



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:13 PM GMT

PDB ID : 1EHY
Title : X-ray structure of the epoxide hydrolase from agrobacterium radiobacter ad1
Authors : Nardini, M.; Ridder, I.S.; Rozeboom, H.J.; Kalk, K.H.; Rink, R.; Janssen, D.B.; Dijkstra, B.W.
Deposited on : 1998-10-17
Resolution : 2.10 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

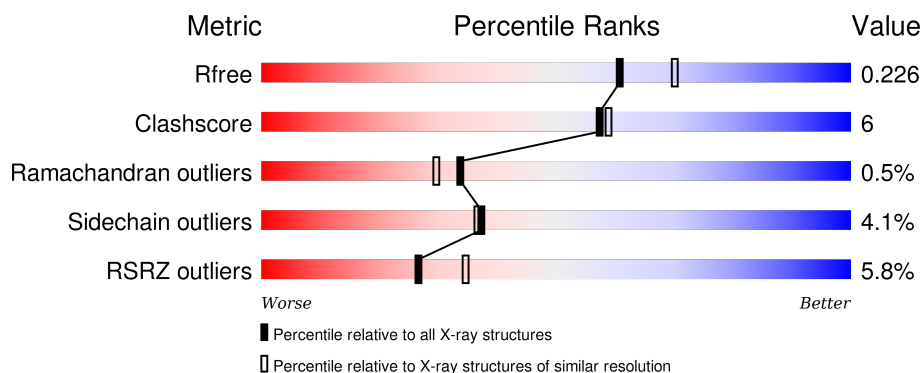
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 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	294	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>17%</div> <div>• •</div> </div> </div>
1	B	294	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>13%</div> <div>• •</div> </div> </div>
1	C	294	<div> <div>6%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>•</div> </div> </div>
1	D	294	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9876 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 PROTEIN (SOLUBLE EPOXIDE HYDROLASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	282	Total	C	N	O	S	0	0	0
			2317	1503	380	424	10			
1	B	282	Total	C	N	O	S	0	0	0
			2317	1503	380	424	10			
1	C	282	Total	C	N	O	S	0	0	0
			2311	1500	377	424	10			
1	D	282	Total	C	N	O	S	0	0	0
			2317	1503	380	424	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	THR	CLONING ARTIFACT	UNP O31243
B	2	ALA	THR	CLONING ARTIFACT	UNP O31243
C	2	ALA	THR	CLONING ARTIFACT	UNP O31243
D	2	ALA	THR	CLONING ARTIFACT	UNP O31243

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	K	0	0
			1	1		
2	A	1	Total	K	0	0
			1	1		
2	D	1	Total	K	0	0
			1	1		
2	C	1	Total	K	0	0
			1	1		

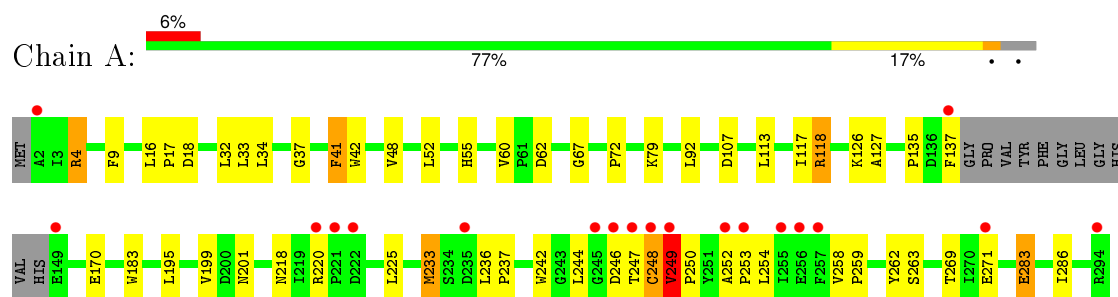
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	134	Total 138	O 138	0	4
3	B	154	Total 167	O 167	0	13
3	C	139	Total 147	O 147	0	8
3	D	150	Total 158	O 158	0	8

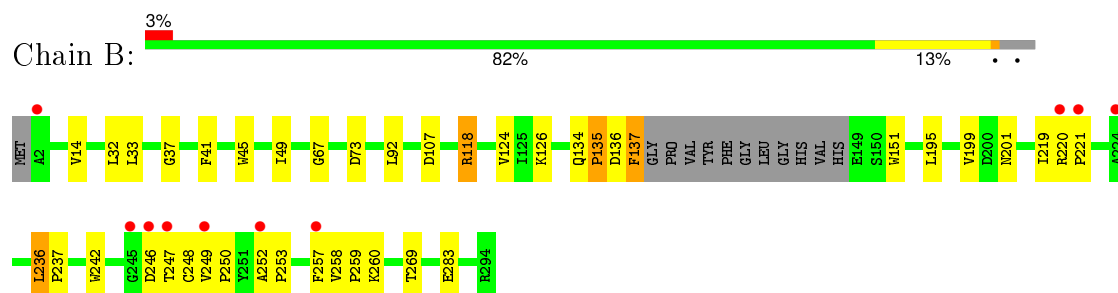
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

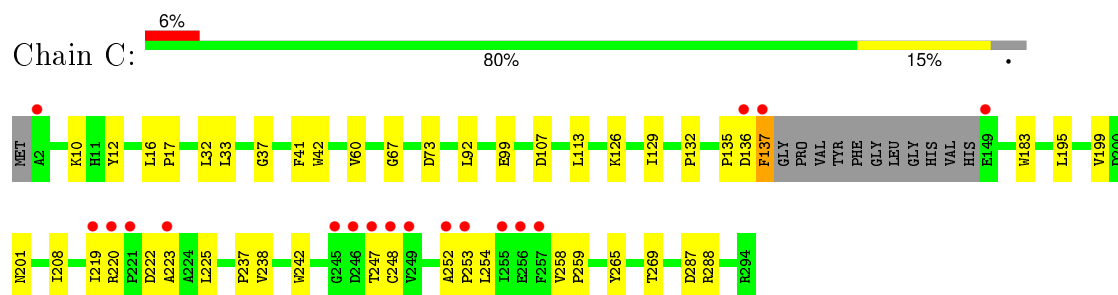
• Molecule 1: PROTEIN (SOLUBLE EPOXIDE HYDROLASE)



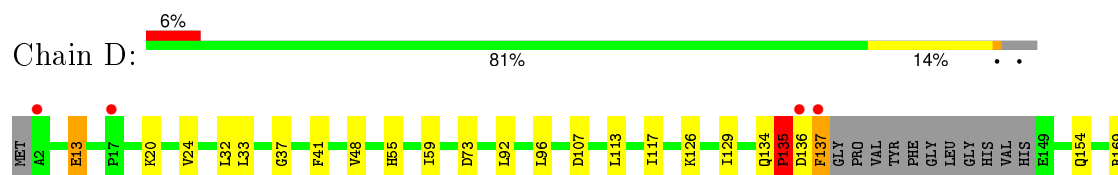
• Molecule 1: PROTEIN (SOLUBLE EPOXIDE HYDROLASE)

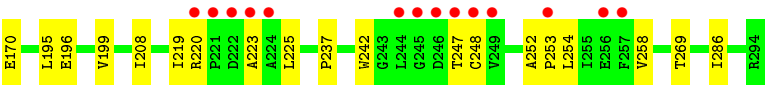


• Molecule 1: PROTEIN (SOLUBLE EPOXIDE HYDROLASE)



• Molecule 1: PROTEIN (SOLUBLE EPOXIDE HYDROLASE)





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	146.62Å 100.20Å 96.88Å 90.00° 100.68° 90.00°	Depositor
Resolution (Å)	25.00 – 2.10 24.38 – 2.10	Depositor EDS
% Data completeness (in resolution range)	91.5 (25.00-2.10) 85.6 (24.38-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.10Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.190 , 0.227 0.195 , 0.226	Depositor DCC
R_{free} test set	3544 reflections (5.16%)	DCC
Wilson B-factor (Å ²)	23.4	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 57.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 73445 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9876	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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, 0.375 respectively for untwinned datasets, and 0.333, 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:
K

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	0.50	0/2390	0.66	1/3248 (0.0%)
1	B	0.45	0/2390	0.65	1/3248 (0.0%)
1	C	0.45	0/2384	0.65	0/3241
1	D	0.46	0/2390	0.64	0/3248
All	All	0.46	0/9554	0.65	2/12985 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	118	ARG	NE-CZ-NH2	5.74	123.17	120.30
1	A	249	VAL	O-C-N	-5.40	110.83	121.10

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	2317	0	2216	39	0
1	B	2317	0	2216	22	0
1	C	2311	0	2204	27	0
1	D	2317	0	2215	23	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	138	0	0	3	0
3	B	167	0	0	0	0
3	C	147	0	0	4	0
3	D	158	0	0	2	0
All	All	9876	0	8851	108	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 (108) 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:135:PRO:HG2	1:C:183:TRP:CD1	2.05	0.91
1:D:220:ARG:HE	1:D:223:ALA:HB2	1.36	0.89
1:A:135:PRO:HG2	1:A:183:TRP:CD1	2.08	0.89
1:C:126:LYS:HG2	1:C:237:PRO:HG2	1.68	0.73
1:B:126:LYS:HG2	1:B:237:PRO:HG2	1.71	0.71
1:D:126:LYS:HG2	1:D:237:PRO:HG2	1.71	0.70
1:A:48:VAL:HG13	1:A:286:ILE:HG12	1.75	0.68
1:D:13:GLU:HG2	1:D:20:LYS:HE2	1.76	0.67
1:C:16:LEU:HB3	1:C:17:PRO:HD2	1.78	0.66
1:A:249:VAL:HG13	1:B:248:CYS:SG	2.36	0.65
1:C:135:PRO:HG2	1:C:183:TRP:CG	2.31	0.65
1:A:126:LYS:HG2	1:A:237:PRO:HG2	1.79	0.65
1:D:113:LEU:HD23	1:D:129:ILE:HD13	1.81	0.62
1:A:233:MET:HE1	1:A:263:SER:HB3	1.80	0.62
1:D:37:GLY:HA3	1:D:107:ASP:HB3	1.82	0.61
1:A:42:TRP:HB2	1:A:60:VAL:HG12	1.82	0.61
1:D:48:VAL:HG22	1:D:286:ILE:HG13	1.82	0.61
1:B:124:VAL:HG13	1:B:236:LEU:HD11	1.83	0.60
1:C:137:PHE:HZ	1:C:219:ILE:HG21	1.66	0.59
1:B:220:ARG:HG3	1:B:221:PRO:HD2	1.83	0.59
1:A:244:LEU:HD11	1:A:271:GLU:HG2	1.85	0.59
1:B:67:GLY:HA2	1:B:201:ASN:OD1	2.04	0.57
1:B:37:GLY:HA3	1:B:107:ASP:HB3	1.86	0.56
1:A:48:VAL:HG12	1:A:52:LEU:HD12	1.86	0.56
1:C:252:ALA:N	1:C:253:PRO:HD2	2.21	0.56
1:A:4:ARG:HD2	1:A:9:PHE:CE1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:PRO:HG2	1:A:183:TRP:CG	2.40	0.55
1:A:48:VAL:HG12	1:A:52:LEU:CD1	2.37	0.55
1:A:244:LEU:CD1	1:A:271:GLU:OE2	2.53	0.55
1:A:254:LEU:O	1:A:258:VAL:HG23	2.07	0.54
1:D:252:ALA:N	1:D:253:PRO:HD2	2.22	0.54
1:A:252:ALA:N	1:A:253:PRO:HD2	2.23	0.54
1:C:67:GLY:HA2	1:C:201:ASN:OD1	2.08	0.53
1:A:248:CYS:O	1:A:249:VAL:HB	2.08	0.53
1:C:113:LEU:HD23	1:C:129:ILE:HD13	1.91	0.52
1:A:244:LEU:CD1	1:A:271:GLU:HG2	2.39	0.52
1:A:242:TRP:O	1:A:269:THR:HA	2.10	0.52
1:C:10:LYS:HE2	3:C:563:HOH:O	2.08	0.52
1:A:37:GLY:HA3	1:A:107:ASP:HB3	1.92	0.52
1:A:233:MET:CE	1:A:263:SER:HB3	2.41	0.51
1:C:242:TRP:NE1	1:C:269:THR:HG22	2.25	0.51
1:D:137:PHE:HZ	1:D:219:ILE:HG21	1.76	0.50
1:D:59:ILE:HD13	1:D:96:LEU:HD12	1.93	0.50
1:C:238:VAL:O	1:C:265:TYR:HA	2.13	0.49
1:B:252:ALA:N	1:B:253:PRO:HD2	2.27	0.48
1:B:126:LYS:HG2	1:B:237:PRO:CG	2.42	0.48
1:C:99:GLU:HG2	3:C:665[B]:HOH:O	2.13	0.48
1:A:170:GLU:HG3	3:A:388:HOH:O	2.11	0.48
1:A:247:THR:O	1:A:248:CYS:HB2	2.12	0.48
1:B:249:VAL:HB	1:B:250:PRO:HD3	1.95	0.48
1:A:55:HIS:HB3	3:A:329:HOH:O	2.13	0.48
1:A:244:LEU:HD12	1:A:271:GLU:HA	1.95	0.47
1:C:208:ILE:HG12	3:C:546:HOH:O	2.14	0.47
1:C:287:ASP:OD2	1:C:288:ARG:NH1	2.47	0.47
1:A:48:VAL:HG13	1:A:286:ILE:CG1	2.44	0.46
1:D:247:THR:HG22	1:D:248:CYS:H	1.80	0.46
1:B:220:ARG:HG3	1:B:221:PRO:CD	2.45	0.46
1:C:37:GLY:HA3	1:C:107:ASP:HB3	1.97	0.46
1:B:137:PHE:HZ	1:B:219:ILE:HG21	1.81	0.46
1:C:254:LEU:O	1:C:258:VAL:HG23	2.16	0.46
1:A:67:GLY:HA2	1:A:201:ASN:OD1	2.15	0.46
1:B:151:TRP:HB3	1:D:154:GLN:OE1	2.16	0.45
1:D:134:GLN:O	1:D:137:PHE:HB2	2.17	0.45
1:C:42:TRP:HB2	1:C:60:VAL:HG12	1.98	0.45
1:D:254:LEU:O	1:D:258:VAL:HG23	2.16	0.45
1:A:283:GLU:H	1:A:283:GLU:CD	2.18	0.44
1:C:12:TYR:HB3	3:C:613:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:TRP:O	1:B:49:ILE:HG13	2.17	0.44
1:A:258:VAL:N	1:A:259:PRO:HD2	2.31	0.44
1:D:208:ILE:HG12	3:D:338:HOH:O	2.17	0.44
1:D:48:VAL:HG22	1:D:286:ILE:CG1	2.48	0.44
1:A:218:ASN:HB3	1:A:225:LEU:HD13	2.00	0.43
1:C:137:PHE:CZ	1:C:219:ILE:HG21	2.51	0.43
1:D:195:LEU:O	1:D:199:VAL:HG23	2.18	0.43
1:B:257:PHE:HD1	1:B:260:LYS:HD2	1.83	0.43
1:C:247:THR:OG1	1:C:248:CYS:N	2.51	0.43
1:A:236:LEU:HD22	1:A:237:PRO:HD2	2.01	0.43
1:A:72:PRO:HB3	1:A:79:LYS:HD3	2.00	0.43
1:A:195:LEU:O	1:A:199:VAL:HG23	2.18	0.43
1:B:195:LEU:O	1:B:199:VAL:HG23	2.18	0.43
1:C:258:VAL:N	1:C:259:PRO:HD2	2.34	0.42
1:D:55:HIS:HB3	3:D:330:HOH:O	2.18	0.42
1:C:220:ARG:HB2	1:C:223:ALA:HB2	2.00	0.42
1:B:246:ASP:O	1:B:247:THR:HG23	2.19	0.42
1:A:250:PRO:HA	3:A:376:HOH:O	2.18	0.42
1:A:113:LEU:HD12	1:A:117:ILE:HG23	2.02	0.42
1:A:113:LEU:HD21	1:A:127:ALA:HB1	2.01	0.42
1:A:117:ILE:HD11	1:A:118:ARG:NH2	2.35	0.42
1:B:283:GLU:H	1:B:283:GLU:CD	2.23	0.42
1:C:195:LEU:O	1:C:199:VAL:HG23	2.19	0.41
1:D:13:GLU:CG	1:D:20:LYS:HE2	2.48	0.41
1:B:242:TRP:NE1	1:B:269:THR:HG22	2.34	0.41
1:C:129:ILE:HG22	1:C:132:PRO:HD3	2.02	0.41
1:D:242:TRP:NE1	1:D:269:THR:HG22	2.36	0.41
1:A:34:LEU:HB2	1:A:60:VAL:HG22	2.02	0.41
1:C:220:ARG:H	1:C:223:ALA:HB2	1.85	0.41
1:B:134:GLN:HA	1:B:135:PRO:HD3	1.89	0.41
1:D:134:GLN:HA	1:D:135:PRO:HD3	1.89	0.41
1:B:258:VAL:N	1:B:259:PRO:HD2	2.36	0.41
1:A:41:PHE:HB2	1:A:62:ASP:OD1	2.20	0.41
1:D:13:GLU:HG2	1:D:20:LYS:CE	2.49	0.40
1:A:118:ARG:NH2	1:A:262:TYR:OH	2.53	0.40
1:A:16:LEU:HB3	1:A:17:PRO:HD2	2.03	0.40
1:B:257:PHE:CE1	1:C:222:ASP:HB3	2.56	0.40
1:D:113:LEU:HD12	1:D:117:ILE:HG23	2.03	0.40
1:B:124:VAL:HG22	1:B:236:LEU:HD21	2.04	0.40
1:C:288:ARG:HD3	1:C:288:ARG:HA	1.86	0.40
1:D:169:ARG:NH2	1:D:196:GLU:OE1	2.48	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	278/294 (95%)	264 (95%)	13 (5%)	1 (0%)	39	37
1	B	278/294 (95%)	265 (95%)	11 (4%)	2 (1%)	26	21
1	C	278/294 (95%)	265 (95%)	12 (4%)	1 (0%)	39	37
1	D	278/294 (95%)	266 (96%)	10 (4%)	2 (1%)	26	21
All	All	1112/1176 (95%)	1060 (95%)	46 (4%)	6 (0%)	34	30

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	249	VAL
1	D	135	PRO
1	B	73	ASP
1	C	73	ASP
1	D	73	ASP
1	B	135	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	247/256 (96%)	234 (95%)	13 (5%)	28	25
1	B	247/256 (96%)	238 (96%)	9 (4%)	42	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	246/256 (96%)	239 (97%)	7 (3%)	51	55
1	D	247/256 (96%)	236 (96%)	11 (4%)	34	32
All	All	987/1024 (96%)	947 (96%)	40 (4%)	37	36

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	18	ASP
1	A	32	LEU
1	A	33	LEU
1	A	41	PHE
1	A	92	LEU
1	A	118	ARG
1	A	137	PHE
1	A	220	ARG
1	A	233	MET
1	A	246	ASP
1	A	248	CYS
1	A	283	GLU
1	B	14	VAL
1	B	32	LEU
1	B	33	LEU
1	B	41	PHE
1	B	92	LEU
1	B	118	ARG
1	B	136	ASP
1	B	137	PHE
1	B	236	LEU
1	C	32	LEU
1	C	33	LEU
1	C	41	PHE
1	C	92	LEU
1	C	136	ASP
1	C	137	PHE
1	C	225	LEU
1	D	13	GLU
1	D	24	VAL
1	D	32	LEU
1	D	33	LEU
1	D	41	PHE

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Mol	Chain	Res	Type
1	D	92	LEU
1	D	135	PRO
1	D	136	ASP
1	D	137	PHE
1	D	170	GLU
1	D	225	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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	282/294 (95%)	0.18	19 (6%) 21 28	16, 28, 54, 74	0
1	B	282/294 (95%)	-0.07	10 (3%) 48 57	12, 22, 48, 66	0
1	C	282/294 (95%)	0.08	18 (6%) 23 30	14, 25, 55, 71	0
1	D	282/294 (95%)	0.01	18 (6%) 23 30	12, 23, 53, 68	0
All	All	1128/1176 (95%)	0.05	65 (5%) 26 34	12, 25, 54, 74	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	247	THR	8.8
1	A	246	ASP	7.3
1	D	2	ALA	7.2
1	C	2	ALA	6.4
1	A	245	GLY	6.4
1	C	221	PRO	6.3
1	C	246	ASP	5.5
1	B	247	THR	5.2
1	D	223	ALA	5.0
1	D	249	VAL	4.8
1	D	221	PRO	4.7
1	A	248	CYS	4.5
1	B	2	ALA	4.3
1	C	137	PHE	4.2
1	D	257	PHE	4.1
1	A	249	VAL	4.0
1	C	220	ARG	4.0
1	C	248	CYS	4.0
1	D	247	THR	4.0
1	C	249	VAL	3.9
1	B	221	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	249	VAL	3.8
1	A	256	GLU	3.7
1	A	221	PRO	3.5
1	C	247	THR	3.5
1	C	257	PHE	3.5
1	B	246	ASP	3.4
1	C	252	ALA	3.4
1	C	253	PRO	3.2
1	C	149	GLU	3.2
1	A	257	PHE	3.2
1	A	137	PHE	3.1
1	D	245	GLY	3.1
1	A	235	ASP	3.1
1	A	2	ALA	3.1
1	B	252	ALA	3.0
1	C	256	GLU	3.0
1	C	219	ILE	3.0
1	B	220	ARG	3.0
1	C	223	ALA	3.0
1	C	245	GLY	2.8
1	B	224	ALA	2.8
1	D	246	ASP	2.8
1	A	220	ARG	2.8
1	A	271	GLU	2.6
1	D	137	PHE	2.5
1	A	252	ALA	2.5
1	B	245	GLY	2.5
1	A	294	ARG	2.5
1	A	149	GLU	2.4
1	D	244	LEU	2.4
1	D	248	CYS	2.4
1	C	255	ILE	2.3
1	D	220	ARG	2.3
1	D	256	GLU	2.3
1	C	136	ASP	2.2
1	A	255	ILE	2.2
1	D	224	ALA	2.2
1	A	253	PRO	2.2
1	D	222	ASP	2.2
1	B	257	PHE	2.2
1	A	222	ASP	2.2
1	D	136	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	17	PRO	2.1
1	D	253	PRO	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(\AA^2)	Q<0.9
2	K	A	295	1/1	0.98	0.11	-0.65	36,36,36,36	0
2	K	C	297	1/1	0.95	0.06	-1.26	33,33,33,33	0
2	K	B	296	1/1	0.93	0.06	-1.28	29,29,29,29	0
2	K	D	298	1/1	0.95	0.04	-2.13	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.