



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:20 PM UTC

PDB ID : 5O78 / pdb\_00005o78  
Title : Crystal structure of Omp35 from Enterobacter aerogenes  
Authors : Ferrara, L.; Naismith, J.  
Deposited on : 2017-06-08  
Resolution : 2.85 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
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

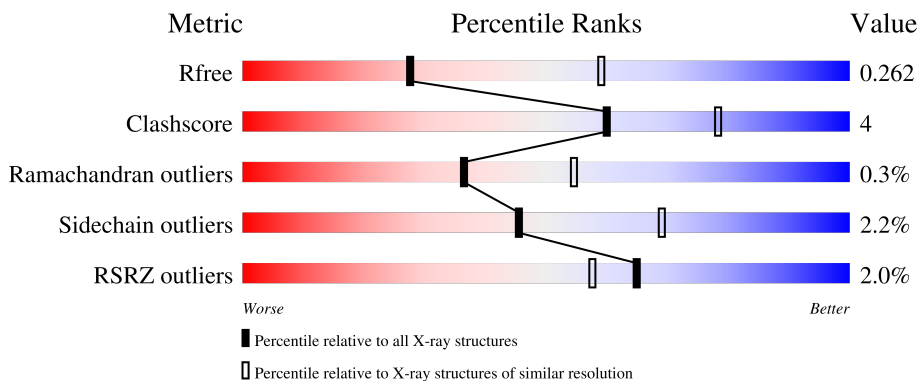
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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  $\geq 3$ , 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	A	337	
1	B	337	
1	C	337	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7765 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 Phosphopirin PhoE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	331	2588	1617	439	525	7	0	0	0
1	B	331	2588	1617	439	525	7	0	0	0
1	C	331	2588	1617	439	525	7	0	0	0

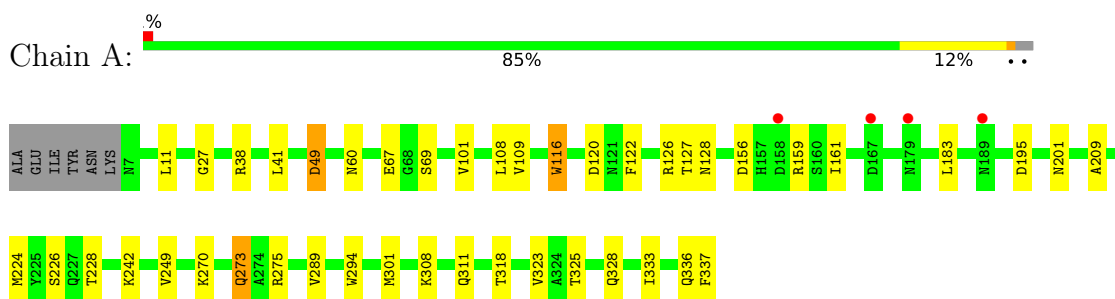
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	O	0	0
			1	1		

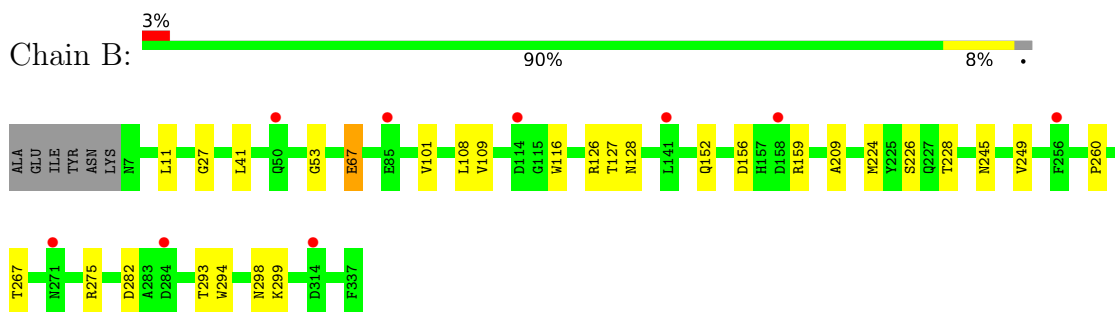
### 3 Residue-property plots [i](#)

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.

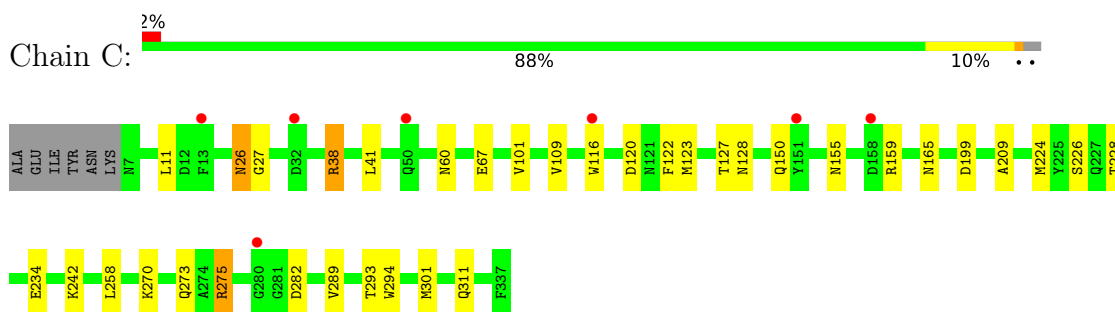
#### • Molecule 1: Phosphoprotein PhoE



#### • Molecule 1: Phosphoprotein PhoE



#### • Molecule 1: Phosphoprotein PhoE



## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.57Å 115.94Å 216.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	108.33 – 2.85 108.33 – 2.85	Depositor EDS
% Data completeness (in resolution range)	82.2 (108.33-2.85) 82.2 (108.33-2.85)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 2.86Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.214 , 0.260 0.217 , 0.262	Depositor DCC
$R_{free}$ test set	1375 reflections (4.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	49.2	Xtrriage
Anisotropy	0.596	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 27.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.022 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7765	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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 i

### 5.1 Standard geometry i

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	0.68	0/2647	0.88	7/3583 (0.2%)
1	B	0.69	0/2647	0.83	2/3583 (0.1%)
1	C	0.69	0/2647	0.84	2/3583 (0.1%)
All	All	0.68	0/7941	0.85	11/10749 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	336	GLN	N-CA-C	-8.15	97.00	109.14
1	A	337	PHE	N-CA-CB	7.62	123.45	110.50
1	A	116	TRP	CA-CB-CG	6.55	126.05	113.60
1	B	67	GLU	N-CA-C	6.42	119.09	111.71
1	A	337	PHE	N-CA-C	-6.26	93.46	111.00
1	C	199	ASP	CB-CA-C	-6.00	98.49	110.42
1	A	156	ASP	N-CA-CB	-5.70	102.74	110.95
1	A	67	GLU	N-CA-C	5.67	119.01	111.75
1	C	38	ARG	CG-CD-NE	5.44	123.97	112.00
1	B	156	ASP	N-CA-CB	-5.37	103.22	110.95
1	A	49	ASP	N-CA-C	-5.21	105.66	112.23

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	2588	0	2362	26	0
1	B	2588	0	2362	17	0
1	C	2588	0	2362	25	0
2	B	1	0	0	0	0
All	All	7765	0	7086	64	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 4.

All (64) 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:C:234:GLU:OE1	1:C:275:ARG:NH2	1.98	0.94
1:B:128:ASN:HD22	1:B:159:ARG:HH22	1.28	0.81
1:C:122:PHE:O	1:C:127:THR:HG21	1.81	0.81
1:A:122:PHE:O	1:A:127:THR:HG21	1.82	0.77
1:A:128:ASN:HD22	1:A:159:ARG:HH22	1.31	0.77
1:C:128:ASN:HD22	1:C:159:ARG:HH12	1.31	0.75
1:A:318:THR:HG21	1:A:325:THR:CG2	2.17	0.75
1:C:128:ASN:HD22	1:C:159:ARG:NH1	1.88	0.72
1:A:318:THR:HG21	1:A:325:THR:HG23	1.71	0.70
1:C:38:ARG:NH1	1:C:60:ASN:ND2	2.40	0.70
1:C:38:ARG:HH11	1:C:60:ASN:HD22	1.41	0.69
1:C:38:ARG:NH1	1:C:60:ASN:HD22	1.91	0.69
1:A:128:ASN:HD22	1:A:159:ARG:NH2	1.90	0.69
1:B:128:ASN:HD22	1:B:159:ARG:NH2	1.90	0.69
1:C:123:MET:HE2	1:C:150:GLN:OE1	1.95	0.66
1:A:289:VAL:HG23	1:A:311:GLN:HE22	1.62	0.65
1:C:26:ASN:HD22	1:C:26:ASN:N	1.97	0.61
1:A:38:ARG:NE	1:A:60:ASN:HD22	1.99	0.61
1:B:108:LEU:HD21	1:B:249:VAL:HG22	1.83	0.59
1:A:108:LEU:HD21	1:A:249:VAL:HG22	1.84	0.59
1:A:38:ARG:HE	1:A:60:ASN:ND2	2.00	0.58
1:C:289:VAL:HG23	1:C:311:GLN:NE2	2.19	0.57
1:B:11:LEU:HD22	1:B:41:LEU:HD11	1.87	0.56
1:C:258:LEU:HD11	1:C:293:THR:HG21	1.89	0.54
1:A:38:ARG:HE	1:A:60:ASN:HD22	1.56	0.54
1:A:11:LEU:HD22	1:A:41:LEU:HD11	1.88	0.54
1:A:120:ASP:HA	1:A:127:THR:HG22	1.91	0.52
1:C:11:LEU:HD22	1:C:41:LEU:HD11	1.91	0.52
1:A:109:VAL:HA	1:A:294:TRP:CZ2	2.44	0.52
1:C:120:ASP:HA	1:C:127:THR:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:VAL:HA	1:B:294:TRP:CZ2	2.45	0.51
1:C:275:ARG:HG2	1:C:275:ARG:O	2.08	0.51
1:A:161:ILE:HD12	1:A:195:ASP:HB3	1.91	0.51
1:C:109:VAL:HA	1:C:294:TRP:CZ2	2.45	0.51
1:A:318:THR:HG23	1:A:323:VAL:HB	1.93	0.50
1:C:116:TRP:CZ3	1:C:224:MET:HE3	2.46	0.49
1:B:116:TRP:CZ3	1:B:224:MET:HE3	2.47	0.49
1:A:126:ARG:NH1	1:B:67:GLU:OE1	2.46	0.49
1:C:101:VAL:HG11	1:C:209:ALA:HB1	1.95	0.48
1:A:101:VAL:HG11	1:A:209:ALA:HB1	1.95	0.48
1:B:224:MET:HE1	1:B:226:SER:HB3	1.95	0.48
1:B:101:VAL:HG11	1:B:209:ALA:HB1	1.96	0.48
1:A:224:MET:HE1	1:A:226:SER:HB3	1.94	0.47
1:A:38:ARG:NE	1:A:60:ASN:ND2	2.61	0.47
1:B:53:GLY:CA	1:C:301:MET:HE3	2.45	0.47
1:C:224:MET:HE1	1:C:226:SER:HB3	1.96	0.47
1:A:289:VAL:CG2	1:A:311:GLN:HE22	2.29	0.46
1:A:224:MET:HE1	1:A:226:SER:CB	2.46	0.45
1:C:155:ASN:HD22	1:C:165:ASN:HD21	1.63	0.45
1:C:224:MET:HE1	1:C:226:SER:CB	2.48	0.44
1:B:126:ARG:NH1	1:C:67:GLU:OE2	2.51	0.44
1:B:224:MET:HE1	1:B:226:SER:CB	2.47	0.44
1:C:116:TRP:CZ3	1:C:224:MET:CE	3.01	0.43
1:B:116:TRP:CZ3	1:B:224:MET:CE	3.02	0.43
1:B:53:GLY:HA3	1:C:301:MET:HE3	2.01	0.42
1:A:161:ILE:HD12	1:A:195:ASP:CB	2.48	0.42
1:B:127:THR:OG1	1:B:152:GLN:NE2	2.53	0.42
1:A:308:LYS:HE2	1:A:328:GLN:HE21	1.84	0.42
1:C:242:LYS:HB3	1:C:270:LYS:HB2	2.01	0.41
1:A:201:ASN:HD21	1:A:273:GLN:HE22	1.69	0.41
1:A:301:MET:CE	1:A:333:ILE:HD11	2.50	0.41
1:B:260:PRO:HA	1:B:293:THR:HG22	2.03	0.40
1:A:242:LYS:HB3	1:A:270:LYS:HB2	2.04	0.40
1:B:245:ASN:ND2	1:B:267:THR:HG23	2.36	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	329/337 (98%)	314 (95%)	14 (4%)	1 (0%)	36	54
1	B	329/337 (98%)	313 (95%)	15 (5%)	1 (0%)	36	54
1	C	329/337 (98%)	313 (95%)	15 (5%)	1 (0%)	36	54
All	All	987/1011 (98%)	940 (95%)	44 (4%)	3 (0%)	36	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	GLY
1	B	27	GLY
1	C	27	GLY

### 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	257/262 (98%)	250 (97%)	7 (3%)	39	63
1	B	257/262 (98%)	252 (98%)	5 (2%)	50	72
1	C	257/262 (98%)	252 (98%)	5 (2%)	50	72
All	All	771/786 (98%)	754 (98%)	17 (2%)	45	69

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASP
1	A	69	SER
1	A	116	TRP
1	A	183	LEU
1	A	228	THR
1	A	273	GLN
1	A	275	ARG
1	B	228	THR
1	B	275	ARG
1	B	282	ASP
1	B	298	ASN
1	B	299	LYS
1	C	26	ASN
1	C	228	THR
1	C	273	GLN
1	C	275	ARG
1	C	282	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	HIS
1	A	60	ASN
1	A	117	ASN
1	A	128	ASN
1	A	189	ASN
1	A	201	ASN
1	A	217	ASN
1	A	227	GLN
1	A	311	GLN
1	A	328	GLN
1	B	121	ASN
1	B	128	ASN
1	B	152	GLN
1	B	217	ASN
1	B	253	GLN
1	B	273	GLN
1	B	298	ASN
1	B	328	GLN
1	C	21	HIS
1	C	26	ASN
1	C	60	ASN
1	C	117	ASN

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Mol	Chain	Res	Type
1	C	128	ASN
1	C	155	ASN
1	C	165	ASN
1	C	217	ASN
1	C	311	GLN
1	C	328	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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	A	331/337 (98%)	0.03	4 (1%) 76 71	32, 58, 87, 110	0
1	B	331/337 (98%)	0.16	9 (2%) 56 47	37, 54, 85, 108	0
1	C	331/337 (98%)	0.04	7 (2%) 63 55	35, 51, 80, 98	0
All	All	993/1011 (98%)	0.08	20 (2%) 65 57	32, 54, 85, 110	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	158	ASP	3.6
1	B	284	ASP	3.5
1	B	256	PHE	3.5
1	B	85	GLU	2.9
1	B	141	LEU	2.9
1	C	116	TRP	2.6
1	C	50	GLN	2.6
1	B	314	ASP	2.5
1	B	114	ASP	2.4
1	C	13	PHE	2.3
1	A	189	ASN	2.3
1	B	271	ASN	2.3
1	C	32	ASP	2.3
1	C	280	GLY	2.3
1	A	167	ASP	2.2
1	C	151	TYR	2.2
1	A	179	ASN	2.2
1	B	158	ASP	2.1
1	A	158	ASP	2.1
1	B	50	GLN	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.