W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 04:06 AM GMT

PDB ID	:	2GE5
Title	:	EcoRV Restriction Endonuclease C-terminal deletion mutant/GATATC/Ca2+
Authors	:	Hiller, D.A.; Perona, J.J.
Deposited on	:	2006-03-17
Resolution	:	2.40 Å(reported)

The following versions of software and data (see references) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 2.40 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	Percentile Ranks	Value
Rfree		0.287
Clashscore		19
Ramachandran outliers		2.1%
Sidechain outliers		5.6%
RSRZ outliers		5.6%

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
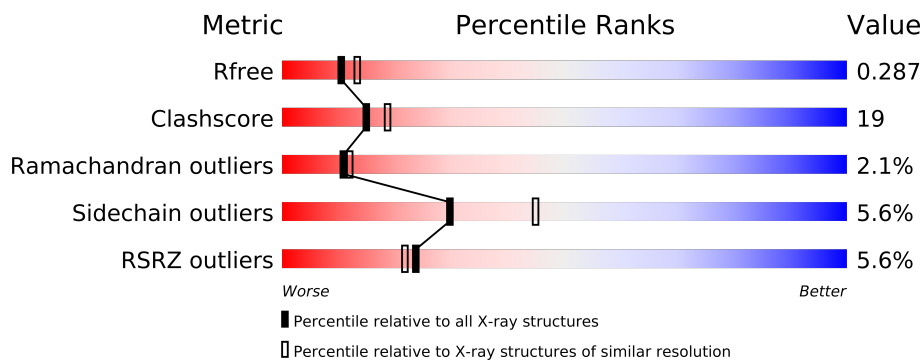
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	C	11	
1	D	11	
2	A	219	
2	B	219	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3967 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called 5'-D(*AP*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	11	Total	C	N	O	P	0	0	0
			223	109	41	63	10			
1	D	11	Total	C	N	O	P	0	0	0
			223	109	41	63	10			

- Molecule 2 is a protein called Type II restriction enzyme EcoRV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	219	Total	C	N	O	S	0	0	0
			1737	1126	281	329	1			
2	B	219	Total	C	N	O	S	0	0	0
			1738	1127	281	329	1			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total	O	0	0
			9	9		
4	B	27	Total	O	0	0
			27	27		
4	C	6	Total	O	0	0
			6	6		
4	D	3	Total	O	0	0
			3	3		

3 Residue-property plots ⓘ

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.

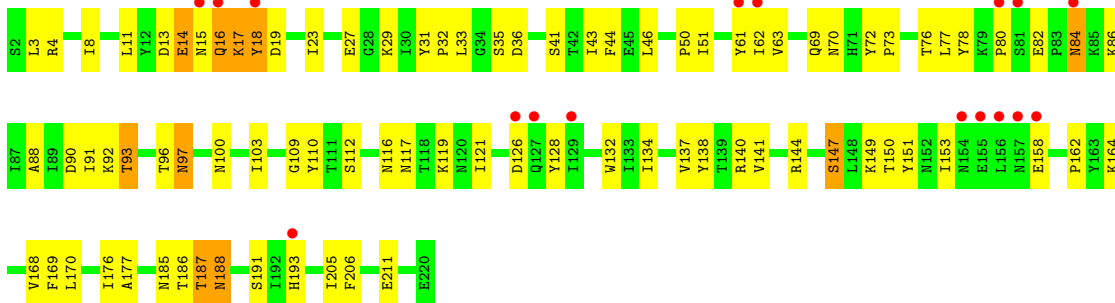• Molecule 1: 5'-D(*AP*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3'

Chain C:
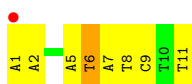
• Molecule 1: 5'-D(*AP*AP*AP*GP*AP*TP*AP*TP*CP*TP*T)-3'
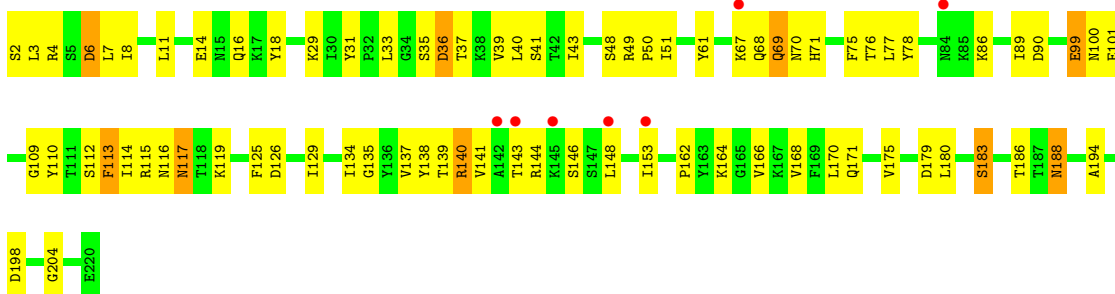
Chain D:

• Molecule 2: Type II restriction enzyme EcoRV

Chain A:

• Molecule 2: Type II restriction enzyme EcoRV

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	67.10Å 67.10Å 259.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 46.68 – 2.40	Depositor EDS
% Data completeness (in resolution range)	64.1 (50.00-2.40) 65.8 (46.68-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.31 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.223 , 0.284 0.235 , 0.287	Depositor DCC
R_{free} test set	1505 reflections (10.38%)	DCC
Wilson B-factor (Å^2)	45.4	Xtriage
Anisotropy	0.476	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 36.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Outliers	0 of 28443 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3967	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	C	0.55	0/250	0.91	0/384
1	D	0.70	0/250	0.97	1/384 (0.3%)
2	A	0.43	0/1783	0.60	1/2426 (0.0%)
2	B	0.42	0/1784	0.60	0/2428
All	All	0.45	0/4067	0.66	2/5622 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	16	GLN	N-CA-C	-5.29	96.72	111.00
1	D	6	DT	N1-C1'-C2'	-5.08	102.95	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	6	DT	Sidechain
1	D	6	DT	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	223	0	127	9	0
1	D	223	0	127	10	0
2	A	1737	0	1652	81	0
2	B	1738	0	1642	66	0
3	A	1	0	0	0	0
4	A	9	0	0	0	0
4	B	27	0	0	2	0
4	C	6	0	0	1	0
4	D	3	0	0	1	0
All	All	3967	0	3548	143	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

All (143) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:17:LYS:HD3	2:A:18:TYR:H	1.22	1.02
2:A:41:SER:HA	2:A:93:THR:HG21	1.55	0.85
2:A:17:LYS:HD3	2:A:18:TYR:N	1.97	0.79
2:B:69:GLN:H	2:B:69:GLN:HE21	1.32	0.78
2:A:132:TRP:HB3	2:A:170:LEU:HD11	1.65	0.77
2:B:183:SER:HB2	2:B:188:ASN:HB2	1.66	0.76
1:C:6:DT:H2"	1:C:7:DA:H5'	1.68	0.74
1:C:5:DA:H2'	1:C:6:DT:H71	1.70	0.73
2:A:14:GLU:OE2	2:A:18:TYR:HB2	1.88	0.73
2:A:69:GLN:NE2	2:B:37:THR:H	1.88	0.72
2:B:2:SER:O	2:B:6:ASP:HB2	1.90	0.71
2:B:35:SER:O	2:B:140:ARG:HD3	1.93	0.69
2:B:40:LEU:HD12	2:B:138:TYR:CZ	2.29	0.67
2:B:117:ASN:HD21	2:B:126:ASP:H	1.42	0.67
2:A:3:LEU:HD22	2:A:61:TYR:CE1	2.30	0.66
2:A:112:SER:HA	2:A:119:LYS:HD2	1.77	0.66
2:A:141:VAL:HB	2:A:162:PRO:O	1.96	0.65
1:D:5:DA:H2'	1:D:6:DT:H72	1.76	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:14:GLU:HG2	2:B:51:ILE:HD11	1.79	0.64
2:B:69:GLN:H	2:B:69:GLN:NE2	1.95	0.63
2:A:17:LYS:CD	2:A:18:TYR:H	2.05	0.63
1:D:5:DA:H2'	1:D:6:DT:C7	2.30	0.62
2:A:35:SER:HB2	2:A:140:ARG:HE	1.65	0.61
2:A:33:LEU:HD22	2:A:43:ILE:HD11	1.83	0.61
2:B:141:VAL:HG23	2:B:143:THR:H	1.66	0.61
2:B:49:ARG:HB2	2:B:50:PRO:HD3	1.83	0.60
1:D:7:DA:H62	2:B:186:THR:HG21	1.66	0.60
1:C:6:DT:H2"	1:C:7:DA:C5'	2.32	0.60
1:C:1:DA:H2"	1:C:2:DA:N7	2.17	0.59
1:D:9:DC:H1'	2:A:70:ASN:ND2	2.18	0.59
2:A:11:LEU:HD23	2:A:51:ILE:HG21	1.85	0.59
2:A:50:PRO:HG3	2:B:31:TYR:HD2	1.70	0.56
2:A:110:TYR:CZ	2:A:187:THR:HB	2.40	0.56
1:D:9:DC:H1'	2:A:70:ASN:HD21	1.69	0.56
1:C:9:DC:H1'	2:B:70:ASN:HD21	1.71	0.56
2:A:36:ASP:HB2	2:B:69:GLN:HG3	1.87	0.55
2:A:27:GLU:HG3	2:B:18:TYR:CD1	2.41	0.55
2:A:27:GLU:HG3	2:B:18:TYR:HD1	1.71	0.55
2:A:14:GLU:CD	2:A:18:TYR:HB2	2.28	0.55
2:A:8:ILE:HD13	2:A:170:LEU:HB3	1.89	0.55
2:B:49:ARG:HG2	2:B:75:PHE:CZ	2.42	0.54
2:B:99:GLU:O	2:B:101:GLU:N	2.41	0.54
2:B:33:LEU:HB2	2:B:162:PRO:HG3	1.90	0.54
2:B:112:SER:HA	2:B:119:LYS:HD3	1.89	0.53
2:A:13:ASP:C	2:A:14:GLU:HG2	2.28	0.53
2:A:27:GLU:HG3	2:B:18:TYR:HA	1.90	0.53
2:B:109:GLY:HA2	2:B:188:ASN:HA	1.90	0.53
1:C:7:DA:H62	2:A:186:THR:HG21	1.73	0.53
2:A:62:ILE:HD11	2:A:80:PRO:HG3	1.91	0.52
2:A:82:GLU:C	2:A:84:ASN:H	2.12	0.52
2:A:76:THR:HG23	2:A:128:TYR:CE2	2.44	0.52
2:B:78:TYR:HB3	2:B:86:LYS:HG2	1.92	0.51
2:B:8:ILE:HG12	2:B:170:LEU:CB	2.41	0.51
2:B:40:LEU:HD12	2:B:138:TYR:CE2	2.45	0.51
2:A:23:ILE:HG13	2:A:23:ILE:O	2.10	0.51
2:B:116:ASN:HB3	2:B:119:LYS:CB	2.41	0.51
1:C:6:DT:H2'	4:C:17:HOH:O	2.10	0.51
2:A:18:TYR:OH	2:A:44:PHE:HD1	1.94	0.50
2:B:114:ILE:HG23	4:B:221:HOH:O	2.09	0.50
2:A:153:ILE:HD13	2:B:153:ILE:CG2	2.42	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:11:LEU:HD11	2:B:134:ILE:HD13	1.92	0.50
2:B:175:VAL:O	2:B:204:GLY:HA3	2.12	0.50
2:B:116:ASN:HB3	2:B:119:LYS:HB2	1.93	0.50
2:A:18:TYR:OH	2:A:44:PHE:CD1	2.64	0.49
2:A:96:THR:HG22	2:A:138:TYR:O	2.13	0.49
2:B:117:ASN:ND2	2:B:125:PHE:HB3	2.28	0.49
2:A:14:GLU:HG3	2:A:17:LYS:HD3	1.95	0.48
2:B:8:ILE:HG12	2:B:170:LEU:HB3	1.94	0.48
2:A:63:VAL:HG22	2:A:77:LEU:HD11	1.96	0.48
2:A:193:HIS:CD2	2:A:193:HIS:N	2.81	0.48
2:A:50:PRO:HG2	2:A:51:ILE:HD12	1.96	0.48
2:A:91:ILE:CD1	2:A:134:ILE:HB	2.44	0.48
2:A:51:ILE:HD12	2:A:51:ILE:N	2.29	0.47
1:D:7:DA:N6	2:B:186:THR:HG21	2.29	0.47
2:B:49:ARG:HG2	2:B:75:PHE:HZ	1.79	0.47
2:B:113:PHE:HA	2:B:116:ASN:O	2.15	0.47
2:B:76:THR:C	2:B:77:LEU:HD12	2.35	0.47
2:B:36:ASP:OD2	2:B:39:VAL:HG23	2.15	0.47
1:C:11:DT:H3	1:D:2:DA:H61	1.63	0.47
1:C:8:DT:OP2	2:A:92:LYS:HD2	2.14	0.47
2:A:91:ILE:HD12	2:A:134:ILE:HB	1.97	0.46
2:A:15:ASN:CB	2:B:29:LYS:HE2	2.45	0.46
2:A:29:LYS:HE3	2:A:150:THR:HG21	1.97	0.46
2:B:129:ILE:HD12	2:B:129:ILE:C	2.36	0.46
2:A:15:ASN:O	2:A:17:LYS:N	2.48	0.46
2:B:170:LEU:HD23	2:B:171:GLN:N	2.31	0.46
2:B:137:VAL:O	2:B:166:VAL:HA	2.15	0.46
2:A:50:PRO:HG3	2:B:31:TYR:CD2	2.48	0.46
2:B:179:ASP:OD1	2:B:180:LEU:HG	2.16	0.46
2:A:141:VAL:CG2	2:A:164:LYS:HG3	2.46	0.46
2:A:46:LEU:HD11	2:B:39:VAL:HG13	1.98	0.45
1:D:8:DT:O3'	2:B:37:THR:HG21	2.17	0.45
2:B:48:SER:HA	2:B:51:ILE:HD12	1.99	0.45
2:A:109:GLY:HA2	2:A:188:ASN:HA	1.99	0.45
1:D:5:DA:N7	2:A:185:ASN:ND2	2.60	0.45
2:A:90:ASP:OD2	2:A:92:LYS:HE2	2.17	0.45
2:B:39:VAL:O	2:B:43:ILE:HD13	2.18	0.44
2:A:132:TRP:HB3	2:A:170:LEU:CD1	2.43	0.44
1:D:9:DC:C1'	2:A:70:ASN:HD21	2.31	0.44
2:B:4:ARG:O	2:B:8:ILE:HG13	2.18	0.44
2:A:205:ILE:HG13	2:A:206:PHE:N	2.32	0.44
2:B:3:LEU:HD22	2:B:61:TYR:CE2	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:40:LEU:HD12	2:B:138:TYR:CE1	2.53	0.44
2:B:139:THR:HB	2:B:164:LYS:HB3	2.00	0.44
2:A:18:TYR:O	2:A:19:ASP:OD2	2.35	0.44
2:A:4:ARG:O	2:A:8:ILE:HG22	2.18	0.43
2:A:73:PRO:HG3	2:A:88:ALA:HB1	2.00	0.43
2:B:69:GLN:N	2:B:69:GLN:HE21	2.09	0.43
2:A:63:VAL:HG22	2:A:77:LEU:CD1	2.48	0.43
2:A:97:ASN:HD22	2:A:97:ASN:HA	1.61	0.43
2:A:206:PHE:HD1	2:A:211:GLU:HG2	1.83	0.43
2:A:168:VAL:HG22	2:A:169:PHE:N	2.33	0.43
2:B:194:ALA:HB1	2:B:198:ASP:OD2	2.19	0.43
2:A:158:GLU:HA	2:A:158:GLU:OE1	2.18	0.43
2:A:149:LYS:HG3	2:A:151:TYR:CE1	2.54	0.43
4:D:23:HOH:O	2:B:41:SER:HB2	2.19	0.43
2:A:103:ILE:HD13	2:A:137:VAL:HG21	2.01	0.42
2:A:35:SER:HB2	2:A:140:ARG:NE	2.32	0.42
2:A:31:TYR:HD2	2:B:50:PRO:HG2	1.83	0.42
2:B:67:LYS:HB2	2:B:68:GLN:OE1	2.20	0.42
2:A:176:ILE:O	2:A:191:SER:HB2	2.19	0.42
2:B:140:ARG:NE	4:B:222:HOH:O	2.53	0.42
2:A:86:LYS:O	2:A:128:TYR:HA	2.19	0.42
2:A:33:LEU:HD22	2:A:43:ILE:CD1	2.48	0.42
2:A:62:ILE:CD1	2:A:80:PRO:HG3	2.49	0.42
2:B:114:ILE:HG13	2:B:115:ARG:HG3	2.02	0.41
2:B:135:GLY:O	2:B:168:VAL:HA	2.20	0.41
2:A:31:TYR:HA	2:A:32:PRO:HD3	1.87	0.41
2:B:75:PHE:HB2	2:B:89:ILE:HB	2.02	0.41
2:A:29:LYS:CE	2:A:150:THR:HG21	2.51	0.41
2:A:88:ALA:HB2	2:A:128:TYR:CE2	2.56	0.41
2:A:103:ILE:CD1	2:A:137:VAL:HG21	2.51	0.41
2:A:14:GLU:HB2	2:A:15:ASN:H	1.53	0.41
2:B:112:SER:O	2:B:114:ILE:N	2.54	0.41
2:A:76:THR:HG23	2:A:128:TYR:HE2	1.86	0.41
2:A:177:ALA:HA	2:A:191:SER:HA	2.03	0.40
2:A:144:ARG:O	2:A:147:SER:HB2	2.21	0.40
2:A:116:ASN:HB3	2:A:119:LYS:CB	2.51	0.40
2:B:110:TYR:O	2:B:114:ILE:HD11	2.21	0.40
2:A:78:TYR:CB	2:A:86:LYS:HG2	2.51	0.40
2:A:153:ILE:HD13	2:B:153:ILE:HG23	2.02	0.40
2:B:148:LEU:HD12	2:B:148:LEU:N	2.36	0.40
2:A:72:TYR:O	2:A:121:ILE:HG13	2.21	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	
2	A	217/219 (99%)	192 (88%)	22 (10%)	3 (1%)	16	22
2	B	217/219 (99%)	195 (90%)	16 (7%)	6 (3%)	8	6
All	All	434/438 (99%)	387 (89%)	38 (9%)	9 (2%)	11	12

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	117	ASN
2	B	100	ASN
2	B	113	PHE
2	B	146	SER
2	B	144	ARG
2	B	99	GLU
2	A	16	GLN
2	A	187	THR
2	B	117	ASN

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	
2	A	181/196 (92%)	171 (94%)	10 (6%)	30	46
2	B	179/196 (91%)	169 (94%)	10 (6%)	30	45
All	All	360/392 (92%)	340 (94%)	20 (6%)	30	45

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	14	GLU
2	A	17	LYS
2	A	18	TYR
2	A	84	ASN
2	A	93	THR
2	A	97	ASN
2	A	100	ASN
2	A	126	ASP
2	A	147	SER
2	A	188	ASN
2	B	6	ASP
2	B	7	LEU
2	B	16	GLN
2	B	36	ASP
2	B	69	GLN
2	B	71	HIS
2	B	90	ASP
2	B	140	ARG
2	B	183	SER
2	B	188	ASN

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

Mol	Chain	Res	Type
2	A	69	GLN
2	A	70	ASN
2	A	97	ASN
2	A	193	HIS
2	B	16	GLN
2	B	69	GLN
2	B	70	ASN
2	B	117	ASN
2	B	157	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 1 ligands modelled in this entry, 1 is 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.

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	C	11/11 (100%)	0.26	1 (9%)	9	8	33, 41, 71, 77	0
1	D	11/11 (100%)	0.76	1 (9%)	9	8	32, 36, 64, 93	0
2	A	219/219 (100%)	0.65	17 (7%)	13	11	32, 54, 69, 74	0
2	B	219/219 (100%)	0.21	7 (3%)	45	43	29, 44, 67, 78	0
All	All	460/460 (100%)	0.44	26 (5%)	24	21	29, 49, 69, 93	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1	DA	11.6
2	A	61	TYR	4.4
2	A	154	ASN	4.1
2	A	80	PRO	3.9
2	A	193	HIS	3.9
2	A	18	TYR	3.8
2	B	142	ALA	3.3
2	A	126	ASP	3.0
2	A	15	ASN	3.0
2	A	155	GLU	3.0
2	A	156	LEU	2.9
2	A	84	ASN	2.7
2	A	81	SER	2.7
2	B	67	LYS	2.6
2	A	158	GLU	2.5
2	A	62	ILE	2.5
2	A	157	ASN	2.3
2	B	143	THR	2.3
2	B	145	LYS	2.2
2	B	84	ASN	2.2
1	C	1	DA	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	153	ILE	2.2
2	A	127	GLN	2.1
2	A	129	ILE	2.1
2	A	16	GLN	2.1
2	B	148	LEU	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å²)	Q<0.9
3	CA	A	283	1/1	0.13	-1.74	86,86,86,86	0

6.5 Other polymers ⓘ

There are no such residues in this entry.