



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 02:30 am GMT

PDB ID : 3EHF
Title : Crystal structure of DesKC in complex with AMP-PCP
Authors : Albanesi, D.; Alzari, P.M.; Buschiazzo, 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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

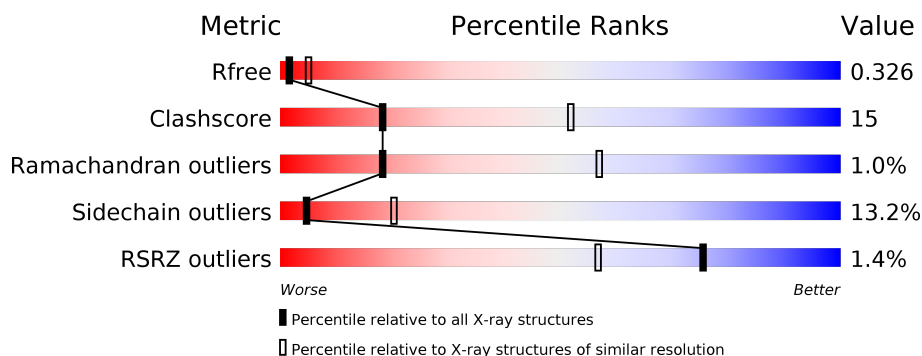
1 Overall quality at a glance

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}	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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	197	<div> <div>2%</div> <div>57% 27% 7% 9%</div> </div>
1	B	197	<div> <div>%</div> <div>37% 11% 6% 47%</div> </div>
1	C	197	<div> <div></div> <div>24% 5% 71%</div> </div>
1	D	197	<div> <div>%</div> <div>59% 31% 8%</div> </div>

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.

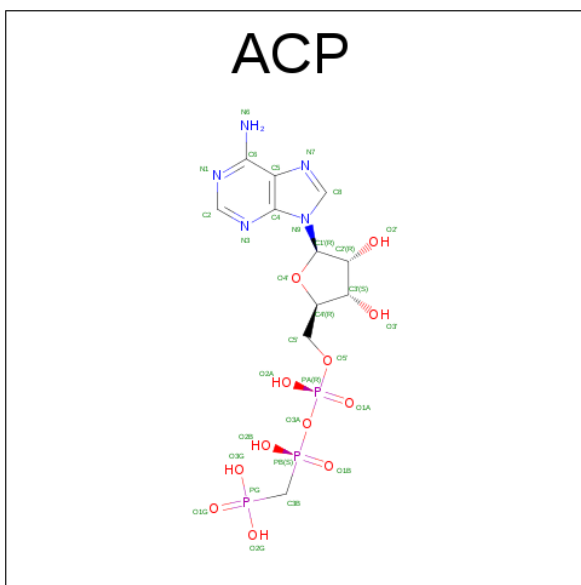
- Molecule 1 is a protein called Sensor kinase (YocF protein).

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 (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



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

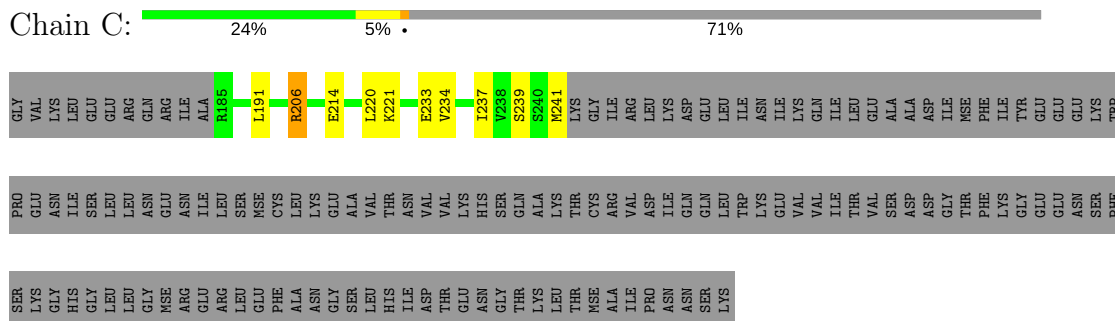
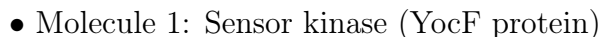
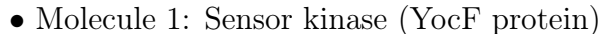
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

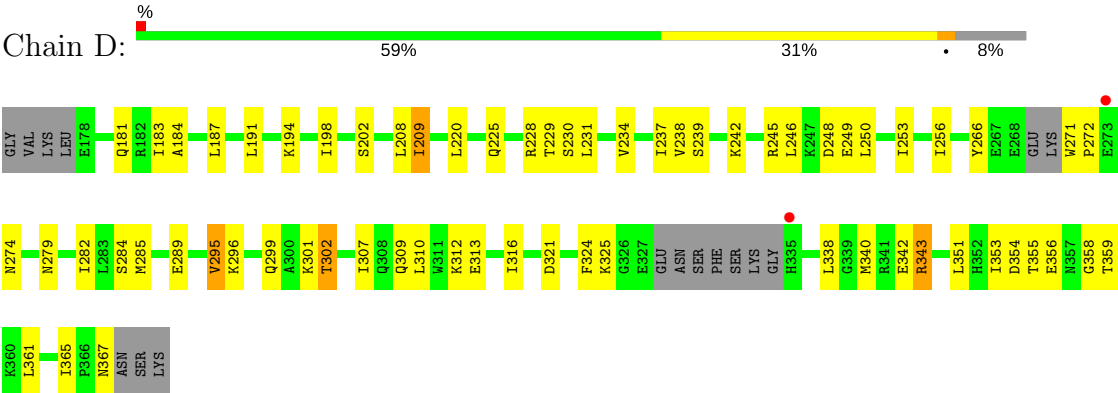
- Molecule 4 is water.

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

- Molecule 1: Sensor kinase (YocF protein)



● Molecule 1: Sensor kinase (YocF protein)



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 14.97 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (15.00-3.10) 99.2 (14.97-3.10)	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 5.5.0070	Depositor
R, R_{free}	0.242 , 0.297 0.280 , 0.326	Depositor DCC
R_{free} test set	815 reflections (5.17%)	DCC
Wilson B-factor (Å ²)	60.4	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 52.1	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	0.65	0/1396	0.82	0/1867
1	B	0.73	0/756	0.77	0/1008
1	C	0.57	0/430	0.72	0/576
1	D	0.62	0/1385	0.72	0/1857
All	All	0.65	0/3967	0.77	0/5308

There are no bond length outliers.

There are no bond angle outliers.

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	47	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	121	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 (121) 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:HG2	1:C:206:ARG:HH11	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:N	1:A:367:ASN:HD22	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:H3'	2:D:500:ACP:O1B	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
1:B:178:GLU:HG3	1:B:178:GLU:O	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:HA	1:B:225:GLN:HE21	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:ND2	1:A:367:ASN:N	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:B:204:LEU:HD23	1:B:219:GLU:CG	2.35	0.57
1:A:247:LYS:HD2	1:A:247:LYS:H	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: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:N	1:A:277:LEU:HD23	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:312:LYS:C	1:D:367:ASN:ND2	2.62	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:NH1	1:C:206:ARG:CG	2.63	0.50
1:D:208:LEU:O	1:D:209:ILE:C	2.49	0.50
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:HD22	1:D:367:ASN:H	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:356:GLU:C	1:D:358:GLY:H	2.16	0.48
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HB3	1:C:206:ARG:NH1	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:198:ILE:O	1:D:202:SER:OG	2.22	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: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
1:D:194:LYS:O	1:D:198:ILE:HG13	2.19	0.43
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:344:LEU:O	1:A:347:ALA:HB3	2.19	0.42
1:D:250:LEU:HD21	1:D:266:TYR:CZ	2.55	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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%)	17	54
1	B	92/197 (47%)	83 (90%)	7 (8%)	2 (2%)	8	35
1	C	55/197 (28%)	52 (94%)	3 (6%)	0	100	100
1	D	175/197 (89%)	158 (90%)	16 (9%)	1 (1%)	28	67
All	All	498/788 (63%)	449 (90%)	44 (9%)	5 (1%)	18	57

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%)	130 (85%)	23 (15%)	3	15
1	B	73/170 (43%)	56 (77%)	17 (23%)	1	4
1	C	46/170 (27%)	42 (91%)	4 (9%)	12	43
1	D	147/170 (86%)	136 (92%)	11 (8%)	16	49
All	All	419/680 (62%)	364 (87%)	55 (13%)	5	20

All (55) 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	193	GLN
1	A	202	SER
1	A	222	SER
1	A	226	THR
1	A	228	ARG
1	A	236	LYS
1	A	239	SER
1	A	247	LYS
1	A	262	ILE
1	A	276	SER
1	A	277	LEU
1	A	295	VAL
1	A	302	THR
1	A	304	ARG
1	A	306	ASP
1	A	320	ASP
1	A	321	ASP
1	A	363	MSE
1	A	367	ASN
1	B	178	GLU

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Mol	Chain	Res	Type
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	211	LYS
1	B	219	GLU
1	B	222	SER
1	B	225	GLN
1	B	226	THR
1	B	231	LEU
1	B	255	GLN
1	B	264	PHE
1	B	266	TYR
1	B	319	SER
1	C	206	ARG
1	C	214	GLU
1	C	221	LYS
1	C	239	SER
1	D	228	ARG
1	D	231	LEU
1	D	239	SER
1	D	253	ILE
1	D	295	VAL
1	D	299	GLN
1	D	301	LYS
1	D	302	THR
1	D	310	LEU
1	D	343	ARG
1	D	351	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	215	GLN
1	A	225	GLN
1	A	309	GLN
1	A	367	ASN
1	B	193	GLN
1	B	225	GLN
1	D	348	ASN

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Mol	Chain	Res	Type
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 carbohydrates 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	A	500	3	27,33,33	1.15	1 (3%)	30,52,52	2.23	6 (20%)
2	ACP	B	500	3	6,11,33	1.83	1 (16%)	9,17,52	1.80	2 (22%)
2	ACP	D	500	3	27,33,33	1.10	1 (3%)	30,52,52	2.19	7 (23%)

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	A	500	3	-	0/15/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACP	B	500	3	-	0/6/11/38	0/0/0/3
2	ACP	D	500	3	-	0/15/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	ACP	PB-O3A	3.81	1.62	1.58
2	A	500	ACP	PB-O3A	3.82	1.62	1.58
2	D	500	ACP	PB-O3A	4.32	1.63	1.58

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	ACP	N3-C2-N1	-9.73	120.38	128.86
2	D	500	ACP	N3-C2-N1	-8.77	121.22	128.86
2	B	500	ACP	O1G-PG-C3B	-3.99	102.41	111.22
2	D	500	ACP	O1G-PG-C3B	-3.43	103.64	111.22
2	A	500	ACP	O1G-PG-C3B	-3.39	103.74	111.22
2	D	500	ACP	PA-O3A-PB	-3.00	122.72	132.39
2	A	500	ACP	PA-O3A-PB	-2.68	123.75	132.39
2	A	500	ACP	C4-C5-N7	-2.55	106.94	109.41
2	D	500	ACP	C4-C5-N7	-2.22	107.27	109.41
2	D	500	ACP	O2G-PG-C3B	-2.13	101.23	106.40
2	A	500	ACP	O3G-PG-O2G	2.13	114.39	108.14
2	B	500	ACP	O2B-PB-O1B	2.52	118.53	110.09
2	D	500	ACP	O3G-PG-O2G	2.67	115.96	108.14
2	D	500	ACP	O2B-PB-O1B	2.88	119.72	110.09
2	A	500	ACP	O2B-PB-O1B	2.88	119.73	110.09

There are no chirality outliers.

There are no torsion outliers.

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

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 [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	174/197 (88%)	-0.17	4 (2%) 61 39	14, 55, 85, 95	0
1	B	101/197 (51%)	-0.16	1 (0%) 82 67	16, 49, 93, 101	0
1	C	56/197 (28%)	-0.42	0 100 100	47, 66, 85, 96	0
1	D	176/197 (89%)	-0.16	2 (1%) 80 65	34, 61, 85, 109	0
All	All	507/788 (64%)	-0.19	7 (1%) 75 57	14, 59, 89, 109	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	335	HIS	4.2
1	A	327	GLU	3.1
1	B	293	ASN	2.6
1	A	349	GLY	2.2
1	A	261	ASP	2.2
1	D	273	GLU	2.1
1	A	274	ASN	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	ACP	D	500	31/31	0.85	0.23	-0.25	54,81,96,97	0
2	ACP	A	500	31/31	0.93	0.16	-0.65	51,62,80,83	0
3	MG	A	501	1/1	0.73	0.10	-	64,64,64,64	0
3	MG	D	501	1/1	0.81	0.09	-	73,73,73,73	0
3	MG	B	501	1/1	0.94	0.09	-	90,90,90,90	0
2	ACP	B	500	12/31	0.80	0.25	-	95,103,108,109	0

6.5 Other polymers [i](#)

There are no such residues in this entry.