



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 06:43 PM EDT

PDB ID : 3X3G / pdb_00003x3g
Title : Fab fragment from anti TRAIL-R2 Human Agonist Antibody KMTR2
Authors : Tamada, T.
Deposited on : 2015-01-20
Resolution : 2.51 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

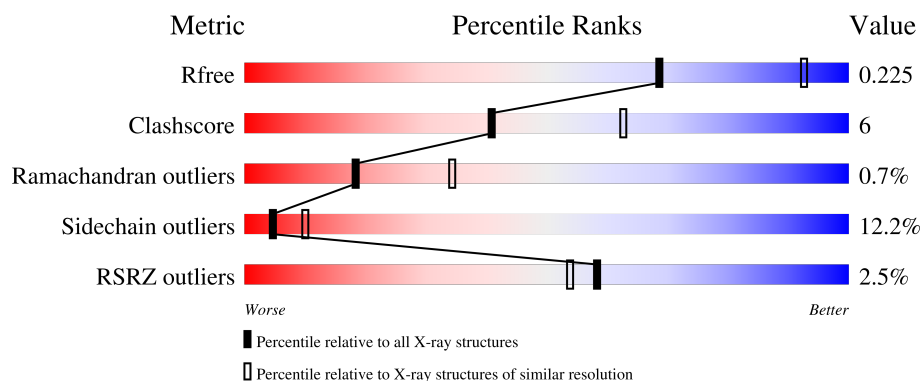
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 $\leq 5\%$. 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	H	229	4% 79% 16% • •
2	L	214	% 79% 18% •

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3424 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 Heavy chain of KMTR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	224	1706	1070	285	340	11	0	0	0

- Molecule 2 is a protein called Light chain of KMTR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	214	1649	1031	279	334	5	0	1	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	H	1	14	8	1	5	0	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total Cl 1 1	0	0
4	L	2	Total Cl 2 2	0	0

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	1	Total O S 5 4 1	0	0
5	H	1	Total O S 5 4 1	0	0

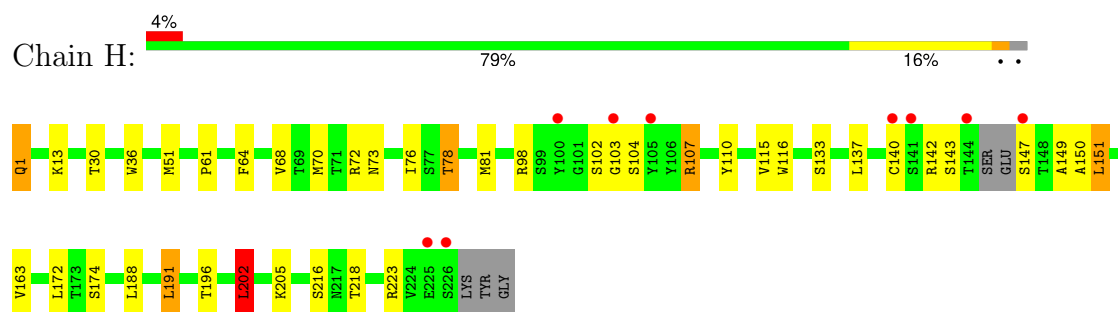
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	29	Total O 29 29	0	0
6	L	13	Total O 13 13	0	0

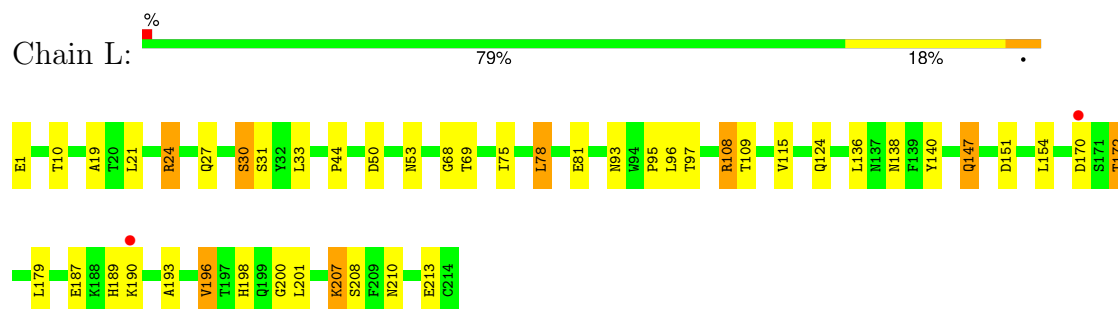
3 Residue-property plots [i](#)

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: Heavy chain of KMTR2



- Molecule 2: Light chain of KMTR2



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	153.00Å 165.38Å 65.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.25 – 2.51 38.25 – 2.51	Depositor EDS
% Data completeness (in resolution range)	95.0 (38.25-2.51) 95.1 (38.25-2.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.32 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.186 , 0.224 0.186 , 0.225	Depositor DCC
R_{free} test set	1382 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	63.8	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3424	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SO4, NAG

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	H	0.82	0/1748	1.03	2/2379 (0.1%)
2	L	0.74	0/1688	0.99	0/2294
All	All	0.78	0/3436	1.01	2/4673 (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	H	202	LEU	N-CA-C	5.24	117.42	111.02
1	H	143	SER	N-CA-C	5.23	117.28	110.43

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	H	1706	0	1647	23	0
2	L	1649	0	1602	22	0
3	H	14	0	13	4	0
4	H	1	0	0	0	0
4	L	2	0	0	0	0
5	H	10	0	0	0	0
6	H	29	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	L	13	0	0	0	0
All	All	3424	0	3262	43	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 (43) 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:H:73:ASN:HD21	3:H:301:NAG:C1	1.71	1.02
1:H:73:ASN:ND2	3:H:301:NAG:C1	2.34	0.90
2:L:170:ASP:OD1	2:L:172:THR:HB	1.93	0.67
2:L:24:ARG:CG	2:L:24:ARG:HH11	2.10	0.65
1:H:76:ILE:HG13	1:H:78:THR:HG23	1.79	0.64
1:H:107:ARG:CG	1:H:107:ARG:HH21	2.10	0.64
2:L:24:ARG:HH11	2:L:24:ARG:HG3	1.64	0.61
2:L:108:ARG:NH1	2:L:109:THR:O	2.34	0.57
1:H:149:ALA:HB3	1:H:202:LEU:HD11	1.89	0.55
1:H:64:PHE:HB3	1:H:68:VAL:HG23	1.88	0.55
1:H:61:PRO:HB3	2:L:95:PRO:HB3	1.89	0.54
1:H:73:ASN:HD21	3:H:301:NAG:C2	2.21	0.53
1:H:73:ASN:ND2	3:H:301:NAG:N2	2.56	0.53
2:L:24:ARG:CG	2:L:24:ARG:NH1	2.72	0.52
1:H:76:ILE:O	1:H:78:THR:HG22	2.10	0.51
1:H:107:ARG:HH21	1:H:107:ARG:HG2	1.76	0.50
1:H:107:ARG:HA	1:H:110:TYR:HB3	1.96	0.47
2:L:151:ASP:OD2	2:L:189:HIS:HB3	2.14	0.46
2:L:138:ASN:HA	2:L:172:THR:CG2	2.45	0.46
1:H:107:ARG:HG2	1:H:107:ARG:NH2	2.30	0.45
1:H:36:TRP:CE2	1:H:81:MET:HB2	2.51	0.45
2:L:136:LEU:HD11	2:L:196:VAL:HG11	1.99	0.45
1:H:1:GLN:HE21	1:H:1:GLN:HB3	1.49	0.44
1:H:116:TRP:CE3	2:L:44:PRO:HD2	2.51	0.44
2:L:198:HIS:CD2	2:L:200:GLY:H	2.35	0.44
1:H:76:ILE:O	1:H:78:THR:CG2	2.66	0.44
2:L:50:ASP:HB3	2:L:53:ASN:HD22	1.82	0.44
2:L:147:GLN:HG2	2:L:154:LEU:HD13	2.00	0.44
2:L:193:ALA:HB2	2:L:208:SER:HB3	2.00	0.44
1:H:64:PHE:HB3	1:H:68:VAL:CG2	2.49	0.42
1:H:51:MET:HE2	1:H:51:MET:HB3	1.62	0.42
2:L:108:ARG:HD2	2:L:140:TYR:CG	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:191:LEU:C	1:H:191:LEU:HD12	2.44	0.42
1:H:36:TRP:CD1	1:H:70:MET:HE2	2.54	0.42
2:L:124:GLN:O	2:L:124:GLN:HG2	2.19	0.42
2:L:19:ALA:HB3	2:L:75:ILE:HB	2.01	0.41
2:L:30:SER:HB3	2:L:31:SER:H	1.66	0.41
1:H:216:SER:OG	1:H:218:THR:HG23	2.20	0.41
2:L:147:GLN:HG2	2:L:154:LEU:CD1	2.50	0.41
2:L:210:ASN:HB2	2:L:213:GLU:HB3	2.03	0.41
2:L:75:ILE:HG21	2:L:78:LEU:HD12	2.03	0.41
1:H:150:ALA:C	1:H:151:LEU:HD23	2.46	0.40
2:L:115:VAL:HG12	2:L:207:LYS:HG3	2.03	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	H	220/229 (96%)	208 (94%)	10 (4%)	2 (1%)	14	27
2	L	213/214 (100%)	206 (97%)	6 (3%)	1 (0%)	24	43
All	All	433/443 (98%)	414 (96%)	16 (4%)	3 (1%)	18	34

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	104	SER
2	L	68	GLY
1	H	103	GLY

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	H	193/197 (98%)	169 (88%)	24 (12%)	4	9
2	L	186/185 (100%)	164 (88%)	22 (12%)	5	11
All	All	379/382 (99%)	333 (88%)	46 (12%)	5	10

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	1	GLN
1	H	13	LYS
1	H	30	THR
1	H	72	ARG
1	H	78	THR
1	H	98	ARG
1	H	102	SER
1	H	107	ARG
1	H	115	VAL
1	H	133	SER
1	H	137	LEU
1	H	140	CYS
1	H	142	ARG
1	H	147	SER
1	H	151	LEU
1	H	163	VAL
1	H	172	LEU
1	H	174	SER
1	H	188	LEU
1	H	191	LEU
1	H	196	THR
1	H	202	LEU
1	H	205	LYS
1	H	223	ARG
2	L	1	GLU
2	L	10	THR
2	L	21	LEU

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Mol	Chain	Res	Type
2	L	24	ARG
2	L	27	GLN
2	L	30	SER
2	L	33	LEU
2	L	69	THR
2	L	78	LEU
2	L	81	GLU
2	L	93	ASN
2	L	96	LEU
2	L	97	THR
2	L	108	ARG
2	L	147	GLN
2	L	172	THR
2	L	179	LEU
2	L	187	GLU
2	L	190	LYS
2	L	196	VAL
2	L	201	LEU
2	L	207	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	1	GLN
1	H	65	GLN
1	H	73	ASN
1	H	177	HIS
1	H	217	ASN
2	L	42	GLN
2	L	53	ASN
2	L	93	ASN
2	L	137	ASN
2	L	147	GLN
2	L	160	GLN
2	L	198	HIS
2	L	199	GLN
2	L	210	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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$
5	SO4	H	304	-	4,4,4	0.74	0	6,6,6	1.13	0
5	SO4	H	303	-	4,4,4	0.46	0	6,6,6	1.10	0
3	NAG	H	301	-	14,14,15	0.90	1 (7%)	17,19,21	2.18	9 (52%)

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
3	NAG	H	301	-	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	301	NAG	C4-C5	2.25	1.57	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	301	NAG	C1-C2-N2	3.61	116.11	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	301	NAG	C8-C7-N2	3.45	121.85	116.12
3	H	301	NAG	C2-N2-C7	3.02	126.95	122.90
3	H	301	NAG	O7-C7-C8	-3.02	116.67	122.05
3	H	301	NAG	O4-C4-C5	3.02	116.75	109.32
3	H	301	NAG	O5-C1-C2	-2.45	107.50	111.29
3	H	301	NAG	O6-C6-C5	2.36	119.38	111.33
3	H	301	NAG	C1-O5-C5	2.22	115.16	112.19
3	H	301	NAG	O5-C5-C6	2.13	111.82	107.66

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	301	NAG	O5-C5-C6-O6
3	H	301	NAG	C4-C5-C6-O6
3	H	301	NAG	C8-C7-N2-C2
3	H	301	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	301	NAG	4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	H	224/229 (97%)	-0.03	9 (4%) 42 38	47, 69, 131, 179	0
2	L	214/214 (100%)	0.01	2 (0%) 81 78	43, 81, 114, 145	1 (0%)
All	All	438/443 (98%)	-0.01	11 (2%) 58 54	43, 75, 123, 179	1 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	144	THR	4.4
1	H	147	SER	4.1
1	H	103	GLY	3.3
1	H	105	TYR	3.1
1	H	226	SER	3.0
1	H	140	CYS	2.6
1	H	225	GLU	2.4
2	L	170	ASP	2.3
2	L	190	LYS	2.2
1	H	141	SER	2.2
1	H	100	TYR	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 oligosaccharides 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
3	NAG	H	301	14/15	0.83	0.15	75,98,112,114	0
5	SO4	H	304	5/5	0.92	0.13	64,65,80,81	5
4	CL	L	302	1/1	0.94	0.21	82,82,82,82	0
4	CL	H	302	1/1	0.94	0.15	79,79,79,79	0
4	CL	L	301	1/1	0.95	0.11	97,97,97,97	0
5	SO4	H	303	5/5	0.96	0.08	57,64,78,90	0

6.5 Other polymers [i](#)

There are no such residues in this entry.