



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 8, 2016 – 07:32 PM EST

PDB ID : 4NCX  
Title : Crystal Structure of Prolyl-tRNA synthetase (ProRS, Proline-tRNA ligase)  
from Plasmodium falciparum 3D7  
Authors : Seattle Structural Genomics Center for Infectious Disease  
Deposited on : 2013-10-25  
Resolution : 1.85 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028320  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028320

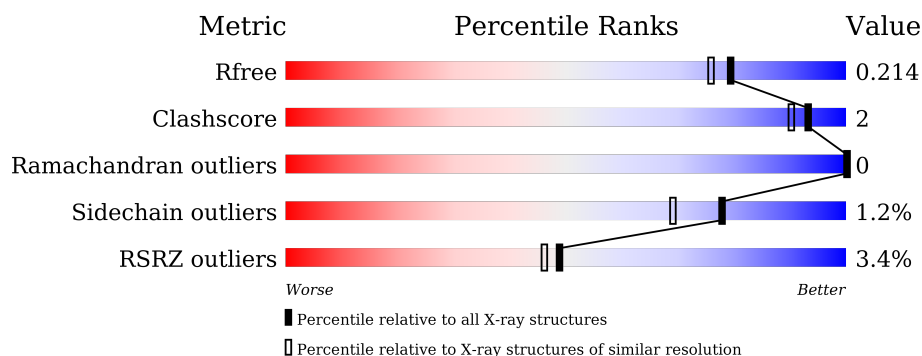
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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))
$R_{free}$	91344	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	506	<div> <div>5%</div> <div>83%</div> <div>5%</div> <div>11%</div> </div>
1	B	506	<div> <div>%</div> <div>82%</div> <div>•</div> <div>14%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	A	803	-	-	-	X
2	EDO	B	802	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7861 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 Proline-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	0	6	0
			3650	2347	607	675	21			
1	B	433	Total	C	N	O	S	0	9	0
			3563	2295	591	656	21			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	MET	-	EXPRESSION TAG	UNP Q8I5R7
A	242	ALA	-	EXPRESSION TAG	UNP Q8I5R7
A	243	HIS	-	EXPRESSION TAG	UNP Q8I5R7
A	244	HIS	-	EXPRESSION TAG	UNP Q8I5R7
A	245	HIS	-	EXPRESSION TAG	UNP Q8I5R7
A	246	HIS	-	EXPRESSION TAG	UNP Q8I5R7
A	247	HIS	-	EXPRESSION TAG	UNP Q8I5R7
A	248	HIS	-	EXPRESSION TAG	UNP Q8I5R7
B	241	MET	-	EXPRESSION TAG	UNP Q8I5R7
B	242	ALA	-	EXPRESSION TAG	UNP Q8I5R7
B	243	HIS	-	EXPRESSION TAG	UNP Q8I5R7
B	244	HIS	-	EXPRESSION TAG	UNP Q8I5R7
B	245	HIS	-	EXPRESSION TAG	UNP Q8I5R7
B	246	HIS	-	EXPRESSION TAG	UNP Q8I5R7
B	247	HIS	-	EXPRESSION TAG	UNP Q8I5R7
B	248	HIS	-	EXPRESSION TAG	UNP Q8I5R7

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	318	Total	O	0	8
			326	326		

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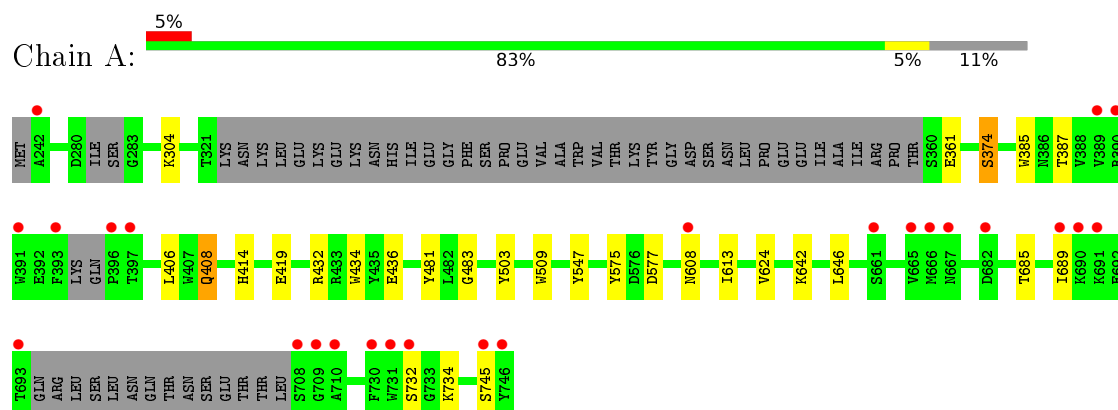
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	286	Total	O	0	9
			295	295		

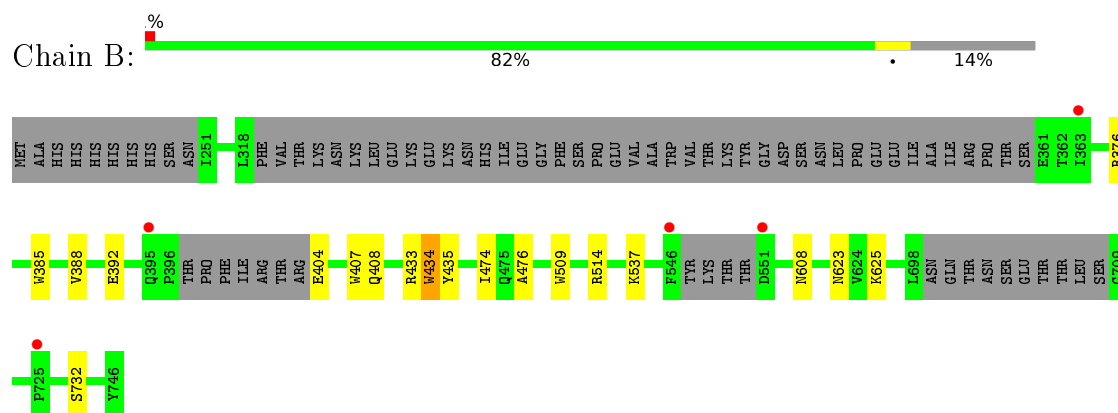
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Proline-tRNA ligase



#### • Molecule 1: Proline-tRNA ligase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	147.96 Å   91.38 Å   110.84 Å 90.00°   129.48°   90.00°	Depositor
Resolution (Å)	46.46 – 1.85 46.46 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.46-1.85) 99.5 (46.46-1.85)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.12 (at 1.86 Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.169   ,   0.206 0.178   ,   0.214	Depositor DCC
$R_{free}$ test set	4832 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36   ,   63.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7861	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, CL

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	0.69	1/3742 (0.0%)	0.75	0/5071
1	B	0.66	0/3656	0.77	3/4947 (0.1%)
All	All	0.68	1/7398 (0.0%)	0.76	3/10018 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	361	GLU	CD-OE1	5.40	1.31	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	433	ARG	NE-CZ-NH2	-9.50	115.55	120.30
1	B	433	ARG	NE-CZ-NH1	8.83	124.72	120.30
1	B	434	TRP	CA-CB-CG	5.33	123.83	113.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	732	SER	Peptide

## 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	3650	0	3523	15	0
1	B	3563	0	3456	8	1
2	A	16	0	24	4	0
2	B	8	0	12	0	0
3	A	2	0	0	1	0
3	B	1	0	0	0	0
4	A	326	0	0	8	1
4	B	295	0	0	2	0
All	All	7861	0	7015	27	2

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 (27) 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:376[A]:ARG:HD2	4:B:1095:HOH:O	1.64	0.97
1:A:642:LYS:O	1:A:646:LEU:HD13	1.82	0.79
1:A:503:TYR:OH	4:A:1059:HOH:O	2.12	0.65
1:A:414:HIS:HD1	1:A:419:GLU:HG2	1.68	0.58
1:A:304:LYS:NZ	4:A:1112:HOH:O	2.39	0.55
2:A:803:EDO:H21	4:A:934:HOH:O	2.09	0.53
1:A:387:THR:HG22	1:A:406:LEU:HD22	1.91	0.52
1:A:414:HIS:ND1	1:A:419:GLU:HG2	2.25	0.52
3:A:806:CL:CL	4:A:1098[A]:HOH:O	2.56	0.52
1:B:388:VAL:HG23	1:B:407:TRP:HZ3	1.74	0.51
1:A:432:ARG:O	1:A:436[A]:GLU:HG3	2.14	0.48
2:A:804:EDO:H12	1:B:537:LYS:HE2	1.97	0.47
1:A:374:SER:HB3	4:A:1168:HOH:O	2.14	0.47
1:B:435:TYR:CZ	1:B:476:ALA:HB1	2.50	0.46
1:B:608:ASN:O	1:B:625:LYS:NZ	2.46	0.46
1:B:404:GLU:CD	4:B:1107:HOH:O	2.54	0.45
2:A:804:EDO:H21	4:A:915:HOH:O	2.16	0.45
1:A:547:TYR:HE1	4:A:1100:HOH:O	1.99	0.45
1:A:613:ILE:HD12	1:A:624:VAL:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:803:EDO:C2	4:A:934:HOH:O	2.65	0.43
1:B:385:TRP:CZ3	1:B:408:GLN:HB2	2.54	0.42
1:A:732:SER:OG	1:A:734:LYS:N	2.47	0.42
1:A:385:TRP:CE3	1:A:408:GLN:HB3	2.56	0.41
1:A:481:TYR:CZ	1:A:483:GLY:HA2	2.56	0.41
1:B:474:ILE:HD11	1:B:514:ARG:HD3	2.03	0.41
1:A:575:TYR:CZ	1:A:577:ASP:HB3	2.55	0.41
1:A:685:THR:O	1:A:689:ILE:HG12	2.21	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:392:GLU:O	1:B:392:GLU:O[2_555]	1.17	1.03
4:A:1033:HOH:O	4:A:1033:HOH:O[2_555]	2.16	0.04

## 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	445/506 (88%)	437 (98%)	8 (2%)	0	100	100
1	B	432/506 (85%)	421 (98%)	11 (2%)	0	100	100
All	All	877/1012 (87%)	858 (98%)	19 (2%)	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	394/460 (86%)	388 (98%)	6 (2%)	72	60
1	B	383/460 (83%)	380 (99%)	3 (1%)	86	82
All	All	777/920 (84%)	768 (99%)	9 (1%)	78	69

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	374	SER
1	A	408	GLN
1	A	434	TRP
1	A	509	TRP
1	A	608	ASN
1	A	745	SER
1	B	434	TRP
1	B	509	TRP
1	B	623	ASN

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

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	$\# Z  > 2$
2	EDO	A	801	-	3,3,3	0.52	0	2,2,2	0.23	0
2	EDO	A	802	-	3,3,3	0.33	0	2,2,2	0.86	0
2	EDO	A	803	-	3,3,3	0.35	0	2,2,2	0.28	0
2	EDO	A	804	-	3,3,3	0.51	0	2,2,2	0.97	0
2	EDO	B	801	-	3,3,3	0.38	0	2,2,2	0.44	0
2	EDO	B	802	-	3,3,3	0.45	0	2,2,2	0.73	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
2	EDO	A	801	-	-	0/1/1/1	0/0/0/0
2	EDO	A	802	-	-	0/1/1/1	0/0/0/0
2	EDO	A	803	-	-	0/1/1/1	0/0/0/0
2	EDO	A	804	-	-	0/1/1/1	0/0/0/0
2	EDO	B	801	-	-	0/1/1/1	0/0/0/0
2	EDO	B	802	-	-	0/1/1/1	0/0/0/0

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.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	803	EDO	2	0
2	A	804	EDO	2	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	449/506 (88%)	0.03	25 (5%) 28 26	15, 29, 61, 79	0
1	B	433/506 (85%)	-0.24	5 (1%) 81 81	15, 31, 55, 91	0
All	All	882/1012 (87%)	-0.10	30 (3%) 49 46	15, 30, 59, 91	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	391	TRP	7.9
1	B	363	ILE	6.8
1	A	393	PHE	5.7
1	A	708	SER	4.2
1	A	730	PHE	3.6
1	A	689	ILE	3.5
1	B	546	PHE	3.5
1	A	731	TRP	3.3
1	A	665	VAL	3.3
1	A	667	ASN	3.3
1	A	242	ALA	3.3
1	A	396	PRO	3.2
1	A	666	MET	3.1
1	A	709	GLY	3.0
1	B	395	GLN	2.9
1	A	682	ASP	2.6
1	A	389	VAL	2.6
1	B	551	ASP	2.6
1	A	732	SER	2.5
1	A	710	ALA	2.4
1	A	661	SER	2.4
1	A	397	THR	2.4
1	A	691	LYS	2.3
1	A	746	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	745	SER	2.2
1	A	608	ASN	2.1
1	B	725	PRO	2.1
1	A	690	LYS	2.0
1	A	390	ARG	2.0
1	A	693	THR	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	EDO	B	802	4/4	0.89	0.16	5.83	42,45,45,49	0
2	EDO	A	803	4/4	0.94	0.17	4.45	29,30,36,40	0
2	EDO	A	802	4/4	0.90	0.15	1.43	33,34,41,46	0
2	EDO	B	801	4/4	0.99	0.11	-0.09	20,23,24,25	0
3	CL	A	805	1/1	0.98	0.08	-0.37	27,27,27,27	0
2	EDO	A	801	4/4	0.98	0.08	-1.24	26,28,29,29	0
3	CL	B	803	1/1	0.98	0.05	-1.81	42,42,42,42	0
2	EDO	A	804	4/4	0.94	0.19	-	32,41,42,43	0
3	CL	A	806	1/1	0.99	0.05	-	46,46,46,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.