



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3UJZ / pdb_00003ujz
Title : Crystal structure of enterohemorrhagic E. coli StcE
Authors : Yu, A.C.Y.; Strynadka, N.C.J.
Deposited on : 2011-11-08
Resolution : 2.50 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

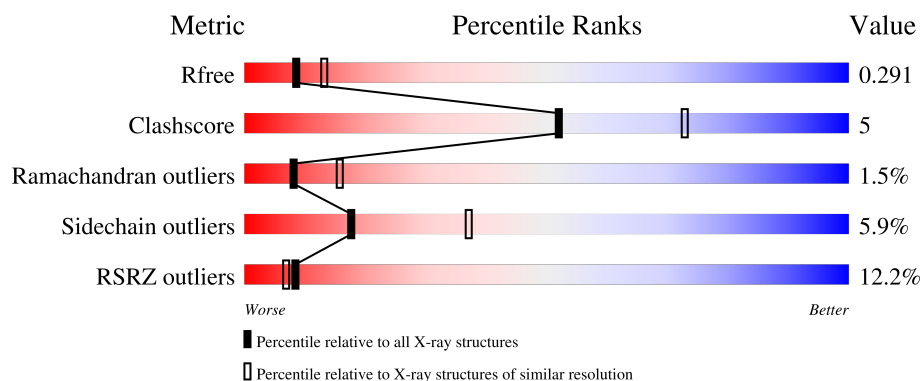
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 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	869	8% 57% 11% • 30%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4868 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 Metalloprotease stcE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	604	Total	C	N	O	S	Se	0	0	0
			4695	2962	817	900	4	12			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	GLY	-	expression tag	UNP O82882
A	31	SER	-	expression tag	UNP O82882
A	32	HIS	-	expression tag	UNP O82882
A	33	MSE	-	expression tag	UNP O82882
A	34	ALA	-	expression tag	UNP O82882
A	35	SER	-	expression tag	UNP O82882
A	318	ALA	LYS	engineered mutation	UNP O82882
A	320	ALA	LYS	engineered mutation	UNP O82882
A	321	ALA	GLU	engineered mutation	UNP O82882
A	447	ASP	GLU	engineered mutation	UNP O82882

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

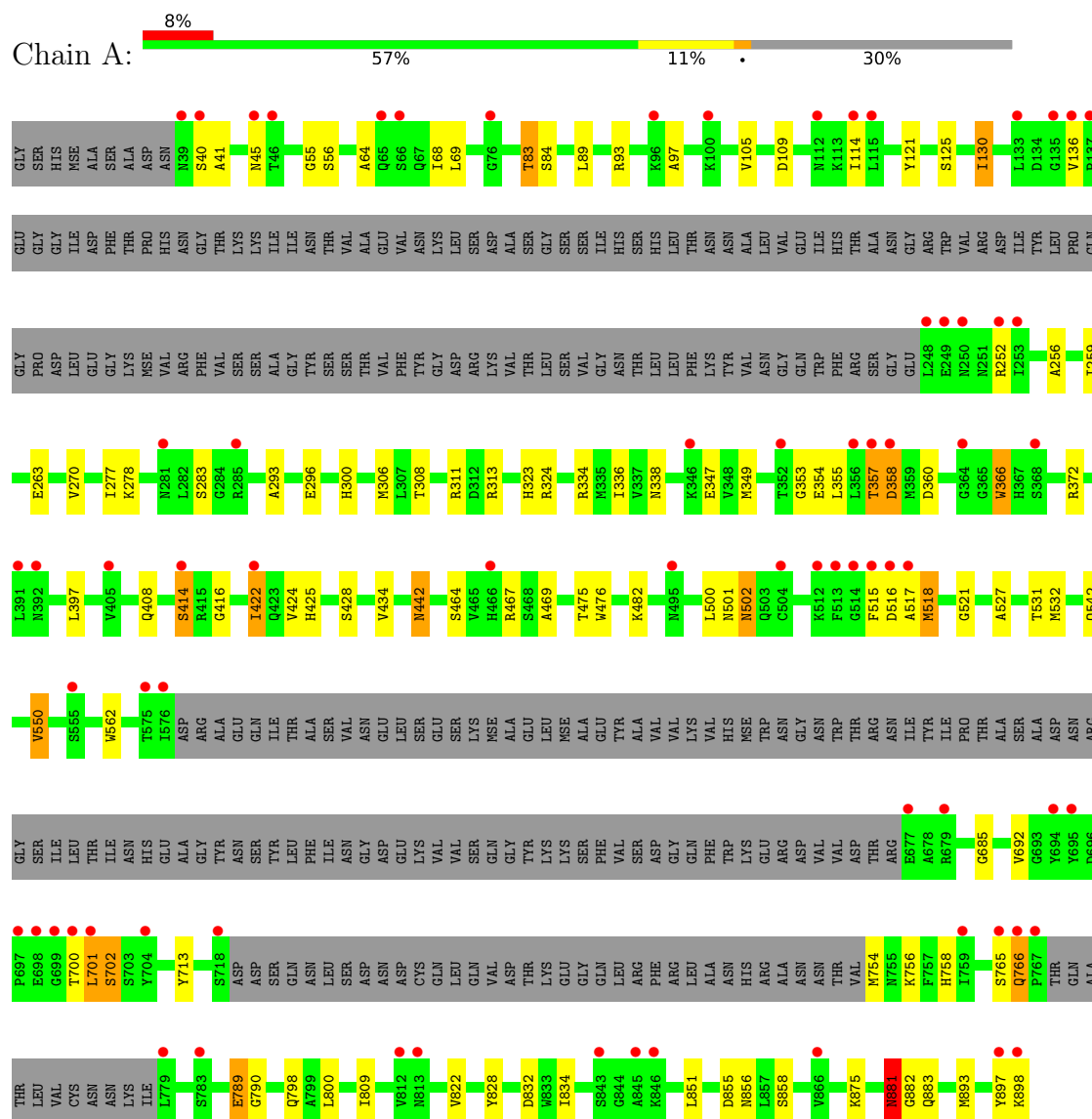
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	172	Total	O	0	0
			172	172		

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: Metalloprotease stcE



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	76.53Å 186.00Å 188.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.17 – 2.50 48.17 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (48.17-2.50) 100.0 (48.17-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.211 , 0.253 0.247 , 0.291	Depositor DCC
R_{free} test set	2349 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	51.0	Xtriage
Anisotropy	0.954	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 73.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4868	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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

5.1 Standard geometry

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	0.85	0/4806	1.26	18/6512 (0.3%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	881	ASN	N-CA-C	-7.92	96.40	108.67
1	A	136	VAL	N-CA-C	7.46	115.29	107.76
1	A	464	SER	N-CA-C	6.93	122.03	113.50
1	A	469	ALA	N-CA-C	6.42	119.09	111.71
1	A	858	SER	N-CA-C	6.33	120.23	110.42
1	A	515	PHE	CA-CB-CG	5.76	119.56	113.80
1	A	55	GLY	CA-C-N	5.69	127.91	120.28
1	A	55	GLY	C-N-CA	5.69	127.91	120.28
1	A	442	ASN	N-CA-C	5.66	117.45	111.28
1	A	422	ILE	N-CA-CB	5.58	117.01	110.82
1	A	323	HIS	CA-C-N	5.54	127.64	120.44
1	A	323	HIS	C-N-CA	5.54	127.64	120.44
1	A	518	MSE	N-CA-C	-5.39	104.97	112.30
1	A	360	ASP	N-CA-C	-5.30	102.97	109.65
1	A	422	ILE	CB-CA-C	5.24	118.35	111.33
1	A	109	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	97	ALA	N-CA-C	5.11	117.71	110.10
1	A	875	LYS	N-CA-C	5.02	119.47	112.90

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	A	4695	0	4503	47	0
2	A	1	0	0	0	0
3	A	172	0	0	0	0
All	All	4868	0	4503	47	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 (47) 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:809:ILE:HG12	1:A:893:MSE:HE1	1.31	1.07
1:A:357:THR:O	1:A:358:ASP:HB2	1.60	1.01
1:A:83:THR:HG22	1:A:542:GLN:HE21	1.34	0.93
1:A:83:THR:HG22	1:A:542:GLN:NE2	1.97	0.79
1:A:300:HIS:HD1	1:A:338:ASN:HD22	1.29	0.76
1:A:516:ASP:OD2	1:A:518:MSE:N	2.22	0.72
1:A:349:MSE:HE1	1:A:353:GLY:HA2	1.70	0.72
1:A:897:TYR:O	1:A:898:LYS:HB2	1.91	0.69
1:A:700:THR:HA	1:A:701:LEU:HB3	1.74	0.68
1:A:105:VAL:HG22	1:A:277:ILE:HG12	1.78	0.65
1:A:130:ILE:HG12	1:A:527:ALA:HB1	1.79	0.64
1:A:822:VAL:HG11	1:A:897:TYR:CD2	2.35	0.62
1:A:93:ARG:HB2	1:A:259:ILE:HG12	1.81	0.62
1:A:357:THR:O	1:A:358:ASP:CB	2.40	0.61
1:A:334:ARG:HD3	1:A:798:GLN:O	2.02	0.60
1:A:501:ASN:O	1:A:502:ASN:HB2	2.03	0.59
1:A:347:GLU:HB3	1:A:355:LEU:HD11	1.84	0.58
1:A:64:ALA:HB3	1:A:89:LEU:HB3	1.85	0.57
1:A:130:ILE:HD11	1:A:482:LYS:HD3	1.88	0.55
1:A:809:ILE:CG1	1:A:893:MSE:HE1	2.22	0.53
1:A:296:GLU:HB2	1:A:550:VAL:HG22	1.91	0.52
1:A:56:SER:HB3	1:A:283:SER:H	1.76	0.51
1:A:881:ASN:O	1:A:883:GLN:N	2.41	0.51
1:A:372:ARG:NH2	1:A:428:SER:OG	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:765:SER:O	1:A:766:GLN:HB2	2.11	0.50
1:A:822:VAL:CG1	1:A:897:TYR:CD2	2.96	0.49
1:A:366:TRP:O	1:A:372:ARG:NH1	2.46	0.48
1:A:40:SER:HA	1:A:252:ARG:HD2	1.95	0.47
1:A:828:TYR:CE2	1:A:855:ASP:HB3	2.51	0.46
1:A:293:ALA:HB2	1:A:562:TRP:CG	2.53	0.44
1:A:517:ALA:HB2	1:A:531:THR:HB	2.00	0.44
1:A:897:TYR:O	1:A:898:LYS:CB	2.60	0.44
1:A:685:GLY:HA3	1:A:713:TYR:CE1	2.53	0.44
1:A:517:ALA:HB2	1:A:531:THR:CG2	2.48	0.43
1:A:442:ASN:CG	1:A:521:GLY:O	2.61	0.42
1:A:68:ILE:HD12	1:A:476:TRP:HB2	2.01	0.42
1:A:121:TYR:HB3	1:A:125:SER:HB2	2.02	0.42
1:A:300:HIS:NE2	1:A:408:GLN:NE2	2.67	0.42
1:A:45:ASN:HB3	1:A:256:ALA:HB2	2.01	0.42
1:A:501:ASN:O	1:A:502:ASN:CB	2.68	0.41
1:A:414:SER:HB3	1:A:425:HIS:HD2	1.85	0.41
1:A:336:ILE:HD11	1:A:800:LEU:HD21	2.02	0.41
1:A:306:MSE:O	1:A:416:GLY:HA2	2.21	0.41
1:A:702:SER:O	1:A:754:MSE:SE	2.89	0.40
1:A:311:ARG:HH11	1:A:424:VAL:HG11	1.87	0.40
1:A:475:THR:HG23	1:A:532:MSE:CE	2.52	0.40
1:A:822:VAL:HG11	1:A:897:TYR:CE2	2.56	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	594/869 (68%)	560 (94%)	25 (4%)	9 (2%)	8 16

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	789	GLU
1	A	882	GLY
1	A	41	ALA
1	A	358	ASP
1	A	702	SER
1	A	790	GLY
1	A	766	GLN
1	A	856	ASN
1	A	502	ASN

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	506/716 (71%)	476 (94%)	30 (6%)	18	37

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	LEU
1	A	83	THR
1	A	84	SER
1	A	114	ILE
1	A	130	ILE
1	A	263	GLU
1	A	270	VAL
1	A	278	LYS
1	A	308	THR
1	A	313	ARG
1	A	324	ARG
1	A	354	GLU
1	A	357	THR
1	A	366	TRP
1	A	397	LEU
1	A	414	SER
1	A	422	ILE
1	A	434	VAL

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Mol	Chain	Res	Type
1	A	467	ARG
1	A	500	LEU
1	A	550	VAL
1	A	692	VAL
1	A	701	LEU
1	A	756	LYS
1	A	758	HIS
1	A	789	GLU
1	A	832	ASP
1	A	834	ILE
1	A	851	LEU
1	A	881	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	257	GLN
1	A	267	HIS
1	A	323	HIS
1	A	408	GLN
1	A	423	GLN
1	A	472	ASN
1	A	502	ASN
1	A	528	ASN
1	A	536	ASN
1	A	798	GLN
1	A	870	ASN
1	A	881	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

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 [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	592/869 (68%)	0.87	72 (12%) 8 7	24, 83, 120, 167	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	248	LEU	9.7
1	A	779	LEU	7.7
1	A	249	GLU	6.6
1	A	767	PRO	6.5
1	A	136	VAL	6.5
1	A	898	LYS	5.8
1	A	700	THR	5.6
1	A	514	GLY	5.6
1	A	697	PRO	5.6
1	A	576	ILE	5.4
1	A	701	LEU	5.4
1	A	517	ALA	4.9
1	A	358	ASP	4.8
1	A	137	PRO	4.8
1	A	718	SER	4.6
1	A	135	GLY	4.1
1	A	515	PHE	3.7
1	A	575	THR	3.4
1	A	783	SER	3.3
1	A	677	GLU	3.3
1	A	512	LYS	3.2
1	A	76	GLY	3.2
1	A	414	SER	3.2
1	A	846	LYS	3.1
1	A	65	GLN	3.0
1	A	679	ARG	3.0
1	A	285	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	699	GLY	3.0
1	A	46	THR	3.0
1	A	866	VAL	2.9
1	A	516	ASP	2.9
1	A	695	TYR	2.9
1	A	250	ASN	2.8
1	A	40	SER	2.7
1	A	766	GLN	2.7
1	A	133	LEU	2.7
1	A	765	SER	2.6
1	A	392	ASN	2.6
1	A	357	THR	2.6
1	A	96	LYS	2.6
1	A	555	SER	2.5
1	A	698	GLU	2.5
1	A	759	ILE	2.5
1	A	39	ASN	2.5
1	A	812	VAL	2.5
1	A	368	SER	2.5
1	A	422	ILE	2.4
1	A	352	THR	2.4
1	A	897	TYR	2.4
1	A	813	ASN	2.4
1	A	513	PHE	2.3
1	A	843	SER	2.3
1	A	100	LYS	2.3
1	A	405	VAL	2.2
1	A	504	CYS	2.2
1	A	346	LYS	2.2
1	A	115	LEU	2.2
1	A	391	LEU	2.2
1	A	252	ARG	2.2
1	A	45	ASN	2.1
1	A	466	HIS	2.1
1	A	845	ALA	2.1
1	A	112	ASN	2.1
1	A	356	LEU	2.1
1	A	364	GLY	2.1
1	A	114	ILE	2.1
1	A	253	ILE	2.1
1	A	704	TYR	2.1
1	A	66	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	694	TYR	2.0
1	A	281	ASN	2.0
1	A	495	ASN	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($\text{\AA}^2$)	Q<0.9
2	ZN	A	1	1/1	0.98	0.03	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.