



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:46 AM GMT

PDB ID : 2BFN
Title : THE CRYSTAL STRUCTURE OF THE COMPLEX OF THE HALOALKANE DEHALOGENASE LINB WITH THE PRODUCT OF DEHALOGENATION REACTION 1,2-DICHLOROPROPANE.
Authors : Banas, P.; Otyepka, M.; Jerabek, P.; Vevodova, J.; Bohac, M.; Damborsky, J.
Deposited on : 2004-12-09
Resolution : 1.60 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

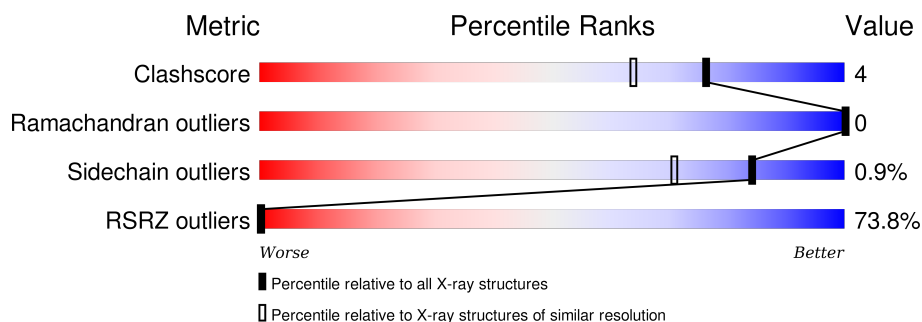
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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	296	

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	D2P	A	1297	-	-	-	X

2 Entry composition [i](#)

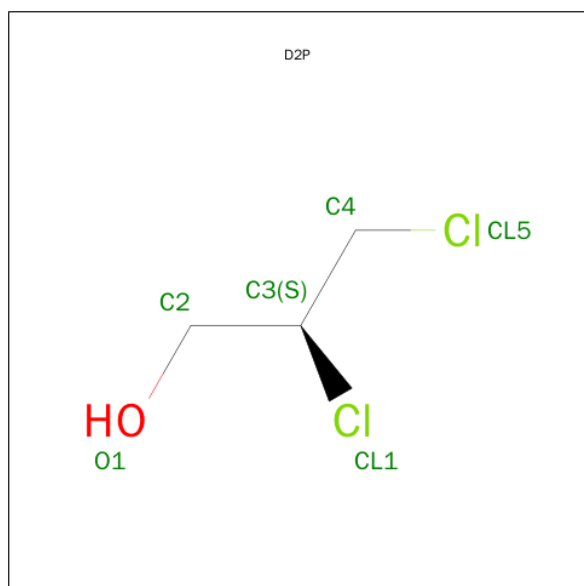
There are 5 unique types of molecules in this entry. The entry contains 2743 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HALOGENALKANE DEHALOGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	8	17	0
			2396	1514	426	446	10			

- Molecule 2 is (2S)-2,3-DICHLOROPROPAN-1-OL (three-letter code: D2P) (formula: $C_3H_6Cl_2O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Cl	O	0	0
			6	3	2	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

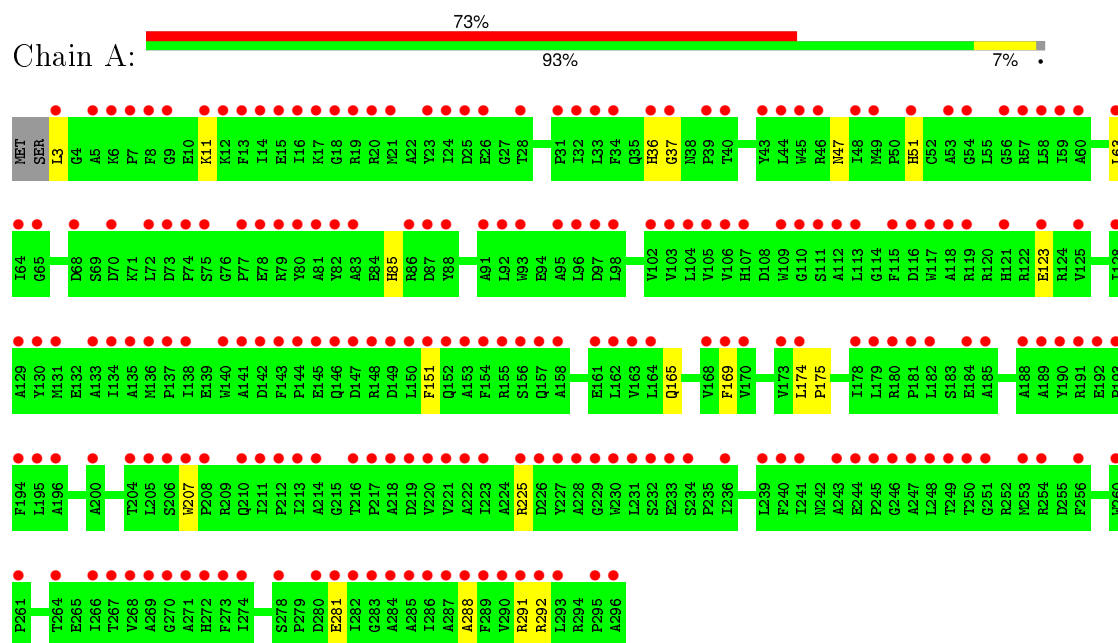
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	337	Total 337	O 337	0	0

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 ($\text{RSRZ} > 2$). 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: HALOGENALKANE DEHALOGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.57Å 72.14Å 73.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.55 – 1.60 29.68 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (72.55-1.60) 99.7 (29.68-1.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.149 , 0.171 0.378 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	8.3	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.8	EDS
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 36003 reflections	Xtriage
F_o, F_c correlation	0.66	EDS
Total number of atoms	2743	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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: D2P, CA, CL

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	0.57	0/2543	0.81	4/3452 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	291[A]	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	A	291[B]	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	A	291[A]	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	291[B]	ARG	NE-CZ-NH2	-5.34	117.63	120.30

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	2396	0	2295	18	0
2	A	6	0	3	1	0
3	A	1	0	0	0	0
4	A	3	0	0	0	0
5	A	337	0	0	9	1
All	All	2743	0	2298	18	1

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 4.

All (18) 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:292[B]:ARG:CD	5:A:2331:HOH:O	2.03	1.02
1:A:292[B]:ARG:NE	5:A:2331:HOH:O	1.96	0.96
1:A:281[B]:GLU:OE1	5:A:2319:HOH:O	1.91	0.89
1:A:292[B]:ARG:NH2	5:A:2330:HOH:O	2.16	0.79
1:A:36:HIS:HE1	1:A:63:LEU:H	1.45	0.63
1:A:165:GLN:NE2	5:A:2202:HOH:O	2.20	0.59
1:A:36:HIS:HD2	1:A:37:GLY:O	1.85	0.58
1:A:36:HIS:CE1	1:A:63:LEU:H	2.23	0.57
1:A:123[B]:GLU:OE2	5:A:2163:HOH:O	2.20	0.49
1:A:3:LEU:HD23	1:A:47:ASN:HB3	1.94	0.48
1:A:151:PHE:HZ	2:A:1297:D2P:H2C1	1.79	0.47
1:A:292[B]:ARG:HD3	5:A:2331:HOH:O	1.94	0.46
1:A:225[A]:ARG:HD3	5:A:2264:HOH:O	2.16	0.46
1:A:288:ALA:O	1:A:292[B]:ARG:HD3	2.17	0.44
1:A:174:LEU:HB3	1:A:175:PRO:HD3	1.99	0.44
1:A:51:HIS:HD2	5:A:2026:HOH:O	2.01	0.43
1:A:85:HIS:CD2	1:A:207:TRP:CZ2	3.08	0.42

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:2086:HOH:O	5:A:2130:HOH:O[3_645]	2.16	0.04

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	
1	A	309/296 (104%)	299 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	251/236 (106%)	249 (99%)	2 (1%)	86	75

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	169	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	51	HIS
1	A	121	HIS

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 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	D2P	A	1297	-	3,5,5	2.79	1 (33%)	0,5,5	0.00	-

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	D2P	A	1297	-	-	0/4/4/4	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1297	D2P	C3-CL1	-4.48	1.70	1.81

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 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1297	D2P	1	0

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	294/296 (99%)	3.07	217 (73%) 0 0	4, 7, 15, 29	5 (1%)

All (217) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	LEU	16.1
1	A	20[A]	ARG	7.4
1	A	266	ILE	7.3
1	A	72[A]	LEU	7.0
1	A	73[A]	ASP	6.8
1	A	244[A]	GLU	6.8
1	A	141	ALA	6.7
1	A	117	TRP	6.5
1	A	221	VAL	6.3
1	A	170	VAL	6.1
1	A	295	PRO	6.0
1	A	286	ILE	6.0
1	A	144	PRO	6.0
1	A	260	TRP	5.9
1	A	105	VAL	5.8
1	A	274	ILE	5.8
1	A	288	ALA	5.5
1	A	229	GLY	5.4
1	A	134	ILE	5.3
1	A	193	PRO	5.3
1	A	282	ILE	5.2
1	A	92	LEU	5.2
1	A	146	GLN	5.2
1	A	185	ALA	5.2
1	A	206	SER	5.1
1	A	93	TRP	5.0
1	A	273	PHE	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	137	PRO	4.9
1	A	214	ALA	4.9
1	A	33	LEU	4.8
1	A	151	PHE	4.8
1	A	32	ILE	4.8
1	A	48	ILE	4.8
1	A	102	VAL	4.8
1	A	195	LEU	4.8
1	A	292[A]	ARG	4.7
1	A	283	GLY	4.6
1	A	17	LYS	4.6
1	A	53	ALA	4.6
1	A	270	GLY	4.6
1	A	82	TYR	4.6
1	A	16	ILE	4.5
1	A	8	PHE	4.5
1	A	130	TYR	4.5
1	A	98	LEU	4.5
1	A	182	LEU	4.5
1	A	194	PHE	4.4
1	A	81	ALA	4.4
1	A	271	ALA	4.4
1	A	241	ILE	4.4
1	A	109	TRP	4.4
1	A	211	ILE	4.4
1	A	115	PHE	4.3
1	A	162	LEU	4.3
1	A	143	PHE	4.3
1	A	289	PHE	4.3
1	A	24	ILE	4.2
1	A	250	THR	4.2
1	A	207	TRP	4.2
1	A	157[A]	GLN	4.2
1	A	45	TRP	4.1
1	A	233[A]	GLU	4.1
1	A	57	ARG	4.1
1	A	31	PRO	4.0
1	A	78[A]	GLU	4.0
1	A	290	VAL	4.0
1	A	196	ALA	4.0
1	A	63	LEU	4.0
1	A	104	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	293	LEU	4.0
1	A	217	PRO	4.0
1	A	95	ALA	4.0
1	A	281[A]	GLU	4.0
1	A	129	ALA	3.9
1	A	113	LEU	3.9
1	A	226[A]	ASP	3.9
1	A	88	TYR	3.9
1	A	208	PRO	3.9
1	A	97[A]	ASP	3.8
1	A	83	ALA	3.8
1	A	154	PHE	3.8
1	A	269	ALA	3.8
1	A	190	TYR	3.8
1	A	5	ALA	3.7
1	A	169	PHE	3.7
1	A	264	THR	3.7
1	A	74	PRO	3.7
1	A	14	ILE	3.7
1	A	245	PRO	3.7
1	A	163	VAL	3.6
1	A	64	ILE	3.6
1	A	112	ALA	3.6
1	A	227	TYR	3.6
1	A	18	GLY	3.6
1	A	213	ILE	3.6
1	A	240	PHE	3.5
1	A	79[A]	ARG	3.5
1	A	230	TRP	3.5
1	A	103	VAL	3.5
1	A	128	ILE	3.5
1	A	247	ALA	3.5
1	A	23	TYR	3.5
1	A	44	LEU	3.5
1	A	80	TYR	3.5
1	A	291[A]	ARG	3.5
1	A	174	LEU	3.4
1	A	228	ALA	3.4
1	A	284	ALA	3.4
1	A	138	ILE	3.4
1	A	7	PRO	3.4
1	A	77	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	216	THR	3.4
1	A	220	VAL	3.4
1	A	256	PHE	3.4
1	A	234	SER	3.4
1	A	168	VAL	3.3
1	A	236	ILE	3.3
1	A	96	LEU	3.3
1	A	248	LEU	3.3
1	A	188	ALA	3.3
1	A	19	ARG	3.3
1	A	232	SER	3.3
1	A	56	GLY	3.3
1	A	225[A]	ARG	3.3
1	A	158	ALA	3.2
1	A	249	THR	3.2
1	A	65	GLY	3.2
1	A	110	GLY	3.2
1	A	267	THR	3.2
1	A	278	SER	3.1
1	A	205	LEU	3.1
1	A	39	PRO	3.1
1	A	12	LYS	3.0
1	A	179	LEU	3.0
1	A	51	HIS	3.0
1	A	118	ALA	2.9
1	A	59	ILE	2.9
1	A	131	MET	2.9
1	A	287	ALA	2.9
1	A	123[A]	GLU	2.9
1	A	223	ILE	2.9
1	A	106	VAL	2.9
1	A	261	PRO	2.8
1	A	28	THR	2.8
1	A	58	LEU	2.8
1	A	140	TRP	2.8
1	A	21	MET	2.8
1	A	150	LEU	2.8
1	A	43	TYR	2.8
1	A	70	ASP	2.8
1	A	13	PHE	2.8
1	A	145	GLU	2.7
1	A	133	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	156	SER	2.7
1	A	91	ALA	2.7
1	A	155	ARG	2.7
1	A	37	GLY	2.7
1	A	25	ASP	2.7
1	A	181	PRO	2.7
1	A	34	PHE	2.7
1	A	173	VAL	2.7
1	A	75	SER	2.6
1	A	121	HIS	2.6
1	A	142	ASP	2.6
1	A	147	ASP	2.6
1	A	60	ALA	2.6
1	A	222	ALA	2.6
1	A	296	ALA	2.6
1	A	239	LEU	2.6
1	A	191	ARG	2.6
1	A	204	THR	2.5
1	A	280	ASP	2.5
1	A	272	HIS	2.5
1	A	219	ASP	2.5
1	A	164	LEU	2.5
1	A	116	ASP	2.5
1	A	253	MET	2.5
1	A	125	VAL	2.4
1	A	148	ARG	2.4
1	A	107	HIS	2.4
1	A	111	SER	2.4
1	A	149[A]	ASP	2.4
1	A	246	GLY	2.4
1	A	251	GLY	2.4
1	A	6	LYS	2.3
1	A	86	ARG	2.3
1	A	178	ILE	2.3
1	A	153	ALA	2.3
1	A	200	ALA	2.3
1	A	36	HIS	2.2
1	A	11	LYS	2.2
1	A	192	GLU	2.2
1	A	254	ARG	2.2
1	A	135	ALA	2.2
1	A	218	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	54	GLY	2.2
1	A	46	ARG	2.2
1	A	49	MET	2.2
1	A	152	GLN	2.2
1	A	9	GLY	2.2
1	A	268	VAL	2.2
1	A	119	ARG	2.1
1	A	87	ASP	2.1
1	A	189	ALA	2.1
1	A	285	ALA	2.1
1	A	212	PRO	2.1
1	A	180	ARG	2.1
1	A	68	ASP	2.1
1	A	26	GLU	2.1
1	A	231	LEU	2.1
1	A	15	GLU	2.1
1	A	40	THR	2.1
1	A	136	MET	2.1
1	A	161[A]	GLU	2.1
1	A	210	GLN	2.1
1	A	243	ALA	2.0
1	A	184	GLU	2.0

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	D2P	A	1297	6/6	0.49	0.51	5.54	61,62,62,63	0
3	CL	A	1298	1/1	0.79	0.23	-0.43	16,16,16,16	1
4	CA	A	1300	1/1	0.94	0.10	-2.42	12,12,12,12	0
4	CA	A	1299	1/1	0.99	0.06	-3.94	5,5,5,5	0
4	CA	A	1301	1/1	0.89	0.18	-	12,12,12,12	1

6.5 Other polymers [i](#)

There are no such residues in this entry.