1	2.31	0.59
1:A:283:MET:HG2	1:A:292:ARG:HD2	1.84	0.59
1:A:188:ARG:HD3	1:A:189:GLN:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ARG:HD3	1:A:189:GLN:H	1.68	0.59
1:A:7:TRP:NE1	1:A:104:ILE:HD12	2.18	0.58
1:A:170:PRO:HG3	1:A:176:THR:CG2	2.33	0.58
1:A:141:ILE:CD1	1:A:144:GLU:HB2	2.34	0.58
1:A:13:VAL:HG13	1:A:32:TRP:CE2	2.39	0.57
1:A:93:ILE:H	1:A:93:ILE:HD13	1.69	0.57
1:A:117:TRP:CD1	1:A:168:CYS:HG	2.22	0.57
1:A:156:GLU:HB3	1:A:184:ILE:CG1	2.35	0.57
1:A:49:ARG:HG2	1:A:49:ARG:HH11	1.69	0.57
1:A:337:PHE:N	1:A:338:PRO:HD2	2.20	0.57
1:A:126:GLU:O	1:A:130:THR:HG23	2.05	0.56
1:A:144:GLU:O	1:A:145:ASN:HB2	2.03	0.56
1:A:190:PRO:C	1:A:192:ALA:H	2.12	0.56
1:A:213:LEU:O	1:A:215:LEU:HG	2.06	0.56
1:A:278:ILE:HD11	1:A:354:MET:HE1	1.86	0.56
1:A:158:THR:HG22	1:A:180:ILE:HB	1.86	0.56
1:A:65:LEU:HD21	1:A:90:LEU:HG	1.87	0.56
1:A:6:THR:HG23	1:A:103:LEU:CD2	2.36	0.55
1:A:297:LYS:HG3	1:A:391:ILE:HG23	1.88	0.55
1:A:54:SER:C	1:A:56:ALA:N	2.61	0.55
1:A:196:LEU:CB	1:A:339:VAL:HG22	2.31	0.55
1:A:296:MET:HE3	1:A:388:MET:HE3	1.88	0.55
1:A:311:HIS:CE1	1:A:314:ASN:ND2	2.74	0.55
1:A:129:LEU:HB3	1:A:228:VAL:HG11	1.87	0.55
1:A:120:LEU:HB2	1:A:167:TRP:O	2.07	0.54
1:A:26:PHE:CE2	1:A:41:LEU:HD12	2.42	0.54
1:A:141:ILE:HD11	1:A:144:GLU:HB2	1.89	0.54
1:A:179:ILE:HG22	1:A:179:ILE:O	2.06	0.54
1:A:200:VAL:HG12	1:A:231:LEU:HB2	1.89	0.54
1:A:370:TYR:HB3	1:A:372:ARG:NH2	2.22	0.54
1:A:170:PRO:HB2	1:A:174:THR:HB	1.89	0.54
1:A:201:ASP:HB3	1:A:414:PHE:CE2	2.42	0.54
1:A:180:ILE:HA	1:A:231:LEU:O	2.06	0.54
1:A:187:ILE:HG22	1:A:188:ARG:N	2.21	0.53
1:A:386:VAL:HG22	1:A:386:VAL:O	2.08	0.53
1:A:262:PRO:HD2	1:A:265:VAL:CG2	2.39	0.53
1:A:311:HIS:CE1	1:A:314:ASN:HD22	2.26	0.53
1:A:347:ILE:HG13	1:A:350:LEU:HD12	1.90	0.53
1:A:243:GLU:O	1:A:244:ARG:HB2	2.09	0.53
1:A:93:ILE:HD13	1:A:93:ILE:N	2.24	0.53
1:A:63:ASN:CB	1:A:257:GLN:HE21	2.16	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:SER:OG	1:A:326:ARG:HA	2.08	0.52
1:A:428:ARG:NH1	1:A:428:ARG:HG2	2.24	0.52
1:A:196:LEU:HB3	1:A:339:VAL:HG21	1.88	0.52
1:A:276:ALA:HA	1:A:381:LEU:HD21	1.90	0.52
1:A:161:LEU:HD22	1:A:174:THR:CG2	2.40	0.52
1:A:277:ARG:O	1:A:277:ARG:HD3	2.10	0.52
1:A:403:LEU:HD13	1:A:423:GLU:HB2	1.91	0.52
1:A:189:GLN:NE2	1:A:194:LEU:HD11	2.25	0.51
1:A:253:GLU:O	1:A:316:SER:HB3	2.10	0.51
1:A:156:GLU:CB	1:A:184:ILE:HG13	2.39	0.51
1:A:182:LEU:N	1:A:182:LEU:HD22	2.26	0.51
1:A:393:SER:O	1:A:394:ASP:C	2.51	0.51
1:A:254:ASP:O	1:A:258:THR:HB	2.10	0.51
1:A:152:ALA:HB3	3:A:500:ACP:H4'	1.93	0.50
1:A:39:ARG:HD2	1:A:321:ALA:HA	1.93	0.50
1:A:57:VAL:O	1:A:57:VAL:HG12	2.11	0.50
1:A:431:GLY:O	1:A:435:ARG:HG3	2.11	0.50
1:A:170:PRO:HG3	1:A:176:THR:HG23	1.94	0.50
1:A:111:THR:HG22	1:A:112:HIS:H	1.77	0.49
1:A:209:LEU:O	1:A:213:LEU:HB2	2.11	0.49
1:A:234:GLU:O	1:A:235:ARG:C	2.54	0.49
1:A:250:LEU:O	1:A:251:PRO:C	2.54	0.49
1:A:252:GLN:HG2	1:A:253:GLU:N	2.28	0.49
1:A:190:PRO:C	1:A:192:ALA:N	2.70	0.49
1:A:188:ARG:CB	1:A:267:TYR:OH	2.61	0.49
1:A:255:MET:HA	1:A:258:THR:CG2	2.43	0.49
1:A:115:MET:HE3	1:A:117:TRP:CZ3	2.45	0.49
1:A:170:PRO:HG3	1:A:176:THR:HG22	1.95	0.48
1:A:180:ILE:H	1:A:180:ILE:CD1	2.23	0.48
1:A:105:PRO:HB2	1:A:108:GLU:CG	2.39	0.48
1:A:84:ARG:HG2	1:A:84:ARG:HH11	1.78	0.48
1:A:124:ARG:O	1:A:127:GLU:HB2	2.12	0.48
1:A:124:ARG:HG2	1:A:124:ARG:NH1	2.26	0.48
1:A:303:TRP:CE3	1:A:304:LEU:HG	2.48	0.48
1:A:120:LEU:HD11	1:A:169:ILE:HG13	1.95	0.48
1:A:220:ALA:HB2	1:A:233:VAL:HG13	1.95	0.48
1:A:318:PHE:CD1	1:A:328:THR:HG22	2.49	0.48
1:A:79:TYR:HB3	1:A:92:GLU:OE1	2.14	0.48
1:A:390:GLU:O	1:A:393:SER:HB3	2.14	0.48
1:A:117:TRP:CD1	1:A:118:GLU:N	2.82	0.48
1:A:170:PRO:CB	1:A:174:THR:HB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:LEU:HD22	1:A:174:THR:HG21	1.95	0.47
1:A:278:ILE:CD1	1:A:354:MET:HE1	2.45	0.47
1:A:262:PRO:HD2	1:A:265:VAL:HG21	1.96	0.47
1:A:300:VAL:HG12	1:A:304:LEU:CD1	2.45	0.47
1:A:78:ARG:C	1:A:78:ARG:CD	2.88	0.47
1:A:117:TRP:CD1	1:A:168:CYS:SG	3.07	0.47
1:A:188:ARG:HB2	1:A:267:TYR:OH	2.15	0.47
1:A:65:LEU:HB2	1:A:72:ARG:HH21	1.80	0.47
1:A:147:PHE:C	1:A:148:ARG:HG2	2.39	0.47
1:A:95:ARG:HD3	1:A:95:ARG:H	1.80	0.47
1:A:378:ALA:HB2	1:A:388:MET:HG3	1.97	0.47
1:A:238:ARG:CZ	1:A:249:ARG:HG2	2.46	0.46
1:A:291:ASP:OD1	1:A:327:LEU:HB3	2.16	0.46
1:A:316:SER:O	1:A:317:VAL:HG13	2.16	0.46
1:A:422:VAL:O	1:A:426:VAL:HG23	2.15	0.46
1:A:428:ARG:HG2	1:A:428:ARG:HH11	1.81	0.46
1:A:7:TRP:HE1	1:A:104:ILE:HB	1.81	0.46
1:A:296:MET:HB3	1:A:388:MET:CE	2.46	0.46
1:A:190:PRO:O	1:A:192:ALA:N	2.49	0.46
1:A:301:PHE:O	1:A:305:ILE:HG12	2.16	0.46
1:A:8:MET:HA	1:A:100:ALA:O	2.16	0.45
1:A:337:PHE:C	1:A:339:VAL:H	2.24	0.45
1:A:65:LEU:CD1	1:A:86:PRO:HA	2.47	0.45
1:A:296:MET:HE1	1:A:377:THR:HG22	1.99	0.45
1:A:430:HIS:O	1:A:433:LEU:HB2	2.16	0.45
1:A:277:ARG:NH1	1:A:277:ARG:HG3	2.31	0.45
1:A:142:ARG:O	1:A:143:GLU:C	2.59	0.45
1:A:279:MET:C	1:A:281:PHE:N	2.73	0.45
1:A:115:MET:CG	1:A:174:THR:HG23	2.47	0.45
1:A:204:TYR:CE2	1:A:208:LEU:HD11	2.52	0.45
1:A:140:MET:HB3	1:A:147:PHE:HB3	1.99	0.45
1:A:146:ASP:CG	1:A:171:LYS:HE3	2.42	0.45
1:A:277:ARG:HG3	1:A:277:ARG:HH11	1.81	0.45
1:A:129:LEU:HD12	1:A:225:ALA:HB3	1.98	0.44
1:A:300:VAL:HG12	1:A:304:LEU:HD12	1.98	0.44
1:A:178:HIS:HA	1:A:235:ARG:HG3	2.00	0.44
1:A:258:THR:HG23	1:A:259:PHE:CE2	2.52	0.44
1:A:357:ASN:OD1	1:A:380:VAL:HG21	2.17	0.44
1:A:42:SER:C	1:A:44:SER:H	2.25	0.44
1:A:378:ALA:CB	1:A:388:MET:HG3	2.47	0.44
1:A:54:SER:C	1:A:56:ALA:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:THR:O	1:A:365:ALA:C	2.61	0.44
1:A:72:ARG:HB3	1:A:84:ARG:HH12	1.83	0.44
1:A:93:ILE:CD1	1:A:93:ILE:N	2.76	0.44
1:A:236:PHE:CD2	3:A:500:ACP:N1	2.86	0.44
1:A:386:VAL:O	1:A:386:VAL:CG2	2.65	0.44
1:A:393:SER:O	1:A:396:ALA:N	2.51	0.44
1:A:320:GLN:N	1:A:324:SER:O	2.51	0.43
1:A:370:TYR:HB3	1:A:372:ARG:CZ	2.48	0.43
1:A:357:ASN:HB3	1:A:377:THR:HA	2.00	0.43
1:A:114:ILE:HG23	1:A:173:ILE:CD1	2.48	0.43
1:A:237:ASP:HA	1:A:250:LEU:HB2	2.01	0.43
1:A:385:GLU:C	1:A:387:GLN:N	2.76	0.43
1:A:407:LYS:HD3	1:A:423:GLU:OE1	2.18	0.43
1:A:188:ARG:O	1:A:189:GLN:HB2	2.19	0.43
1:A:196:LEU:HB2	1:A:197:SER:H	1.37	0.43
1:A:268:GLU:HA	1:A:272:GLY:H	1.82	0.43
1:A:274:GLY:HA2	1:A:354:MET:SD	2.58	0.43
1:A:285:SER:O	1:A:288:ALA:HB2	2.19	0.43
1:A:144:GLU:HB3	1:A:145:ASN:H	1.54	0.43
1:A:286:SER:HB2	1:A:320:GLN:HE22	1.84	0.43
1:A:114:ILE:HG23	1:A:173:ILE:HD11	2.01	0.43
1:A:7:TRP:CD1	1:A:7:TRP:N	2.86	0.42
1:A:337:PHE:N	1:A:338:PRO:CD	2.81	0.42
1:A:147:PHE:CZ	1:A:169:ILE:HG23	2.54	0.42
1:A:216:ASN:C	1:A:216:ASN:ND2	2.77	0.42
1:A:46:PRO:O	1:A:48:GLN:HG2	2.20	0.42
1:A:259:PHE:CE1	1:A:277:ARG:HD2	2.55	0.42
1:A:430:HIS:ND1	1:A:430:HIS:C	2.77	0.42
1:A:3:LYS:HG2	1:A:15:GLU:CD	2.44	0.42
1:A:44:SER:OG	1:A:45:LEU:HD23	2.19	0.42
1:A:78:ARG:HB3	1:A:79:TYR:CD1	2.55	0.42
1:A:104:ILE:HA	1:A:105:PRO:HD3	1.94	0.42
1:A:399:ILE:O	1:A:400:PRO:C	2.62	0.42
1:A:69:PRO:O	1:A:73:ASP:N	2.52	0.42
1:A:160:LEU:O	1:A:177:THR:N	2.50	0.42
1:A:370:TYR:HB3	1:A:371:PRO:HD2	2.01	0.42
1:A:58:PHE:CE1	1:A:86:PRO:HG3	2.55	0.42
1:A:65:LEU:HD21	1:A:90:LEU:CD2	2.50	0.42
1:A:331:TYR:CE1	3:A:500:ACP:H3'	2.54	0.42
1:A:385:GLU:C	1:A:387:GLN:H	2.27	0.42
1:A:63:ASN:HB3	1:A:313:LYS:NZ	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:PHE:HE2	1:A:388:MET:HG2	1.85	0.42
1:A:295:PHE:O	1:A:298:PHE:N	2.49	0.42
1:A:267:TYR:O	1:A:268:GLU:C	2.62	0.41
1:A:278:ILE:O	1:A:281:PHE:HB3	2.19	0.41
1:A:141:ILE:HD12	1:A:144:GLU:HB2	2.01	0.41
1:A:209:LEU:HD13	1:A:403:LEU:HD23	2.01	0.41
1:A:279:MET:O	1:A:282:LEU:N	2.51	0.41
1:A:316:SER:O	1:A:327:LEU:HD12	2.20	0.41
1:A:188:ARG:HD2	1:A:267:TYR:CZ	2.56	0.41
1:A:209:LEU:HG	1:A:213:LEU:HD12	2.02	0.41
1:A:54:SER:O	1:A:55:ASP:C	2.63	0.41
1:A:59:ASN:O	1:A:60:PHE:C	2.63	0.41
1:A:391:ILE:O	1:A:392:LEU:C	2.64	0.41
1:A:120:LEU:HD11	1:A:169:ILE:CG1	2.50	0.41
1:A:205:TYR:CE1	1:A:419:VAL:HG22	2.55	0.41
1:A:210:ALA:O	1:A:215:LEU:HB2	2.20	0.41
1:A:93:ILE:O	1:A:148:ARG:O	2.38	0.41
1:A:161:LEU:HB3	1:A:170:PRO:HD3	2.02	0.41
1:A:182:LEU:HA	1:A:182:LEU:HD13	1.76	0.41
1:A:254:ASP:OD2	1:A:257:GLN:HG3	2.20	0.41
1:A:177:THR:C	1:A:235:ARG:HG3	2.46	0.41
1:A:200:VAL:HG12	1:A:231:LEU:CB	2.51	0.40
1:A:303:TRP:HD1	1:A:366:ILE:HG23	1.86	0.40
1:A:58:PHE:CZ	1:A:86:PRO:HG3	2.56	0.40
1:A:206:CYS:HB3	1:A:333:ILE:CG2	2.48	0.40
1:A:253:GLU:HB2	1:A:257:GLN:OE1	2.20	0.40
1:A:112:HIS:O	1:A:113:PRO:C	2.63	0.40
1:A:188:ARG:CD	1:A:189:GLN:H	2.33	0.40
1:A:363:LYS:CE	1:A:368:LYS:HB3	2.35	0.40

All (6) 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)
1:A:272:GLY:CA	2:B:24:UNK:CB[4_555]	1.51	0.69
1:A:271:GLY:O	2:B:24:UNK:CA[4_555]	1.58	0.62
1:A:272:GLY:C	2:B:24:UNK:CB[4_555]	1.80	0.40
1:A:261:LEU:CD1	2:B:24:UNK:O[4_555]	1.86	0.34
1:A:271:GLY:O	2:B:24:UNK:CB[4_555]	1.86	0.34
1:A:272:GLY:N	2:B:24:UNK:CB[4_555]	2.09	0.11

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	434/437 (99%)	347 (80%)	71 (16%)	16 (4%)	2	21

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	ARG
1	A	144	GLU
1	A	145	ASN
1	A	189	GLN
1	A	286	SER
1	A	332	ASP
1	A	152	ALA
1	A	393	SER
1	A	197	SER
1	A	265	VAL
1	A	415	PRO
1	A	191	ASN
1	A	411	PRO
1	A	54	SER
1	A	306	GLY
1	A	76	VAL

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	371/372 (100%)	330 (89%)	41 (11%)	6 25

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	6	THR
1	A	7	TRP
1	A	8	MET
1	A	13	VAL
1	A	17	THR
1	A	19	LEU
1	A	36	ARG
1	A	39	ARG
1	A	41	LEU
1	A	45	LEU
1	A	51	ASN
1	A	53	THR
1	A	55	ASP
1	A	85	GLN
1	A	93	ILE
1	A	119	LYS
1	A	121	THR
1	A	147	PHE
1	A	166	ASP
1	A	173	ILE
1	A	186	GLU
1	A	188	ARG
1	A	193	THR
1	A	195	ASP
1	A	196	LEU
1	A	200	VAL
1	A	203	GLU
1	A	213	LEU
1	A	227	ASN
1	A	229	ARG
1	A	256	CYS
1	A	283	MET
1	A	287	GLU
1	A	289	LEU

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Mol	Chain	Res	Type
1	A	294	ASP
1	A	317	VAL
1	A	362	LYS
1	A	372	ARG
1	A	388	MET
1	A	408	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	85	GLN
1	A	189	GLN
1	A	216	ASN
1	A	227	ASN
1	A	257	GLN
1	A	302	GLN
1	A	314	ASN
1	A	373	HIS
1	A	425	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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
3	ACP	A	500	-	31,33,33	2.43	9 (29%)	47,52,52	1.67	6 (12%)

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
3	ACP	A	500	-	-	4/19/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	ACP	PA-O3A	8.55	1.68	1.59
3	A	500	ACP	C4-N3	5.25	1.44	1.34
3	A	500	ACP	PB-O2B	-4.24	1.46	1.56
3	A	500	ACP	C2-N3	3.48	1.40	1.33
3	A	500	ACP	PB-O3A	2.61	1.61	1.58
3	A	500	ACP	PG-O2G	-2.50	1.49	1.55
3	A	500	ACP	PA-O2A	-2.50	1.43	1.55
3	A	500	ACP	C1'-N9	2.45	1.53	1.46
3	A	500	ACP	C2-N1	2.34	1.38	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	ACP	O2B-PB-O1B	7.56	134.56	109.95
3	A	500	ACP	C3'-C2'-C1'	3.20	107.52	101.46
3	A	500	ACP	PB-O3A-PA	2.91	141.87	132.37
3	A	500	ACP	C1'-N9-C8	2.51	132.67	127.09
3	A	500	ACP	O5'-C5'-C4'	2.32	116.89	108.99
3	A	500	ACP	N3-C2-N1	-2.23	125.21	128.58

There are no chirality outliers.

All (4) torsion outliers are listed below:

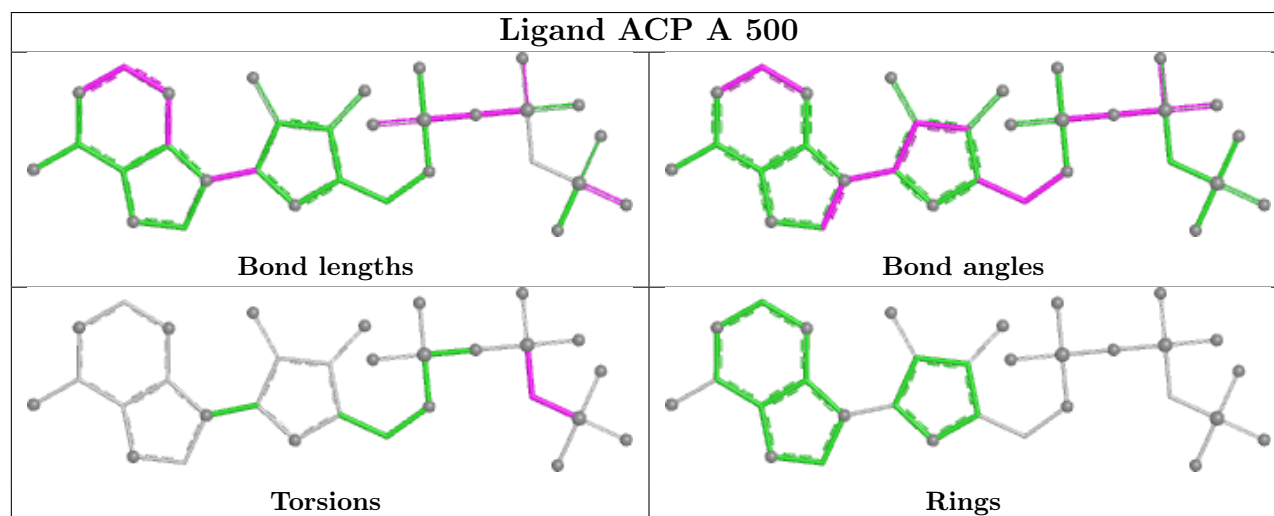
Mol	Chain	Res	Type	Atoms
3	A	500	ACP	PB-C3B-PG-O1G
3	A	500	ACP	PB-C3B-PG-O2G
3	A	500	ACP	PB-C3B-PG-O3G
3	A	500	ACP	PG-C3B-PB-O1B

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	ACP	4	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	436/437 (99%)	0.13	18 (4%) 41 22	19, 45, 73, 83	0
2	B	0/9	-	-	-	-
All	All	436/446 (97%)	0.13	18 (4%) 41 22	19, 45, 73, 83	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	274	GLY	3.1
1	A	353	ALA	3.1
1	A	58	PHE	3.1
1	A	38	ALA	2.9
1	A	241	ASN	2.6
1	A	280	ALA	2.5
1	A	109	THR	2.4
1	A	218	PRO	2.3
1	A	278	ILE	2.3
1	A	367	ASP	2.3
1	A	56	ALA	2.3
1	A	243	GLU	2.2
1	A	377	THR	2.2
1	A	99	GLY	2.2
1	A	154	ALA	2.1
1	A	246	VAL	2.1
1	A	287	GLU	2.0
1	A	111	THR	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](#)

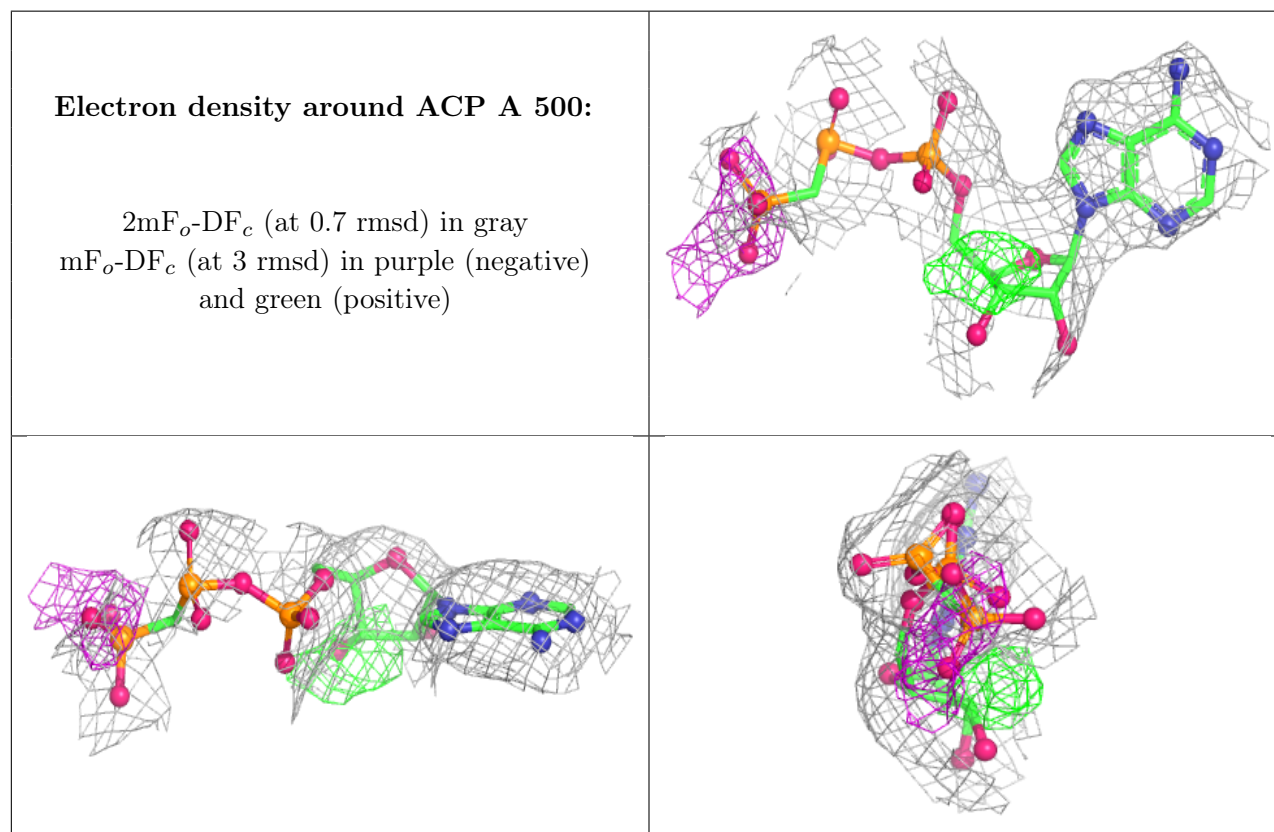
There are no oligosaccharides in this entry.

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
3	ACP	A	500	31/31	0.87	0.14	32,39,80,81	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.