Full wwPDB X-ray Structure Validation Report ⓘ

Feb 18, 2024 – 09:33 AM EST

PDB ID	:	4E4W
Title	:	Structure of the C-terminal domain of the Saccharomyces cerevisiae MUTL alpha (MLH1/PMS1) heterodimer
Authors	:	Gueneau, E.; Legrand, P.; Charbonnier, J.B.
Deposited on	:	2012-03-13
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:

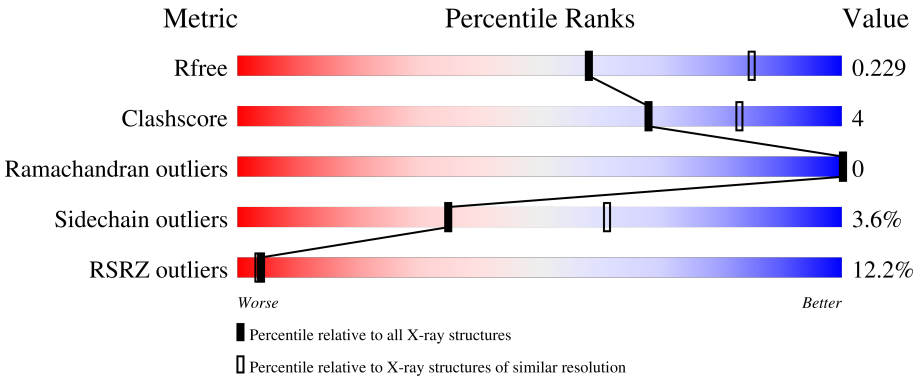
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 <=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	285	5% 78% 14% 8%
2	B	239	19% 81% 8% 11%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4032 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.

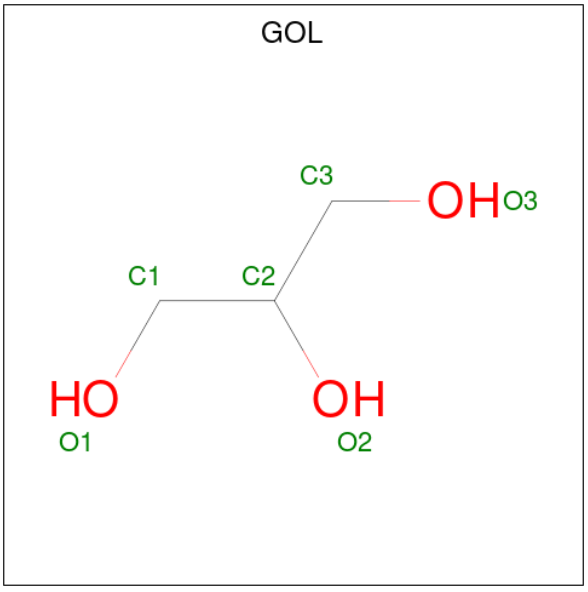
- Molecule 1 is a protein called DNA mismatch repair protein MLH1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	261	2135	1377	346	405	7	0	1	0

- Molecule 2 is a protein called DNA mismatch repair protein PMS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	213	1673	1064	287	312	10	0	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0

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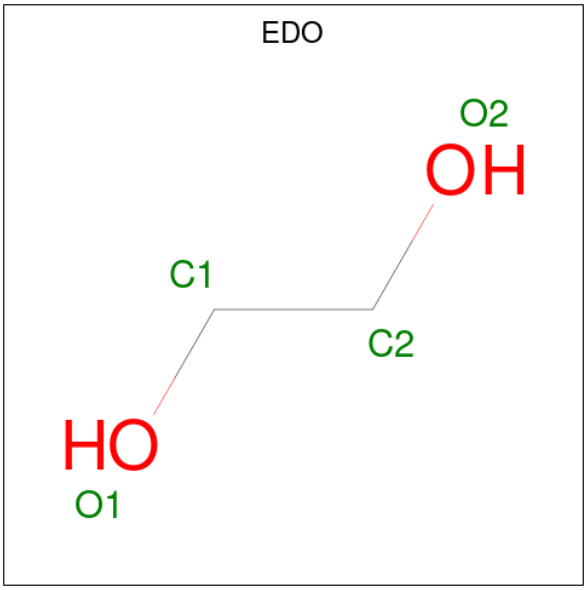
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	2	Total Zn 2 2	0	0

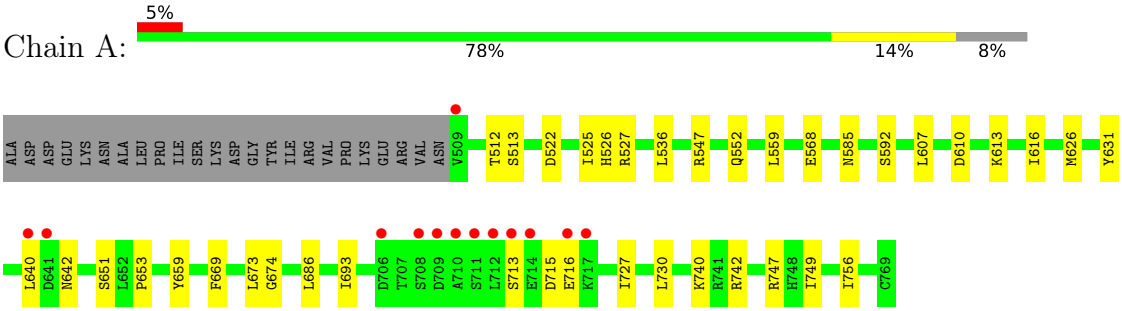
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	128	Total O 128 128	0	0
6	B	52	Total O 52 52	0	0

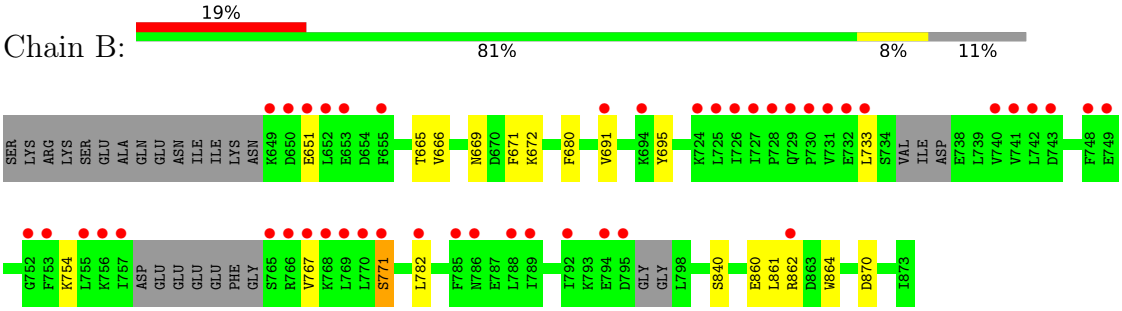
3 Residue-property plots (i)

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: DNA mismatch repair protein MLH1



• Molecule 2: DNA mismatch repair protein PMS1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	187.21Å 66.14Å 74.01Å 90.00° 90.75° 90.00°	Depositor
Resolution (Å)	39.79 – 2.50 39.79 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.79-2.50) 99.7 (39.79-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.33 (at 2.51Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.10.0, BUSTER 2.10.0	Depositor
R, R_{free}	0.170 , 0.210 0.189 , 0.229	Depositor DCC
R_{free} test set	1568 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	41.9	Xtriage
Anisotropy	0.978	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 66.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4032	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: EDO, GOL, 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	0.54	0/2178	0.77	0/2944
2	B	0.47	0/1702	0.67	0/2291
All	All	0.51	0/3880	0.73	0/5235

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

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	2135	0	2152	24	0
2	B	1673	0	1612	9	0
3	A	30	0	40	5	0
4	A	12	0	18	0	0
5	B	2	0	0	0	0
6	A	128	0	0	1	0
6	B	52	0	0	0	0
All	All	4032	0	3822	29	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 4.

All (29) 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:616:ILE:HG23	1:A:674:GLY:HA3	1.60	0.83
1:A:522:ASP:HA	1:A:525:ILE:HD12	1.71	0.73
1:A:713:SER:HB3	1:A:716:GLU:HG2	1.76	0.68
1:A:742:ARG:HD2	3:A:801:GOL:H32	1.81	0.62
2:B:754:LYS:HB2	2:B:771:SER:HB2	1.83	0.61
2:B:665:THR:HG23	2:B:666:VAL:HG23	1.82	0.60
1:A:559:LEU:HD23	2:B:864:TRP:CZ3	2.37	0.59
1:A:640:LEU:HD23	1:A:642:ASN:H	1.68	0.58
1:A:568:GLU:HG3	1:A:749:ILE:CD1	2.37	0.54
1:A:585:ASN:HB3	6:A:977:HOH:O	2.08	0.53
1:A:568:GLU:HG3	1:A:749:ILE:HD11	1.91	0.53
2:B:669:ASN:HA	2:B:672:LYS:HE3	1.94	0.49
1:A:527:ARG:H	3:A:805:GOL:H11	1.78	0.49
1:A:559:LEU:HD13	1:A:756:ILE:HD13	1.97	0.46
2:B:860:GLU:HB3	2:B:862:ARG:HH21	1.81	0.45
1:A:525:ILE:HG22	3:A:802:GOL:H32	1.99	0.45
1:A:653:PRO:HG3	1:A:693:ILE:HD13	1.98	0.44
1:A:547:ARG:NH2	2:B:870:ASP:OD2	2.41	0.43
1:A:526:HIS:HA	3:A:805:GOL:H11	2.00	0.42
1:A:607:LEU:O	1:A:613:LYS:HE3	2.20	0.42
1:A:669:PHE:O	1:A:673:LEU:HB2	2.19	0.42
1:A:747:ARG:HH21	3:A:805:GOL:H12	1.85	0.42
1:A:659:TYR:CE1	1:A:730:LEU:HD21	2.55	0.41
1:A:552:GLN:HG3	2:B:680:PHE:HE2	1.85	0.41
1:A:631:TYR:OH	1:A:686:LEU:HA	2.21	0.41
1:A:536:LEU:HG	1:A:740:LYS:HG3	2.03	0.41
1:A:559:LEU:HD21	2:B:861:LEU:HD21	2.03	0.41
1:A:631:TYR:O	1:A:653:PRO:HB3	2.21	0.40
2:B:671:PHE:HB2	2:B:840:SER:HB3	2.03	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	260/285 (91%)	253 (97%)	7 (3%)	0	100	100
2	B	205/239 (86%)	195 (95%)	10 (5%)	0	100	100
All	All	465/524 (89%)	448 (96%)	17 (4%)	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	243/264 (92%)	235 (97%)	8 (3%)	38	64
2	B	180/224 (80%)	173 (96%)	7 (4%)	32	57
All	All	423/488 (87%)	408 (96%)	15 (4%)	35	62

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	512	THR
1	A	513	SER
1	A	592	SER
1	A	610	ASP
1	A	626	MET
1	A	651	SER
1	A	715	ASP
1	A	727	ILE
2	B	651	GLU
2	B	691	VAL
2	B	695	TYR
2	B	733	LEU
2	B	767	VAL
2	B	771	SER
2	B	782	LEU

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
4	EDO	A	806	-	3,3,3	0.71	0	2,2,2	0.15	0
3	GOL	A	804	-	5,5,5	0.12	0	5,5,5	0.31	0
3	GOL	A	802	-	5,5,5	0.13	0	5,5,5	0.50	0
3	GOL	A	801	-	5,5,5	0.14	0	5,5,5	0.38	0
3	GOL	A	805	-	5,5,5	0.17	0	5,5,5	0.31	0
4	EDO	A	807	-	3,3,3	0.71	0	2,2,2	0.10	0
3	GOL	A	803	-	5,5,5	0.06	0	5,5,5	0.26	0
4	EDO	A	808	-	3,3,3	0.86	0	2,2,2	0.17	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
4	EDO	A	806	-	-	0/1/1/1	-
3	GOL	A	804	-	-	2/4/4/4	-
3	GOL	A	802	-	-	2/4/4/4	-
3	GOL	A	801	-	-	2/4/4/4	-
3	GOL	A	805	-	-	3/4/4/4	-
4	EDO	A	807	-	-	0/1/1/1	-
3	GOL	A	803	-	-	0/4/4/4	-
4	EDO	A	808	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	802	GOL	O1-C1-C2-C3
3	A	804	GOL	C1-C2-C3-O3
3	A	805	GOL	O1-C1-C2-C3
3	A	802	GOL	O1-C1-C2-O2
3	A	804	GOL	O2-C2-C3-O3
4	A	808	EDO	O1-C1-C2-O2
3	A	801	GOL	C1-C2-C3-O3
3	A	805	GOL	C1-C2-C3-O3
3	A	801	GOL	O2-C2-C3-O3
3	A	805	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	GOL	1	0
3	A	801	GOL	1	0
3	A	805	GOL	3	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, 95^{th} 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	261/285 (91%)	-0.00	13 (4%) 28 30	44, 60, 115, 148	0
2	B	213/239 (89%)	0.91	45 (21%) 1 0	46, 85, 158, 200	0
All	All	474/524 (90%)	0.41	58 (12%) 4 3	44, 66, 146, 200	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	733	LEU	8.8
2	B	726	ILE	7.9
2	B	767	VAL	6.9
1	A	509	VAL	6.2
2	B	743	ASP	6.1
2	B	755	LEU	5.6
2	B	785	PHE	5.2
2	B	731	VAL	5.0
2	B	770	LEU	4.9
2	B	792	ILE	4.9
1	A	708	SER	4.8
2	B	652	LEU	4.8
2	B	732	GLU	4.6
2	B	742	LEU	4.6
2	B	728	PRO	4.5
2	B	753	PHE	4.5
2	B	782	LEU	4.4
2	B	756	LYS	4.4
2	B	757	ILE	4.4
2	B	771	SER	4.3
1	A	641	ASP	4.2
2	B	725	LEU	4.2
2	B	769	LEU	4.2
2	B	788	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
2	B	740	VAL	3.8
2	B	786	ASN	3.8
2	B	649	LYS	3.7
2	B	730	PRO	3.5
1	A	711	SER	3.5
2	B	768	LYS	3.4
1	A	709	ASP	3.3
2	B	694	LYS	3.3
2	B	748	PHE	3.3
2	B	651	GLU	3.2
2	B	794	GLU	3.2
2	B	650	ASP	3.2
2	B	729	GLN	3.2
1	A	710	ALA	3.2
1	A	706	ASP	3.1
1	A	712	LEU	3.1
2	B	653	GLU	3.1
2	B	741	VAL	3.0
2	B	789	ILE	3.0
2	B	691	VAL	2.9
2	B	727	ILE	2.7
1	A	714	GLU	2.7
2	B	724	LYS	2.6
2	B	766	ARG	2.6
2	B	862	ARG	2.5
1	A	640	LEU	2.5
1	A	713	SER	2.4
2	B	655	PHE	2.2
1	A	716	GLU	2.2
2	B	765	SER	2.2
1	A	717	LYS	2.2
2	B	752	GLY	2.1
2	B	795	ASP	2.1
2	B	749	GLU	2.1

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, 95^{th} 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	GOL	A	804	6/6	0.81	0.21	76,82,82,84	0
3	GOL	A	802	6/6	0.89	0.24	52,62,67,68	0
3	GOL	A	801	6/6	0.89	0.23	73,79,80,81	0
4	EDO	A	808	4/4	0.90	0.30	53,58,62,64	0
3	GOL	A	805	6/6	0.91	0.21	59,71,75,78	0
3	GOL	A	803	6/6	0.91	0.17	74,77,78,78	0
4	EDO	A	807	4/4	0.92	0.19	73,77,78,80	0
4	EDO	A	806	4/4	0.95	0.11	63,64,65,65	0
5	ZN	B	902	1/1	0.99	0.13	57,57,57,57	0
5	ZN	B	901	1/1	1.00	0.14	58,58,58,58	0

6.5 Other polymers (i)

There are no such residues in this entry.