



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:35 AM UTC

PDB ID : 8XPN / pdb_00008xpn
Title : The Crystal Structure of USP8 from Biortus.
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Deposited on : 2024-01-04
Resolution : 2.10 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

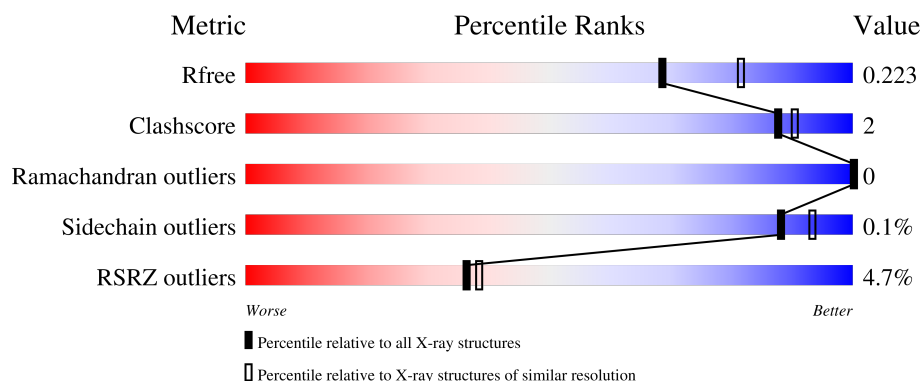
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	377	5% 86% 5% 10%
1	B	377	3% 89% • 8%
1	C	377	5% 79% 8% 13%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8768 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 Ubiquitin carboxyl-terminal hydrolase 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	1	0
			2749	1745	478	510	16			
1	B	347	Total	C	N	O	S	0	1	0
			2827	1795	499	518	15			
1	C	327	Total	C	N	O	S	0	1	0
			2639	1684	456	485	14			

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

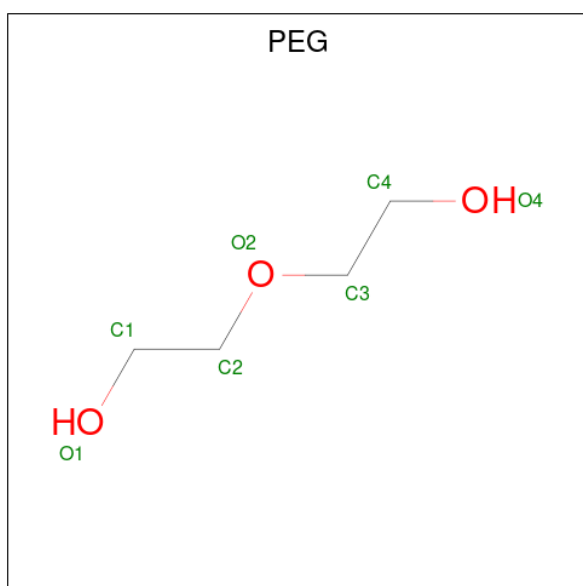
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			7	4	3		

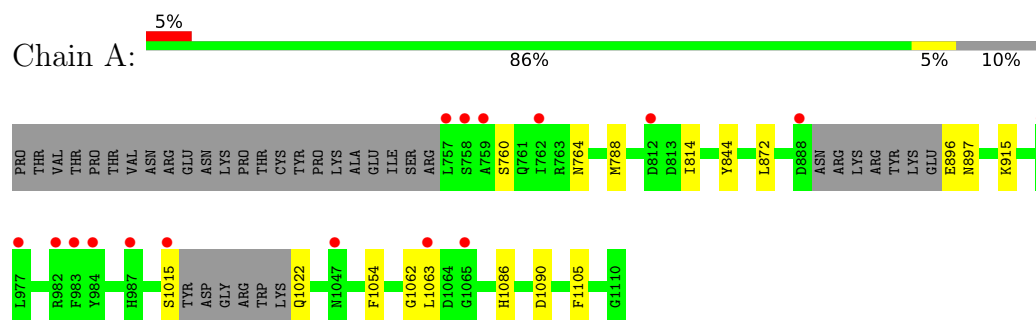
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	152	Total 152	O 152	0	0
5	B	237	Total 237	O 237	0	0
5	C	146	Total 146	O 146	0	0

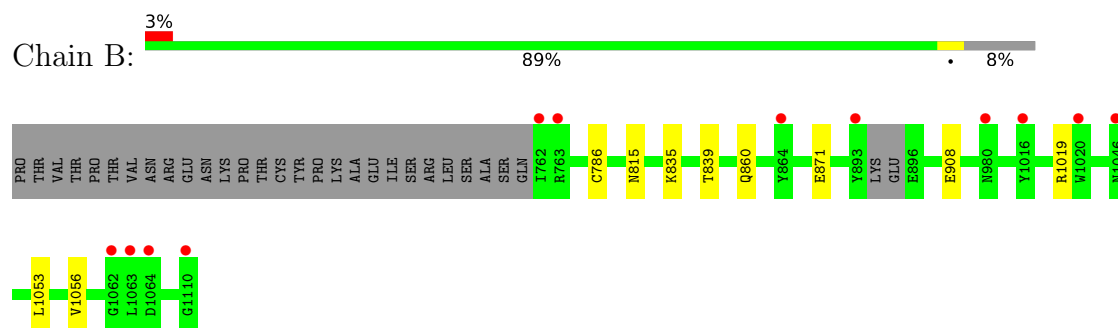
3 Residue-property plots [i](#)

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.

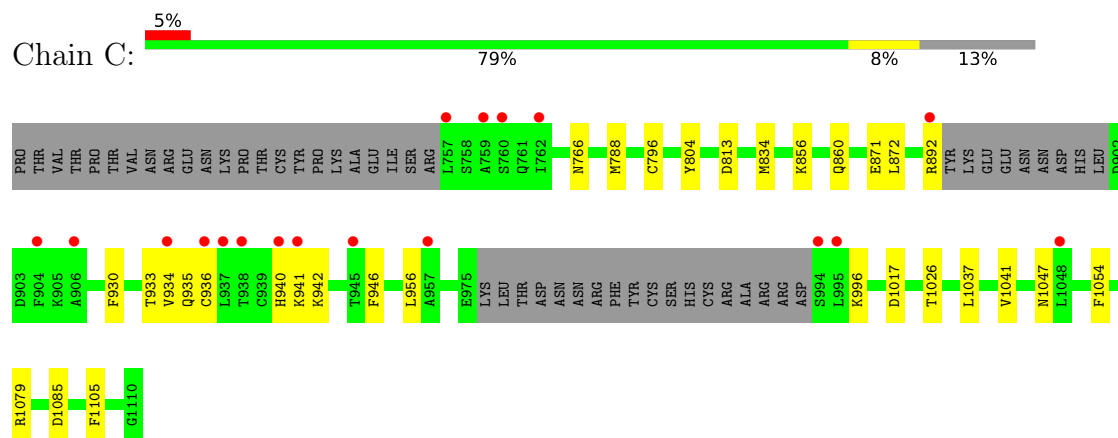
- Molecule 1: Ubiquitin carboxyl-terminal hydrolase 8



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- Molecule 1: Ubiquitin carboxyl-terminal hydrolase 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.83Å 109.34Å 180.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.78 – 2.10 48.78 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.78-2.10) 99.4 (48.78-2.10)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.176 , 0.216 0.185 , 0.223	Depositor DCC
R_{free} test set	3285 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8768	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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, PEG, 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	0.49	0/2812	0.88	1/3788 (0.0%)
1	B	0.52	0/2895	0.90	1/3899 (0.0%)
1	C	0.51	0/2701	0.89	2/3637 (0.1%)
All	All	0.51	0/8408	0.89	4/11324 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	908	GLU	CB-CG-CD	6.24	123.22	112.60
1	C	1085	ASP	CB-CA-C	5.86	122.07	110.42
1	A	1090	ASP	CA-CB-CG	5.32	117.92	112.60
1	C	766	ASN	O-C-N	-5.06	119.20	121.53

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	2749	0	2695	9	0
1	B	2827	0	2772	6	0
1	C	2639	0	2606	18	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	B	8	0	12	1	0
4	C	7	0	10	1	0
5	A	152	0	0	2	0
5	B	237	0	0	1	0
5	C	146	0	0	4	0
All	All	8768	0	8095	32	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 2.

All (32) 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:760:SER:O	1:A:764:ASN:HB2	1.99	0.62
1:A:788:MET:HA	1:A:872:LEU:HD22	1.85	0.58
1:C:860:GLN:NE2	5:C:1302:HOH:O	2.35	0.57
1:C:935:GLN:HA	1:C:941:LYS:O	2.06	0.55
1:C:860:GLN:NE2	1:C:871:GLU:OE1	2.40	0.52
1:B:786:CYS:SG	5:B:1424:HOH:O	2.55	0.52
1:C:892:ARG:NH1	5:C:1306:HOH:O	2.42	0.52
1:C:933:THR:O	1:C:996:LYS:HA	2.11	0.51
1:C:1079:ARG:HG2	5:C:1323:HOH:O	2.10	0.51
1:A:896:GLU:OE1	1:B:1019:ARG:NH2	2.44	0.51
1:B:860:GLN:NE2	1:B:871:GLU:OE2	2.43	0.50
1:C:1017:ASP:OD1	1:C:1017:ASP:C	2.54	0.50
1:C:956:LEU:HD13	1:C:1026:THR:HB	1.94	0.49
1:C:936:CYS:O	1:C:940:HIS:HA	2.13	0.49
1:A:1015:SER:HB3	1:A:1022:GLN:HB2	1.95	0.48
1:C:796:CYS:HB2	1:C:834:MET:HE1	1.96	0.48
1:B:835:LYS:O	1:B:839:THR:HG23	2.13	0.47
1:C:788:MET:HA	1:C:872:LEU:CD2	2.44	0.47
1:C:1047:ASN:O	5:C:1301:HOH:O	2.20	0.47
1:C:934:VAL:O	1:C:942:LYS:HA	2.14	0.47
1:C:1037:LEU:O	1:C:1041:VAL:HG23	2.14	0.47
1:B:1053:LEU:HD21	1:B:1056:VAL:CG2	2.46	0.46
1:B:815:ASN:HD21	3:B:1201:EDO:H11	1.80	0.46
1:C:930:PHE:O	1:C:946:PHE:HA	2.16	0.45
1:A:1054:PHE:CZ	1:A:1105:PHE:HB3	2.52	0.45
1:A:1062:GLY:O	1:A:1063:LEU:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:856:LYS:HA	4:C:1201:PEG:H41	2.01	0.42
1:A:897:ASN:HA	5:A:1395:HOH:O	2.19	0.42
1:C:1054:PHE:CZ	1:C:1105:PHE:HB3	2.55	0.41
1:A:844:TYR:CG	1:A:1086:HIS:HB2	2.56	0.40
1:A:915:LYS:NZ	5:A:1312:HOH:O	2.53	0.40
1:C:804:TYR:OH	1:C:813:ASP:OD2	2.28	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	336/377 (89%)	323 (96%)	13 (4%)	0	100	100
1	B	344/377 (91%)	337 (98%)	7 (2%)	0	100	100
1	C	322/377 (85%)	313 (97%)	9 (3%)	0	100	100
All	All	1002/1131 (89%)	973 (97%)	29 (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	303/336 (90%)	302 (100%)	1 (0%)	86	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	309/336 (92%)	309 (100%)	0	100	100
1	C	289/336 (86%)	289 (100%)	0	100	100
All	All	901/1008 (89%)	900 (100%)	1 (0%)	88	93

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	814	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	841	GLN
1	A	860	GLN
1	A	866	GLN
1	A	867	GLN
1	A	1034	ASN
1	B	815	ASN
1	B	866	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 3 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
3	EDO	B	1201	-	3,3,3	0.21	0	2,2,2	0.21	0
4	PEG	C	1201	-	6,6,6	0.29	0	5,5,5	0.20	0
3	EDO	B	1202	-	3,3,3	0.21	0	2,2,2	0.18	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
3	EDO	B	1201	-	-	1/1/1/1	-
4	PEG	C	1201	-	-	3/4/4/4	-
3	EDO	B	1202	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1201	PEG	O1-C1-C2-O2
3	B	1202	EDO	O1-C1-C2-O2
4	C	1201	PEG	O2-C3-C4-O4
3	B	1201	EDO	O1-C1-C2-O2
4	C	1201	PEG	C4-C3-O2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1201	EDO	1	0
4	C	1201	PEG	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

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	341/377 (90%)	0.33	18 (5%) 32 34	18, 37, 77, 93	1 (0%)
1	B	347/377 (92%)	-0.07	12 (3%) 47 49	18, 28, 54, 96	1 (0%)
1	C	327/377 (86%)	0.31	18 (5%) 30 32	16, 34, 76, 101	1 (0%)
All	All	1015/1131 (89%)	0.19	48 (4%) 36 38	16, 33, 73, 101	3 (0%)

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	762	ILE	6.2
1	C	757	LEU	6.0
1	A	757	LEU	5.0
1	C	762	ILE	4.9
1	A	762	ILE	4.8
1	B	1020	TRP	4.5
1	C	759	ALA	4.2
1	A	759	ALA	3.9
1	C	937	LEU	3.7
1	A	1063	LEU	3.6
1	C	904	PHE	3.5
1	A	983	PHE	3.4
1	C	995	LEU	3.3
1	A	977	LEU	3.2
1	A	987	HIS	3.0
1	C	940	HIS	2.9
1	C	760	SER	2.9
1	C	938	THR	2.9
1	C	936	CYS	2.7
1	C	1048	LEU	2.7
1	B	1046	ASN	2.7
1	A	940	HIS	2.7
1	B	1016	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1065	GLY	2.6
1	C	957	ALA	2.6
1	B	1063	LEU	2.6
1	B	980	ASN	2.5
1	B	864	TYR	2.5
1	C	994	SER	2.4
1	A	982	ARG	2.3
1	C	945	THR	2.3
1	A	888	ASP	2.3
1	A	1015	SER	2.2
1	C	941	LYS	2.2
1	C	906	ALA	2.2
1	A	984	TYR	2.2
1	B	1064	ASP	2.2
1	B	763	ARG	2.2
1	C	934	VAL	2.2
1	A	936	CYS	2.2
1	B	1110	GLY	2.1
1	B	1062	GLY	2.1
1	A	812	ASP	2.1
1	B	893	TYR	2.1
1	A	758	SER	2.1
1	C	892	ARG	2.0
1	A	1047	ASN	2.0
1	A	941	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	C	1202	1/1	0.79	0.12	99,99,99,99	0
3	EDO	B	1201	4/4	0.81	0.18	49,49,51,52	0
3	EDO	B	1202	4/4	0.81	0.15	41,46,51,55	0
4	PEG	C	1201	7/7	0.84	0.15	38,48,51,52	0
2	ZN	A	1201	1/1	0.95	0.08	56,56,56,56	0
2	ZN	B	1203	1/1	1.00	0.01	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.