



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 02:07 PM BST

PDB ID : 4OGY
Title : Crystal structure of Fab DX-2930 in complex with human plasma kallikrein at 2.1 Angstrom resolution
Authors : Edwards, T.E.; Clifton, M.C.; Abendroth, J.; Nixon, A.; Ladner, R.
Deposited on : 2014-01-16
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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

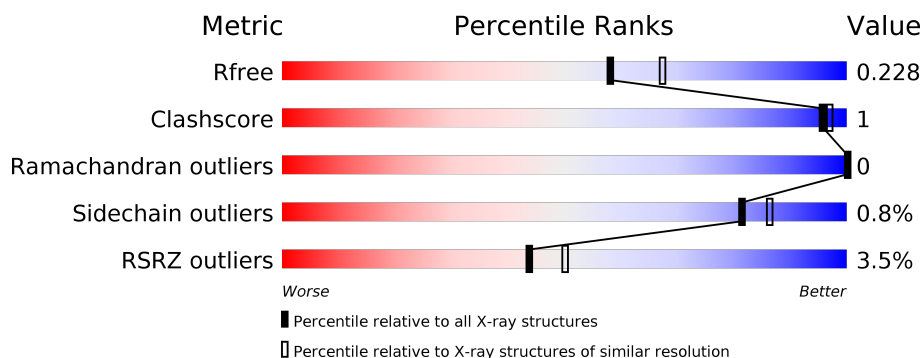
1 Overall quality at a glance

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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (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 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 $\leq 5\%$. 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	241	<div> <div style="width: 95%;"></div> <div>95%</div> </div>
1	B	241	<div> <div style="width: 95%;"></div> <div>95%</div> <div style="width: 5%;"></div> <div>5%</div> </div>
2	H	225	<div> <div style="width: 96%;"></div> <div>96%</div> </div>
2	M	225	<div> <div style="width: 87%;"></div> <div>87%</div> <div style="width: 11%;"></div> <div>11%</div> </div>
3	L	213	<div> <div style="width: 97%;"></div> <div>97%</div> </div>
3	N	213	<div> <div style="width: 95%;"></div> <div>95%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11073 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 Plasma kallikrein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	0	2	0
			1871	1194	318	348	11			
1	B	239	Total	C	N	O	S	0	3	0
			1883	1201	316	356	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	396	GLU	ASN	ENGINEERED MUTATION	UNP P03952
A	453	GLU	ASN	ENGINEERED MUTATION	UNP P03952
A	494	GLU	ASN	ENGINEERED MUTATION	UNP P03952
A	503	SER	CYS	ENGINEERED MUTATION	UNP P03952
B	396	GLU	ASN	ENGINEERED MUTATION	UNP P03952
B	453	GLU	ASN	ENGINEERED MUTATION	UNP P03952
B	494	GLU	ASN	ENGINEERED MUTATION	UNP P03952
B	503	SER	CYS	ENGINEERED MUTATION	UNP P03952

- Molecule 2 is a protein called DX-2930 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	219	Total	C	N	O	S	0	2	0
			1631	1028	279	316	8			
2	M	200	Total	C	N	O	S	0	0	0
			1448	911	248	281	8			

- Molecule 3 is a protein called DX-2930 LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	3	0
			1624	1021	266	332	5			
3	N	212	Total	C	N	O	S	0	0	0
			1584	993	262	324	5			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

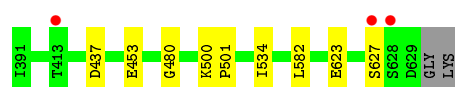
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	228	Total	O	0	0
			228	228		
5	B	201	Total	O	0	0
			201	201		
5	H	160	Total	O	0	0
			160	160		
5	L	185	Total	O	0	0
			185	185		
5	M	86	Total	O	0	0
			86	86		
5	N	160	Total	O	0	0
			160	160		

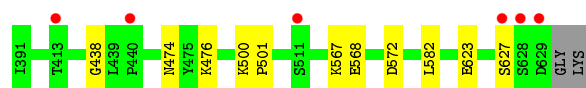
3 Residue-property plots [i](#)

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 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.

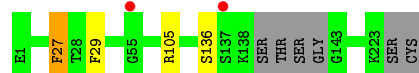
- Molecule 1: Plasma kallikrein



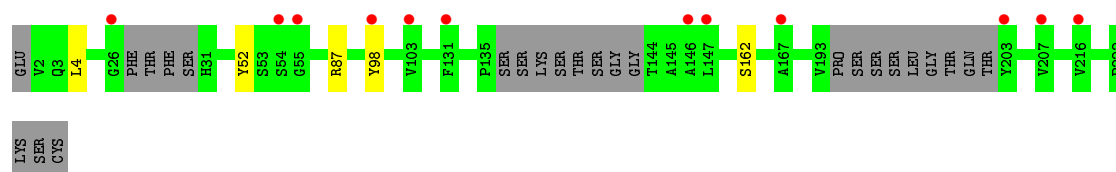
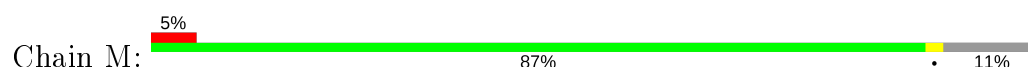
- Molecule 1: Plasma kallikrein



- Molecule 2: DX-2930 HEAVY CHAIN



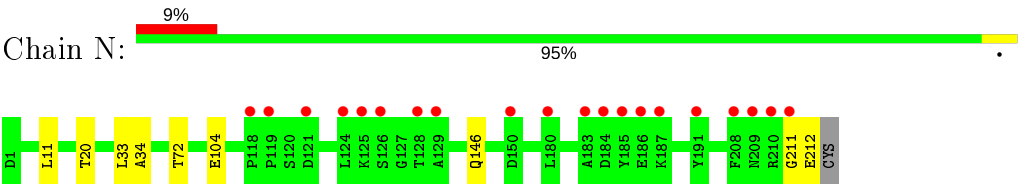
- Molecule 2: DX-2930 HEAVY CHAIN



- Molecule 3: DX-2930 LIGHT CHAIN



● Molecule 3: DX-2930 LIGHT CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.12Å 113.76Å 89.05Å 90.00° 94.70° 90.00°	Depositor
Resolution (Å)	40.59 – 2.10 40.56 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.59-2.10) 99.8 (40.56-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.97 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.183 , 0.221 0.190 , 0.228	Depositor DCC
R_{free} test set	4757 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11073	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.60	0/1924	0.71	0/2615
1	B	0.60	0/1939	0.69	1/2634 (0.0%)
2	H	0.54	0/1676	0.68	1/2286 (0.0%)
2	M	0.49	0/1479	0.66	0/2019
3	L	0.53	0/1670	0.70	1/2277 (0.0%)
3	N	0.55	0/1621	0.69	0/2214
All	All	0.56	0/10309	0.69	3/14045 (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	B	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	141	ARG	NE-CZ-NH1	5.46	123.03	120.30
2	H	105	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	B	572	ASP	CB-CG-OD1	5.10	122.89	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	438	GLY	Peptide

5.2 Too-close contacts ⓘ

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	1871	0	1813	6	0
1	B	1883	0	1823	6	0
2	H	1631	0	1567	2	0
2	M	1448	0	1352	5	0
3	L	1624	0	1546	1	0
3	N	1584	0	1467	3	0
4	A	8	0	12	1	0
4	L	4	0	6	0	0
5	A	228	0	0	1	0
5	B	201	0	0	2	0
5	H	160	0	0	0	0
5	L	185	0	0	0	0
5	M	86	0	0	2	0
5	N	160	0	0	0	0
All	All	11073	0	9586	22	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 1.

All (22) 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:476:LYS:NZ	5:B:897:HOH:O	2.33	0.55
1:B:568:GLU:OE1	5:B:899:HOH:O	2.18	0.54
2:M:52:TYR:O	5:M:371:HOH:O	2.19	0.51
1:A:623:GLU:O	1:A:627:SER:HB3	2.11	0.51
1:B:623:GLU:O	1:B:627:SER:HB3	2.10	0.50
1:A:453:GLU:HG2	1:A:534:ILE:HG12	1.95	0.48
1:A:500:LYS:HB2	1:A:501:PRO:HD2	1.96	0.47
2:M:98:TYR:CD2	2:M:98:TYR:N	2.82	0.46
1:B:582:LEU:HD23	1:B:582:LEU:C	2.36	0.46
3:N:211:GLY:O	3:N:212:GLU:C	2.53	0.46
2:M:87:ARG:NH2	5:M:339:HOH:O	2.49	0.46
3:N:20:THR:HG23	3:N:72:THR:CG2	2.45	0.46
2:M:98:TYR:HD2	2:M:98:TYR:N	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:27:PHE:CD1	2:H:27:PHE:N	2.85	0.44
3:N:33:LEU:HG	3:N:34:ALA:N	2.31	0.44
1:B:500:LYS:HB2	1:B:501:PRO:HD2	1.99	0.43
2:M:4:LEU:HD11	2:M:98:TYR:CD2	2.53	0.43
1:A:480:GLY:HA3	4:A:702:EDO:H11	2.01	0.43
5:A:876:HOH:O	1:B:474:ASN:HB3	2.19	0.42
1:A:582:LEU:HD23	1:A:582:LEU:C	2.39	0.42
3:L:33:LEU:HG	3:L:34:ALA:N	2.35	0.42
1:A:437:ASP:HB2	2:H:29:PHE:O	2.21	0.41

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	239/241 (99%)	234 (98%)	5 (2%)	0	100	100
1	B	240/241 (100%)	235 (98%)	5 (2%)	0	100	100
2	H	217/225 (96%)	212 (98%)	5 (2%)	0	100	100
2	M	192/225 (85%)	186 (97%)	6 (3%)	0	100	100
3	L	213/213 (100%)	204 (96%)	9 (4%)	0	100	100
3	N	210/213 (99%)	201 (96%)	9 (4%)	0	100	100
All	All	1311/1358 (96%)	1272 (97%)	39 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	200/207 (97%)	200 (100%)	0	100	100
1	B	203/207 (98%)	202 (100%)	1 (0%)	88	92
2	H	178/189 (94%)	176 (99%)	2 (1%)	73	79
2	M	150/189 (79%)	149 (99%)	1 (1%)	84	88
3	L	182/188 (97%)	180 (99%)	2 (1%)	73	79
3	N	171/188 (91%)	168 (98%)	3 (2%)	59	65
All	All	1084/1168 (93%)	1075 (99%)	9 (1%)	81	86

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	567	LYS
2	H	27	PHE
2	H	136	SER
3	L	11	LEU
3	L	104	GLU
2	M	162	SER
3	N	11	LEU
3	N	104	GLU
3	N	146	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	473	GLN
3	N	209	ASN

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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
4	EDO	L	301	-	3,3,3	0.34	0	2,2,2	0.87	0
4	EDO	A	701	-	3,3,3	0.60	0	2,2,2	0.23	0
4	EDO	A	702	-	3,3,3	0.48	0	2,2,2	0.13	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
4	EDO	L	301	-	-	1/1/1/1	-
4	EDO	A	701	-	-	0/1/1/1	-
4	EDO	A	702	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	301	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	702	EDO	1	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 ⓘ

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	239/241 (99%)	-0.14	3 (1%) 77 80	12, 17, 32, 64	0
1	B	239/241 (99%)	-0.05	6 (2%) 57 62	13, 18, 44, 70	0
2	H	219/225 (97%)	-0.29	2 (0%) 84 86	15, 25, 43, 54	0
2	M	200/225 (88%)	0.32	12 (6%) 21 27	20, 35, 66, 81	0
3	L	212/213 (99%)	-0.22	3 (1%) 75 78	14, 22, 47, 53	0
3	N	212/213 (99%)	0.22	20 (9%) 8 11	14, 26, 77, 87	0
All	All	1321/1358 (97%)	-0.03	46 (3%) 44 50	12, 23, 59, 87	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	N	124	LEU	5.0
1	B	627	SER	5.0
1	B	628	SER	4.7
2	M	167	ALA	4.2
3	N	183	ALA	3.9
2	M	216	VAL	3.8
3	N	128	THR	3.7
1	B	413	THR	3.6
1	B	629	ASP	3.5
2	M	147	LEU	3.3
3	N	126	SER	3.3
1	A	413	THR	3.2
3	N	191	TYR	3.2
2	M	203	TYR	3.1
1	A	628	SER	3.1
3	N	209	ASN	3.0
2	M	131	PHE	2.9
1	B	440	PRO	2.8
3	N	121	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
2	H	137	SER	2.8
3	N	118	PRO	2.8
3	N	187	LYS	2.8
3	N	211	GLY	2.7
3	N	125	LYS	2.7
3	N	208	PHE	2.6
2	M	146	ALA	2.5
3	N	185	TYR	2.5
2	M	207	VAL	2.5
2	M	54	SER	2.4
3	L	124	LEU	2.3
3	N	119	PRO	2.3
2	M	26	GLY	2.3
3	N	186	GLU	2.3
2	M	55	GLY	2.2
1	A	627	SER	2.2
3	N	129	ALA	2.2
3	N	210	ARG	2.2
2	M	98	TYR	2.1
3	L	211	GLY	2.1
1	B	511	SER	2.1
3	N	180	LEU	2.1
3	L	190	VAL	2.1
3	N	150	ASP	2.1
3	N	184	ASP	2.1
2	H	55	GLY	2.0
2	M	103	VAL	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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
4	EDO	A	701	4/4	0.82	0.20	30,33,33,34	0
4	EDO	L	301	4/4	0.95	0.13	24,25,27,32	0
4	EDO	A	702	4/4	0.97	0.12	19,23,25,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.