Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 01:52 AM EDT

PDB ID	:	2DHC
Title	:	CRYSTALLOGRAPHIC ANALYSIS OF THE CATALYTIC MECHANISM OF HALOALKANE DEHALOGENASE
Authors	:	Verschueren, K.H.G.; Dijkstra, B.W.
Deposited on	:	1993-09-08
Resolution	:	2.30 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:

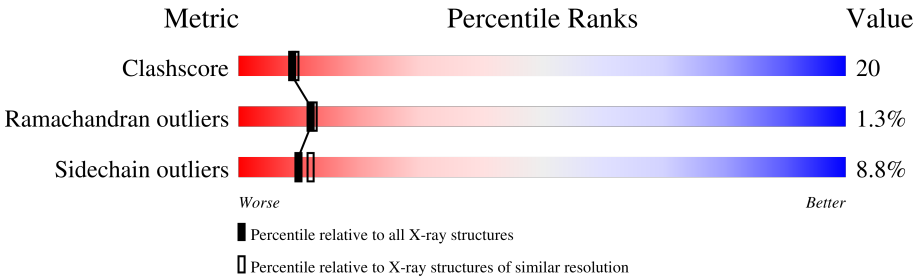
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	310	54% 35% 11%

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	DCE	A	600	-	-	X	-

2 Entry composition

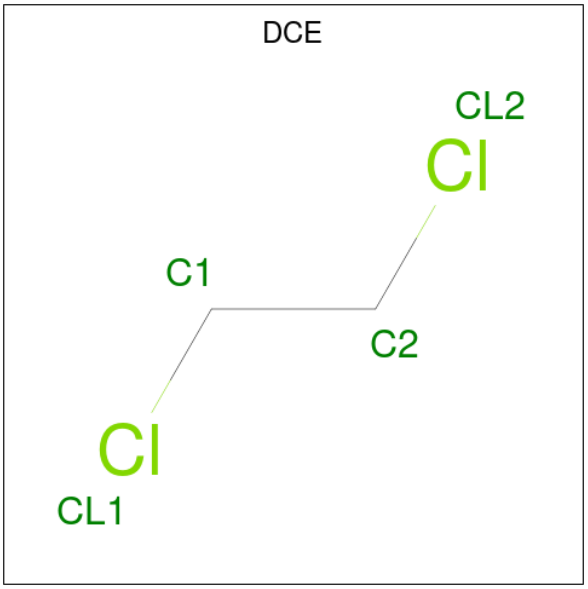
There are 3 unique types of molecules in this entry. The entry contains 2605 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HALOALKANE DEHALOGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2479	1596	406	462	15			

- Molecule 2 is 1,2-DICHLOROETHANE (three-letter code: DCE) (formula: $C_2H_4Cl_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	Cl	0	0
			4	2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	122	Total	O	0	0
			122	122		

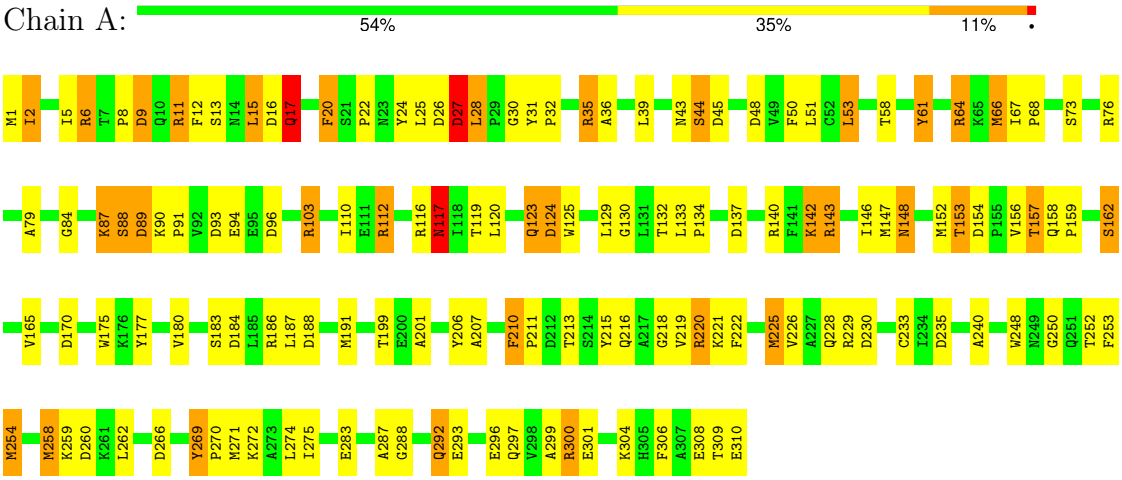
3 Residue-property plots (i)

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: HALOALKANE DEHALOGENASE

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	94.90Å 72.80Å 41.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.195 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2605	wwPDB-VP
Average B, all atoms (Å^2)	9.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.84	0/2552	1.90	73/3470 (2.1%)

There are no bond length outliers.

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	116	ARG	NE-CZ-NH2	-14.04	113.28	120.30
1	A	116	ARG	NE-CZ-NH1	11.56	126.08	120.30
1	A	230	ASP	CB-CG-OD1	11.26	128.43	118.30
1	A	124	ASP	CB-CG-OD1	-11.19	108.23	118.30
1	A	220	ARG	NE-CZ-NH1	10.56	125.58	120.30
1	A	184	ASP	CB-CG-OD2	-9.90	109.39	118.30
1	A	103	ARG	NE-CZ-NH1	-9.46	115.57	120.30
1	A	235	ASP	CB-CG-OD2	-9.34	109.89	118.30
1	A	89	ASP	CB-CG-OD1	9.00	126.40	118.30
1	A	89	ASP	CB-CG-OD2	-8.84	110.34	118.30
1	A	11	ARG	NE-CZ-NH1	8.80	124.70	120.30
1	A	143	ARG	NE-CZ-NH1	8.63	124.62	120.30
1	A	112	ARG	NE-CZ-NH1	8.57	124.59	120.30
1	A	124	ASP	CB-CG-OD2	8.44	125.89	118.30
1	A	35	ARG	NE-CZ-NH1	-8.32	116.14	120.30
1	A	137	ASP	CB-CG-OD2	-8.14	110.97	118.30
1	A	48	ASP	CB-CG-OD1	8.02	125.52	118.30
1	A	230	ASP	CB-CG-OD2	-7.96	111.13	118.30
1	A	274	LEU	CB-CG-CD2	-7.88	97.60	111.00
1	A	9	ASP	CB-CG-OD1	-7.58	111.48	118.30
1	A	6	ARG	NE-CZ-NH2	7.33	123.97	120.30
1	A	229	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	A	300	ARG	NE-CZ-NH2	7.06	123.83	120.30
1	A	266	ASP	CB-CG-OD2	-7.06	111.95	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	35	ARG	NE-CZ-NH2	6.94	123.77	120.30
1	A	201	ALA	CB-CA-C	6.94	120.51	110.10
1	A	53	LEU	CB-CG-CD2	-6.85	99.36	111.00
1	A	235	ASP	CB-CG-OD1	6.79	124.41	118.30
1	A	180	VAL	CG1-CB-CG2	-6.72	100.15	110.90
1	A	93	ASP	CB-CG-OD1	6.67	124.30	118.30
1	A	201	ALA	N-CA-CB	6.63	119.38	110.10
1	A	140	ARG	NE-CZ-NH2	6.54	123.57	120.30
1	A	87	LYS	N-CA-CB	6.44	122.20	110.60
1	A	170	ASP	CB-CG-OD1	6.44	124.09	118.30
1	A	225	MET	CG-SD-CE	6.38	110.40	100.20
1	A	76	ARG	NE-CZ-NH2	6.25	123.42	120.30
1	A	143	ARG	CD-NE-CZ	6.22	132.30	123.60
1	A	258	MET	CG-SD-CE	6.05	109.88	100.20
1	A	48	ASP	CB-CG-OD2	-6.00	112.90	118.30
1	A	177	TYR	CB-CA-C	5.92	122.25	110.40
1	A	191	MET	CG-SD-CE	5.88	109.61	100.20
1	A	254	MET	CB-CA-C	5.83	122.06	110.40
1	A	117	ASN	N-CA-CB	5.82	121.07	110.60
1	A	187	LEU	CB-CG-CD1	-5.79	101.16	111.00
1	A	186	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	269	TYR	CB-CG-CD1	-5.74	117.55	121.00
1	A	9	ASP	CB-CG-OD2	5.74	123.46	118.30
1	A	152	MET	CG-SD-CE	5.69	109.30	100.20
1	A	218	GLY	O-C-N	5.65	131.74	122.70
1	A	228	GLN	C-N-CA	5.62	135.75	121.70
1	A	117	ASN	CB-CA-C	5.57	121.53	110.40
1	A	220	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	260	ASP	CB-CG-OD1	5.56	123.30	118.30
1	A	147	MET	CG-SD-CE	5.54	109.07	100.20
1	A	143	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	A	199	THR	CA-CB-OG1	-5.49	97.47	109.00
1	A	22	PRO	CB-CA-C	-5.42	98.44	112.00
1	A	24	TYR	CB-CG-CD2	5.41	124.25	121.00
1	A	61	TYR	CB-CG-CD2	5.39	124.24	121.00
1	A	96	ASP	CB-CG-OD1	5.34	123.11	118.30
1	A	17	GLN	CB-CA-C	5.33	121.06	110.40
1	A	184	ASP	CB-CG-OD1	5.32	123.09	118.30
1	A	188	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	27	ASP	N-CA-CB	-5.27	101.11	110.60
1	A	26	ASP	CB-CG-OD2	-5.27	113.56	118.30
1	A	16	ASP	CB-CG-OD2	-5.23	113.60	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	96	ASP	CB-CG-OD2	-5.22	113.60	118.30
1	A	20	PHE	O-C-N	5.19	131.01	122.70
1	A	219	VAL	CG1-CB-CG2	-5.17	102.62	110.90
1	A	28	LEU	CB-CA-C	5.12	119.94	110.20
1	A	159	PRO	O-C-N	-5.10	114.53	122.70
1	A	93	ASP	CB-CG-OD2	-5.08	113.72	118.30
1	A	240	ALA	O-C-N	-5.01	114.68	122.70

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	2479	0	2379	99	0
2	A	4	0	0	3	0
3	A	122	0	0	13	0
All	All	2605	0	2379	99	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 20.

All (99) 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:153:THR:HG21	1:A:158:GLN:HB2	1.33	1.10
1:A:292:GLN:HE21	1:A:292:GLN:H	1.04	0.99
1:A:133:LEU:HB2	1:A:134:PRO:HD3	1.59	0.84
1:A:304:LYS:O	1:A:308:GLU:HG3	1.79	0.82
1:A:84:GLY:HA2	1:A:90:LYS:HG2	1.64	0.80
1:A:308:GLU:HB2	3:A:461:HOH:O	1.83	0.79
1:A:258:MET:SD	1:A:283:GLU:HG2	2.22	0.79
1:A:306:PHE:O	1:A:310:GLU:HG3	1.84	0.78
1:A:153:THR:CG2	1:A:158:GLN:HB2	2.14	0.74
1:A:148:ASN:ND2	3:A:522:HOH:O	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:PHE:HB3	1:A:15:LEU:HD21	1.71	0.73
1:A:2:ILE:CG2	1:A:91:PRO:HB3	2.20	0.72
1:A:27:ASP:HB3	3:A:517:HOH:O	1.90	0.71
1:A:58:THR:HG22	1:A:206:TYR:CD1	2.26	0.70
1:A:112:ARG:HG3	1:A:112:ARG:HH11	1.56	0.70
1:A:292:GLN:H	1:A:292:GLN:NE2	1.85	0.69
1:A:288:GLY:O	3:A:522:HOH:O	2.12	0.68
1:A:292:GLN:HE21	1:A:292:GLN:N	1.86	0.67
1:A:58:THR:HG22	1:A:206:TYR:CE1	2.31	0.65
1:A:66:MET:HG2	1:A:299:ALA:HB2	1.79	0.64
1:A:262:LEU:HD12	1:A:262:LEU:N	2.12	0.64
1:A:5:ILE:HD12	1:A:215:TYR:CE2	2.32	0.64
1:A:12:PHE:HB3	1:A:15:LEU:CD2	2.29	0.62
1:A:36:ALA:HA	1:A:88:SER:HB3	1.82	0.62
1:A:103:ARG:HD3	3:A:405:HOH:O	2.01	0.60
1:A:50:PHE:CE2	1:A:119:THR:HG21	2.38	0.59
1:A:25:LEU:HB2	3:A:518:HOH:O	2.02	0.58
1:A:12:PHE:O	1:A:15:LEU:HD22	2.04	0.57
1:A:51:LEU:CD2	1:A:110:ILE:HD11	2.34	0.57
1:A:297:GLN:O	1:A:301:GLU:HG2	2.06	0.55
1:A:124:ASP:OD1	1:A:125:TRP:N	2.39	0.55
1:A:309:THR:O	1:A:309:THR:HG22	2.07	0.54
1:A:67:ILE:HG22	1:A:68:PRO:N	2.21	0.54
1:A:112:ARG:HG3	1:A:112:ARG:NH1	2.19	0.53
1:A:142:LYS:HG2	1:A:143:ARG:HG3	1.91	0.53
1:A:248:TRP:CZ2	1:A:250:GLY:HA3	2.44	0.53
1:A:133:LEU:CB	1:A:134:PRO:HD3	2.36	0.53
1:A:258:MET:CE	1:A:283:GLU:HG2	2.38	0.53
1:A:112:ARG:NH1	1:A:112:ARG:CG	2.71	0.53
1:A:129:LEU:O	1:A:132:THR:OG1	2.25	0.53
1:A:269:TYR:N	1:A:270:PRO:HD2	2.25	0.52
1:A:36:ALA:HB3	3:A:518:HOH:O	2.10	0.52
1:A:84:GLY:CA	1:A:90:LYS:HG2	2.38	0.52
1:A:20:PHE:HB3	1:A:39:LEU:HD22	1.93	0.51
1:A:89:ASP:C	1:A:90:LYS:HG3	2.30	0.51
1:A:133:LEU:HB2	1:A:134:PRO:CD	2.38	0.51
1:A:2:ILE:HG23	1:A:91:PRO:HB3	1.93	0.51
1:A:142:LYS:CG	1:A:143:ARG:HG3	2.41	0.50
1:A:39:LEU:HB2	1:A:79:ALA:HB3	1.95	0.49
1:A:221:LYS:O	1:A:225:MET:HG3	2.13	0.49
1:A:5:ILE:HD12	1:A:215:TYR:CD2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ARG:HH11	1:A:64:ARG:HG2	1.78	0.48
1:A:153:THR:HG22	3:A:425:HOH:O	2.12	0.48
1:A:11:ARG:NH2	1:A:207:ALA:O	2.47	0.48
1:A:183:SER:O	1:A:213:THR:HG21	2.14	0.48
1:A:2:ILE:N	1:A:2:ILE:HD13	2.29	0.47
1:A:206:TYR:OH	1:A:293:GLU:OE2	2.28	0.47
1:A:262:LEU:HD12	1:A:262:LEU:H	1.79	0.47
1:A:175:TRP:NE1	2:A:600:DCE:C1	2.78	0.47
1:A:175:TRP:HE1	2:A:600:DCE:C1	2.28	0.46
1:A:269:TYR:N	1:A:270:PRO:CD	2.79	0.46
1:A:153:THR:HG21	1:A:158:GLN:CB	2.24	0.46
1:A:220:ARG:HD3	3:A:434:HOH:O	2.15	0.46
1:A:120:LEU:HD21	1:A:130:GLY:O	2.15	0.46
1:A:213:THR:HA	1:A:216:GLN:OE1	2.16	0.45
1:A:269:TYR:CB	1:A:270:PRO:HD3	2.46	0.45
1:A:252:THR:HG22	1:A:253:PHE:N	2.31	0.45
1:A:53:LEU:HD23	1:A:53:LEU:HA	1.69	0.45
1:A:296:GLU:O	1:A:300:ARG:HG3	2.16	0.45
1:A:30:GLY:C	1:A:32:PRO:HD3	2.37	0.45
1:A:31:TYR:N	1:A:32:PRO:HD3	2.30	0.45
1:A:123:GLN:HE21	1:A:123:GLN:C	2.21	0.45
1:A:103:ARG:HD3	1:A:103:ARG:HH11	1.50	0.44
1:A:20:PHE:CB	1:A:39:LEU:HD22	2.47	0.44
1:A:271:MET:O	1:A:272:LYS:C	2.56	0.44
1:A:43:ASN:C	1:A:45:ASP:H	2.22	0.43
1:A:64:ARG:HG2	1:A:64:ARG:NH1	2.31	0.43
1:A:226:VAL:HG21	2:A:600:DCE:C2	2.47	0.43
1:A:94:GLU:HB3	1:A:221:LYS:HB2	2.01	0.43
1:A:259:LYS:HB2	1:A:287:ALA:O	2.19	0.42
1:A:154:ASP:OD1	1:A:157:THR:HG23	2.19	0.42
1:A:36:ALA:CB	3:A:518:HOH:O	2.67	0.42
1:A:31:TYR:N	1:A:32:PRO:CD	2.83	0.42
1:A:6:ARG:HD3	1:A:35:ARG:NH2	2.35	0.41
1:A:28:LEU:HD11	3:A:518:HOH:O	2.20	0.41
1:A:117:ASN:O	3:A:421:HOH:O	2.21	0.41
1:A:210:PHE:HA	1:A:211:PRO:HD2	1.54	0.41
1:A:61:TYR:CE1	1:A:64:ARG:HD3	2.55	0.41
1:A:17:GLN:HE21	1:A:17:GLN:HB3	1.75	0.41
1:A:28:LEU:CD1	3:A:518:HOH:O	2.68	0.41
1:A:133:LEU:CB	1:A:134:PRO:CD	2.98	0.41
1:A:154:ASP:OD2	1:A:157:THR:CG2	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:GLN:C	1:A:123:GLN:NE2	2.74	0.41
1:A:30:GLY:C	1:A:32:PRO:CD	2.90	0.40
1:A:262:LEU:N	1:A:262:LEU:CD1	2.84	0.40
1:A:269:TYR:CB	1:A:270:PRO:CD	2.99	0.40
1:A:275:ILE:HG21	1:A:275:ILE:HD13	1.85	0.40
1:A:162:SER:O	1:A:165:VAL:HG23	2.20	0.40
1:A:146:ILE:HG23	1:A:254:MET:HB2	2.04	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	308/310 (99%)	273 (89%)	31 (10%)	4 (1%)	12 12

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	ARG
1	A	148	ASN
1	A	44	SER
1	A	156	VAL

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	262/262 (100%)	239 (91%)	23 (9%)	10 12

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	2	ILE
1	A	8	PRO
1	A	9	ASP
1	A	13	SER
1	A	15	LEU
1	A	17	GLN
1	A	27	ASP
1	A	44	SER
1	A	66	MET
1	A	73	SER
1	A	87	LYS
1	A	88	SER
1	A	117	ASN
1	A	123	GLN
1	A	142	LYS
1	A	153	THR
1	A	157	THR
1	A	162	SER
1	A	210	PHE
1	A	222	PHE
1	A	233	CYS
1	A	292	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	17	GLN
1	A	104	ASN
1	A	123	GLN
1	A	292	GLN
1	A	297	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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	$\#\|Z\| > 2$
2	DCE	A	600	-	3,3,3	0.48	0	2,2,2	0.71	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
2	DCE	A	600	-	-	0/1/1/1	-

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.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	DCE	3	0

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

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.