



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2023 – 04:10 PM EDT

PDB ID : 6WZB
Title : Crystal structure of the GltPh V216C-G388C mutant cross-linked with divalent mercury
Authors : Chen, I.; Font, J.; Ryan, R.
Deposited on : 2020-05-13
Resolution : 3.45 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

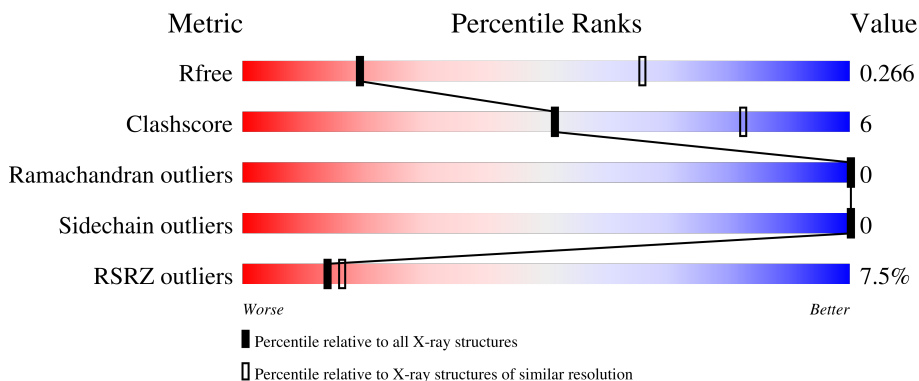
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


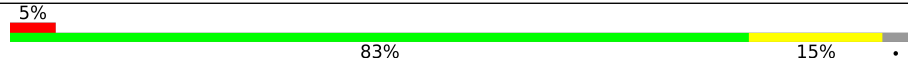
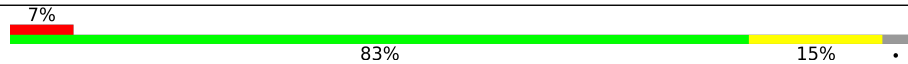
The reported resolution of this entry is 3.45 Å.

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	1291 (3.52-3.40)
Clashscore	141614	1372 (3.52-3.40)
Ramachandran outliers	138981	1337 (3.52-3.40)
Sidechain outliers	138945	1338 (3.52-3.40)
RSRZ outliers	127900	1205 (3.52-3.40)

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	A	422	
1	B	422	
1	C	422	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9144 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 Glutamate transporter homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	411	3034	2000	479	537	18	0	0	0
1	B	411	3038	2002	480	538	18	0	0	0
1	C	411	3036	2001	481	536	18	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

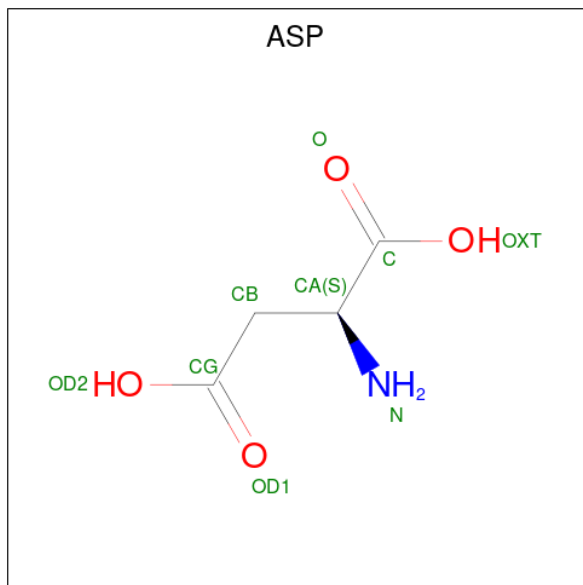
Chain	Residue	Modelled	Actual	Comment	Reference
A	216	CYS	VAL	engineered mutation	UNP O59010
A	321	SER	CYS	engineered mutation	UNP O59010
A	388	CYS	GLY	engineered mutation	UNP O59010
A	418	THR	-	expression tag	UNP O59010
A	419	LEU	-	expression tag	UNP O59010
A	420	VAL	-	expression tag	UNP O59010
A	421	PRO	-	expression tag	UNP O59010
A	422	ARG	-	expression tag	UNP O59010
B	216	CYS	VAL	engineered mutation	UNP O59010
B	321	SER	CYS	engineered mutation	UNP O59010
B	388	CYS	GLY	engineered mutation	UNP O59010
B	418	THR	-	expression tag	UNP O59010
B	419	LEU	-	expression tag	UNP O59010
B	420	VAL	-	expression tag	UNP O59010
B	421	PRO	-	expression tag	UNP O59010
B	422	ARG	-	expression tag	UNP O59010
C	216	CYS	VAL	engineered mutation	UNP O59010
C	321	SER	CYS	engineered mutation	UNP O59010
C	388	CYS	GLY	engineered mutation	UNP O59010
C	418	THR	-	expression tag	UNP O59010
C	419	LEU	-	expression tag	UNP O59010
C	420	VAL	-	expression tag	UNP O59010
C	421	PRO	-	expression tag	UNP O59010

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	422	ARG	-	expression tag	UNP O59010

- Molecule 2 is ASPARTIC ACID (three-letter code: ASP) (formula: $C_4H_7NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	9	4	1	4	0	0
2	B	1	9	4	1	4	0	0
2	C	1	9	4	1	4	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
3	A	2	2	2	0	0
3	B	2	2	2	0	0
3	C	2	2	2	0	0

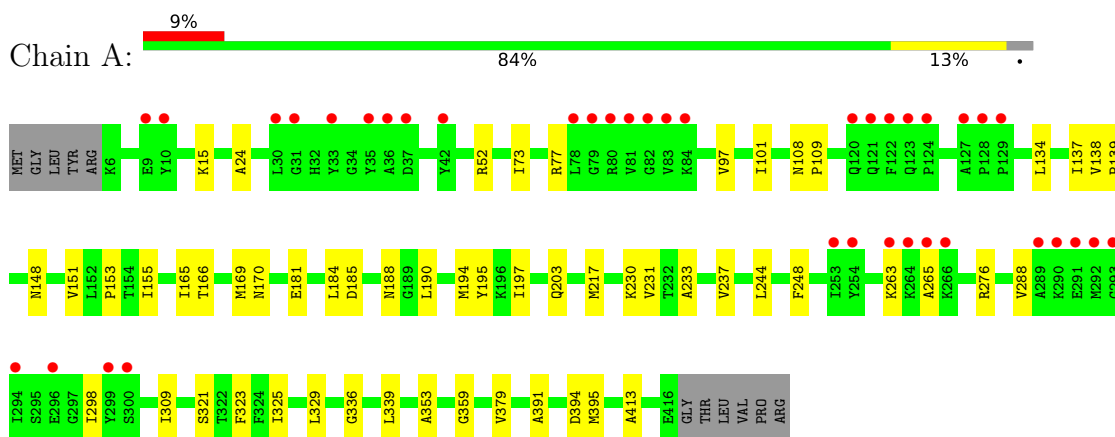
- Molecule 4 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Hg 1	0	0
4	B	1	Total 1	Hg 1	0	0
4	C	1	Total 1	Hg 1	0	0

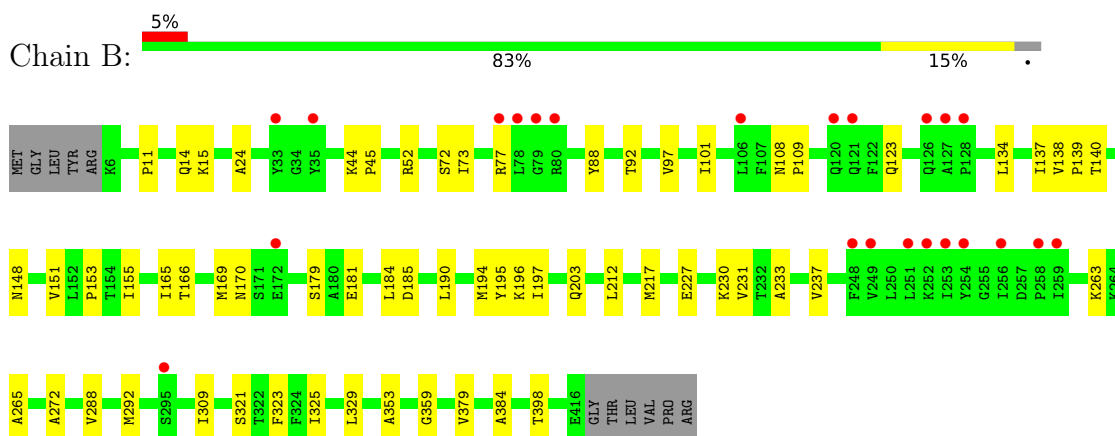
3 Residue-property plots [i](#)

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.

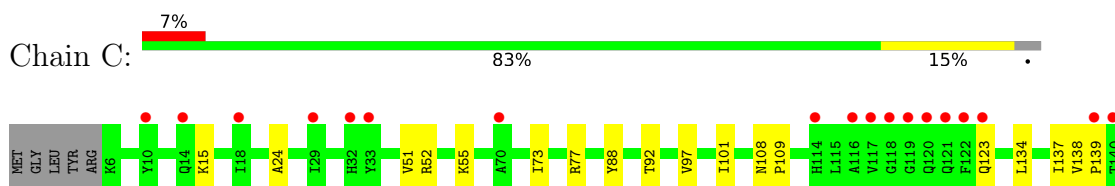
- Molecule 1: Glutamate transporter homolog

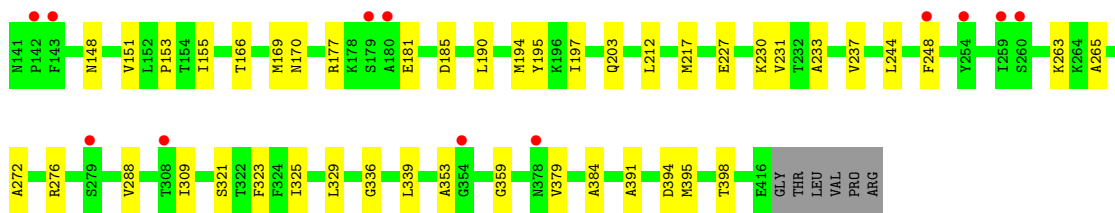


- Molecule 1: Glutamate transporter homolog



- Molecule 1: Glutamate transporter homolog





4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	112.11Å 204.57Å 207.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.31 – 3.45 49.31 – 3.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.31-3.45) 99.9 (49.31-3.45)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 3.48Å)	Xtrriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.233 , 0.268 0.233 , 0.266	Depositor DCC
R_{free} test set	1555 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	113.1	Xtrriage
Anisotropy	0.258	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 64.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.005 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.025 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	9144	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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: HG, NA

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	0.25	0/3087	0.42	0/4205
1	B	0.25	0/3091	0.42	0/4210
1	C	0.25	0/3089	0.42	0/4207
All	All	0.25	0/9267	0.42	0/12622

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 [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	3034	0	3233	34	0
1	B	3038	0	3239	39	0
1	C	3036	0	3238	37	0
2	A	9	0	3	1	0
2	B	9	0	3	1	0
2	C	9	0	3	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
4	A	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	C	1	0	0	0	0
All	All	9144	0	9719	105	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.

The worst 5 of 105 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:166:THR:HA	1:B:169:MET:HE2	1.76	0.68
1:B:329:LEU:HD21	1:B:379:VAL:HG22	1.78	0.65
1:B:194:MET:HA	1:B:197:ILE:HD12	1.79	0.65
1:A:194:MET:HA	1:A:197:ILE:HD12	1.79	0.64
1:A:329:LEU:HD21	1:A:379:VAL:HG22	1.79	0.64

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	409/422 (97%)	395 (97%)	14 (3%)	0	100	100
1	B	409/422 (97%)	396 (97%)	13 (3%)	0	100	100
1	C	409/422 (97%)	395 (97%)	14 (3%)	0	100	100
All	All	1227/1266 (97%)	1186 (97%)	41 (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	320/331 (97%)	320 (100%)	0	100	100
1	B	321/331 (97%)	321 (100%)	0	100	100
1	C	320/331 (97%)	320 (100%)	0	100	100
All	All	961/993 (97%)	961 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 9 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
2	ASP	C	501	-	6,8,8	1.21	1 (16%)	8,10,10	1.33	2 (25%)
2	ASP	A	501	-	6,8,8	1.21	1 (16%)	8,10,10	1.38	2 (25%)
2	ASP	B	501	-	6,8,8	1.20	1 (16%)	8,10,10	1.32	2 (25%)

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	ASP	C	501	-	-	2/8/8/8	-
2	ASP	A	501	-	-	2/8/8/8	-
2	ASP	B	501	-	-	2/8/8/8	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	ASP	OXT-C	-2.21	1.23	1.30
2	C	501	ASP	OXT-C	-2.20	1.23	1.30
2	B	501	ASP	OXT-C	-2.14	1.23	1.30

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	ASP	OXT-C-O	-2.57	118.25	124.09
2	C	501	ASP	OXT-C-O	-2.37	118.70	124.09
2	B	501	ASP	OXT-C-O	-2.28	118.92	124.09
2	B	501	ASP	OXT-C-CA	2.15	120.71	113.38
2	A	501	ASP	OXT-C-CA	2.11	120.58	113.38

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	ASP	CA-CB-CG-OD1
2	B	501	ASP	CA-CB-CG-OD1
2	B	501	ASP	CA-CB-CG-OD2
2	C	501	ASP	CA-CB-CG-OD1
2	C	501	ASP	CA-CB-CG-OD2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	ASP	1	0
2	A	501	ASP	1	0
2	B	501	ASP	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 [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	A	411/422 (97%)	0.22	39 (9%) 8 10	69, 107, 151, 204	0
1	B	411/422 (97%)	0.13	23 (5%) 24 24	69, 99, 148, 198	0
1	C	411/422 (97%)	0.23	30 (7%) 15 17	74, 112, 159, 208	0
All	All	1233/1266 (97%)	0.19	92 (7%) 14 16	69, 107, 156, 208	0

The worst 5 of 92 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	252	LYS	4.8
1	A	291	GLU	4.8
1	B	126	GLN	4.6
1	A	300	SER	4.5
1	C	120	GLN	4.5

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(\AA^2)	Q<0.9
2	ASP	C	501	9/9	0.88	0.41	109,115,122,122	0
2	ASP	B	501	9/9	0.92	0.22	85,100,104,104	0
4	HG	C	504	1/1	0.92	0.06	200,200,200,200	0
3	NA	A	503	1/1	0.93	0.20	126,126,126,126	0
3	NA	B	502	1/1	0.93	0.26	84,84,84,84	0
4	HG	B	504	1/1	0.93	0.08	185,185,185,185	0
2	ASP	A	501	9/9	0.93	0.15	89,100,102,104	0
3	NA	A	502	1/1	0.94	0.24	101,101,101,101	0
4	HG	A	504	1/1	0.94	0.10	184,184,184,184	0
3	NA	C	502	1/1	0.95	0.31	100,100,100,100	0
3	NA	B	503	1/1	0.96	0.43	76,76,76,76	0
3	NA	C	503	1/1	0.97	0.61	113,113,113,113	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.