



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 11:57 pm BST

PDB ID : 6MYI
Title : Pleurotus ostreatus OstreolysinA
Authors : Tomchick, D.R.; Radhakrishnan, A.; Endapally, S.
Deposited on : 2018-11-01
Resolution : 1.15 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

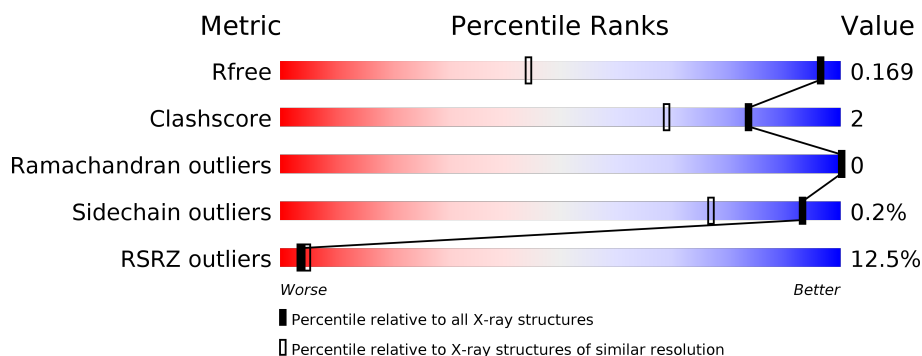
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.15 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	1492 (1.18-1.10)
Clashscore	141614	1537 (1.18-1.10)
Ramachandran outliers	138981	1483 (1.18-1.10)
Sidechain outliers	138945	1480 (1.18-1.10)
RSRZ outliers	127900	1464 (1.18-1.10)

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 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	139	<div> <div>15%</div> <div> <div></div> <div>94%</div> <div>5%</div> </div> </div>
1	B	139	<div> <div>10%</div> <div> <div></div> <div>90%</div> <div>7%</div> </div> </div>
1	C	139	<div> <div>12%</div> <div> <div></div> <div>94%</div> <div></div> </div> </div>
1	D	139	<div> <div>12%</div> <div> <div></div> <div>96%</div> <div></div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4956 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 Ostreolysin A6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	137	Total	C	N	O	S	0	3	0
			1071	675	182	213	1			
1	B	135	Total	C	N	O	S	0	5	0
			1059	665	180	213	1			
1	C	136	Total	C	N	O	S	0	7	0
			1085	683	183	218	1			
1	D	137	Total	C	N	O	S	0	3	0
			1070	676	181	211	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P83467
A	62	SER	CYS	engineered mutation	UNP P83467
A	94	SER	CYS	engineered mutation	UNP P83467
B	0	GLY	-	expression tag	UNP P83467
B	62	SER	CYS	engineered mutation	UNP P83467
B	94	SER	CYS	engineered mutation	UNP P83467
C	0	GLY	-	expression tag	UNP P83467
C	62	SER	CYS	engineered mutation	UNP P83467
C	94	SER	CYS	engineered mutation	UNP P83467
D	0	GLY	-	expression tag	UNP P83467
D	62	SER	CYS	engineered mutation	UNP P83467
D	94	SER	CYS	engineered mutation	UNP P83467

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Na	0	0
			1	1		
2	C	1	Total	Na	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 4 is water.

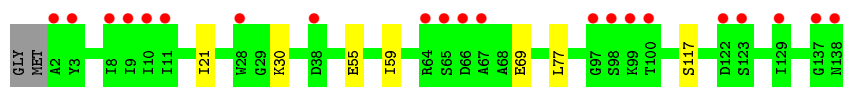
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	166	Total	O		0	0
			166	166			
4	B	158	Total	O		0	0
			158	158			
4	C	157	Total	O		0	0
			157	157			
4	D	142	Total	O		0	0
			142	142			

3 Residue-property plots [i](#)

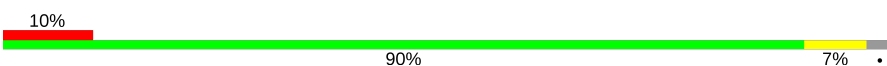
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

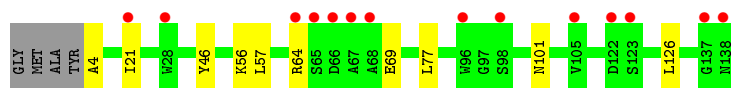
• Molecule 1: Ostreolysin A6

Chain A: 



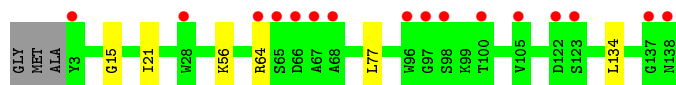
• Molecule 1: Ostreolysin A6

Chain B: 



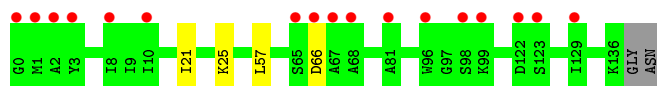
• Molecule 1: Ostreolysin A6

Chain C: 



• Molecule 1: Ostreolysin A6

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.43 Å 100.33 Å 59.02 Å 90.00° 106.43° 90.00°	Depositor
Resolution (Å)	33.30 – 1.15 33.30 – 1.15	Depositor EDS
% Data completeness (in resolution range)	90.7 (33.30-1.15) 90.1 (33.30-1.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 1.15 Å)	Xtriage
Refinement program	PHENIX (1.12_2829)	Depositor
R, R_{free}	0.142 , 0.161 0.153 , 0.169	Depositor DCC
R_{free} test set	1451 reflections (0.87%)	wwPDB-VP
Wilson B-factor (Å ²)	15.1	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.9	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	0.98	EDS
Total number of atoms	4956	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.85 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6914e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: NA, 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	0.55	1/1103 (0.1%)	0.69	0/1494
1	B	0.51	0/1096	0.67	0/1485
1	C	0.52	0/1126	0.73	0/1525
1	D	0.54	0/1102	0.73	0/1493
All	All	0.53	1/4427 (0.0%)	0.71	0/5997

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	55	GLU	CD-OE1	6.02	1.32	1.25

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	1071	0	1048	4	0
1	B	1059	0	1037	9	0
1	C	1085	0	1062	5	0
1	D	1070	0	1054	3	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	12	0	18	1	0
3	B	8	0	12	0	0
3	C	16	0	24	0	0
3	D	8	0	12	0	0
4	A	166	0	0	1	0
4	B	158	0	0	1	0
4	C	157	0	0	1	0
4	D	142	0	0	1	0
All	All	4956	0	4267	21	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 (21) 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:21[A]:ILE:HD12	1:B:57:LEU:HD23	1.78	0.66
1:D:25[B]:LYS:HG3	4:D:356:HOH:O	2.07	0.55
1:B:21[A]:ILE:CD1	1:B:57:LEU:HD23	2.37	0.54
1:B:4:ALA:N	4:B:302:HOH:O	2.43	0.50
1:B:21[A]:ILE:HD12	1:B:57:LEU:CD2	2.41	0.48
1:A:21[A]:ILE:CD1	1:A:59:ILE:HD11	2.43	0.48
1:D:21[B]:ILE:HD12	1:D:57:LEU:HD23	1.96	0.48
1:C:21[B]:ILE:HD13	1:C:77:LEU:CD2	2.46	0.45
1:B:64:ARG:HB2	1:B:69:GLU:HG2	1.98	0.45
1:D:66:ASP:OD1	1:D:66:ASP:N	2.50	0.44
1:B:101:ASN:HB3	1:B:126:LEU:HD13	1.99	0.44
1:C:21[B]:ILE:HD13	1:C:77:LEU:HD23	2.00	0.44
1:A:21[B]:ILE:HD13	1:A:77:LEU:CD2	2.48	0.43
1:A:117:SER:OG	3:A:204:EDO:H21	2.19	0.43
1:B:21[B]:ILE:CD1	1:B:46:TYR:HB3	2.50	0.41
1:B:21[B]:ILE:HG22	1:B:77:LEU:HD23	2.01	0.41
1:A:69:GLU:HB3	4:A:333:HOH:O	2.20	0.41
1:C:64:ARG:NH1	4:C:310:HOH:O	2.55	0.40
1:C:15:GLY:HA3	1:C:134:LEU:HD12	2.04	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	138/139 (99%)	135 (98%)	3 (2%)	0	100	100
1	B	138/139 (99%)	136 (99%)	2 (1%)	0	100	100
1	C	141/139 (101%)	136 (96%)	5 (4%)	0	100	100
1	D	138/139 (99%)	136 (99%)	2 (1%)	0	100	100
All	All	555/556 (100%)	543 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	115/113 (102%)	114 (99%)	1 (1%)	78	46
1	B	116/113 (103%)	116 (100%)	0	100	100
1	C	119/113 (105%)	119 (100%)	0	100	100
1	D	115/113 (102%)	115 (100%)	0	100	100
All	All	465/452 (103%)	464 (100%)	1 (0%)	93	77

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

Mol	Chain	Res	Type
1	A	30	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no

such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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	C	202	-	3,3,3	0.47	0	2,2,2	0.12	0
3	EDO	D	202	-	3,3,3	0.40	0	2,2,2	0.41	0
3	EDO	D	203	-	3,3,3	0.42	0	2,2,2	0.24	0
3	EDO	B	203	-	3,3,3	0.47	0	2,2,2	0.19	0
3	EDO	C	205	-	3,3,3	0.49	0	2,2,2	0.25	0
3	EDO	C	204	-	3,3,3	0.36	0	2,2,2	0.79	0
3	EDO	A	204	-	3,3,3	0.41	0	2,2,2	0.68	0
3	EDO	C	203	-	3,3,3	0.56	0	2,2,2	0.38	0
3	EDO	A	203	-	3,3,3	0.30	0	2,2,2	0.48	0
3	EDO	A	202	-	3,3,3	0.43	0	2,2,2	0.97	0
3	EDO	B	202	-	3,3,3	0.40	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
3	EDO	C	202	-	-	0/1/1/1	-
3	EDO	D	202	-	-	0/1/1/1	-
3	EDO	D	203	-	-	0/1/1/1	-
3	EDO	B	203	-	-	0/1/1/1	-
3	EDO	C	205	-	-	0/1/1/1	-
3	EDO	C	204	-	-	0/1/1/1	-
3	EDO	A	204	-	-	1/1/1/1	-
3	EDO	C	203	-	-	1/1/1/1	-
3	EDO	A	203	-	-	1/1/1/1	-
3	EDO	A	202	-	-	0/1/1/1	-
3	EDO	B	202	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	203	EDO	O1-C1-C2-O2
3	A	204	EDO	O1-C1-C2-O2
3	C	203	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	204	EDO	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	137/139 (98%)	1.02	21 (15%) 2 3	11, 15, 34, 46	0
1	B	135/139 (97%)	0.76	14 (10%) 6 7	13, 18, 40, 56	0
1	C	136/139 (97%)	1.03	16 (11%) 4 6	12, 19, 39, 60	0
1	D	137/139 (98%)	0.90	17 (12%) 4 5	11, 18, 32, 45	0
All	All	545/556 (98%)	0.93	68 (12%) 3 5	11, 18, 38, 60	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	TYR	12.8
1	C	66	ASP	12.1
1	A	138	ASN	8.7
1	B	66	ASP	8.7
1	C	3	TYR	7.3
1	D	66	ASP	7.2
1	B	138	ASN	6.7
1	C	137	GLY	6.4
1	C	65	SER	6.4
1	C	138	ASN	6.3
1	C	123	SER	6.3
1	D	123	SER	6.2
1	B	123	SER	6.1
1	A	2	ALA	5.9
1	B	65	SER	5.7
1	A	98	SER	5.6
1	C	122	ASP	5.4
1	C	96	TRP	5.1
1	D	3	TYR	4.6
1	D	96	TRP	4.5
1	C	67	ALA	4.5

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Mol	Chain	Res	Type	RSRZ
1	D	68	ALA	4.4
1	A	38	ASP	4.3
1	D	67	ALA	4.2
1	A	97	GLY	4.1
1	A	99	LYS	4.0
1	B	67	ALA	3.9
1	D	0	GLY	3.9
1	B	28	TRP	3.8
1	A	64	ARG	3.7
1	D	2	ALA	3.7
1	D	1	MET	3.6
1	A	123	SER	3.6
1	C	98	SER	3.5
1	D	98	SER	3.3
1	B	64	ARG	3.3
1	A	137	GLY	3.3
1	A	28	TRP	3.2
1	A	65	SER	3.1
1	A	122	ASP	3.1
1	D	99	LYS	3.1
1	B	96	TRP	3.0
1	D	8	ILE	3.0
1	D	65	SER	3.0
1	D	122	ASP	3.0
1	B	137	GLY	3.0
1	B	98	SER	2.9
1	C	28	TRP	2.9
1	A	11[A]	ILE	2.8
1	B	68	ALA	2.8
1	D	81	ALA	2.8
1	C	97	GLY	2.7
1	A	8	ILE	2.7
1	C	68	ALA	2.6
1	A	100	THR	2.5
1	C	64	ARG	2.4
1	C	100	THR	2.3
1	B	122	ASP	2.3
1	A	67	ALA	2.2
1	A	66	ASP	2.2
1	A	10	ILE	2.2
1	D	10	ILE	2.2
1	D	129	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	9	ILE	2.2
1	B	105	VAL	2.1
1	A	129	ILE	2.0
1	B	21[A]	ILE	2.0
1	C	105	VAL	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 carbohydrates 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	EDO	C	203	4/4	0.57	0.38	33,35,38,43	0
3	EDO	B	202	4/4	0.69	0.17	23,29,29,36	0
3	EDO	D	203	4/4	0.70	0.19	25,29,35,43	0
3	EDO	A	204	4/4	0.78	0.14	24,29,30,32	0
3	EDO	C	204	4/4	0.79	0.20	24,29,29,33	0
3	EDO	A	202	4/4	0.81	0.19	20,25,30,37	0
3	EDO	A	203	4/4	0.81	0.16	35,35,36,41	0
3	EDO	C	205	4/4	0.86	0.20	31,31,34,40	0
3	EDO	D	202	4/4	0.86	0.16	22,24,28,29	0
3	EDO	B	203	4/4	0.91	0.18	22,27,27,27	0
2	NA	D	201	1/1	0.91	0.10	43,43,43,43	0
2	NA	B	201	1/1	0.93	0.10	42,42,42,42	0
2	NA	C	201	1/1	0.93	0.14	34,34,34,34	0
3	EDO	C	202	4/4	0.95	0.11	14,14,19,20	0
2	NA	A	201	1/1	0.96	0.12	22,22,22,22	0

6.5 Other polymers

There are no such residues in this entry.