



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2023 – 03:37 AM EDT

PDB ID : 3GIE
Title : Crystal structure of DesKC_H188E in complex with AMP-PCP
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Deposited on : 2009-03-05
Resolution : 2.65 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

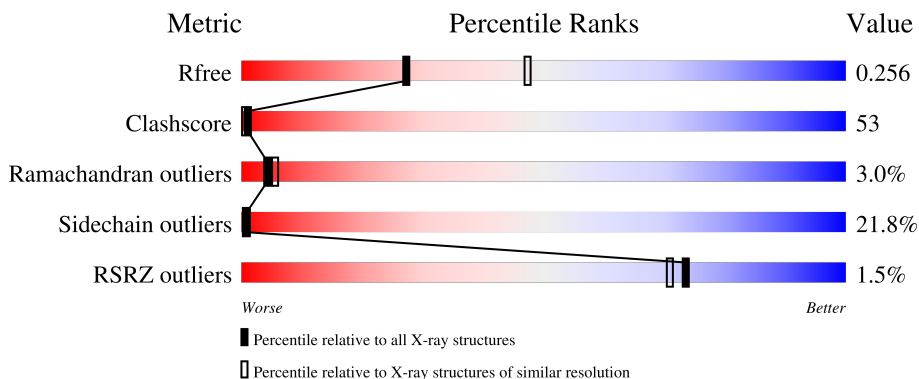
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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	218	
1	B	218	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACP	B	1303	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3375 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.

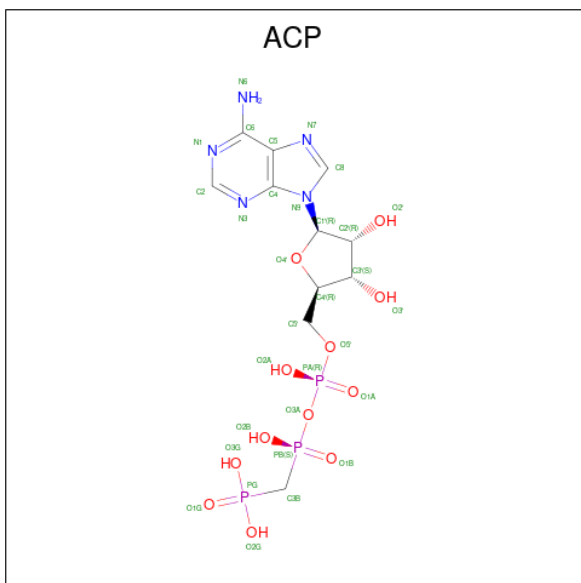
- Molecule 1 is a protein called Sensor histidine kinase desK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	202	Total 1621	C 1010	N 289	O 315	S 7	0	0	0
1	B	211	Total 1687	C 1051	N 298	O 331	S 7	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	GLY	-	expression tag	UNP O34757
A	188	GLU	HIS	engineered mutation	UNP O34757
B	153	GLY	-	expression tag	UNP O34757
B	188	GLU	HIS	engineered mutation	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	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	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

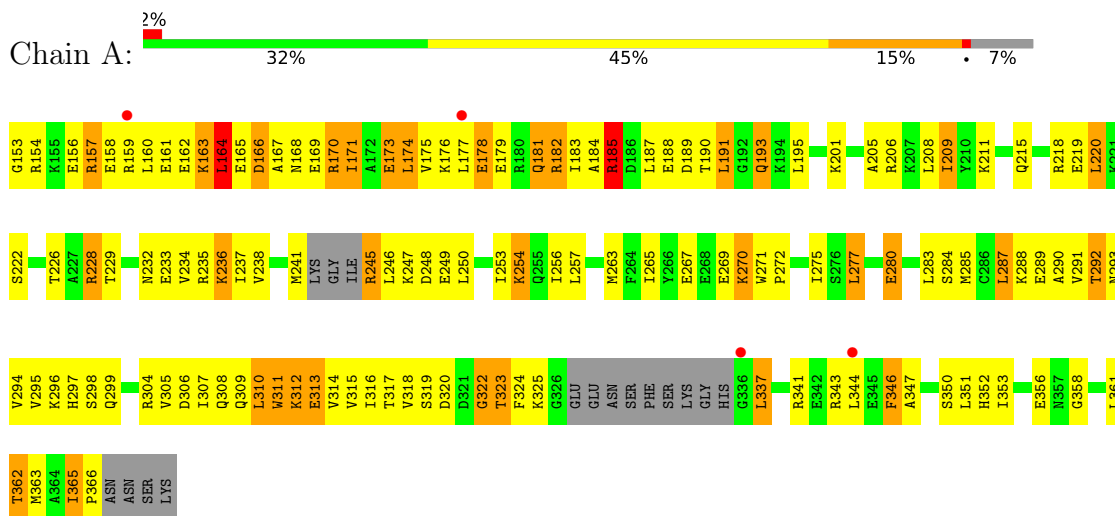
- Molecule 4 is water.

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

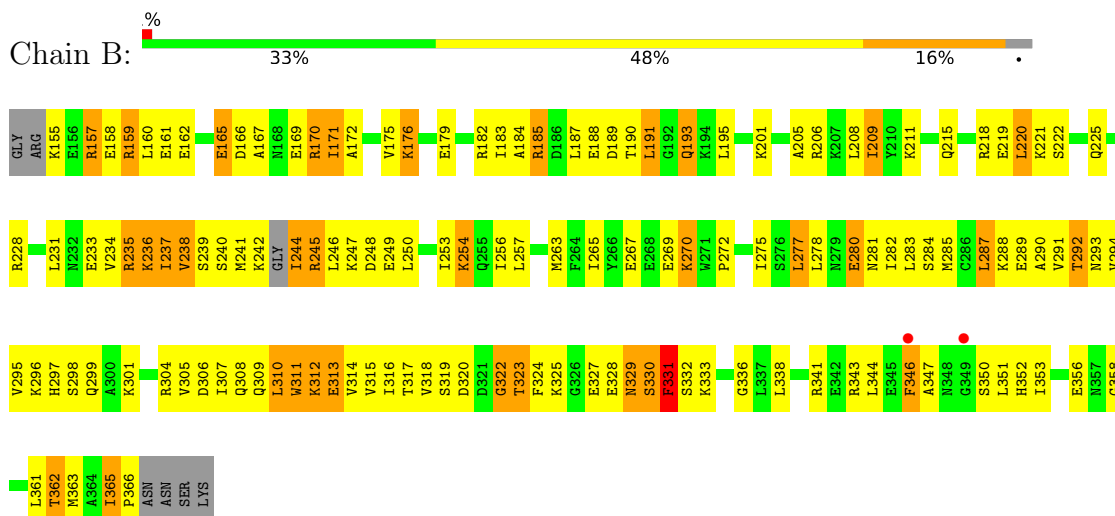
3 Residue-property plots [i](#)

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 histidine kinase desK



• Molecule 1: Sensor histidine kinase desK



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	99.89Å 94.05Å 44.62Å 90.00° 90.02° 90.00°	Depositor
Resolution (Å)	27.16 – 2.65 27.17 – 2.65	Depositor EDS
% Data completeness (in resolution range)	97.7 (27.16-2.65) 97.6 (27.17-2.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.64Å)	Xtrriage
Refinement program	PHENIX 2009_02_15_2320_3	Depositor
R, R_{free}	0.194 , 0.243 0.195 , 0.256	Depositor DCC
R_{free} test set	1076 reflections (9.15%)	wwPDB-VP
Wilson B-factor (Å ²)	53.5	Xtrriage
Anisotropy	0.158	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 69.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.478 for -h,-k,l	Xtrriage
Reported twinning fraction	0.528 for -h,-k,l	Depositor
Outliers	0 of 11757 reflections	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3375	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.51% 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 [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	0.40	0/1632	0.79	5/2185 (0.2%)
1	B	0.39	0/1700	0.74	3/2277 (0.1%)
All	All	0.40	0/3332	0.77	8/4462 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	185	ARG	NE-CZ-NH1	-12.04	114.28	120.30
1	A	185	ARG	NE-CZ-NH2	-11.87	114.36	120.30
1	B	185	ARG	NE-CZ-NH2	11.69	126.14	120.30
1	A	185	ARG	NE-CZ-NH1	11.31	125.96	120.30
1	A	164	LEU	CB-CG-CD2	-8.84	95.97	111.00
1	A	164	LEU	CA-CB-CG	-6.14	101.18	115.30
1	B	185	ARG	CD-NE-CZ	6.06	132.08	123.60
1	A	185	ARG	CD-NE-CZ	5.81	131.74	123.60

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	1621	0	1679	186	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1687	0	1734	187	0
2	A	31	0	14	8	0
2	B	31	0	14	13	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	2	0	0	1	0
4	B	1	0	0	0	0
All	All	3375	0	3441	364	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 53.

All (364) 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:154:ARG:O	1:A:158:GLU:HB2	1.23	1.36
1:B:244:ILE:HD13	1:B:245:ARG:H	1.14	1.12
1:A:249:GLU:OE1	1:A:288:LYS:HD2	1.57	1.03
1:A:154:ARG:O	1:A:158:GLU:CB	2.08	1.02
1:B:249:GLU:OE1	1:B:288:LYS:HD2	1.59	1.02
1:A:253:ILE:HD13	1:A:287:LEU:HD11	1.38	1.01
1:A:232:ASN:O	1:A:236:LYS:HE2	1.61	1.00
1:A:317:THR:HG22	1:A:362:THR:HG23	1.44	1.00
1:B:235:ARG:HG3	1:B:235:ARG:HH11	1.22	1.00
1:B:253:ILE:HD13	1:B:287:LEU:HD11	1.39	0.99
1:B:166:ASP:O	1:B:170:ARG:HG3	1.62	0.99
1:A:157:ARG:HG3	1:A:157:ARG:HH11	1.22	0.99
1:B:317:THR:HG22	1:B:362:THR:HG23	1.48	0.95
1:B:244:ILE:CD1	1:B:245:ARG:H	1.79	0.94
1:A:245:ARG:HB3	1:A:248:ASP:HB2	1.52	0.90
1:A:171:ILE:O	1:A:174:LEU:HG	1.71	0.89
1:B:284:SER:HB3	1:B:288:LYS:HZ1	1.38	0.89
1:B:245:ARG:HB3	1:B:248:ASP:HB2	1.54	0.88
1:A:175:VAL:O	1:A:179:GLU:HB2	1.72	0.87
1:A:182:ARG:HH11	1:A:182:ARG:CG	1.87	0.87
1:A:171:ILE:HA	1:A:174:LEU:HD11	1.55	0.87
1:A:284:SER:HB3	1:A:288:LYS:HZ1	1.39	0.87
1:B:336:GLY:HA3	2:B:1303:ACP:O3G	1.74	0.86
1:A:285:MET:SD	1:A:343:ARG:NH1	2.49	0.86
1:B:305:VAL:HG22	1:B:318:VAL:HG22	1.57	0.84
1:A:157:ARG:HH11	1:A:157:ARG:CG	1.91	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:VAL:HG22	1:A:318:VAL:HG22	1.58	0.84
1:B:285:MET:SD	1:B:343:ARG:NH1	2.50	0.84
1:B:171:ILE:O	1:B:175:VAL:HG23	1.77	0.84
1:A:157:ARG:HG3	1:A:157:ARG:NH1	1.93	0.82
1:A:168:ASN:HA	1:A:171:ILE:CG1	2.10	0.82
1:A:297:HIS:ND1	2:A:1303:ACP:H2'	1.94	0.82
1:B:346:PHE:CD2	1:B:347:ALA:N	2.49	0.81
1:B:298:SER:O	1:B:299:GLN:HB2	1.80	0.81
1:B:284:SER:HB3	1:B:288:LYS:NZ	1.95	0.81
1:B:285:MET:HA	1:B:288:LYS:HE2	1.64	0.80
1:A:163:LYS:O	1:A:164:LEU:HD23	1.82	0.79
1:A:168:ASN:HA	1:A:171:ILE:HD11	1.65	0.79
1:A:346:PHE:CD2	1:A:347:ALA:N	2.51	0.79
1:A:176:LYS:HE2	1:B:278:LEU:HD22	1.64	0.79
1:A:346:PHE:HD2	1:A:347:ALA:N	1.80	0.79
1:B:346:PHE:HD2	1:B:347:ALA:N	1.79	0.79
1:A:181:GLN:CD	1:A:185:ARG:HH12	1.86	0.78
1:A:298:SER:O	1:A:299:GLN:HB2	1.82	0.78
1:A:285:MET:HA	1:A:288:LYS:HE2	1.66	0.77
1:A:284:SER:HB3	1:A:288:LYS:NZ	1.98	0.77
1:A:249:GLU:OE2	1:A:253:ILE:HG23	1.85	0.77
1:A:277:LEU:O	1:A:277:LEU:HD12	1.86	0.76
1:B:249:GLU:OE2	1:B:253:ILE:HG23	1.86	0.76
1:B:244:ILE:HD13	1:B:245:ARG:N	1.96	0.76
1:B:277:LEU:HD12	1:B:277:LEU:O	1.86	0.75
1:B:235:ARG:HG3	1:B:235:ARG:NH1	1.94	0.75
1:A:182:ARG:HH11	1:A:182:ARG:HG2	1.52	0.75
1:B:244:ILE:O	1:B:281:ASN:OD1	2.05	0.75
1:A:168:ASN:HA	1:A:171:ILE:CD1	2.18	0.73
1:A:153:GLY:HA2	1:A:157:ARG:HB2	1.70	0.73
1:A:184:ALA:O	1:A:188:GLU:HB2	1.88	0.73
1:B:184:ALA:O	1:B:188:GLU:HB2	1.87	0.73
1:B:330:SER:HB2	2:B:1303:ACP:H4'	1.71	0.73
1:B:346:PHE:HD2	1:B:347:ALA:H	1.36	0.72
1:A:163:LYS:C	1:A:164:LEU:HD23	2.09	0.72
1:A:324:PHE:HA	2:A:1303:ACP:H2	1.70	0.72
1:B:333:LYS:HG3	1:B:333:LYS:O	1.88	0.72
1:B:155:LYS:HG3	1:B:158:GLU:OE2	1.89	0.71
1:A:313:GLU:HB3	1:A:365:ILE:C	2.11	0.71
1:B:244:ILE:N	1:B:281:ASN:OD1	2.24	0.71
1:A:153:GLY:N	1:A:156:GLU:HG2	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:GLU:HB3	1:A:365:ILE:O	1.91	0.71
1:B:298:SER:HB2	1:B:320:ASP:OD1	1.91	0.71
1:B:313:GLU:HB3	1:B:365:ILE:C	2.12	0.70
1:A:253:ILE:HG21	1:A:287:LEU:HD12	1.72	0.70
1:B:312:LYS:HG3	1:B:313:GLU:HG3	1.74	0.70
1:A:298:SER:HB2	1:A:320:ASP:OD1	1.91	0.70
1:A:322:GLY:O	1:A:358:GLY:HA2	1.92	0.69
1:A:311:TRP:HE3	1:A:312:LYS:N	1.90	0.69
1:B:311:TRP:HE3	1:B:312:LYS:N	1.90	0.69
1:A:170:ARG:O	1:A:174:LEU:HD21	1.92	0.69
1:A:153:GLY:O	1:A:157:ARG:N	2.26	0.69
1:B:253:ILE:HG21	1:B:287:LEU:HD12	1.73	0.69
1:B:313:GLU:HB3	1:B:365:ILE:O	1.93	0.68
1:B:322:GLY:O	1:B:358:GLY:HA2	1.93	0.68
1:A:168:ASN:HA	1:A:171:ILE:HG12	1.76	0.68
1:A:296:LYS:HB3	1:A:297:HIS:CD2	2.29	0.68
1:A:346:PHE:HD2	1:A:347:ALA:H	1.40	0.67
1:A:344:LEU:HD12	1:A:351:LEU:HB2	1.75	0.67
1:B:296:LYS:HB3	1:B:297:HIS:CD2	2.29	0.67
1:A:312:LYS:HG3	1:A:313:GLU:HG3	1.77	0.67
1:B:256:ILE:HG22	1:B:295:VAL:HG21	1.77	0.66
1:B:344:LEU:HD12	1:B:351:LEU:HB2	1.76	0.66
1:B:253:ILE:HG21	1:B:287:LEU:CD1	2.25	0.66
1:A:297:HIS:HE1	2:A:1303:ACP:O1B	1.78	0.65
1:A:171:ILE:O	1:A:174:LEU:CG	2.43	0.65
1:A:234:VAL:HG21	1:B:191:LEU:HD23	1.79	0.65
1:A:157:ARG:O	1:A:160:LEU:HG	1.95	0.65
1:A:253:ILE:HG21	1:A:287:LEU:CD1	2.26	0.65
1:B:238:VAL:HG13	1:B:242:LYS:HE2	1.80	0.64
1:A:256:ILE:HG22	1:A:295:VAL:HG21	1.78	0.64
1:A:288:LYS:O	1:A:292:THR:HB	1.97	0.64
1:A:191:LEU:HD21	1:B:191:LEU:HD21	1.79	0.64
1:A:337:LEU:HD11	2:A:1303:ACP:O5'	1.97	0.64
1:A:313:GLU:CB	1:A:365:ILE:O	2.44	0.63
1:B:190:THR:HG21	1:B:233:GLU:HG2	1.81	0.63
1:B:288:LYS:O	1:B:292:THR:HB	1.98	0.63
1:A:284:SER:O	1:A:287:LEU:HB3	1.99	0.63
1:A:181:GLN:OE1	1:A:181:GLN:HA	1.98	0.63
1:B:284:SER:O	1:B:287:LEU:HB3	1.99	0.63
1:A:190:THR:HG21	1:A:233:GLU:HG2	1.82	0.62
1:B:313:GLU:CB	1:B:365:ILE:O	2.46	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:239:SER:C	1:B:241:MET:H	2.00	0.62
1:A:176:LYS:HD2	1:B:278:LEU:HD13	1.81	0.62
1:A:309:GLN:NE2	1:A:311:TRP:O	2.33	0.62
1:B:244:ILE:CA	1:B:281:ASN:OD1	2.48	0.62
1:B:309:GLN:NE2	1:B:311:TRP:O	2.32	0.61
1:B:172:ALA:O	1:B:176:LYS:HG3	2.00	0.61
1:B:331:PHE:CD1	1:B:331:PHE:N	2.67	0.61
1:B:323:THR:O	2:B:1303:ACP:H2	2.01	0.61
1:A:160:LEU:HA	1:A:163:LYS:HG2	1.83	0.60
1:B:272:PRO:HA	1:B:309:GLN:HB2	1.84	0.60
1:A:296:LYS:CB	1:A:297:HIS:CD2	2.85	0.60
1:A:233:GLU:O	1:A:237:ILE:HG13	2.02	0.60
1:A:272:PRO:HA	1:A:309:GLN:HB2	1.84	0.60
1:A:257:LEU:HD23	1:A:295:VAL:HG22	1.83	0.59
1:B:175:VAL:HG11	1:B:346:PHE:HD1	1.67	0.59
1:B:257:LEU:HD23	1:B:295:VAL:HG22	1.83	0.59
1:A:171:ILE:O	1:A:174:LEU:CD1	2.51	0.59
1:B:159:ARG:HA	1:B:162:GLU:HG2	1.85	0.59
1:B:330:SER:O	1:B:332:SER:N	2.36	0.59
1:A:182:ARG:HH11	1:A:182:ARG:HG3	1.65	0.59
1:B:244:ILE:HG23	1:B:245:ARG:N	2.18	0.59
1:A:249:GLU:HG2	1:A:288:LYS:NZ	2.18	0.59
1:A:306:ASP:O	1:A:316:ILE:HA	2.03	0.59
1:B:185:ARG:NH2	1:B:188:GLU:OE1	2.35	0.58
1:B:296:LYS:CB	1:B:297:HIS:CD2	2.86	0.58
1:A:160:LEU:HD12	1:A:161:GLU:N	2.18	0.58
1:B:292:THR:O	1:B:296:LYS:HB2	2.03	0.58
1:B:244:ILE:C	1:B:281:ASN:OD1	2.42	0.58
1:A:245:ARG:HB3	1:A:248:ASP:CB	2.28	0.58
1:B:325:LYS:HG2	2:B:1303:ACP:C2	2.34	0.57
1:A:179:GLU:O	1:A:183:ILE:HG13	2.03	0.57
1:A:311:TRP:HE3	1:A:312:LYS:H	1.51	0.57
1:A:311:TRP:CE3	1:A:312:LYS:N	2.73	0.57
1:B:306:ASP:O	1:B:316:ILE:HA	2.05	0.57
1:B:245:ARG:HB3	1:B:248:ASP:CB	2.29	0.57
1:A:324:PHE:HD1	2:A:1303:ACP:C2	2.17	0.56
1:A:215:GLN:NE2	1:A:218:ARG:HE	2.02	0.56
1:B:244:ILE:HD13	1:B:245:ARG:HB2	1.87	0.56
1:B:249:GLU:HG2	1:B:288:LYS:NZ	2.20	0.56
1:B:311:TRP:CE3	1:B:312:LYS:N	2.73	0.56
1:B:312:LYS:CG	1:B:313:GLU:HG3	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:ASN:O	1:A:235:ARG:HB2	2.06	0.56
1:B:329:ASN:CG	1:B:330:SER:N	2.58	0.56
1:A:269:GLU:HG2	1:A:270:LYS:H	1.71	0.56
1:B:179:GLU:O	1:B:183:ILE:HG13	2.05	0.56
1:A:178:GLU:O	1:A:182:ARG:HD2	2.05	0.55
1:A:311:TRP:CE3	1:A:312:LYS:HG2	2.42	0.55
1:B:269:GLU:HG2	1:B:270:LYS:H	1.71	0.55
1:B:215:GLN:NE2	1:B:218:ARG:HE	2.04	0.55
1:A:153:GLY:CA	1:A:157:ARG:HB2	2.37	0.55
1:A:237:ILE:O	1:A:241:MET:HG2	2.06	0.55
1:A:312:LYS:CG	1:A:313:GLU:HG3	2.36	0.55
1:B:285:MET:CE	1:B:343:ARG:HH12	2.19	0.54
1:A:181:GLN:CD	1:A:185:ARG:NH1	2.60	0.54
1:B:239:SER:C	1:B:241:MET:N	2.61	0.54
1:A:185:ARG:HA	1:A:185:ARG:NE	2.21	0.54
1:B:298:SER:HA	2:B:1303:ACP:N1	2.22	0.54
1:A:292:THR:O	1:A:296:LYS:HB2	2.07	0.54
1:A:208:LEU:O	1:A:209:ILE:C	2.44	0.54
1:A:293:ASN:HB3	2:A:1303:ACP:N7	2.22	0.54
1:B:167:ALA:HA	1:B:170:ARG:HD2	1.90	0.54
1:A:162:GLU:C	1:A:164:LEU:H	2.11	0.54
1:B:346:PHE:CE2	1:B:347:ALA:HB2	2.42	0.54
1:A:269:GLU:OE2	1:A:308:GLN:HG2	2.08	0.54
1:A:285:MET:CE	1:A:343:ARG:HH12	2.20	0.54
1:A:346:PHE:CE2	1:A:347:ALA:HB2	2.42	0.54
1:B:161:GLU:O	1:B:165:GLU:HB2	2.09	0.53
1:B:324:PHE:HA	2:B:1303:ACP:C2	2.37	0.53
1:A:351:LEU:HD21	1:A:361:LEU:HD11	1.91	0.53
1:B:311:TRP:CE3	1:B:312:LYS:HG2	2.43	0.53
1:B:190:THR:CG2	1:B:233:GLU:HG2	2.38	0.53
1:B:365:ILE:O	1:B:365:ILE:CG2	2.57	0.53
1:A:253:ILE:CD1	1:A:287:LEU:HD11	2.27	0.53
1:B:231:LEU:O	1:B:235:ARG:HG2	2.09	0.53
1:B:311:TRP:HE3	1:B:312:LYS:H	1.55	0.53
1:A:185:ARG:HA	1:A:185:ARG:HE	1.73	0.53
1:A:189:ASP:O	1:A:193:GLN:HB3	2.09	0.53
1:B:351:LEU:HD21	1:B:361:LEU:HD11	1.91	0.53
1:A:167:ALA:O	1:A:171:ILE:HD13	2.08	0.52
1:B:269:GLU:OE2	1:B:308:GLN:HG2	2.10	0.52
1:B:315:VAL:HA	1:B:363:MET:O	2.10	0.52
1:A:249:GLU:OE1	1:A:288:LYS:CD	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:ILE:O	1:A:365:ILE:CG2	2.58	0.52
1:A:190:THR:CG2	1:A:233:GLU:HG2	2.40	0.52
1:A:173:GLU:CA	1:A:173:GLU:OE1	2.58	0.52
1:A:181:GLN:NE2	1:A:185:ARG:HH12	2.07	0.52
1:B:167:ALA:HA	1:B:170:ARG:CD	2.39	0.52
1:B:272:PRO:HB3	1:B:309:GLN:OE1	2.11	0.51
1:B:329:ASN:OD1	1:B:329:ASN:C	2.48	0.51
1:A:315:VAL:HA	1:A:363:MET:O	2.10	0.51
1:B:175:VAL:HG11	1:B:346:PHE:CD1	2.44	0.51
1:B:189:ASP:O	1:B:193:GLN:HB3	2.11	0.51
1:A:173:GLU:OE1	1:A:173:GLU:HA	2.10	0.51
1:A:272:PRO:HB3	1:A:309:GLN:OE1	2.11	0.51
1:B:208:LEU:O	1:B:209:ILE:C	2.47	0.51
1:B:253:ILE:CD1	1:B:287:LEU:HD11	2.28	0.51
1:A:219:GLU:O	1:A:222:SER:HB3	2.11	0.51
1:B:313:GLU:HB3	1:B:366:PRO:HA	1.93	0.51
1:B:332:SER:C	1:B:338:LEU:HD12	2.31	0.51
1:B:332:SER:O	1:B:338:LEU:HD12	2.11	0.51
1:A:191:LEU:HD23	1:B:234:VAL:HG21	1.93	0.51
1:B:332:SER:O	1:B:333:LYS:C	2.48	0.51
1:B:157:ARG:HG3	1:B:157:ARG:HH11	1.76	0.51
1:B:256:ILE:CG2	1:B:295:VAL:HG21	2.39	0.51
1:B:333:LYS:HA	1:B:338:LEU:CD1	2.41	0.51
1:B:277:LEU:HA	1:B:280:GLU:HB3	1.93	0.50
1:A:267:GLU:HG3	1:A:304:ARG:NH2	2.27	0.50
1:A:277:LEU:HA	1:A:280:GLU:HB3	1.94	0.50
1:A:313:GLU:HB3	1:A:366:PRO:HA	1.93	0.50
1:B:341:ARG:HB2	1:B:351:LEU:HD13	1.94	0.50
1:A:168:ASN:O	1:A:171:ILE:HG12	2.12	0.50
1:B:159:ARG:O	1:B:162:GLU:HG2	2.12	0.49
1:A:171:ILE:HA	1:A:174:LEU:CD1	2.36	0.49
1:A:256:ILE:CG2	1:A:295:VAL:HG21	2.40	0.49
1:A:265:ILE:HG22	1:A:304:ARG:HG3	1.94	0.49
1:A:176:LYS:HE2	1:B:278:LEU:CD2	2.37	0.49
1:A:249:GLU:HG2	1:A:288:LYS:HZ3	1.76	0.49
1:A:291:VAL:O	1:A:295:VAL:HG23	2.13	0.49
1:A:325:LYS:HD3	1:A:325:LYS:N	2.27	0.49
1:B:249:GLU:HG2	1:B:288:LYS:HZ3	1.77	0.49
1:B:330:SER:HB2	2:B:1303:ACP:C4'	2.41	0.49
1:A:284:SER:O	1:A:287:LEU:CB	2.61	0.49
1:A:308:GLN:OE1	1:A:310:LEU:HD11	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:LYS:HD3	1:B:236:LYS:C	2.33	0.49
1:A:246:LEU:HB2	1:A:280:GLU:OE1	2.12	0.49
1:B:179:GLU:HA	1:B:182:ARG:NH1	2.28	0.49
1:B:267:GLU:HG3	1:B:304:ARG:NH2	2.28	0.49
1:B:310:LEU:O	1:B:313:GLU:O	2.31	0.48
1:B:325:LYS:HG2	2:B:1303:ACP:N3	2.28	0.48
1:B:325:LYS:HD3	1:B:325:LYS:N	2.27	0.48
1:A:310:LEU:O	1:A:313:GLU:O	2.31	0.48
1:B:236:LYS:HD3	1:B:236:LYS:O	2.12	0.48
1:B:324:PHE:HE1	2:B:1303:ACP:C8	2.26	0.48
1:A:159:ARG:O	1:A:162:GLU:HB2	2.13	0.48
1:B:235:ARG:HH11	1:B:235:ARG:CG	2.09	0.48
1:A:265:ILE:CG2	1:A:304:ARG:HG3	2.44	0.48
1:B:327:GLU:O	1:B:330:SER:N	2.47	0.48
1:A:168:ASN:C	1:A:171:ILE:HG12	2.34	0.48
1:B:284:SER:O	1:B:287:LEU:CB	2.62	0.48
1:B:291:VAL:O	1:B:295:VAL:HG23	2.14	0.48
1:A:205:ALA:CB	1:A:220:LEU:HD13	2.44	0.48
1:A:166:ASP:O	1:A:170:ARG:HG2	2.13	0.48
1:A:162:GLU:O	1:A:164:LEU:N	2.47	0.47
1:A:176:LYS:CE	1:B:278:LEU:HD22	2.41	0.47
1:B:244:ILE:CD1	1:B:245:ARG:HB2	2.44	0.47
1:B:246:LEU:HB2	1:B:280:GLU:OE1	2.13	0.47
1:B:308:GLN:OE1	1:B:310:LEU:HD11	2.12	0.47
1:A:346:PHE:CD2	1:A:346:PHE:C	2.85	0.47
1:A:307:ILE:HD13	1:A:316:ILE:CD1	2.44	0.47
1:A:167:ALA:O	1:A:171:ILE:CD1	2.63	0.47
1:B:265:ILE:HG22	1:B:304:ARG:HG3	1.96	0.47
1:A:297:HIS:CD2	1:A:297:HIS:N	2.82	0.47
1:A:310:LEU:O	1:A:313:GLU:OE1	2.32	0.47
1:A:181:GLN:O	1:A:185:ARG:HB2	2.14	0.47
1:A:246:LEU:N	1:A:280:GLU:OE1	2.46	0.47
1:A:269:GLU:CD	1:A:308:GLN:HG2	2.35	0.47
1:B:236:LYS:C	1:B:236:LYS:CD	2.82	0.47
1:B:249:GLU:CD	1:B:288:LYS:HD2	2.31	0.47
1:B:290:ALA:O	1:B:294:VAL:HG23	2.14	0.47
1:B:329:ASN:O	1:B:330:SER:C	2.53	0.47
1:A:307:ILE:HD13	1:A:316:ILE:HG12	1.97	0.47
1:B:297:HIS:CD2	1:B:297:HIS:N	2.83	0.47
1:B:307:ILE:HD13	1:B:316:ILE:HG12	1.96	0.47
1:B:310:LEU:O	1:B:313:GLU:OE1	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLU:OE2	4:A:371:HOH:O	2.21	0.47
1:A:162:GLU:C	1:A:164:LEU:N	2.68	0.46
1:B:205:ALA:CB	1:B:220:LEU:HD13	2.45	0.46
1:B:246:LEU:N	1:B:280:GLU:OE1	2.47	0.46
1:A:160:LEU:O	1:A:161:GLU:C	2.54	0.46
1:A:290:ALA:O	1:A:294:VAL:HG23	2.15	0.46
1:B:307:ILE:HD13	1:B:316:ILE:CD1	2.44	0.46
1:A:341:ARG:HB2	1:A:351:LEU:HD13	1.98	0.46
1:A:249:GLU:HG3	1:A:287:LEU:HG	1.97	0.46
1:A:153:GLY:O	1:A:154:ARG:C	2.54	0.46
1:A:249:GLU:CD	1:A:288:LYS:HD2	2.31	0.46
1:A:350:SER:OG	1:A:352:HIS:HE1	1.99	0.46
1:B:325:LYS:H	2:B:1303:ACP:C2	2.27	0.46
1:B:346:PHE:CD2	1:B:346:PHE:C	2.85	0.46
1:B:269:GLU:CD	1:B:308:GLN:HG2	2.36	0.45
1:B:344:LEU:HD13	1:B:350:SER:O	2.16	0.45
1:A:168:ASN:CA	1:A:171:ILE:HG12	2.42	0.45
1:B:249:GLU:HG3	1:B:287:LEU:HG	1.98	0.45
1:A:337:LEU:HD12	2:A:1303:ACP:O2A	2.16	0.45
1:B:333:LYS:HA	1:B:338:LEU:HD13	1.99	0.45
1:A:201:LYS:HE3	1:A:222:SER:OG	2.16	0.45
1:A:296:LYS:CB	1:A:297:HIS:HD2	2.27	0.45
1:B:284:SER:C	1:B:288:LYS:NZ	2.70	0.45
1:A:344:LEU:HD13	1:A:350:SER:O	2.16	0.45
1:B:219:GLU:O	1:B:222:SER:HB3	2.17	0.45
1:B:289:GLU:O	1:B:293:ASN:CG	2.55	0.45
1:B:235:ARG:NH1	1:B:235:ARG:CG	2.72	0.45
1:A:284:SER:C	1:A:288:LYS:HZ3	2.20	0.44
1:A:182:ARG:HG2	1:A:182:ARG:NH1	2.25	0.44
1:B:220:LEU:HD12	1:B:220:LEU:HA	1.78	0.44
1:B:284:SER:C	1:B:288:LYS:HZ3	2.21	0.44
1:B:239:SER:O	1:B:241:MET:N	2.50	0.44
1:A:361:LEU:HD12	1:A:362:THR:H	1.83	0.44
1:B:221:LYS:O	1:B:225:GLN:HG3	2.18	0.44
1:B:265:ILE:CG2	1:B:304:ARG:HG3	2.48	0.44
1:A:289:GLU:O	1:A:293:ASN:CG	2.56	0.44
1:A:235:ARG:O	1:A:236:LYS:C	2.56	0.44
1:B:336:GLY:HA3	2:B:1303:ACP:PG	2.58	0.44
1:B:350:SER:OG	1:B:352:HIS:HE1	2.01	0.43
1:B:172:ALA:O	1:B:176:LYS:CG	2.65	0.43
1:B:323:THR:OG1	1:B:325:LYS:HE2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:LYS:CB	1:B:297:HIS:HD2	2.29	0.43
1:A:253:ILE:HG13	1:A:254:LYS:N	2.32	0.43
1:B:206:ARG:CZ	1:B:206:ARG:HB3	2.47	0.43
1:A:284:SER:C	1:A:288:LYS:NZ	2.72	0.43
1:A:160:LEU:HD12	1:A:160:LEU:C	2.39	0.43
1:A:275:ILE:HD11	1:A:283:LEU:HD12	2.00	0.43
1:A:220:LEU:HA	1:A:220:LEU:HD12	1.76	0.43
1:B:253:ILE:HG13	1:B:254:LYS:N	2.33	0.43
1:B:325:LYS:HG2	2:B:1303:ACP:H2	2.00	0.42
1:B:275:ILE:HD12	1:B:314:VAL:HG21	2.00	0.42
1:A:275:ILE:HD12	1:A:314:VAL:HG21	2.00	0.42
1:B:155:LYS:N	1:B:157:ARG:NH1	2.68	0.42
1:B:275:ILE:HD11	1:B:283:LEU:HD12	2.01	0.42
1:A:337:LEU:CD1	2:A:1303:ACP:PA	3.08	0.42
1:B:249:GLU:OE1	1:B:288:LYS:CD	2.48	0.42
1:B:272:PRO:CA	1:B:309:GLN:HB2	2.48	0.42
1:B:185:ARG:HD3	1:B:185:ARG:HA	1.82	0.42
1:A:290:ALA:CB	1:A:361:LEU:HD23	2.49	0.42
1:B:290:ALA:CB	1:B:361:LEU:HD23	2.50	0.42
1:B:311:TRP:HB3	1:B:312:LYS:H	1.63	0.42
1:A:272:PRO:CA	1:A:309:GLN:HB2	2.48	0.42
1:A:298:SER:O	1:A:299:GLN:CB	2.59	0.42
1:B:175:VAL:CG1	1:B:346:PHE:HD1	2.32	0.42
1:B:365:ILE:O	1:B:365:ILE:HG22	2.19	0.42
1:B:201:LYS:HE3	1:B:222:SER:OG	2.20	0.42
1:A:163:LYS:O	1:A:167:ALA:HB2	2.20	0.41
1:A:234:VAL:HG21	1:B:191:LEU:CD2	2.49	0.41
1:B:298:SER:CB	1:B:320:ASP:OD1	2.64	0.41
1:A:271:TRP:HA	1:A:272:PRO:HD3	1.70	0.41
1:B:159:ARG:CG	1:B:160:LEU:N	2.83	0.41
1:B:328:GLU:HA	1:B:331:PHE:CZ	2.55	0.41
1:A:323:THR:OG1	1:A:325:LYS:HE2	2.21	0.41
1:A:206:ARG:CZ	1:A:206:ARG:HB3	2.50	0.41
1:B:272:PRO:CB	1:B:314:VAL:HG22	2.51	0.41
1:A:163:LYS:HA	1:A:163:LYS:HD3	1.84	0.41
1:A:171:ILE:O	1:A:174:LEU:HD12	2.19	0.41
1:B:361:LEU:HD12	1:B:362:THR:H	1.85	0.41
1:A:226:THR:HA	1:A:229:THR:HG1	1.86	0.41
1:B:249:GLU:OE2	1:B:249:GLU:O	2.39	0.41
1:A:249:GLU:OE2	1:A:249:GLU:O	2.39	0.40
1:A:298:SER:CB	1:A:320:ASP:OD1	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:ILE:HG23	1:B:343:ARG:HG2	2.03	0.40
1:B:285:MET:CA	1:B:288:LYS:HE2	2.44	0.40
1:A:232:ASN:O	1:A:236:LYS:CE	2.50	0.40
1:A:236:LYS:HA	1:A:236:LYS:HD3	1.87	0.40
1:A:238:VAL:O	1:A:241:MET:HB2	2.21	0.40
1:B:301:LYS:HD3	1:B:301:LYS:HA	1.93	0.40
1:A:195:LEU:HD21	1:B:195:LEU:HD21	2.03	0.40
1:B:179:GLU:HG2	1:B:183:ILE:HD11	2.03	0.40
1:B:237:ILE:O	1:B:238:VAL:C	2.60	0.40
1:B:297:HIS:ND1	2:B:1303:ACP:H2'	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	196/218 (90%)	171 (87%)	20 (10%)	5 (3%)	5	7
1	B	207/218 (95%)	179 (86%)	21 (10%)	7 (3%)	3	4
All	All	403/436 (92%)	350 (87%)	41 (10%)	12 (3%)	4	5

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	ILE
1	B	209	ILE
1	B	240	SER
1	B	331	PHE
1	A	163	LYS
1	A	187	LEU
1	A	228	ARG
1	B	187	LEU

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Mol	Chain	Res	Type
1	B	330	SER
1	A	322	GLY
1	B	238	VAL
1	B	322	GLY

5.3.2 Protein sidechains [i](#)

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	180/194 (93%)	139 (77%)	41 (23%)	1	0
1	B	187/194 (96%)	148 (79%)	39 (21%)	1	1
All	All	367/388 (95%)	287 (78%)	80 (22%)	1	1

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	157	ARG
1	A	164	LEU
1	A	165	GLU
1	A	166	ASP
1	A	170	ARG
1	A	171	ILE
1	A	173	GLU
1	A	174	LEU
1	A	177	LEU
1	A	178	GLU
1	A	181	GLN
1	A	182	ARG
1	A	185	ARG
1	A	191	LEU
1	A	193	GLN
1	A	211	LYS
1	A	220	LEU
1	A	228	ARG
1	A	236	LYS

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Mol	Chain	Res	Type
1	A	245	ARG
1	A	247	LYS
1	A	250	LEU
1	A	254	LYS
1	A	263	MET
1	A	270	LYS
1	A	277	LEU
1	A	280	GLU
1	A	287	LEU
1	A	292	THR
1	A	310	LEU
1	A	311	TRP
1	A	312	LYS
1	A	313	GLU
1	A	319	SER
1	A	323	THR
1	A	337	LEU
1	A	346	PHE
1	A	353	ILE
1	A	356	GLU
1	A	362	THR
1	A	365	ILE
1	B	157	ARG
1	B	159	ARG
1	B	165	GLU
1	B	169	GLU
1	B	170	ARG
1	B	171	ILE
1	B	176	LYS
1	B	191	LEU
1	B	193	GLN
1	B	211	LYS
1	B	220	LEU
1	B	228	ARG
1	B	235	ARG
1	B	236	LYS
1	B	237	ILE
1	B	244	ILE
1	B	245	ARG
1	B	247	LYS
1	B	250	LEU
1	B	254	LYS

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Mol	Chain	Res	Type
1	B	263	MET
1	B	270	LYS
1	B	277	LEU
1	B	280	GLU
1	B	287	LEU
1	B	292	THR
1	B	310	LEU
1	B	311	TRP
1	B	312	LYS
1	B	313	GLU
1	B	319	SER
1	B	323	THR
1	B	329	ASN
1	B	331	PHE
1	B	346	PHE
1	B	353	ILE
1	B	356	GLU
1	B	362	THR
1	B	365	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	215	GLN
1	A	279	ASN
1	A	297	HIS
1	A	352	HIS
1	B	215	GLN
1	B	279	ASN
1	B	297	HIS
1	B	352	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	1303	3	27,33,33	1.05	2 (7%)	32,52,52	1.56	6 (18%)
2	ACP	B	1303	3	27,33,33	1.16	2 (7%)	32,52,52	1.61	5 (15%)

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	1303	3	-	0/15/38/38	0/3/3/3
2	ACP	B	1303	3	-	4/15/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1303	ACP	PB-O3A	3.52	1.62	1.58
2	A	1303	ACP	PB-O3A	2.79	1.61	1.58
2	A	1303	ACP	PB-O2B	-2.15	1.51	1.56
2	B	1303	ACP	O4'-C1'	2.06	1.44	1.41

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1303	ACP	N3-C2-N1	-4.87	121.07	128.68
2	B	1303	ACP	N3-C2-N1	-4.69	121.35	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1303	ACP	PB-O3A-PA	-4.10	119.57	132.56
2	B	1303	ACP	O1G-PG-C3B	-3.39	103.94	111.24
2	A	1303	ACP	PB-O3A-PA	-3.13	122.64	132.56
2	A	1303	ACP	C3'-C2'-C1'	2.87	105.29	100.98
2	A	1303	ACP	O2B-PB-O1B	2.80	119.41	110.07
2	B	1303	ACP	O2B-PB-O1B	2.76	119.28	110.07
2	A	1303	ACP	O1G-PG-C3B	-2.59	105.66	111.24
2	A	1303	ACP	O3G-PG-O2G	2.19	114.49	108.08
2	B	1303	ACP	C3'-C2'-C1'	2.05	104.06	100.98

There are no chirality outliers.

All (4) torsion outliers are listed below:

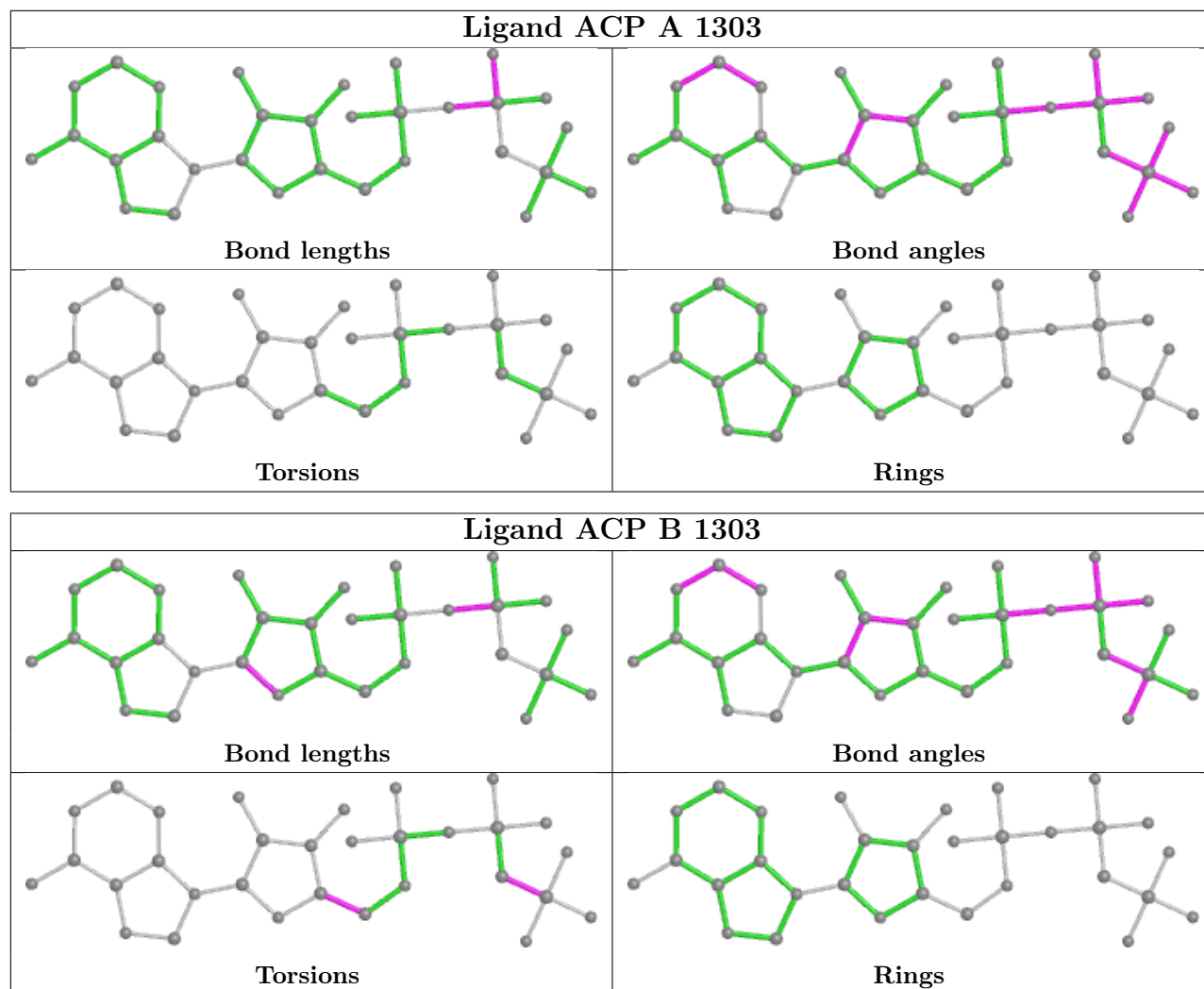
Mol	Chain	Res	Type	Atoms
2	B	1303	ACP	PB-C3B-PG-O1G
2	B	1303	ACP	PB-C3B-PG-O2G
2	B	1303	ACP	PB-C3B-PG-O3G
2	B	1303	ACP	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1303	ACP	8	0
2	B	1303	ACP	13	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 [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	202/218 (92%)	-0.39	4 (1%) 65 60	38, 96, 148, 197	0
1	B	211/218 (96%)	-0.40	2 (0%) 84 83	38, 98, 147, 195	0
All	All	413/436 (94%)	-0.40	6 (1%) 73 71	38, 97, 148, 197	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	336	GLY	3.1
1	A	177	LEU	2.4
1	A	344	LEU	2.2
1	B	349	GLY	2.2
1	A	159	ARG	2.2
1	B	346	PHE	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](#)

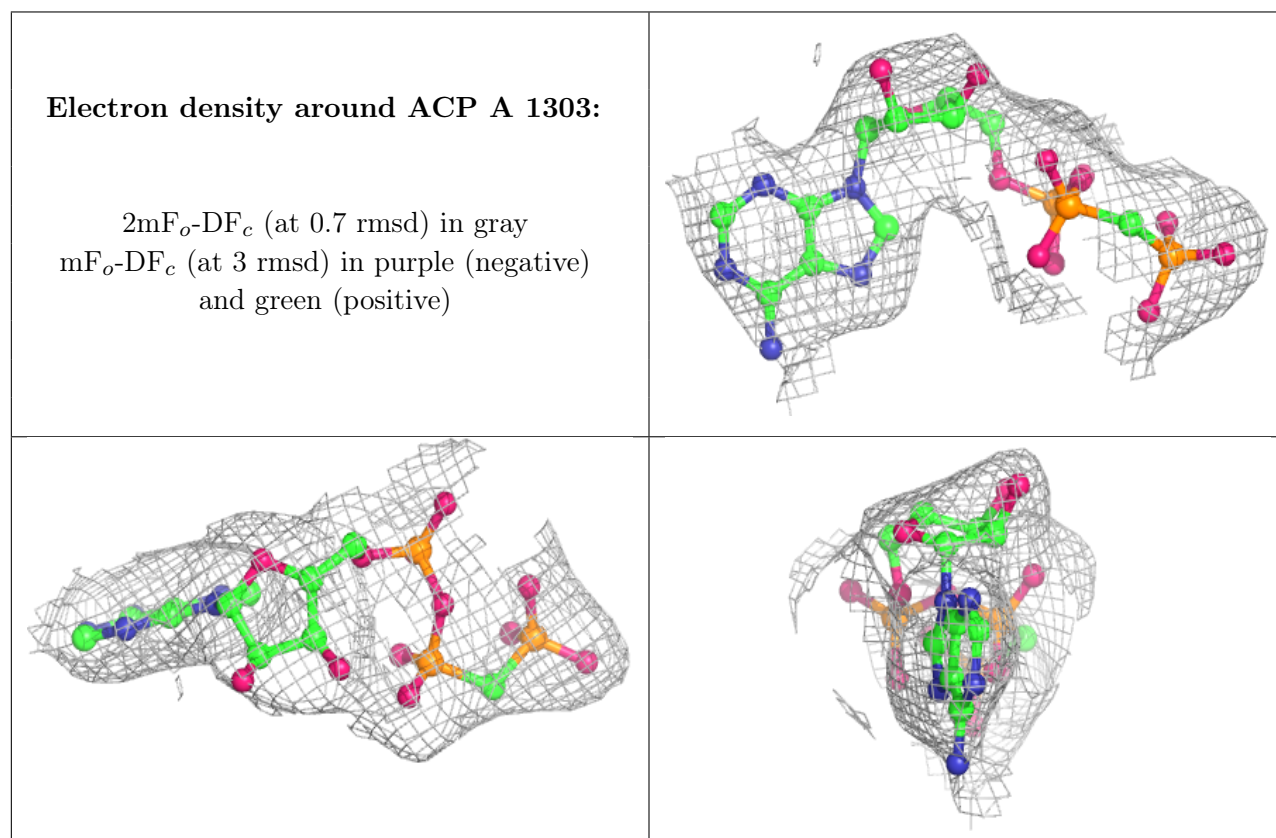
There are no monosaccharides in this entry.

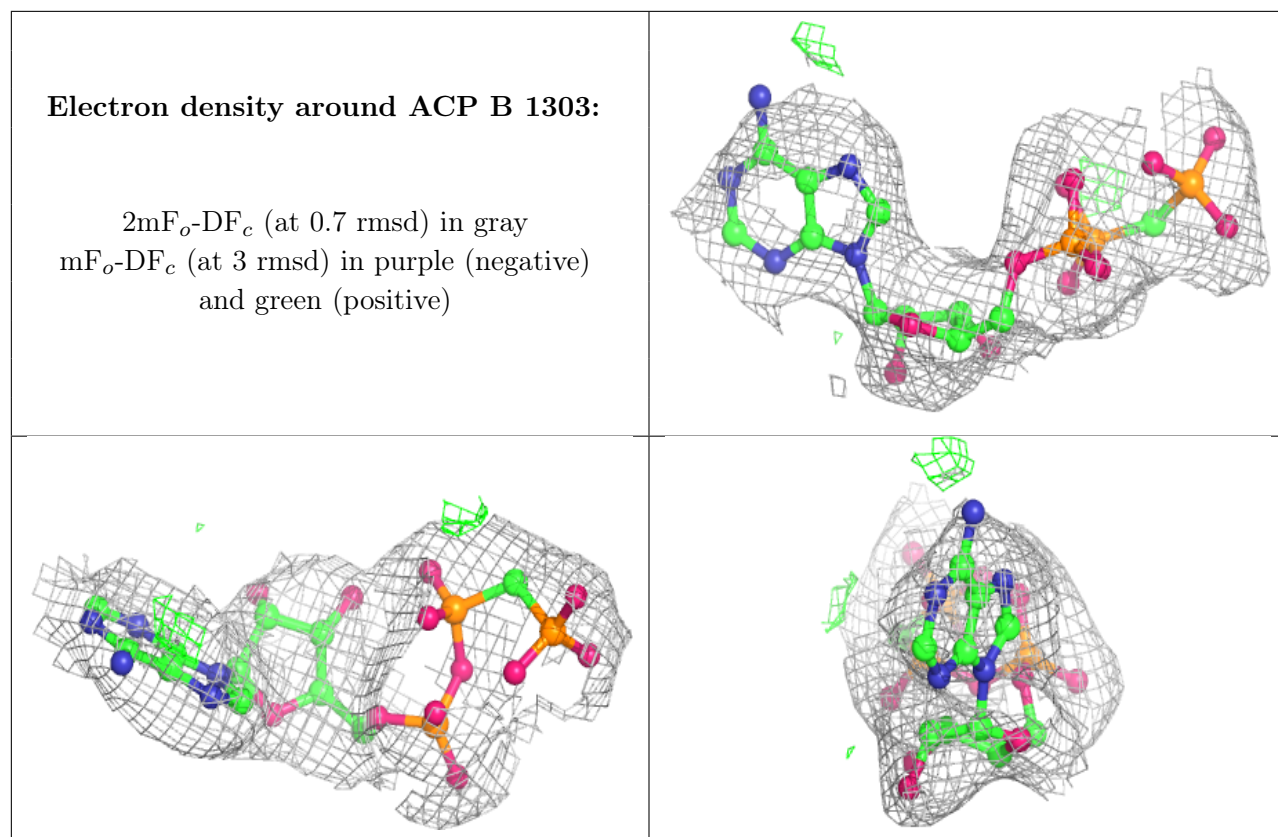
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
3	MG	A	1	1/1	0.89	0.06	134,134,134,134	0
2	ACP	A	1303	31/31	0.95	0.10	68,104,125,251	0
2	ACP	B	1303	31/31	0.96	0.11	41,125,144,162	0
3	MG	B	1	1/1	0.97	0.12	198,198,198,198	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.