



Full wwPDB X-ray Structure Validation Report ⓘ

May 7, 2026 – 09:40 AM EDT

PDB ID : 3EHF / pdb_00003ehf
Title : Crystal structure of DesKC in complex with AMP-PCP
Authors : Albanesi, D.; Alzari, P.M.; Buschiazzi, A.
Deposited on : 2008-09-12
Resolution : 3.10 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

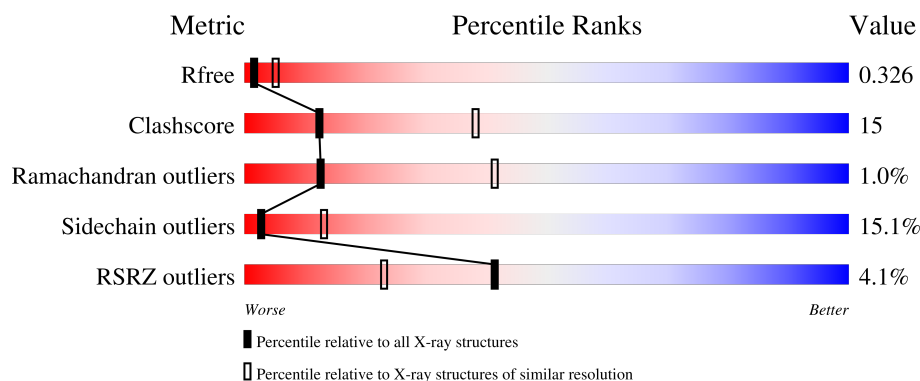
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	197	3% 52% 30% 8% 9%
1	B	197	5% 36% 11% 6% 47%
1	C	197	% 24% 5% 71%
1	D	197	3% 56% 32% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4035 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.

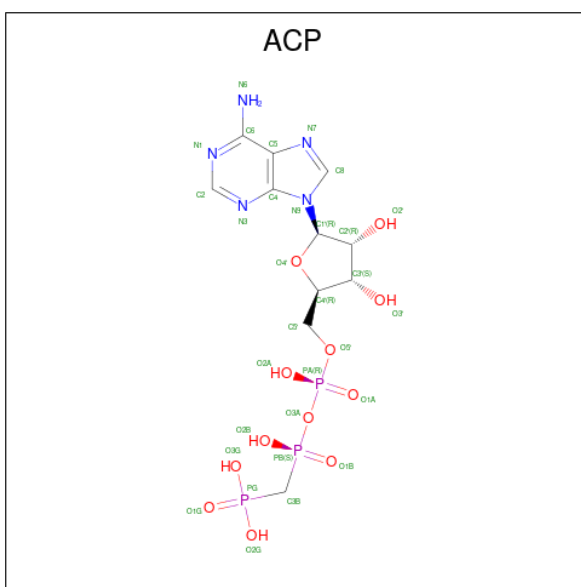
- Molecule 1 is a protein called Sensor kinase (YocF protein).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	Se	0	1	0
			1388	866	247	267	2	6			
1	B	104	Total	C	N	O	Se		0	0	0
			760	474	137	147	2				
1	C	57	Total	C	N	O	Se		0	0	0
			429	268	78	82	1				
1	D	181	Total	C	N	O	S	Se	0	0	0
			1378	865	240	266	2	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	174	GLY	-	expression tag	UNP O34757
B	174	GLY	-	expression tag	UNP O34757
C	174	GLY	-	expression tag	UNP O34757
D	174	GLY	-	expression tag	UNP O34757

- Molecule 2 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O P 31 11 5 12 3	0	0
2	B	1	Total C O P 12 1 8 3	0	0
2	D	1	Total C N O P 31 11 5 12 3	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0

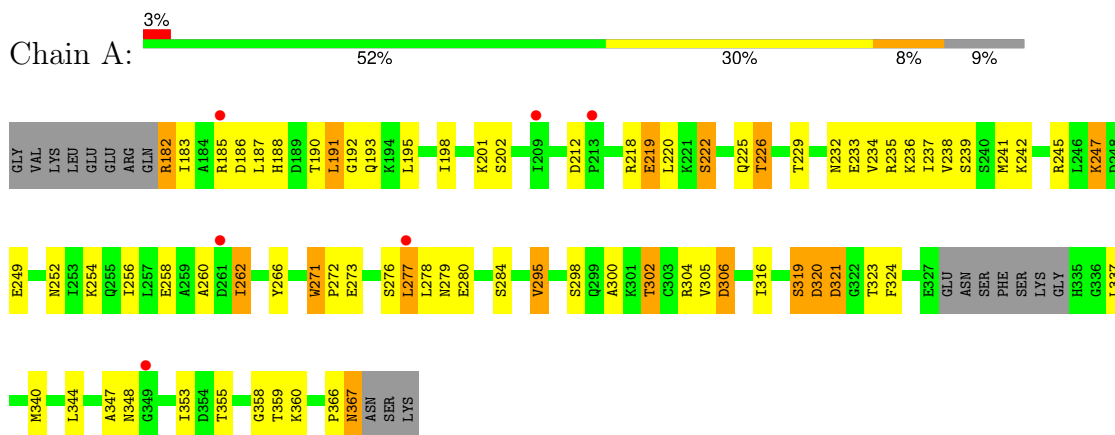
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O 1 1	0	0
4	D	2	Total O 2 2	0	0

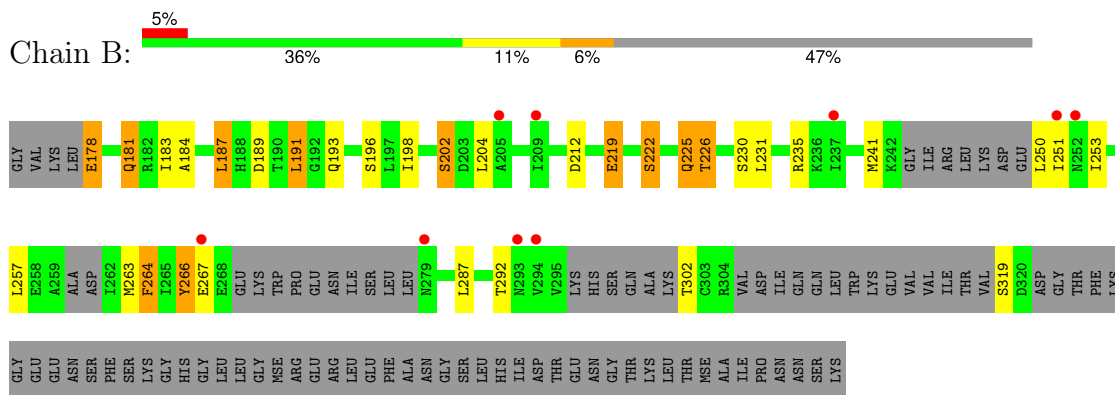
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

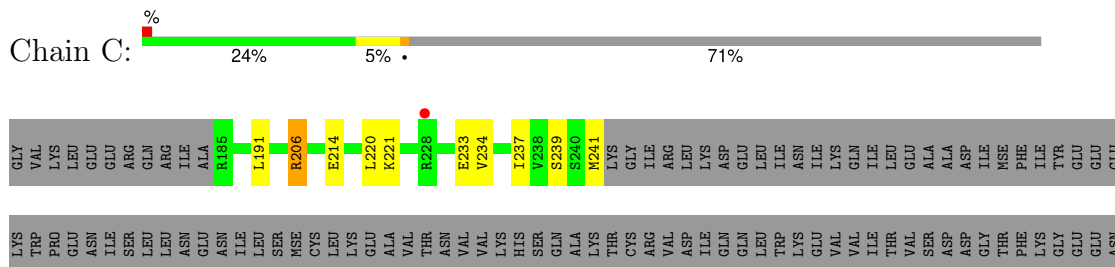
- Molecule 1: Sensor kinase (YocF protein)



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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.80Å 44.70Å 131.45Å 90.00° 103.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.10 15.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (15.00-3.10) 98.2 (15.00-3.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.10 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.5.0053	Depositor
R, R_{free}	0.242 , 0.297 0.282 , 0.326	Depositor DCC
R_{free} test set	816 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	60.4	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 53.6	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	0.87	EDS
Total number of atoms	4035	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.70 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.6365e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.88	0/1396	1.15	7/1867 (0.4%)
1	B	0.95	0/756	1.17	2/1008 (0.2%)
1	C	0.78	0/430	1.05	0/576
1	D	0.81	0/1385	1.06	2/1857 (0.1%)
All	All	0.86	0/3967	1.11	11/5308 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	ASP	CA-C-N	6.47	126.69	119.32
1	A	212	ASP	C-N-CA	6.47	126.69	119.32
1	D	301	LYS	N-CA-C	-6.01	105.60	113.12
1	A	271	TRP	CA-C-N	5.41	126.60	119.84
1	A	271	TRP	C-N-CA	5.41	126.60	119.84
1	D	264	PHE	N-CA-C	5.38	117.29	108.52
1	A	220	LEU	N-CA-C	5.31	117.15	111.36
1	B	212	ASP	CA-C-N	5.25	125.06	119.28
1	B	212	ASP	C-N-CA	5.25	125.06	119.28
1	A	298	SER	N-CA-C	5.16	116.90	111.28
1	A	232	ASN	N-CA-C	5.14	117.55	111.33

There are no chirality outliers.

There are no planarity outliers.

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	1388	0	1431	50	0
1	B	760	0	726	23	0
1	C	429	0	445	12	0
1	D	1378	0	1382	52	0
2	A	31	0	14	0	0
2	B	12	0	2	0	0
2	D	31	0	14	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	D	2	0	0	0	0
All	All	4035	0	4014	124	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 15.

All (124) 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:206:ARG:HH11	1:C:206:ARG:HG2	1.30	0.93
1:A:254:LYS:O	1:A:258:GLU:HG3	1.69	0.92
1:D:230:SER:O	1:D:234:VAL:HG23	1.70	0.91
1:C:220:LEU:HD21	1:D:220:LEU:CD2	2.01	0.91
1:A:201:LYS:NZ	1:A:219:GLU:OE2	2.07	0.86
1:C:220:LEU:HD21	1:D:220:LEU:HD21	1.60	0.80
1:B:222:SER:O	1:B:226:THR:HG22	1.81	0.79
1:C:206:ARG:HH11	1:C:206:ARG:CG	1.95	0.79
1:A:247:LYS:H	1:A:247:LYS:CD	1.94	0.79
1:A:367:ASN:HD22	1:A:367:ASN:N	1.83	0.77
1:D:324:PHE:HA	2:D:500:ACP:C2	2.17	0.75
1:D:353:ILE:HG13	1:D:361:LEU:CD2	2.18	0.74
1:A:347:ALA:O	1:A:348:ASN:HB2	1.89	0.72
2:D:500:ACP:O1B	2:D:500:ACP:H3'	1.89	0.71
1:D:307:ILE:HG12	1:D:316:ILE:HG12	1.73	0.70
1:C:233:GLU:O	1:C:237:ILE:HD12	1.93	0.69
1:A:302:THR:HB	1:A:321:ASP:OD2	1.92	0.69
1:A:277:LEU:H	1:A:277:LEU:HD23	1.57	0.69
1:D:353:ILE:HG13	1:D:361:LEU:HD23	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:178:GLU:O	1:B:178:GLU:HG3	1.94	0.67
1:D:312:LYS:O	1:D:367:ASN:ND2	2.27	0.66
1:D:302:THR:HG23	1:D:321:ASP:OD2	1.97	0.65
1:B:225:GLN:HE21	1:B:225:GLN:HA	1.62	0.65
1:D:353:ILE:CG2	1:D:355:THR:HG23	2.27	0.64
1:D:353:ILE:HG22	1:D:355:THR:HG23	1.80	0.64
1:A:367:ASN:HD22	1:A:367:ASN:H	1.44	0.64
1:B:178:GLU:HA	1:B:181:GLN:HB2	1.80	0.63
1:A:367:ASN:N	1:A:367:ASN:ND2	2.47	0.63
1:D:282:ILE:HG12	1:D:343:ARG:HD3	1.80	0.61
1:A:241:MSE:HE3	1:B:183:ILE:HG22	1.82	0.61
1:A:266:TYR:HD1	1:A:305:VAL:O	1.85	0.60
1:D:272:PRO:HA	1:D:309:GLN:HB2	1.82	0.60
1:A:182:ARG:CG	1:A:183:ILE:H	2.17	0.58
1:D:312:LYS:C	1:D:367:ASN:ND2	2.62	0.57
1:B:204:LEU:HD23	1:B:219:GLU:CG	2.35	0.57
1:A:247:LYS:H	1:A:247:LYS:HD2	1.67	0.57
1:B:222:SER:O	1:B:226:THR:CG2	2.52	0.56
1:B:204:LEU:HD23	1:B:219:GLU:HG2	1.87	0.56
1:A:225:GLN:O	1:A:229:THR:HG23	2.06	0.56
1:C:241:MSE:CE	1:D:183:ILE:HB	2.36	0.55
1:D:353:ILE:HG22	1:D:354:ASP:N	2.22	0.55
1:A:355:THR:HA	1:A:358:GLY:O	2.06	0.55
1:D:208:LEU:O	1:D:209:ILE:C	2.49	0.55
1:D:313:GLU:HA	1:D:367:ASN:ND2	2.22	0.55
1:A:225:GLN:NE2	1:A:225:GLN:HA	2.22	0.55
1:A:277:LEU:HD23	1:A:277:LEU:N	2.21	0.54
1:A:225:GLN:HA	1:A:225:GLN:HE21	1.72	0.54
1:A:182:ARG:CG	1:A:183:ILE:N	2.71	0.54
1:A:187:LEU:HD11	1:B:187:LEU:HD21	1.89	0.54
1:D:356:GLU:C	1:D:358:GLY:H	2.16	0.53
1:A:249:GLU:HG2	1:A:284:SER:O	2.09	0.52
1:D:353:ILE:HG13	1:D:361:LEU:HD21	1.88	0.52
1:A:247:LYS:H	1:A:247:LYS:HD3	1.70	0.52
1:D:324:PHE:HD1	1:D:359:THR:HG1	1.57	0.52
1:D:353:ILE:CG2	1:D:354:ASP:N	2.73	0.52
1:C:191:LEU:HD11	1:C:234:VAL:HG22	1.91	0.51
1:B:253:ILE:HD13	1:B:287:LEU:HD21	1.93	0.51
1:A:262:ILE:CD1	1:A:300:ALA:O	2.58	0.51
1:D:187:LEU:HD13	1:D:237:ILE:HG21	1.93	0.51
1:C:206:ARG:CG	1:C:206:ARG:NH1	2.63	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:296:LYS:HG2	1:D:296:LYS:O	2.12	0.50
1:D:271:TRP:CD2	1:D:272:PRO:HD2	2.46	0.50
1:D:367:ASN:H	1:D:367:ASN:HD22	1.58	0.50
1:B:263:MSE:O	1:B:302:THR:HA	2.12	0.50
1:D:256:ILE:HG22	1:D:295:VAL:HG11	1.93	0.49
1:A:279:ASN:ND2	1:A:366:PRO:O	2.45	0.49
1:A:241:MSE:HE1	1:B:187:LEU:HD23	1.95	0.49
1:A:195:LEU:HD22	1:B:230:SER:HB2	1.95	0.49
1:A:188:HIS:O	1:A:192:GLY:HA3	2.13	0.49
1:D:353:ILE:CG2	1:D:355:THR:CG2	2.92	0.48
1:A:241:MSE:CE	1:B:183:ILE:HG22	2.43	0.48
1:B:198:ILE:O	1:B:202:SER:HB2	2.13	0.48
1:B:266:TYR:O	1:B:267:GLU:HG3	2.13	0.48
1:A:260:ALA:CB	1:A:295:VAL:HB	2.44	0.48
1:D:274:ASN:O	1:D:367:ASN:HB3	2.14	0.48
1:B:250:LEU:O	1:B:253:ILE:HG12	2.13	0.47
1:A:233:GLU:O	1:A:237:ILE:HG13	2.14	0.47
1:B:253:ILE:O	1:B:257:LEU:HD12	2.14	0.47
1:A:191:LEU:HD21	1:B:191:LEU:HD21	1.96	0.47
1:D:181:GLN:O	1:D:184:ALA:HB3	2.14	0.47
1:C:241:MSE:HB3	1:D:184:ALA:HB2	1.96	0.47
1:D:338:LEU:O	1:D:342:GLU:HG3	2.14	0.47
1:D:289:GLU:HG3	1:D:340:MSE:HE2	1.98	0.46
1:D:191:LEU:HD11	1:D:234:VAL:HG22	1.98	0.46
1:A:300:ALA:HB2	1:A:320:ASP:OD1	2.15	0.46
1:A:262:ILE:HD12	1:A:300:ALA:O	2.16	0.46
1:C:206:ARG:NH1	1:C:206:ARG:HB3	2.31	0.45
1:A:222:SER:O	1:A:226:THR:HG22	2.17	0.45
1:A:324:PHE:HD1	1:A:359:THR:OG1	1.99	0.45
1:A:238:VAL:HG13	1:B:184:ALA:HB1	1.99	0.45
1:B:191:LEU:HD11	1:B:230:SER:HB3	2.00	0.44
1:D:245:ARG:HB2	1:D:248:ASP:OD2	2.17	0.44
1:A:324:PHE:CD1	1:A:359:THR:OG1	2.70	0.44
1:D:238:VAL:O	1:D:242:LYS:HB2	2.17	0.44
1:D:367:ASN:HD22	1:D:367:ASN:N	2.16	0.44
1:A:319:SER:HB3	1:A:360:LYS:HG3	1.99	0.44
1:A:306:ASP:O	1:A:316:ILE:HA	2.18	0.44
1:A:234:VAL:O	1:A:235:ARG:C	2.60	0.43
1:A:337:LEU:HA	1:A:340:MSE:HE3	1.99	0.43
1:C:220:LEU:HD21	1:D:220:LEU:HD22	1.93	0.43
1:B:257:LEU:HD13	1:B:264:PHE:CB	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:194:LYS:O	1:D:198:ILE:HG13	2.19	0.43
1:A:218:ARG:O	1:A:219:GLU:C	2.62	0.42
1:A:276:SER:HB3	1:A:279:ASN:HB2	1.99	0.42
1:D:324:PHE:HD1	1:D:359:THR:OG1	2.01	0.42
1:A:245:ARG:HH21	1:A:280:GLU:CD	2.28	0.42
1:A:344:LEU:O	1:A:347:ALA:HB3	2.19	0.42
1:D:246:LEU:HA	1:D:284:SER:OG	2.20	0.42
1:D:246:LEU:HD21	1:D:316:ILE:HD11	2.01	0.42
1:D:250:LEU:HD21	1:D:266:TYR:CZ	2.55	0.42
1:A:271:TRP:HA	1:A:272:PRO:HD2	1.84	0.42
1:D:353:ILE:HG21	1:D:355:THR:CG2	2.49	0.42
1:C:241:MSE:HE2	1:D:183:ILE:HB	2.01	0.42
1:A:191:LEU:HD11	1:A:234:VAL:HG23	2.01	0.41
1:D:353:ILE:HG21	1:D:355:THR:HG23	2.02	0.41
1:A:252:ASN:O	1:A:256:ILE:HD13	2.20	0.41
1:D:225:GLN:O	1:D:229:THR:HG23	2.20	0.41
1:D:279:ASN:OD1	1:D:365:ILE:HD11	2.21	0.41
1:D:285:MSE:HG3	1:D:343:ARG:NH2	2.36	0.41
1:D:267:GLU:O	1:D:268:GLU:C	2.64	0.41
1:D:249:GLU:HG2	1:D:284:SER:O	2.21	0.40
1:A:183:ILE:HB	1:B:241:MSE:HE1	2.03	0.40
1:D:325:LYS:HB2	2:D:500:ACP:O2'	2.22	0.40
1:A:277:LEU:H	1:A:277:LEU:CD2	2.24	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	176/197 (89%)	156 (89%)	18 (10%)	2 (1%)	11	39
1	B	92/197 (47%)	83 (90%)	7 (8%)	2 (2%)	5	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	55/197 (28%)	52 (94%)	3 (6%)	0	100	100
1	D	175/197 (89%)	158 (90%)	16 (9%)	1 (1%)	21	52
All	All	498/788 (63%)	449 (90%)	44 (9%)	5 (1%)	12	41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	GLU
1	A	323	THR
1	B	251	ILE
1	B	189	ASP
1	D	209	ILE

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	153/170 (90%)	126 (82%)	27 (18%)	2	9
1	B	73/170 (43%)	56 (77%)	17 (23%)	1	4
1	C	46/170 (27%)	42 (91%)	4 (9%)	9	34
1	D	147/170 (86%)	132 (90%)	15 (10%)	7	28
All	All	419/680 (62%)	356 (85%)	63 (15%)	3	13

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	ARG
1	A	185	ARG
1	A	186	ASP
1	A	190	THR
1	A	191	LEU
1	A	193	GLN
1	A	198	ILE

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Mol	Chain	Res	Type
1	A	202	SER
1	A	219	GLU
1	A	222	SER
1	A	226	THR
1	A	236	LYS
1	A	239	SER
1	A	242	LYS
1	A	247	LYS
1	A	262	ILE
1	A	277	LEU
1	A	278	LEU
1	A	295	VAL
1	A	302	THR
1	A	304	ARG
1	A	306	ASP
1	A	319	SER
1	A	320	ASP
1	A	321	ASP
1	A	353	ILE
1	A	367	ASN
1	B	178	GLU
1	B	181	GLN
1	B	187	LEU
1	B	191	LEU
1	B	193	GLN
1	B	196	SER
1	B	202	SER
1	B	219	GLU
1	B	222	SER
1	B	225	GLN
1	B	226	THR
1	B	231	LEU
1	B	235	ARG
1	B	264	PHE
1	B	266	TYR
1	B	292	THR
1	B	319	SER
1	C	206	ARG
1	C	214	GLU
1	C	221	LYS
1	C	239	SER
1	D	228	ARG

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Mol	Chain	Res	Type
1	D	231	LEU
1	D	239	SER
1	D	253	ILE
1	D	262	ILE
1	D	295	VAL
1	D	299	GLN
1	D	301	LYS
1	D	302	THR
1	D	304	ARG
1	D	308	GLN
1	D	310	LEU
1	D	343	ARG
1	D	351	LEU
1	D	367	ASN

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	215	GLN
1	A	225	GLN
1	A	367	ASN
1	B	193	GLN
1	B	225	GLN
1	C	224	GLN
1	D	308	GLN
1	D	348	ASN
1	D	357	ASN
1	D	367	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACP	D	500	3	31,33,33	1.31	5 (16%)	47,52,52	2.00	13 (27%)
2	ACP	A	500	3	31,33,33	1.27	4 (12%)	47,52,52	2.00	12 (25%)
2	ACP	B	500	3	6,11,33	1.87	1 (16%)	9,17,52	1.86	2 (22%)

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	ACP	D	500	3	-	1/19/38/38	0/3/3/3
2	ACP	A	500	3	-	5/19/38/38	0/3/3/3
2	ACP	B	500	3	-	3/6/11/38	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	ACP	PB-O3A	4.38	1.63	1.58
2	A	500	ACP	PB-O3A	3.88	1.62	1.58
2	B	500	ACP	PB-O3A	3.87	1.62	1.58
2	D	500	ACP	PA-O3A	2.72	1.62	1.59
2	A	500	ACP	PA-O3A	2.39	1.62	1.59
2	A	500	ACP	C8-N7	2.30	1.36	1.31
2	D	500	ACP	C8-N9	-2.20	1.33	1.37
2	A	500	ACP	C4-N3	2.18	1.38	1.34
2	D	500	ACP	C4-N9	-2.10	1.33	1.37
2	D	500	ACP	C8-N7	2.03	1.35	1.31

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	ACP	C5-C4-N3	-5.68	118.89	126.72
2	A	500	ACP	N3-C2-N1	-5.42	120.38	128.58
2	D	500	ACP	C5-C4-N3	-5.01	119.81	126.72
2	D	500	ACP	N3-C2-N1	-4.86	121.22	128.58
2	A	500	ACP	C2-N3-C4	4.12	121.90	111.83
2	B	500	ACP	O1G-PG-C3B	-4.11	102.41	111.37
2	A	500	ACP	N3-C4-N9	3.77	133.58	127.17
2	D	500	ACP	N9-C8-N7	-3.72	108.66	113.94
2	D	500	ACP	C2-N3-C4	3.55	120.49	111.83
2	D	500	ACP	O1G-PG-C3B	-3.55	103.64	111.37
2	A	500	ACP	O1G-PG-C3B	-3.50	103.74	111.37
2	A	500	ACP	N9-C8-N7	-3.30	109.25	113.94
2	D	500	ACP	N3-C4-N9	3.23	132.65	127.17
2	A	500	ACP	C4-C5-N7	-3.18	106.94	110.58
2	D	500	ACP	C4-N9-C8	3.16	109.06	105.74
2	A	500	ACP	O2B-PB-O1B	3.00	119.73	109.95
2	D	500	ACP	O2B-PB-O1B	3.00	119.72	109.95
2	D	500	ACP	PB-O3A-PA	-2.96	122.72	132.37
2	D	500	ACP	C4-C5-N7	-2.90	107.27	110.58
2	A	500	ACP	C5-N7-C8	2.86	107.95	103.45
2	D	500	ACP	O3G-PG-O2G	2.81	115.96	107.96
2	A	500	ACP	PB-O3A-PA	-2.64	123.75	132.37
2	B	500	ACP	O2B-PB-O1B	2.64	118.53	109.95
2	D	500	ACP	C5-N7-C8	2.56	107.48	103.45
2	A	500	ACP	C4-N9-C8	2.49	108.35	105.74
2	A	500	ACP	O3G-PG-O2G	2.26	114.39	107.96
2	D	500	ACP	O2G-PG-C3B	-2.13	101.23	106.40

There are no chirality outliers.

All (9) torsion outliers are listed below:

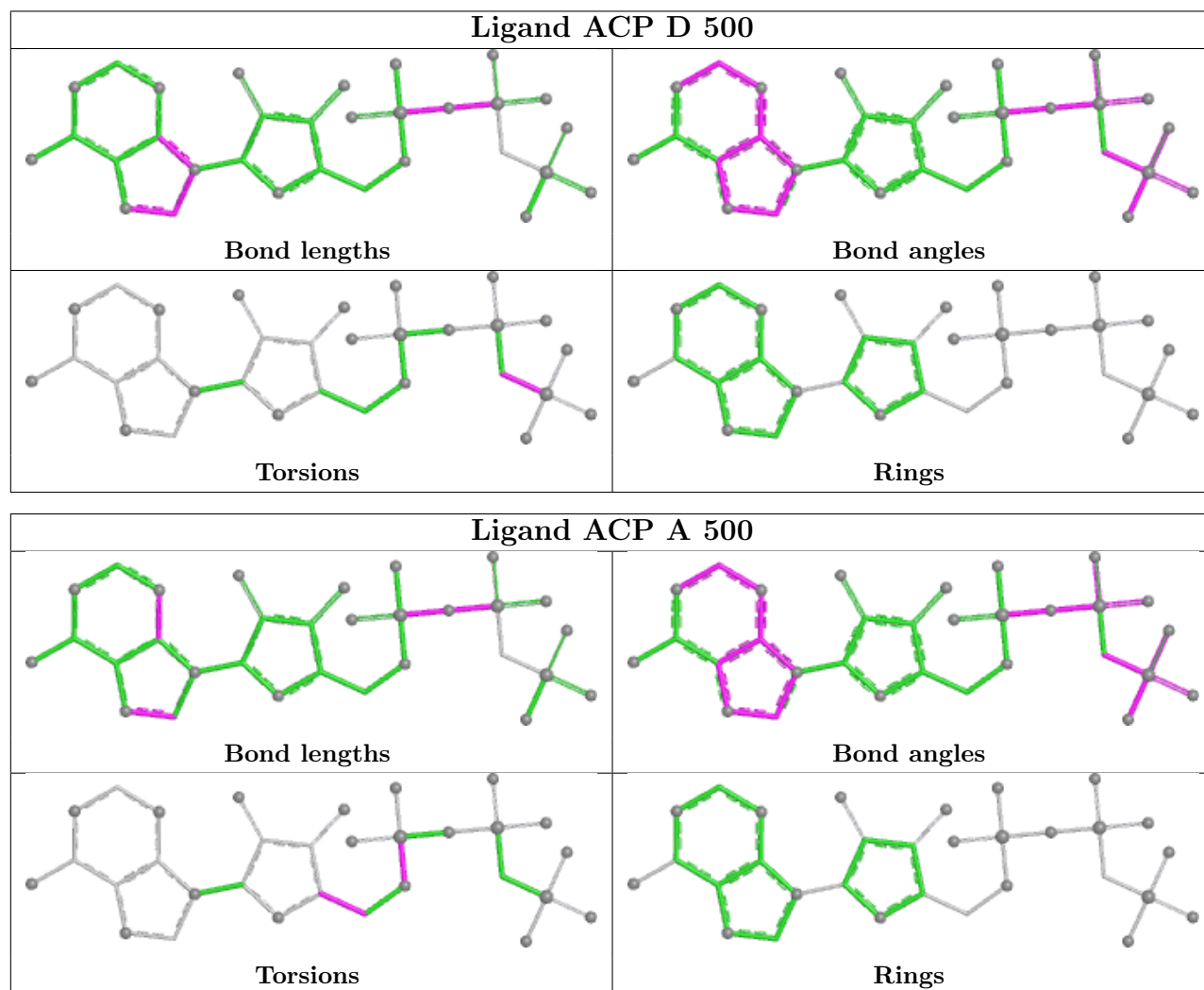
Mol	Chain	Res	Type	Atoms
2	A	500	ACP	C5'-O5'-PA-O3A
2	B	500	ACP	PG-C3B-PB-O1B
2	B	500	ACP	PG-C3B-PB-O3A
2	A	500	ACP	O4'-C4'-C5'-O5'
2	A	500	ACP	C3'-C4'-C5'-O5'
2	A	500	ACP	C5'-O5'-PA-O1A
2	A	500	ACP	C5'-O5'-PA-O2A
2	B	500	ACP	PG-C3B-PB-O2B
2	D	500	ACP	PB-C3B-PG-O1G

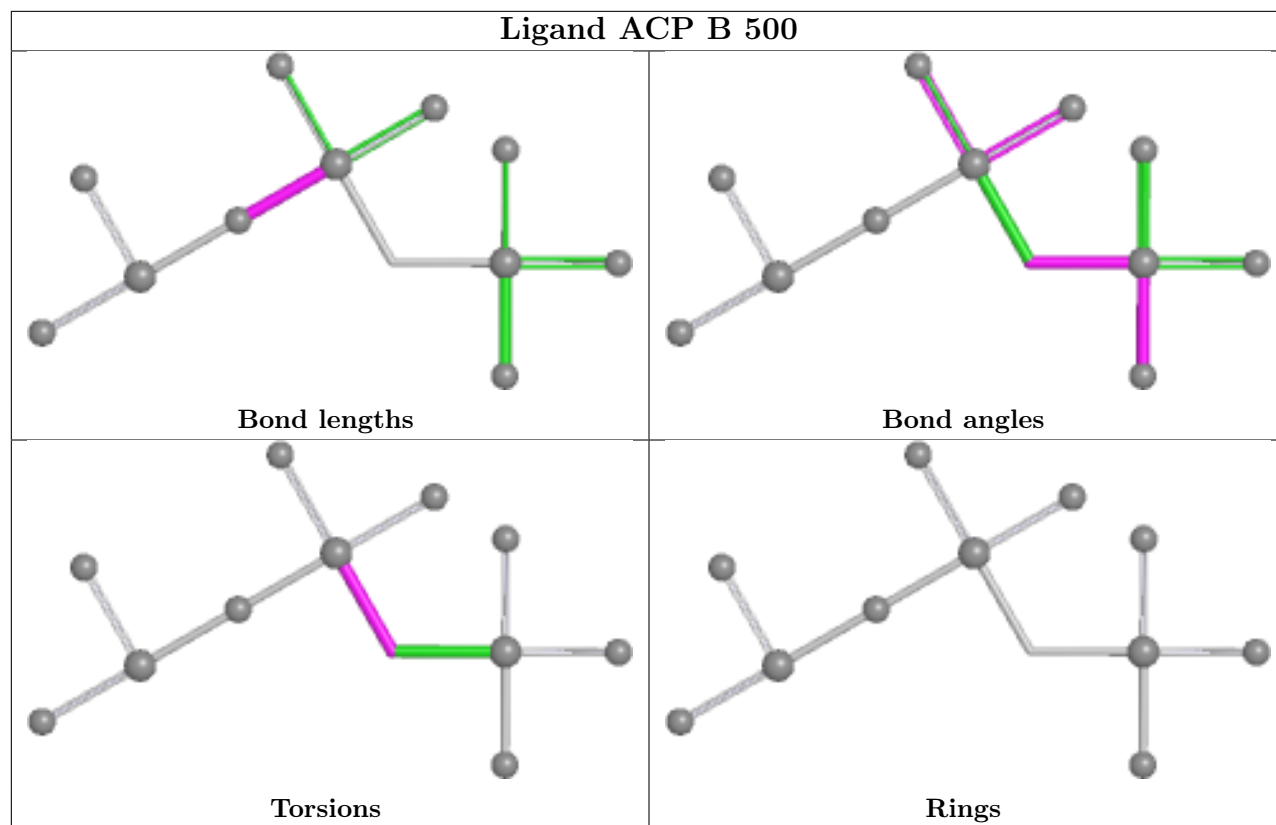
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	500	ACP	3	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 [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	174/197 (88%)	0.32	6 (3%) 48 28	14, 55, 85, 95	0
1	B	101/197 (51%)	0.45	9 (8%) 15 8	16, 49, 93, 101	0
1	C	56/197 (28%)	0.23	1 (1%) 67 47	47, 66, 85, 96	0
1	D	176/197 (89%)	0.25	5 (2%) 55 34	34, 61, 85, 109	0
All	All	507/788 (64%)	0.31	21 (4%) 41 23	14, 59, 89, 109	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	293	ASN	4.3
1	D	327	GLU	3.4
1	A	261	ASP	3.1
1	B	294	VAL	2.6
1	B	252	ASN	2.5
1	B	267	GLU	2.4
1	D	232	ASN	2.4
1	B	209	ILE	2.4
1	B	251	ILE	2.3
1	D	275	ILE	2.3
1	C	228	ARG	2.3
1	A	277	LEU	2.2
1	A	209	ILE	2.2
1	B	237	ILE	2.2
1	D	273	GLU	2.2
1	A	349	GLY	2.2
1	D	335	HIS	2.1
1	A	213	PRO	2.1
1	B	279	ASN	2.1
1	A	185	ARG	2.0
1	B	205	ALA	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](#)

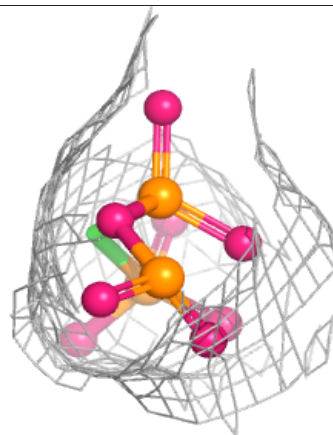
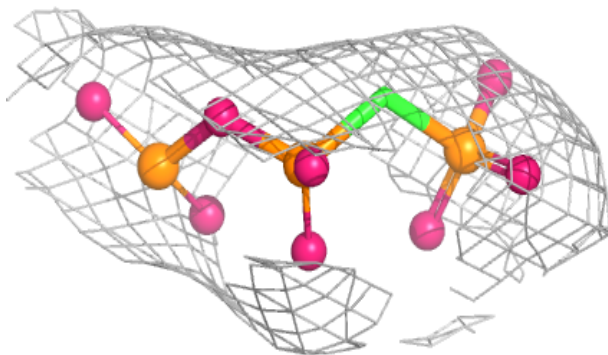
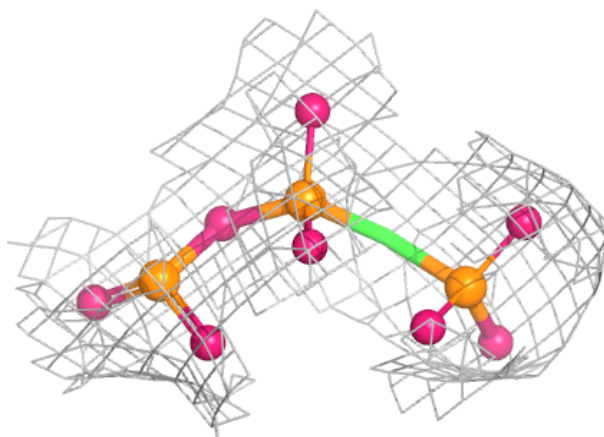
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	ACP	B	500	12/31	0.78	0.11	95,103,108,109	0
2	ACP	D	500	31/31	0.89	0.11	54,81,96,97	0
2	ACP	A	500	31/31	0.90	0.10	51,62,80,83	0
3	MG	A	501	1/1	0.94	0.07	64,64,64,64	0
3	MG	D	501	1/1	0.96	0.09	73,73,73,73	0
3	MG	B	501	1/1	0.97	0.08	90,90,90,90	0

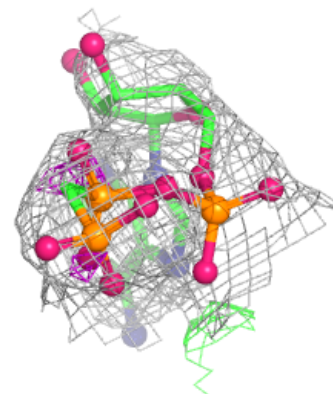
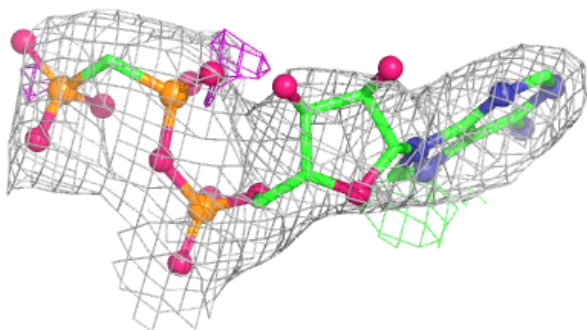
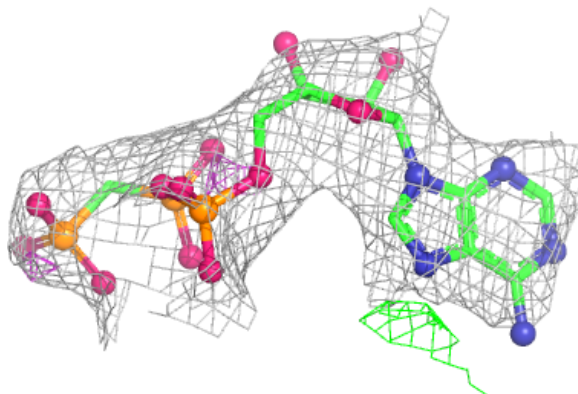
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

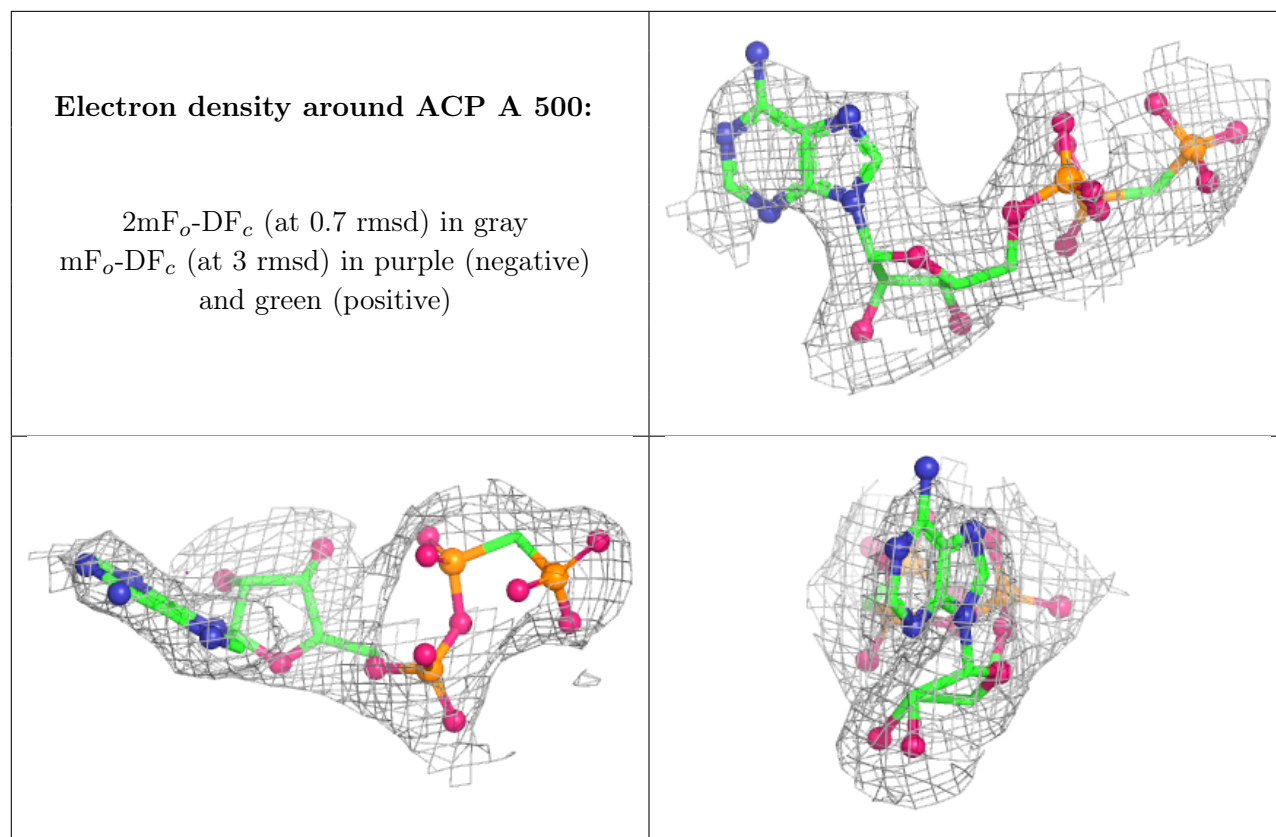
Electron density around ACP B 500:

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

**Electron density around ACP D 500:**

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





6.5 Other polymers [i](#)

There are no such residues in this entry.