



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:58 AM UTC

PDB ID : 3C4E / pdb_00003c4e
Title : Pim-1 Kinase Domain in Complex with 3-aminophenyl-7-azaindole
Authors : Zhang, K.Y.J.; Wang, W.
Deposited on : 2008-01-29
Resolution : 1.98 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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

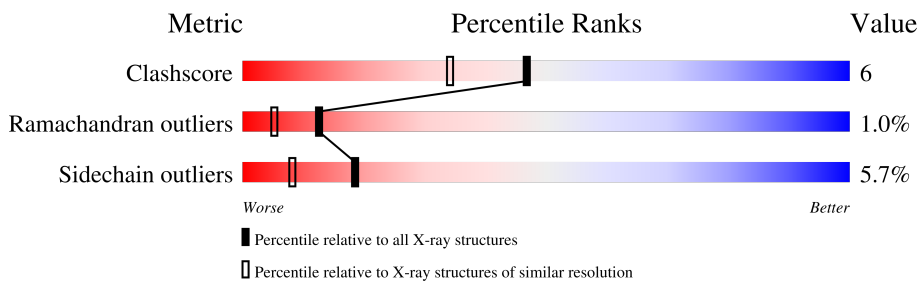
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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))
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	273	
1	B	273	
1	C	273	
1	D	273	

2 Entry composition [i](#)

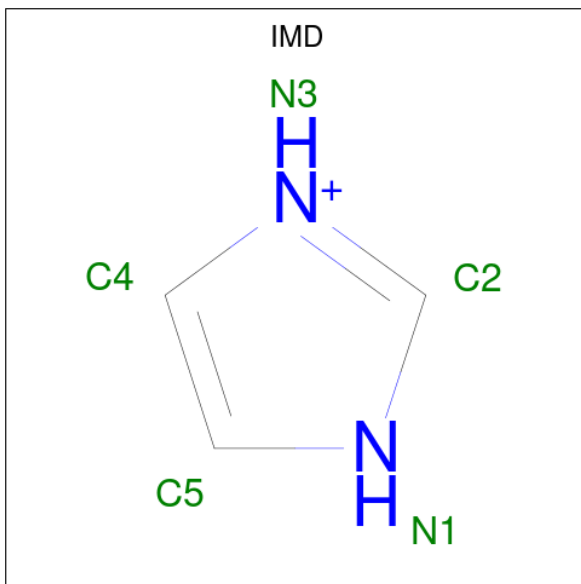
There are 4 unique types of molecules in this entry. The entry contains 9643 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Proto-oncogene serine/threonine-protein kinase Pim-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	273	Total 2225	C 1423	N 389	O 405	S 8	0	0	0
1	B	273	Total 2225	C 1423	N 389	O 405	S 8	0	0	0
1	C	272	Total 2218	C 1418	N 388	O 404	S 8	0	0	0
1	D	273	Total 2225	C 1423	N 389	O 405	S 8	0	0	0

- Molecule 2 is IMIDAZOLE (CCD ID: IMD) (formula: C₃H₅N₂).



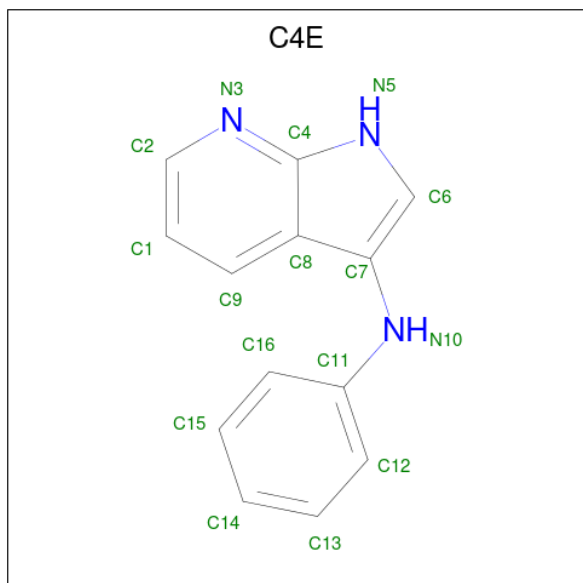
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	N		
2	A	1	Total 5	C 3	N 2	0	0
2	B	1	Total 5	C 3	N 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	N	0	0
			5	3	2		
2	D	1	Total	C	N	0	0
			5	3	2		

- Molecule 3 is N-phenyl-1H-pyrrolo[2,3-b]pyridin-3-amine (CCD ID: C4E) (formula: C₁₃H₁₁N₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			16	13	3		
3	B	1	Total	C	N	0	0
			16	13	3		
3	C	1	Total	C	N	0	0
			16	13	3		
3	D	1	Total	C	N	0	0
			16	13	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	175	Total	O	0	0
			175	175		
4	B	173	Total	O	0	0
			173	173		
4	C	159	Total	O	0	0
			159	159		

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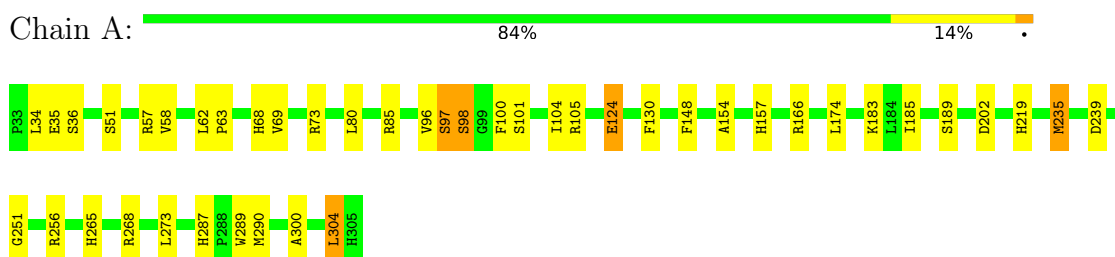
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	159	Total 159	O 159	0	0

3 Residue-property plots [i](#)

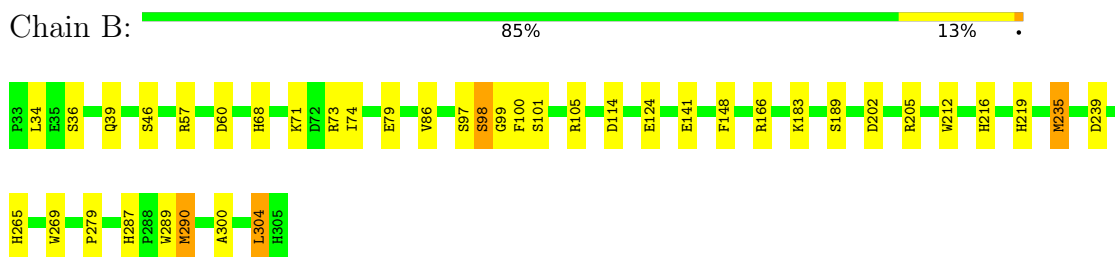
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

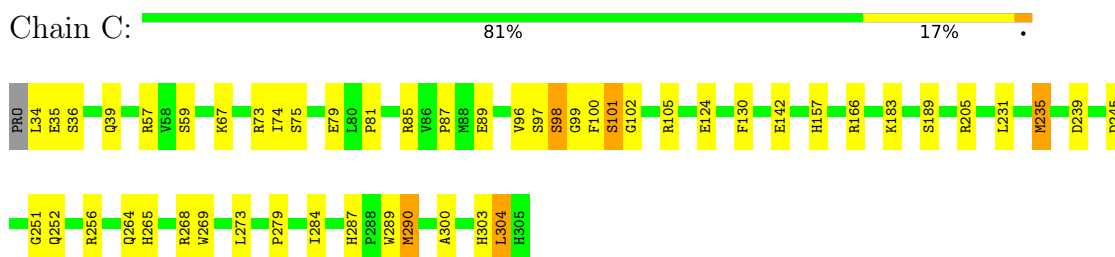
- Molecule 1: Proto-oncogene serine/threonine-protein kinase Pim-1



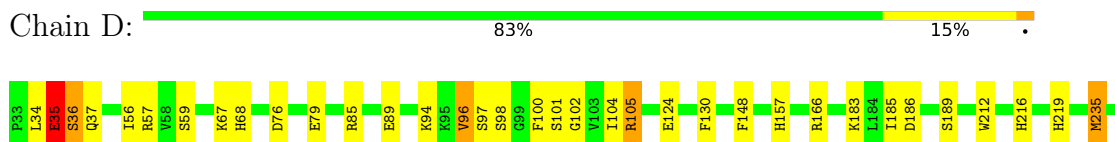
- Molecule 1: Proto-oncogene serine/threonine-protein kinase Pim-1



- Molecule 1: Proto-oncogene serine/threonine-protein kinase Pim-1



- Molecule 1: Proto-oncogene serine/threonine-protein kinase Pim-1





4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	197.46Å 197.46Å 80.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	182.57 – 1.98	Depositor
% Data completeness (in resolution range)	99.1 (182.57-1.98)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	REFMAC 5.1.25	Depositor
R, R_{free}	0.214 , 0.245	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	9643	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

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: C4E, IMD

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	1/2285 (0.0%)	0.83	0/3100
1	B	0.62	2/2285 (0.1%)	0.82	2/3100 (0.1%)
1	C	0.59	1/2277 (0.0%)	0.82	1/3089 (0.0%)
1	D	0.62	1/2285 (0.0%)	0.83	1/3100 (0.0%)
All	All	0.63	5/9132 (0.1%)	0.82	4/12389 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	235	MET	SD-CE	-10.23	1.53	1.79
1	B	235	MET	SD-CE	-8.37	1.58	1.79
1	D	235	MET	SD-CE	-7.71	1.60	1.79
1	C	235	MET	SD-CE	-6.60	1.63	1.79
1	B	290	MET	SD-CE	-5.04	1.67	1.79

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	99	GLY	N-CA-C	6.26	120.47	112.83
1	B	86	VAL	N-CA-C	5.22	113.47	109.19
1	B	141	GLU	N-CA-C	5.07	116.81	111.28
1	D	96	VAL	N-CA-C	5.02	117.80	112.83

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	2225	0	2170	25	0
1	B	2225	0	2170	23	0
1	C	2218	0	2162	24	0
1	D	2225	0	2170	28	0
2	A	5	0	5	1	0
2	B	5	0	5	1	0
2	C	5	0	5	1	0
2	D	5	0	5	2	0
3	A	16	0	11	0	0
3	B	16	0	11	1	0
3	C	16	0	11	2	0
3	D	16	0	11	4	0
4	A	175	0	0	7	0
4	B	173	0	0	3	0
4	C	159	0	0	2	0
4	D	159	0	0	3	0
All	All	9643	0	8736	100	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 6.

All (100) 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:B:265:HIS:CD2	1:B:287:HIS:HE1	1.73	1.06
1:B:265:HIS:HD2	1:B:287:HIS:CE1	1.82	0.95
1:A:101:SER:O	1:A:183:LYS:NZ	2.06	0.88
1:B:265:HIS:HD2	1:B:287:HIS:HE1	0.93	0.87
1:A:104:ILE:HD11	1:A:174:LEU:HD12	1.57	0.87
1:B:97:SER:O	1:B:98:SER:HB3	1.73	0.86
1:A:268:ARG:NH1	4:A:417:HOH:O	2.17	0.77
1:B:101:SER:O	1:B:183:LYS:NZ	2.18	0.74
1:B:265:HIS:CD2	1:B:287:HIS:CE1	2.65	0.74
1:A:104:ILE:CD1	1:A:174:LEU:HD12	2.17	0.74
1:C:287:HIS:HD2	1:C:289:TRP:H	1.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:265:HIS:ND1	1:D:287:HIS:HE1	1.88	0.71
1:B:71:LYS:HA	1:B:74:ILE:HD12	1.72	0.70
1:C:166:ARG:HD3	1:C:189:SER:O	1.91	0.70
1:B:166:ARG:HD3	1:B:189:SER:O	1.92	0.70
1:B:287:HIS:HD2	1:B:289:TRP:H	1.39	0.70
1:C:265:HIS:ND1	1:C:287:HIS:HE1	1.91	0.69
1:A:97:SER:HB2	4:A:316:HOH:O	1.93	0.69
1:C:101:SER:O	1:C:183:LYS:NZ	2.27	0.68
1:C:300:ALA:HA	1:C:304:LEU:HB2	1.77	0.66
1:D:287:HIS:HD2	1:D:289:TRP:H	1.42	0.66
1:A:287:HIS:HD2	1:A:289:TRP:H	1.43	0.65
1:B:205:ARG:NH2	4:B:366:HOH:O	2.29	0.65
1:D:166:ARG:HD3	1:D:189:SER:O	1.98	0.63
1:C:264:GLN:OE1	1:C:268:ARG:NH2	2.32	0.63
1:D:68:HIS:HD2	4:D:345:HOH:O	1.81	0.63
1:A:96:VAL:O	1:A:157:HIS:HE1	1.84	0.61
1:D:100:PHE:CE2	1:D:102:GLY:HA3	2.36	0.60
1:A:287:HIS:CD2	1:A:289:TRP:H	2.20	0.59
1:D:67:LYS:HZ2	3:D:306:C4E:H13	1.67	0.58
1:B:57:ARG:HD2	1:B:60:ASP:OD2	2.03	0.58
1:D:287:HIS:CD2	1:D:289:TRP:H	2.21	0.57
1:A:104:ILE:HD12	1:A:185:ILE:CG2	2.34	0.57
1:A:265:HIS:ND1	1:A:287:HIS:HE1	2.02	0.57
1:B:300:ALA:HA	1:B:304:LEU:HB2	1.87	0.57
1:C:287:HIS:CD2	1:C:289:TRP:H	2.19	0.57
1:B:287:HIS:CD2	1:B:289:TRP:H	2.21	0.56
1:D:300:ALA:HA	1:D:304:LEU:HB2	1.88	0.56
1:C:96:VAL:O	1:C:157:HIS:HE1	1.90	0.54
1:A:97:SER:O	1:A:98:SER:HB3	2.08	0.54
1:D:264:GLN:OE1	1:D:268:ARG:NH2	2.41	0.53
1:B:269:TRP:CD1	1:B:279:PRO:HD3	2.43	0.53
1:B:68:HIS:HD2	4:B:342:HOH:O	1.93	0.52
1:C:205:ARG:NH2	4:C:438:HOH:O	2.41	0.52
1:A:166:ARG:HD3	1:A:189:SER:O	2.08	0.52
1:B:148:PHE:HB2	1:B:235:MET:HE1	1.91	0.52
1:A:148:PHE:HB2	1:A:235:MET:HE1	1.92	0.51
1:B:97:SER:O	1:B:98:SER:CB	2.51	0.51
1:B:101:SER:HB2	1:B:183:LYS:NZ	2.26	0.51
3:B:306:C4E:H12	3:B:306:C4E:H6	1.94	0.50
1:A:68:HIS:HD2	4:A:412:HOH:O	1.95	0.50
1:D:284:ILE:O	1:D:290:MET:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:LYS:NZ	1:C:89:GLU:OE2	2.46	0.49
1:D:67:LYS:NZ	1:D:89:GLU:OE2	2.44	0.49
1:D:219:HIS:HD2	4:D:402:HOH:O	1.96	0.48
1:C:74:ILE:HD13	1:C:87:PRO:HG3	1.96	0.48
1:D:239:ASP:OD1	2:D:4:IMD:H4	2.13	0.48
1:D:258:ARG:HD3	1:D:258:ARG:C	2.39	0.48
1:D:98:SER:O	1:D:105:ARG:NH2	2.46	0.48
1:D:35:GLU:C	1:D:37:GLN:H	2.22	0.48
1:B:212:TRP:CE3	1:B:216:HIS:HA	2.49	0.47
1:A:51:SER:OG	1:B:219:HIS:HE1	1.98	0.47
1:D:67:LYS:HZ2	3:D:306:C4E:C13	2.28	0.47
1:D:34:LEU:HD23	1:D:35:GLU:HB2	1.97	0.47
1:A:219:HIS:HD2	4:A:413:HOH:O	1.98	0.47
1:D:96:VAL:O	1:D:157:HIS:HE1	1.97	0.46
1:D:130:PHE:O	2:D:4:IMD:H2	2.15	0.46
1:A:300:ALA:HA	1:A:304:LEU:HB2	1.97	0.46
1:C:205:ARG:NH1	1:C:245:ASP:OD2	2.49	0.45
1:C:303:HIS:HD2	4:C:356:HOH:O	1.98	0.45
1:C:289:TRP:CZ3	1:C:290:MET:HE3	2.51	0.45
1:D:101:SER:HB2	1:D:183:LYS:NZ	2.31	0.45
1:C:231:LEU:HG	1:C:235:MET:HE2	1.99	0.45
1:C:100:PHE:CE2	1:C:102:GLY:HA3	2.52	0.45
1:B:101:SER:HB2	1:B:183:LYS:HZ2	1.82	0.45
1:D:97:SER:HB2	4:D:407:HOH:O	2.17	0.45
1:D:148:PHE:HB2	1:D:235:MET:HE1	2.00	0.44
1:C:67:LYS:HZ3	3:C:306:C4E:H13	1.82	0.44
1:D:104:ILE:HD13	1:D:185:ILE:HG22	2.00	0.44
1:A:124:GLU:HG2	4:A:424:HOH:O	2.17	0.43
1:C:130:PHE:O	2:C:3:IMD:H4	2.18	0.43
1:B:239:ASP:OD1	2:B:2:IMD:H4	2.18	0.43
1:C:67:LYS:HZ3	3:C:306:C4E:C13	2.31	0.43
1:C:284:ILE:O	1:C:290:MET:HG3	2.18	0.43
1:D:186:ASP:CG	3:D:306:C4E:H14	2.43	0.43
1:C:251:GLY:HA3	1:C:273:LEU:HD21	2.01	0.42
1:D:186:ASP:HB2	3:D:306:C4E:C14	2.49	0.42
1:A:62:LEU:HA	1:A:63:PRO:HD3	1.93	0.42
1:A:100:PHE:HZ	4:A:334:HOH:O	2.02	0.42
1:C:97:SER:O	1:C:98:SER:HB3	2.19	0.42
1:A:130:PHE:O	2:A:1:IMD:H2	2.20	0.42
1:C:142:GLU:OE1	1:C:303:HIS:HE1	2.02	0.42
1:C:269:TRP:CD1	1:C:279:PRO:HD3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:GLY:HA3	1:A:273:LEU:HD21	2.02	0.41
1:D:212:TRP:CE3	1:D:216:HIS:HA	2.55	0.41
1:A:97:SER:CB	4:A:316:HOH:O	2.59	0.41
1:B:100:PHE:HZ	4:B:325:HOH:O	2.03	0.41
1:A:100:PHE:HE2	1:A:154:ALA:HA	1.85	0.41
1:D:104:ILE:O	1:D:104:ILE:HG23	2.21	0.40
1:A:98:SER:H	1:A:105:ARG:HE	1.67	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	271/273 (99%)	264 (97%)	5 (2%)	2 (1%)	18	9
1	B	271/273 (99%)	262 (97%)	5 (2%)	4 (2%)	8	2
1	C	270/273 (99%)	263 (97%)	4 (2%)	3 (1%)	11	4
1	D	271/273 (99%)	265 (98%)	4 (2%)	2 (1%)	18	9
All	All	1083/1092 (99%)	1054 (97%)	18 (2%)	11 (1%)	12	5

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	98	SER
1	C	98	SER
1	A	98	SER
1	B	36	SER
1	B	99	GLY
1	D	36	SER
1	A	36	SER
1	B	34	LEU

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Mol	Chain	Res	Type
1	C	36	SER
1	D	35	GLU
1	C	81	PRO

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	244/244 (100%)	229 (94%)	15 (6%)	17	7
1	B	244/244 (100%)	234 (96%)	10 (4%)	27	16
1	C	243/244 (100%)	226 (93%)	17 (7%)	14	5
1	D	244/244 (100%)	230 (94%)	14 (6%)	18	8
All	All	975/976 (100%)	919 (94%)	56 (6%)	18	8

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LEU
1	A	35	GLU
1	A	57	ARG
1	A	58	VAL
1	A	69	VAL
1	A	73	ARG
1	A	80	LEU
1	A	85	ARG
1	A	97	SER
1	A	124	GLU
1	A	202	ASP
1	A	239	ASP
1	A	256	ARG
1	A	290	MET
1	A	304	LEU
1	B	39	GLN
1	B	46	SER
1	B	73	ARG

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Mol	Chain	Res	Type
1	B	79	GLU
1	B	105	ARG
1	B	114	ASP
1	B	124	GLU
1	B	202	ASP
1	B	290	MET
1	B	304	LEU
1	C	34	LEU
1	C	35	GLU
1	C	39	GLN
1	C	57	ARG
1	C	59	SER
1	C	73	ARG
1	C	75	SER
1	C	79	GLU
1	C	85	ARG
1	C	101	SER
1	C	105	ARG
1	C	124	GLU
1	C	239	ASP
1	C	252	GLN
1	C	256	ARG
1	C	290	MET
1	C	304	LEU
1	D	35	GLU
1	D	36	SER
1	D	56	ILE
1	D	57	ARG
1	D	59	SER
1	D	76	ASP
1	D	79	GLU
1	D	85	ARG
1	D	94	LYS
1	D	105	ARG
1	D	124	GLU
1	D	252	GLN
1	D	290	MET
1	D	304	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	68	HIS
1	A	157	HIS
1	A	219	HIS
1	A	252	GLN
1	A	287	HIS
1	A	291	GLN
1	A	303	HIS
1	B	39	GLN
1	B	61	ASN
1	B	68	HIS
1	B	157	HIS
1	B	219	HIS
1	B	265	HIS
1	B	287	HIS
1	B	291	GLN
1	C	39	GLN
1	C	68	HIS
1	C	157	HIS
1	C	219	HIS
1	C	287	HIS
1	C	291	GLN
1	C	303	HIS
1	D	37	GLN
1	D	68	HIS
1	D	157	HIS
1	D	219	HIS
1	D	287	HIS
1	D	291	GLN
1	D	303	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	C4E	C	306	-	18,18,18	1.12	1 (5%)	20,24,24	1.68	4 (20%)
2	IMD	B	2	-	5,5,5	0.69	0	5,5,5	0.37	0
3	C4E	D	306	-	18,18,18	1.13	1 (5%)	20,24,24	1.51	3 (15%)
2	IMD	C	3	-	5,5,5	0.65	0	5,5,5	0.36	0
3	C4E	A	306	-	18,18,18	1.09	1 (5%)	20,24,24	1.45	3 (15%)
2	IMD	D	4	-	5,5,5	0.69	0	5,5,5	0.43	0
3	C4E	B	306	-	18,18,18	1.08	1 (5%)	20,24,24	1.42	4 (20%)
2	IMD	A	1	-	5,5,5	0.59	0	5,5,5	0.45	0

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	C4E	C	306	-	-	0/4/4/4	0/3/3/3
3	C4E	D	306	-	-	0/4/4/4	0/3/3/3
2	IMD	B	2	-	-	-	0/1/1/1
2	IMD	C	3	-	-	-	0/1/1/1
3	C4E	A	306	-	-	0/4/4/4	0/3/3/3
2	IMD	D	4	-	-	-	0/1/1/1
3	C4E	B	306	-	-	0/4/4/4	0/3/3/3
2	IMD	A	1	-	-	-	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	306	C4E	C8-C7	-2.84	1.42	1.46
3	D	306	C4E	C8-C7	-2.76	1.42	1.46
3	A	306	C4E	C8-C7	-2.73	1.42	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	306	C4E	C8-C7	-2.57	1.42	1.46

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	306	C4E	C4-N5-C6	3.93	110.33	108.48
3	D	306	C4E	C9-C8-C7	3.47	135.93	131.07
3	A	306	C4E	C11-N10-C7	3.27	135.51	127.72
3	C	306	C4E	C11-N10-C7	3.26	135.47	127.72
3	B	306	C4E	C4-N5-C6	3.14	109.96	108.48
3	D	306	C4E	C4-N5-C6	3.00	109.89	108.48
3	C	306	C4E	C9-C8-C7	2.99	135.26	131.07
3	D	306	C4E	C11-N10-C7	2.97	134.78	127.72
3	A	306	C4E	C9-C8-C7	2.81	135.01	131.07
3	B	306	C4E	C9-C8-C7	2.80	135.00	131.07
3	A	306	C4E	C4-N5-C6	2.71	109.76	108.48
3	B	306	C4E	C2-N3-C4	-2.18	112.51	116.74
3	B	306	C4E	C11-N10-C7	2.02	132.51	127.72
3	C	306	C4E	C1-C2-N3	2.00	126.59	123.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	306	C4E	2	0
2	B	2	IMD	1	0
3	D	306	C4E	4	0
2	C	3	IMD	1	0
2	D	4	IMD	2	0
3	B	306	C4E	1	0
2	A	1	IMD	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.