



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 03:16 am BST

PDB ID : 6CR1  
Title : adalimumab EFab  
Authors : Arndt, J.W.  
Deposited on : 2018-03-16  
Resolution : 1.52 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](mailto: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.

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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 : 2.11  
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) : 2.11

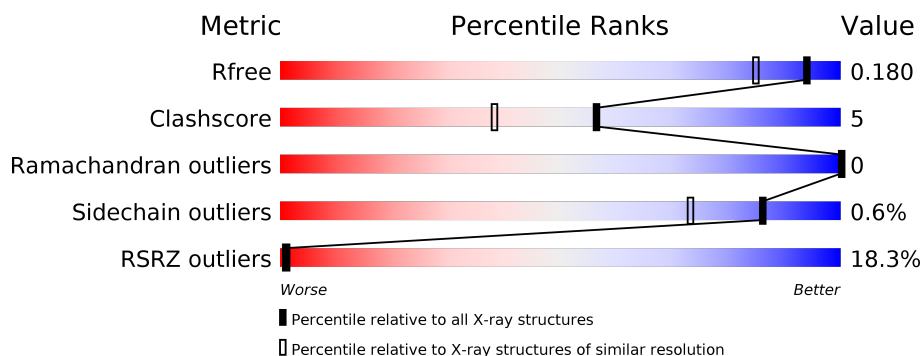
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.52 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	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	L	211	<div> <div>18%</div> <div> <div></div> <div>88%</div> <div>12%</div> </div> </div>
2	H	231	<div> <div>18%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div></div> </div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3883 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.

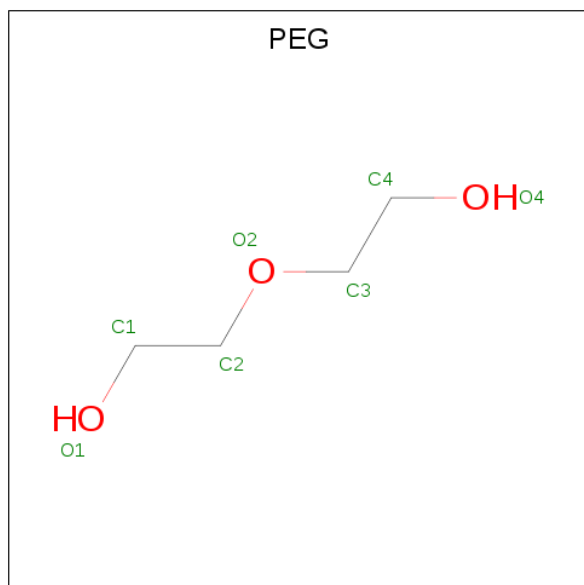
- Molecule 1 is a protein called Light chain of adalimumab EFab (VL-IgE CH2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	7	0
			1646	1024	279	335	8			

- Molecule 2 is a protein called Heavy chain of adalimumab EFab (VH-IgE CH2).

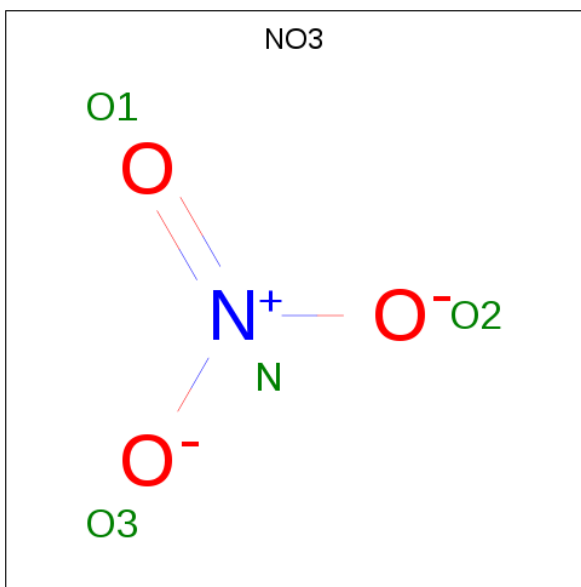
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	225	Total	C	N	O	S	0	3	0
			1731	1082	293	347	9			

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	L	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	N	O	0	0
			4	1	3		
4	H	1	Total	N	O	0	0
			4	1	3		

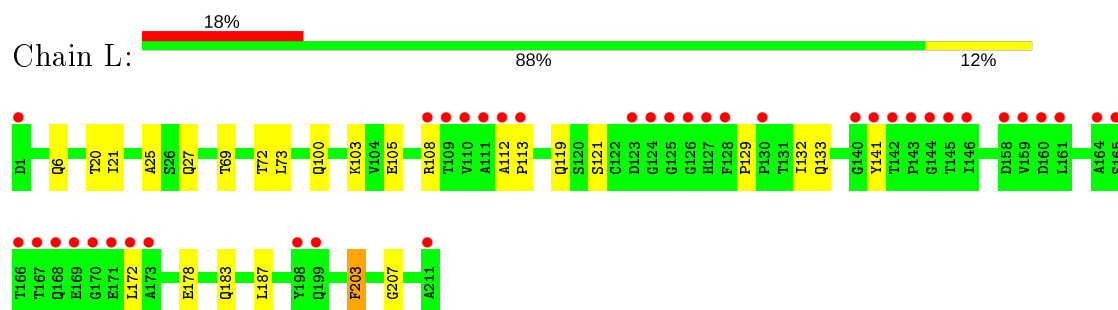
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	223	Total	O	0	0
			223	223		
5	H	268	Total	O	0	0
			268	268		

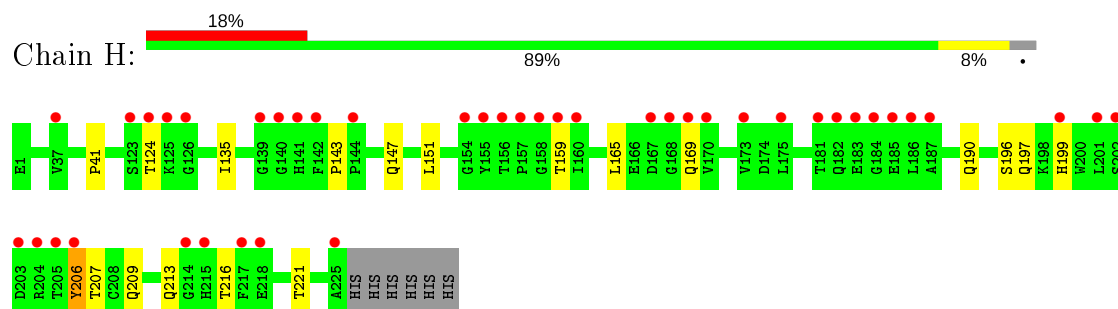
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Light chain of adalimumab EFab (VL-IgE CH2)



- Molecule 2: Heavy chain of adalimumab EFab (VH-IgE CH2)



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	125.41Å 195.85Å 48.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.90 – 1.52 24.90 – 1.52	Depositor EDS
% Data completeness (in resolution range)	99.5 (24.90-1.52) 99.6 (24.90-1.52)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 1.52Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.153 , 0.179 0.157 , 0.180	Depositor DCC
$R_{free}$ test set	4698 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.5	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3883	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PEG, NO3

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	L	0.89	0/1679	0.81	0/2286
2	H	0.86	0/1769	0.81	0/2412
All	All	0.87	0/3448	0.81	0/4698

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	L	1646	0	1592	19	0
2	H	1731	0	1633	16	0
3	L	7	0	10	1	0
4	H	8	0	0	0	0
5	H	268	0	0	3	0
5	L	223	0	0	3	0
All	All	3883	0	3235	33	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 5.

All (33) 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:L:6:GLN:H	1:L:100:GLN:HE21	1.25	0.84
1:L:207:GLY:HA3	2:H:135:ILE:HD12	1.75	0.68
1:L:27:GLN:HG3	5:L:412:HOH:O	1.95	0.66
1:L:108:ARG:HD2	1:L:172:LEU:HD21	1.81	0.61
2:H:169:GLN:NE2	5:H:403:HOH:O	2.33	0.60
2:H:209:GLN:HE21	2:H:216:THR:HG21	1.67	0.60
1:L:133:GLN:HG2	1:L:178:GLU:OE2	2.03	0.59
2:H:196:SER:OG	2:H:199:HIS:HB2	2.06	0.55
1:L:112:ALA:HB1	1:L:203:PHE:CE2	2.41	0.55
2:H:213:GLN:N	5:H:401:HOH:O	2.22	0.54
2:H:165:LEU:HB2	2:H:207:THR:HB	1.90	0.54
2:H:151:LEU:HD23	2:H:190:GLN:HG2	1.92	0.52
1:L:203:PHE:CD1	1:L:203:PHE:N	2.76	0.52
2:H:124:THR:OG1	2:H:213:GLN:HG3	2.10	0.52
1:L:113:PRO:HB3	1:L:141:TYR:HB3	1.92	0.51
1:L:103:LYS:HD2	5:L:553:HOH:O	2.08	0.51
2:H:143:PRO:O	2:H:197:GLN:NE2	2.42	0.50
2:H:151:LEU:CD2	2:H:190:GLN:HG2	2.41	0.50
1:L:103:LYS:HE2	1:L:105:GLU:OE2	2.14	0.47
2:H:206:TYR:CD1	2:H:206:TYR:N	2.83	0.47
1:L:20:THR:HG23	1:L:72[B]:THR:CG2	2.44	0.47
1:L:129:PRO:HG2	1:L:132:ILE:HD13	1.97	0.46
2:H:147:GLN:HG3	5:H:592:HOH:O	2.16	0.45
1:L:119:GLN:HB3	2:H:135:ILE:HG22	1.97	0.45
1:L:21:ILE:HG21	1:L:21:ILE:HD13	1.73	0.44
1:L:121:SER:HB3	2:H:221:THR:OG1	2.17	0.43
1:L:25:ALA:O	1:L:69[B]:THR:HG23	2.19	0.43
1:L:73:LEU:HD23	1:L:73:LEU:C	2.39	0.43
1:L:183:GLN:O	1:L:187:LEU:HD23	2.18	0.43
3:L:301:PEG:H42	5:L:481:HOH:O	2.18	0.43
1:L:203:PHE:HD1	1:L:203:PHE:N	2.17	0.43
2:H:206:TYR:N	2:H:206:TYR:HD1	2.16	0.42
2:H:41:PRO:HG3	2:H:159:THR:HG23	2.02	0.42

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	
1	L	216/211 (102%)	210 (97%)	6 (3%)	0	100	100
2	H	226/231 (98%)	223 (99%)	3 (1%)	0	100	100
All	All	442/442 (100%)	433 (98%)	9 (2%)	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	L	185/180 (103%)	184 (100%)	1 (0%)	88	78
2	H	187/196 (95%)	186 (100%)	1 (0%)	88	78
All	All	372/376 (99%)	370 (100%)	2 (0%)	86	78

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

Mol	Chain	Res	Type
1	L	203	PHE
2	H	206	TYR

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

Mol	Chain	Res	Type
1	L	100	GLN

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Mol	Chain	Res	Type
2	H	209	GLN

### 5.3.3 RNA [i](#)

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 carbohydrates 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	NO3	H	302	-	1,3,3	0.13	0	0,3,3	0.00	-
3	PEG	L	301	-	6,6,6	0.62	0	5,5,5	0.89	0
4	NO3	H	301	-	1,3,3	1.03	0	0,3,3	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
3	PEG	L	301	-	-	1/4/4/4	-

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
3	L	301	PEG	O2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	301	PEG	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	L	211/211 (100%)	0.85	38 (18%) 1 1	11, 28, 74, 83	0
2	H	225/231 (97%)	0.89	42 (18%) 1 1	11, 24, 71, 81	0
All	All	436/442 (98%)	0.87	80 (18%) 1 1	11, 28, 74, 83	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	186	LEU	9.7
1	L	170	GLY	9.1
1	L	167	THR	8.2
1	L	168	GLN	7.7
1	L	171	GLU	7.6
1	L	110	VAL	7.5
2	H	203	ASP	7.4
1	L	172	LEU	7.3
1	L	144	GLY	6.7
2	H	184	GLY	6.6
1	L	112	ALA	6.5
2	H	215	HIS	6.4
2	H	183	GLU	6.1
2	H	201	LEU	6.1
2	H	157	PRO	6.1
1	L	145	THR	6.1
1	L	127	HIS	6.1
2	H	123	SER	5.9
1	L	108	ARG	5.6
1	L	109	THR	5.6
2	H	154	GLY	5.5
2	H	159	THR	5.3
1	L	173	ALA	5.3
1	L	125	GLY	5.3

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Mol	Chain	Res	Type	RSRZ
2	H	187	ALA	5.1
1	L	141	TYR	4.8
2	H	141	HIS	4.6
2	H	185	GLU	4.4
1	L	111	ALA	4.4
1	L	143	PRO	4.3
1	L	1	ASP	4.3
2	H	182	GLN	4.2
1	L	159	VAL	4.1
2	H	160	ILE	4.1
2	H	167	ASP	4.0
1	L	140	GLY	4.0
2	H	156	THR	4.0
2	H	217	PHE	4.0
1	L	160	ASP	4.0
1	L	166	THR	3.9
2	H	181	THR	3.7
1	L	211	ALA	3.7
2	H	126	GLY	3.7
1	L	169	GLU	3.6
2	H	202	SER	3.6
2	H	168	GLY	3.5
1	L	198	TYR	3.5
2	H	169	GLN	3.4
2	H	155	TYR	3.3
2	H	124	THR	3.3
2	H	199	HIS	3.3
2	H	204	ARG	3.3
2	H	225	ALA	3.1
1	L	128	PHE	3.0
1	L	164	ALA	3.0
1	L	130	PRO	3.0
2	H	170	VAL	2.9
1	L	165	SER	2.9
1	L	146	ILE	2.9
2	H	125	LYS	2.8
2	H	175	LEU	2.8
1	L	158	ASP	2.8
2	H	173	VAL	2.7
1	L	124	GLY	2.7
2	H	214	GLY	2.7
1	L	142	THR	2.7

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Mol	Chain	Res	Type	RSRZ
2	H	140	GLY	2.7
2	H	139	GLY	2.6
2	H	142	PHE	2.6
2	H	218	GLU	2.5
1	L	161	LEU	2.5
1	L	113	PRO	2.5
2	H	205	THR	2.5
2	H	158	GLY	2.3
1	L	126	GLY	2.3
2	H	206	TYR	2.2
1	L	199	GLN	2.2
1	L	123	ASP	2.1
2	H	144	PRO	2.0
2	H	37	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 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	PEG	L	301	7/7	0.93	0.08	24,26,32,33	0
4	NO3	H	302	4/4	0.97	0.11	27,42,43,59	0
4	NO3	H	301	4/4	0.99	0.05	15,15,17,19	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.