



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:27 PM UTC

PDB ID : 7LVO / pdb_00007lvo
Title : Cryptococcus neoformans GAR synthetase
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Deposited on : 2021-02-26
Resolution : 2.00 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

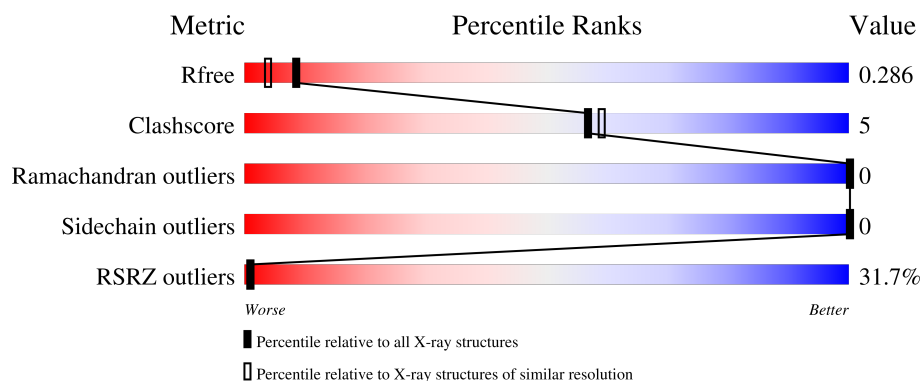
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	476	29% 82% 9% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6186 atoms, of which 2817 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 phosphoribosyl-glycinamide (GAR) synthetase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	435	6053	2071	2799	546	621	16	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP J9VYP5
A	2	HIS	-	expression tag	UNP J9VYP5
A	3	HIS	-	expression tag	UNP J9VYP5
A	4	HIS	-	expression tag	UNP J9VYP5
A	5	HIS	-	expression tag	UNP J9VYP5
A	6	HIS	-	expression tag	UNP J9VYP5
A	7	HIS	-	expression tag	UNP J9VYP5
A	8	SER	-	expression tag	UNP J9VYP5
A	9	SER	-	expression tag	UNP J9VYP5
A	10	GLY	-	expression tag	UNP J9VYP5
A	11	VAL	-	expression tag	UNP J9VYP5
A	12	ASP	-	expression tag	UNP J9VYP5
A	13	LEU	-	expression tag	UNP J9VYP5
A	14	GLY	-	expression tag	UNP J9VYP5
A	15	THR	-	expression tag	UNP J9VYP5
A	16	GLU	-	expression tag	UNP J9VYP5
A	17	ASN	-	expression tag	UNP J9VYP5
A	18	LEU	-	expression tag	UNP J9VYP5
A	19	TYR	-	expression tag	UNP J9VYP5
A	20	PHE	-	expression tag	UNP J9VYP5
A	21	GLN	-	expression tag	UNP J9VYP5
A	22	SER	-	expression tag	UNP J9VYP5
A	23	ASN	-	expression tag	UNP J9VYP5
A	24	ALA	-	expression tag	UNP J9VYP5

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		

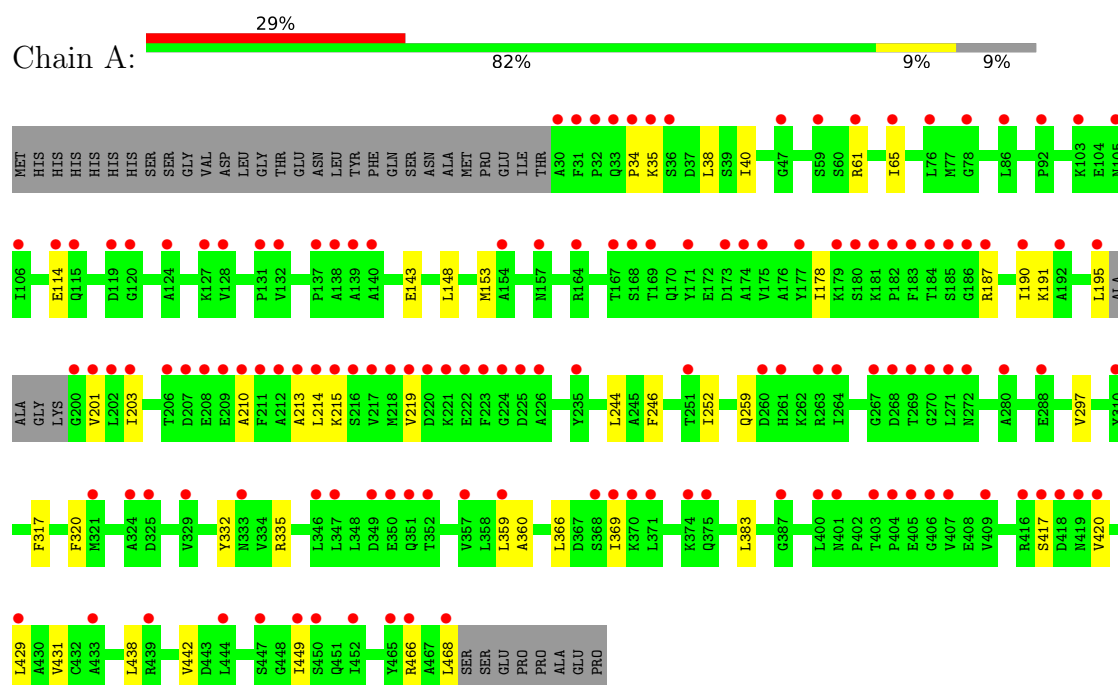
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	103	Total	O	0	0
			103	103		

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: phosphoribosyl-glycinamide (GAR) synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	87.10Å 76.49Å 74.97Å 90.00° 107.57° 90.00°	Depositor
Resolution (Å)	38.24 – 2.00 38.24 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (38.24-2.00) 97.6 (38.24-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.242 , 0.285 0.242 , 0.286	Depositor DCC
R_{free} test set	3172 reflections (7.27%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6186	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.37% 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: 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	0.18	0/3322	0.25	0/4507

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	3254	2799	3260	30	0
2	A	12	18	18	0	0
3	A	103	0	0	1	0
All	All	3369	2817	3278	30	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 (30) 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:A:360:ALA:CB	1:A:369:ILE:HD13	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:GLU:OE2	1:A:195:LEU:HD22	1.98	0.63
1:A:431:VAL:HG21	1:A:449:ILE:HD13	1.83	0.59
1:A:34:PRO:HB2	1:A:61:ARG:NH1	2.18	0.58
1:A:383:LEU:HD11	1:A:449:ILE:HD12	1.86	0.57
1:A:215:LYS:HG3	1:A:219:VAL:HB	1.85	0.57
1:A:259:GLN:NE2	1:A:466:ARG:HH12	2.03	0.55
1:A:190:ILE:HD12	1:A:213:ALA:HB3	1.89	0.55
1:A:360:ALA:HB3	1:A:369:ILE:HD13	1.88	0.54
1:A:417:SER:O	1:A:420:VAL:HG12	2.08	0.53
1:A:153:MET:HE2	1:A:332:TYR:CE2	2.47	0.49
1:A:438:LEU:O	1:A:442:VAL:HG23	2.14	0.48
1:A:148:LEU:HD23	1:A:148:LEU:C	2.38	0.48
1:A:178:ILE:HD13	1:A:210:ALA:HB1	1.96	0.47
1:A:34:PRO:C	1:A:61:ARG:HH12	2.22	0.47
1:A:187:ARG:HH21	1:A:203:ILE:HG22	1.78	0.47
1:A:178:ILE:CD1	1:A:214:LEU:HD11	2.45	0.46
1:A:187:ARG:NH2	1:A:203:ILE:HG22	2.30	0.46
1:A:178:ILE:HD12	1:A:214:LEU:HD11	1.96	0.46
1:A:191:LYS:HG2	1:A:201:VAL:HG22	1.98	0.45
1:A:297:VAL:HG21	1:A:320:PHE:HE2	1.82	0.45
1:A:246:PHE:O	1:A:252:ILE:HA	2.18	0.44
1:A:35:LYS:HB2	3:A:642:HOH:O	2.17	0.43
1:A:429:LEU:C	1:A:429:LEU:HD12	2.44	0.43
1:A:438:LEU:HG	1:A:468:LEU:HD21	2.01	0.43
1:A:40:ILE:HB	1:A:65:ILE:HD13	2.02	0.41
1:A:38:LEU:HD13	1:A:359:LEU:HD11	2.01	0.41
1:A:143:GLU:OE2	1:A:335:ARG:NH2	2.54	0.41
1:A:244:LEU:HD11	1:A:317:PHE:CE2	2.56	0.40
1:A:366:LEU:HD12	1:A:369:ILE:HD11	2.03	0.40

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	A	431/476 (90%)	410 (95%)	21 (5%)	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	343/377 (91%)	343 (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 oligosaccharides 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	$\# Z > 2$
2	EDO	A	501	-	3,3,3	0.42	0	2,2,2	0.34	0
2	EDO	A	502	-	3,3,3	0.44	0	2,2,2	0.32	0
2	EDO	A	503	-	3,3,3	0.43	0	2,2,2	0.37	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
2	EDO	A	501	-	-	0/1/1/1	-
2	EDO	A	502	-	-	0/1/1/1	-
2	EDO	A	503	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	435/476 (91%)	1.75	138 (31%) 1 1	20, 33, 61, 82	0

All (138) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	465	TYR	8.4
1	A	418	ASP	8.0
1	A	419	ASN	7.6
1	A	195	LEU	7.0
1	A	466	ARG	6.6
1	A	184	THR	6.0
1	A	34	PRO	5.9
1	A	216	SER	5.8
1	A	420	VAL	5.5
1	A	186	GLY	5.3
1	A	206	THR	5.2
1	A	35	LYS	5.1
1	A	417	SER	5.1
1	A	140	ALA	5.1
1	A	226	ALA	5.0
1	A	32	PRO	5.0
1	A	127	LYS	4.9
1	A	350	GLU	4.9
1	A	400	LEU	4.8
1	A	30	ALA	4.5
1	A	169	THR	4.3
1	A	183	PHE	4.2
1	A	175	VAL	4.2
1	A	213	ALA	4.2
1	A	222	GLU	4.2
1	A	208	GLU	4.2
1	A	185	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	203	ILE	4.0
1	A	406	GLY	4.0
1	A	168	SER	3.9
1	A	202	LEU	3.9
1	A	33	GLN	3.8
1	A	349	ASP	3.7
1	A	214	LEU	3.6
1	A	409	VAL	3.5
1	A	201	VAL	3.4
1	A	439	ARG	3.4
1	A	223	PHE	3.4
1	A	219	VAL	3.3
1	A	369	ILE	3.3
1	A	270	GLY	3.3
1	A	351	GLN	3.3
1	A	36	SER	3.3
1	A	225	ASP	3.3
1	A	182	PRO	3.2
1	A	224	GLY	3.2
1	A	468	LEU	3.2
1	A	359	LEU	3.1
1	A	405	GLU	3.1
1	A	449	ILE	3.1
1	A	212	ALA	3.1
1	A	179	LYS	3.1
1	A	370	LYS	3.1
1	A	371	LEU	3.1
1	A	180	SER	3.1
1	A	171	TYR	3.0
1	A	187	ARG	3.0
1	A	352	THR	3.0
1	A	209	GLU	3.0
1	A	106	ILE	3.0
1	A	105	ASN	3.0
1	A	210	ALA	2.9
1	A	404	PRO	2.9
1	A	211	PHE	2.9
1	A	103	LYS	2.9
1	A	329	VAL	2.8
1	A	325	ASP	2.8
1	A	114	GLU	2.8
1	A	387	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	59	SER	2.7
1	A	374	LYS	2.7
1	A	190	ILE	2.7
1	A	31	PHE	2.7
1	A	65	ILE	2.7
1	A	269	THR	2.6
1	A	137	PRO	2.6
1	A	215	LYS	2.6
1	A	263	ARG	2.6
1	A	271	LEU	2.6
1	A	268	ASP	2.6
1	A	221	LYS	2.5
1	A	272	ASN	2.5
1	A	124	ALA	2.5
1	A	192	ALA	2.5
1	A	324	ALA	2.5
1	A	403	THR	2.5
1	A	47	GLY	2.5
1	A	181	LYS	2.5
1	A	220	ASP	2.5
1	A	78	GLY	2.5
1	A	310	TYR	2.5
1	A	76	LEU	2.5
1	A	444	LEU	2.5
1	A	416	ARG	2.5
1	A	200	GLY	2.5
1	A	119	ASP	2.4
1	A	368	SER	2.4
1	A	450	SER	2.4
1	A	164	ARG	2.4
1	A	429	LEU	2.4
1	A	260	ASP	2.4
1	A	217	VAL	2.4
1	A	218	MET	2.4
1	A	264	ILE	2.3
1	A	375	GLN	2.3
1	A	139	ALA	2.3
1	A	407	VAL	2.3
1	A	207	ASP	2.3
1	A	267	GLY	2.3
1	A	261	HIS	2.3
1	A	447	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	346	LEU	2.3
1	A	347	LEU	2.3
1	A	288	GLU	2.2
1	A	132	VAL	2.2
1	A	86	LEU	2.2
1	A	157	ASN	2.2
1	A	333	ASN	2.2
1	A	138	ALA	2.2
1	A	401	ASN	2.2
1	A	92	PRO	2.2
1	A	120	GLY	2.2
1	A	154	ALA	2.2
1	A	433	ALA	2.2
1	A	61	ARG	2.2
1	A	321	MET	2.2
1	A	115	GLN	2.1
1	A	235	TYR	2.1
1	A	128	VAL	2.1
1	A	177	TYR	2.1
1	A	131	PRO	2.1
1	A	452	ILE	2.1
1	A	174	ALA	2.1
1	A	280	ALA	2.1
1	A	251	THR	2.0
1	A	357	VAL	2.0
1	A	173	ASP	2.0
1	A	167	THR	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 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
2	EDO	A	503	4/4	0.57	0.25	18,18,63,63	0
2	EDO	A	502	4/4	0.67	0.18	18,18,46,46	0
2	EDO	A	501	4/4	0.81	0.24	16,16,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.