



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2020 – 03:44 PM BST

PDB ID : 6F2G
Title : Bacterial asc transporter crystal structure in open to in conformation
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Deposited on : 2017-11-24
Resolution : 2.92 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.13
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)	:	2.13

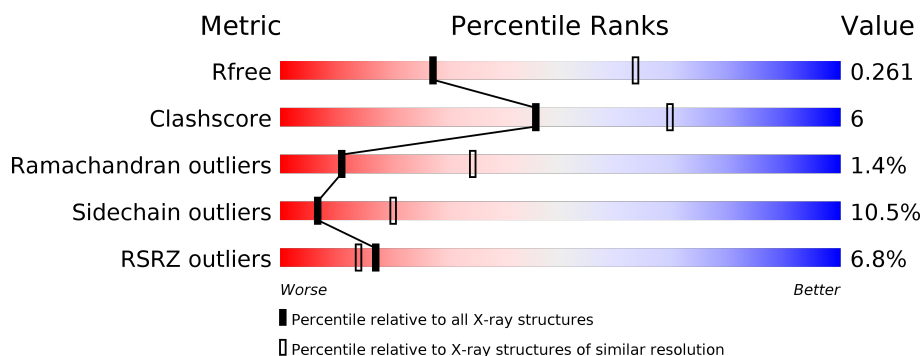
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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 ≥ 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	444	<div> <div>7%</div> <div> <div></div> <div>73%</div> <div>20%</div> <div>• •</div> </div> </div>
2	B	134	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4253 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 Putative amino acid/polyamine transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	0	0
			3258	2200	500	547	11			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A8UCQ5
A	436	GLY	-	expression tag	UNP A8UCQ5
A	437	GLY	-	expression tag	UNP A8UCQ5
A	438	GLY	-	expression tag	UNP A8UCQ5
A	439	LEU	-	expression tag	UNP A8UCQ5
A	440	GLU	-	expression tag	UNP A8UCQ5
A	441	VAL	-	expression tag	UNP A8UCQ5
A	442	LEU	-	expression tag	UNP A8UCQ5
A	443	PHE	-	expression tag	UNP A8UCQ5
A	444	GLN	-	expression tag	UNP A8UCQ5

- Molecule 2 is a protein called Nanobody 74.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	131	Total	C	N	O	S	0	0	0
			994	612	186	192	4			

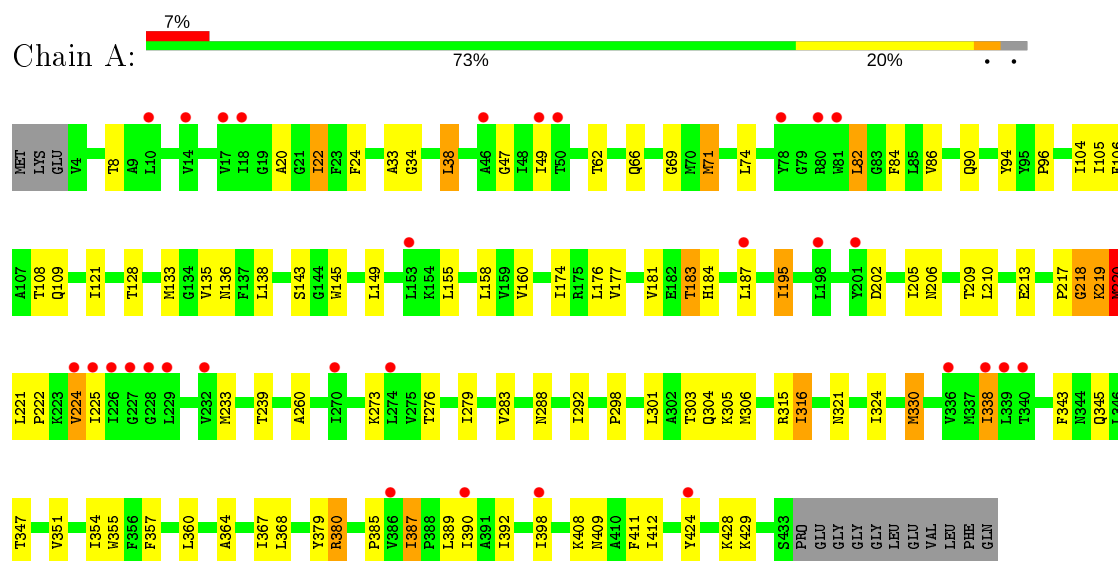
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

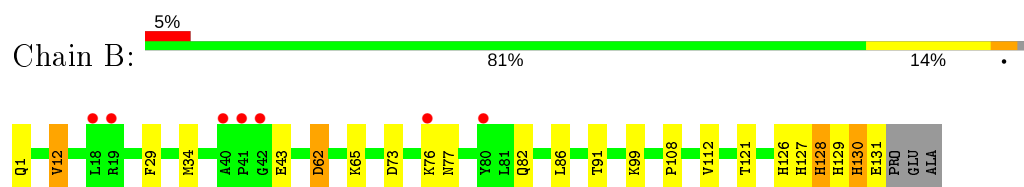
3 Residue-property plots [i](#)

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: Putative amino acid/polyamine transport protein



- Molecule 2: Nanobody 74



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	85.83Å 85.83Å 321.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.05 – 2.92 82.93 – 2.92	Depositor EDS
% Data completeness (in resolution range)	74.1 (83.05-2.92) 74.1 (82.93-2.92)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.238 , 0.261 0.240 , 0.261	Depositor DCC
R_{free} test set	972 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	93.7	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 64.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	4253	wwPDB-VP
Average B, all atoms (Å ²)	119.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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: ZN

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	0.84	0/3341	0.94	4/4569 (0.1%)
2	B	0.90	0/1019	0.99	3/1381 (0.2%)
All	All	0.85	0/4360	0.96	7/5950 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	34	MET	CG-SD-CE	-7.67	87.93	100.20
1	A	380	ARG	NE-CZ-NH2	6.94	123.77	120.30
2	B	62	ASP	CB-CG-OD2	6.03	123.72	118.30
1	A	315	ARG	CG-CD-NE	-5.44	100.38	111.80
1	A	380	ARG	NE-CZ-NH1	-5.23	117.68	120.30
1	A	133	MET	CG-SD-CE	5.06	108.29	100.20
2	B	73	ASP	CB-CG-OD1	-5.02	113.78	118.30

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	3258	0	3457	49	0
2	B	994	0	928	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
All	All	4253	0	4385	55	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 (55) 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:316:ILE:HD13	2:B:108:PRO:HG2	1.79	0.65
1:A:74:LEU:HD12	1:A:86:VAL:HG21	1.81	0.63
1:A:109:GLN:HE22	1:A:260:ALA:HB2	1.64	0.61
2:B:29:PHE:HB3	2:B:77:ASN:HD22	1.67	0.60
1:A:74:LEU:HD12	1:A:86:VAL:CG2	2.34	0.57
1:A:143:SER:HB3	1:A:292:ILE:HD11	1.86	0.57
1:A:355:TRP:HB3	1:A:398:ILE:HD11	1.85	0.57
1:A:389:LEU:HA	1:A:392:ILE:HG22	1.88	0.56
1:A:47:GLY:HA3	1:A:233:MET:HG3	1.86	0.56
2:B:127:HIS:O	2:B:128:HIS:HB2	2.04	0.56
1:A:276:THR:HA	1:A:279:ILE:HD12	1.87	0.56
1:A:343:PHE:O	1:A:347:THR:HG23	2.06	0.55
1:A:387:ILE:HA	1:A:390:ILE:HD12	1.89	0.54
1:A:158:LEU:HD22	1:A:239:THR:HG21	1.90	0.54
1:A:104:ILE:HD11	1:A:338:ILE:HA	1.90	0.54
2:B:131:GLU:N	2:B:131:GLU:OE1	2.41	0.53
1:A:347:THR:O	1:A:351:VAL:HG23	2.09	0.53
1:A:181:VAL:HG12	1:A:183:THR:HG22	1.91	0.53
1:A:108:THR:HA	1:A:121:ILE:HD12	1.91	0.52
1:A:20:ALA:HB1	1:A:283:VAL:HG22	1.91	0.52
1:A:96:PRO:HG3	1:A:330:MET:HG3	1.93	0.51
1:A:298:PRO:HA	1:A:301:LEU:HD12	1.92	0.51
1:A:174:ILE:HA	1:A:177:VAL:HG13	1.92	0.50
1:A:135:VAL:HA	1:A:138:LEU:HD12	1.93	0.49
1:A:195:ILE:O	1:A:351:VAL:HG21	2.11	0.49
1:A:62:THR:HG21	1:A:379:TYR:HB3	1.93	0.49
1:A:351:VAL:O	1:A:355:TRP:HB2	2.12	0.49
1:A:24:PHE:CD1	1:A:105:ILE:HG13	2.49	0.48
1:A:218:GLY:O	1:A:222:PRO:HD3	2.14	0.48
1:A:82:LEU:O	1:A:86:VAL:HG23	2.15	0.47
1:A:357:PHE:HA	1:A:360:LEU:HD12	1.97	0.46
1:A:364:ALA:HA	1:A:367:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ALA:HB1	1:A:38:LEU:HB3	1.98	0.46
1:A:213:GLU:OE2	2:B:99:LYS:NZ	2.49	0.45
1:A:385:PRO:O	1:A:389:LEU:HD13	2.17	0.45
1:A:219:LYS:O	1:A:220:MET:CB	2.64	0.45
1:A:409:ASN:HA	1:A:412:ILE:HD12	1.99	0.44
1:A:69:GLY:C	1:A:71:MET:H	2.20	0.44
1:A:219:LYS:HG3	1:A:219:LYS:O	2.17	0.44
1:A:90:GLN:HA	1:A:94:TYR:HB3	1.98	0.44
1:A:221:LEU:O	1:A:224:VAL:HG12	2.18	0.44
1:A:355:TRP:HB3	1:A:398:ILE:CD1	2.47	0.43
1:A:181:VAL:CG1	1:A:183:THR:HG22	2.49	0.43
1:A:84:PHE:CE2	1:A:424:TYR:HB2	2.53	0.43
1:A:304:GLN:HA	2:B:62:ASP:HB2	2.00	0.43
1:A:136:ASN:HD21	1:A:288:ASN:ND2	2.16	0.42
1:A:22:ILE:HD13	1:A:158:LEU:HD21	2.02	0.42
1:A:209:THR:O	1:A:213:GLU:HB2	2.20	0.42
1:A:183:THR:HG23	1:A:184:HIS:CD2	2.55	0.41
1:A:34:GLY:HA3	1:A:184:HIS:CD2	2.56	0.41
2:B:12:VAL:HG21	2:B:86:LEU:HD13	2.03	0.41
2:B:91:THR:HG23	2:B:121:THR:HA	2.03	0.41
1:A:221:LEU:O	1:A:225:ILE:HG12	2.22	0.40
2:B:29:PHE:HB3	2:B:77:ASN:ND2	2.33	0.40
1:A:106:PHE:CE2	1:A:128:THR:HG21	2.57	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	428/444 (96%)	401 (94%)	22 (5%)	5 (1%)	13	38
2	B	129/134 (96%)	120 (93%)	6 (5%)	3 (2%)	6	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	557/578 (96%)	521 (94%)	28 (5%)	8 (1%)	11	34

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	128	HIS
1	A	206	ASN
1	A	217	PRO
1	A	306	MET
2	B	129	HIS
1	A	218	GLY
1	A	220	MET
2	B	130	HIS

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	A	344/356 (97%)	306 (89%)	38 (11%)	6	18
2	B	102/104 (98%)	93 (91%)	9 (9%)	10	28
All	All	446/460 (97%)	399 (90%)	47 (10%)	7	20

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	THR
1	A	22	ILE
1	A	38	LEU
1	A	49	ILE
1	A	66	GLN
1	A	71	MET
1	A	82	LEU
1	A	145	TRP
1	A	149	LEU
1	A	155	LEU

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Mol	Chain	Res	Type
1	A	160	VAL
1	A	176	LEU
1	A	183	THR
1	A	187	LEU
1	A	195	ILE
1	A	202	ASP
1	A	205	ILE
1	A	210	LEU
1	A	219	LYS
1	A	220	MET
1	A	224	VAL
1	A	273	LYS
1	A	303	THR
1	A	305	LYS
1	A	316	ILE
1	A	321	ASN
1	A	324	ILE
1	A	330	MET
1	A	338	ILE
1	A	345	GLN
1	A	354	ILE
1	A	368	LEU
1	A	380	ARG
1	A	387	ILE
1	A	408	LYS
1	A	411	PHE
1	A	428	LYS
1	A	429	LYS
2	B	1	GLN
2	B	12	VAL
2	B	43	GLU
2	B	65	LYS
2	B	76	LYS
2	B	82	GLN
2	B	112	VAL
2	B	126	HIS
2	B	130	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	GLN

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Mol	Chain	Res	Type
1	A	184	HIS
1	A	240	ASN
1	A	288	ASN
1	A	321	ASN
1	A	345	GLN
1	A	401	ASN
2	B	1	GLN
2	B	77	ASN

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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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	430/444 (96%)	0.43	31 (7%) 15 12	85, 120, 167, 203	1 (0%)
2	B	131/134 (97%)	0.33	7 (5%) 26 23	69, 98, 159, 227	0
All	All	561/578 (97%)	0.41	38 (6%) 17 14	69, 115, 165, 227	1 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	224	VAL	6.9
2	B	41	PRO	5.7
1	A	270	ILE	5.4
1	A	80	ARG	5.2
1	A	229	LEU	3.8
1	A	81	TRP	3.8
1	A	201	TYR	3.7
2	B	42	GLY	3.6
2	B	40	ALA	3.6
1	A	274	LEU	3.4
1	A	50	THR	3.4
1	A	226	ILE	3.4
1	A	390	ILE	3.3
1	A	398	ILE	3.2
1	A	386	VAL	3.1
1	A	339	LEU	3.0
1	A	18	ILE	2.9
1	A	49	ILE	2.8
1	A	228	GLY	2.6
2	B	76	LYS	2.6
1	A	17	VAL	2.5
1	A	340	THR	2.5
1	A	153	LEU	2.5
1	A	187	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	18	LEU	2.5
1	A	232	VAL	2.4
1	A	46	ALA	2.4
1	A	225	ILE	2.4
1	A	227	GLY	2.4
1	A	78	TYR	2.2
1	A	424	TYR	2.2
2	B	19	ARG	2.2
1	A	14	VAL	2.1
1	A	336	VAL	2.1
1	A	338	ILE	2.1
1	A	198	LEU	2.1
1	A	10	LEU	2.0
2	B	80	TYR	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 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(Å ²)	Q<0.9
3	ZN	B	201	1/1	0.96	0.25	118,118,118,118	0

6.5 Other polymers [i](#)

There are no such residues in this entry.