wwPDB X-ray Structure Validation Summary Report (i)

Aug 30, 2023 – 03:53 AM EDT

PDB ID	:	3OCE
Title	:	Crystal structure of fumarate lyase:delta crystallin from Brucella melitensis bound to cobalt
Authors	:	Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2010-08-09
Resolution	:	2.58 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

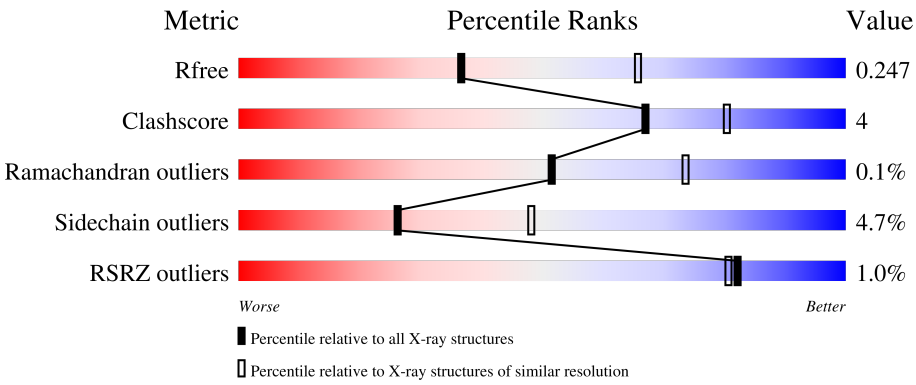
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

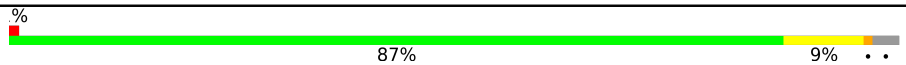
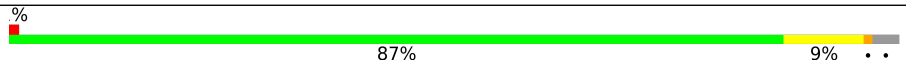
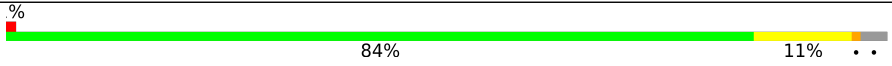
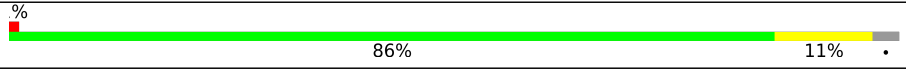
The reported resolution of this entry is 2.58 Å.

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	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

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	474	
1	B	474	
1	C	474	
1	D	474	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 14371 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 Fumarate lyase:Delta crystallin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	3461	2169	613	663	16	0	1	0
1	B	461	3451	2164	608	663	16	0	0	0
1	C	460	3433	2153	607	657	16	0	1	0
1	D	460	3462	2166	617	663	16	0	2	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q2YLW1
A	-2	PRO	-	expression tag	UNP Q2YLW1
A	-1	GLY	-	expression tag	UNP Q2YLW1
A	0	SER	-	expression tag	UNP Q2YLW1
A	1	MET	-	expression tag	UNP Q2YLW1
B	-3	GLY	-	expression tag	UNP Q2YLW1
B	-2	PRO	-	expression tag	UNP Q2YLW1
B	-1	GLY	-	expression tag	UNP Q2YLW1
B	0	SER	-	expression tag	UNP Q2YLW1
B	1	MET	-	expression tag	UNP Q2YLW1
C	-3	GLY	-	expression tag	UNP Q2YLW1
C	-2	PRO	-	expression tag	UNP Q2YLW1
C	-1	GLY	-	expression tag	UNP Q2YLW1
C	0	SER	-	expression tag	UNP Q2YLW1
C	1	MET	-	expression tag	UNP Q2YLW1
D	-3	GLY	-	expression tag	UNP Q2YLW1
D	-2	PRO	-	expression tag	UNP Q2YLW1
D	-1	GLY	-	expression tag	UNP Q2YLW1
D	0	SER	-	expression tag	UNP Q2YLW1
D	1	MET	-	expression tag	UNP Q2YLW1

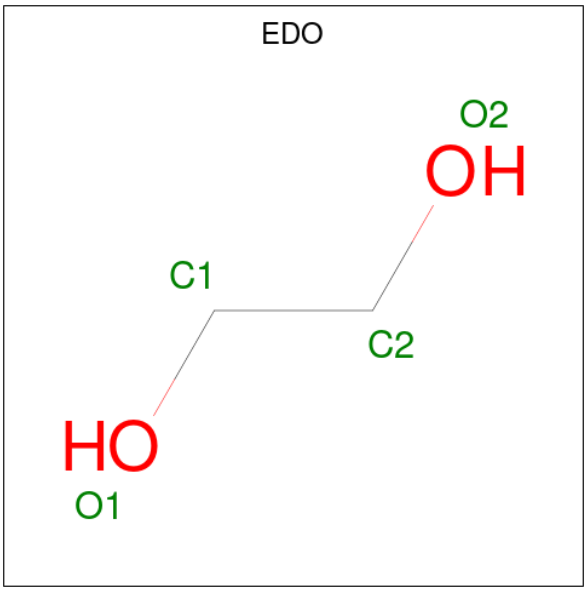
- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Co		
2	A	3	3	3	0	0
2	B	3	3	3	0	0
2	C	3	3	3	0	0
2	D	3	3	3	0	0

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

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

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



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

- Molecule 5 is water.

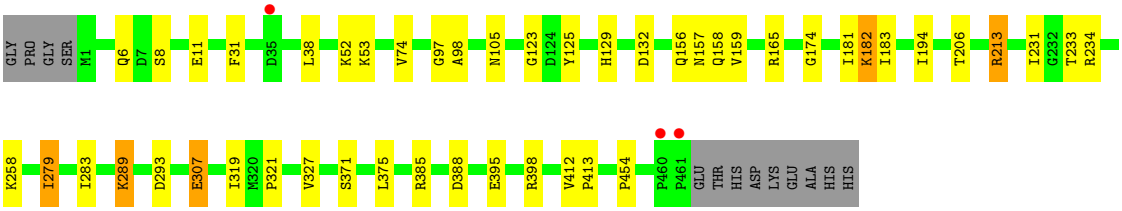
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	152	152	152	0	0
			Total	O		
5	B	135	135	135	0	0
			Total	O		
5	C	125	125	125	0	0
			Total	O		
5	D	132	132	132	0	0

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.

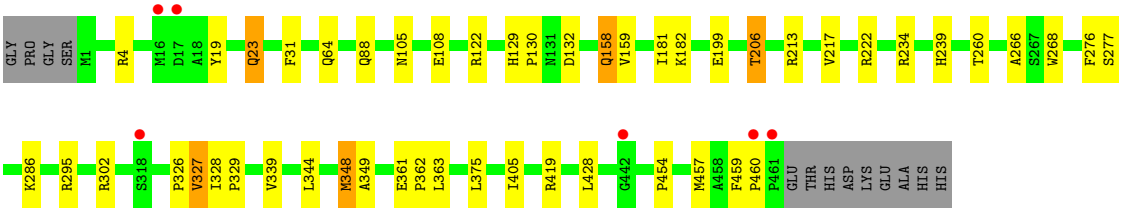
• Molecule 1: Fumarate lyase:Delta crystallin

Chain A:



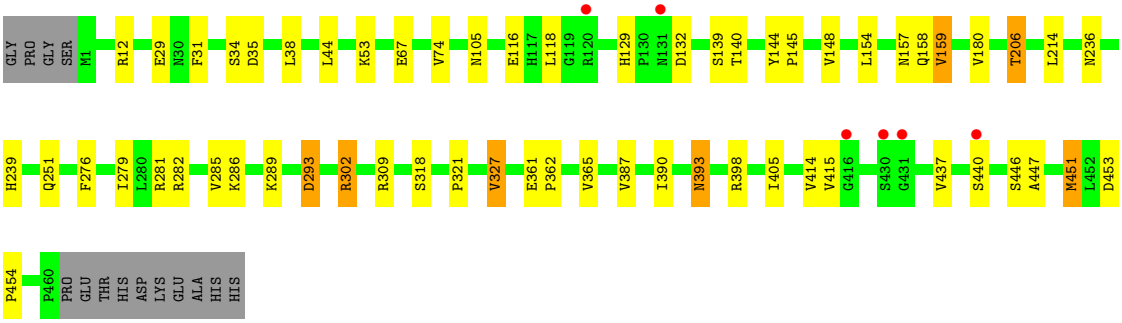
• Molecule 1: Fumarate lyase:Delta crystallin

Chain B:



• Molecule 1: Fumarate lyase:Delta crystallin

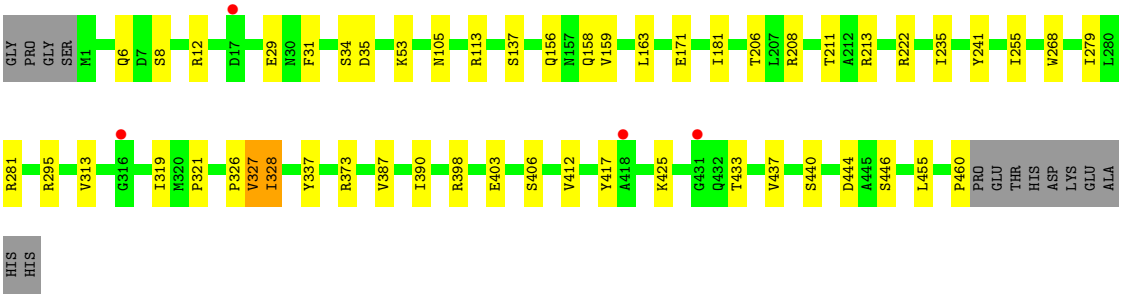
Chain C:



• Molecule 1: Fumarate lyase:Delta crystallin

Chain D:

%
86%
11%


GLY PRO GLY SER M1 Q6 D7 S8 R12 D17 E29 N30 F31 S34 D35 K53 N105 R113 S137 Q156 N157 Q158 V159 L163 E171 I181 T206 L207 R208 T211 A212 R213 R222 I235 Y241 I255 W268 I279 L280
R281 R295 V313 G316 I319 M320 P321 P326 V327 I328 Y337 R373 V387 I390 R398 E403 S406 V412 Y417 A418 K425 G431 Q432 T433 V437 S440 D444 A445 S446 L455 P460 PRO GLU THR HIS ASP LYS GLU ALA
HIS HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	95.33Å 113.55Å 236.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.58 19.95 – 2.58	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-2.58) 99.1 (19.95-2.58)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.32 (at 2.59Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.196 , 0.245 0.198 , 0.247	Depositor DCC
R_{free} test set	4054 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	24.6	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 33.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	14371	wwPDB-VP
Average B, all atoms (Å^2)	29.0	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 48.49 % 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 8.5396e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, CO, 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	0.70	1/3511 (0.0%)	0.78	1/4769 (0.0%)
1	B	0.69	0/3498	0.75	0/4752
1	C	0.68	0/3482	0.76	2/4732 (0.0%)
1	D	0.68	0/3514	0.73	0/4770
All	All	0.69	1/14005 (0.0%)	0.75	3/19023 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	395	GLU	CG-CD	5.29	1.59	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	293	ASP	CB-CG-OD2	6.10	123.79	118.30
1	C	293	ASP	CB-CG-OD2	5.11	122.90	118.30
1	C	154	LEU	CB-CG-CD1	-5.06	102.39	111.00

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	3461	0	3510	28	0
1	B	3451	0	3497	34	0
1	C	3433	0	3469	37	0
1	D	3462	0	3507	31	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	4	0	6	1	0
5	A	152	0	0	1	0
5	B	135	0	0	3	0
5	C	125	0	0	1	0
5	D	132	0	0	2	0
All	All	14371	0	13989	107	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.

The worst 5 of 107 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:327:VAL:HG13	1:D:31:PHE:CZ	2.11	0.85
1:B:327:VAL:HG13	1:D:31:PHE:HZ	1.40	0.85
1:B:31:PHE:CZ	1:D:327:VAL:HG13	2.14	0.83
1:D:171:GLU:OE2	1:D:208:ARG:NH1	2.13	0.81
1:B:31:PHE:HZ	1:D:327:VAL:HG13	1.48	0.77

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	460/474 (97%)	447 (97%)	12 (3%)	1 (0%)	47	69
1	B	459/474 (97%)	449 (98%)	10 (2%)	0	100	100
1	C	459/474 (97%)	443 (96%)	15 (3%)	1 (0%)	47	69
1	D	460/474 (97%)	450 (98%)	10 (2%)	0	100	100
All	All	1838/1896 (97%)	1789 (97%)	47 (3%)	2 (0%)	51	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	SER
1	C	180	VAL

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	363/377 (96%)	345 (95%)	18 (5%)	24	45
1	B	362/377 (96%)	347 (96%)	15 (4%)	30	54
1	C	357/377 (95%)	342 (96%)	15 (4%)	30	53
1	D	362/377 (96%)	341 (94%)	21 (6%)	20	38
All	All	1444/1508 (96%)	1375 (95%)	69 (5%)	26	47

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	235	ILE
1	D	281	ARG
1	D	406	SER
1	B	159	VAL
1	B	158	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	GLN
1	B	239	HIS
1	C	131	ASN
1	D	426	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 17 ligands modelled in this entry, 16 are monoatomic - leaving 1 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	475	-	3,3,3	0.59	0	2,2,2	0.51	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	475	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	475	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
4	A	475	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 (i)

6.1 Protein, DNA and RNA chains (i)

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	461/474 (97%)	-0.49	3 (0%)	87	86	12, 24, 49, 67	0
1	B	461/474 (97%)	-0.44	6 (1%)	77	74	12, 26, 49, 69	0
1	C	460/474 (97%)	-0.31	6 (1%)	77	74	13, 29, 57, 74	0
1	D	460/474 (97%)	-0.30	4 (0%)	84	83	13, 29, 63, 74	0
All	All	1842/1896 (97%)	-0.39	19 (1%)	82	81	12, 27, 55, 74	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	431	GLY	3.6
1	C	440	SER	3.0
1	B	17	ASP	2.8
1	D	316	GLY	2.7
1	C	416	GLY	2.6

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, 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
2	CO	B	473	1/1	0.84	0.15	54,54,54,54	0
4	EDO	A	475	4/4	0.88	0.23	27,30,31,35	0
2	CO	A	473	1/1	0.89	0.13	56,56,56,56	0
2	CO	C	473	1/1	0.94	0.10	44,44,44,44	0
2	CO	D	473	1/1	0.97	0.12	50,50,50,50	0
3	CL	A	474	1/1	0.97	0.14	42,42,42,42	0
3	CL	D	474	1/1	0.97	0.12	27,27,27,27	0
2	CO	B	472	1/1	0.97	0.13	33,33,33,33	0
2	CO	A	472	1/1	0.98	0.08	38,38,38,38	0
3	CL	C	474	1/1	0.98	0.08	23,23,23,23	0
2	CO	C	471	1/1	0.99	0.03	14,14,14,14	0
2	CO	C	472	1/1	0.99	0.06	33,33,33,33	0
3	CL	B	474	1/1	0.99	0.08	23,23,23,23	0
2	CO	B	471	1/1	0.99	0.05	9,9,9,9	0
2	CO	D	471	1/1	0.99	0.02	8,8,8,8	0
2	CO	D	472	1/1	0.99	0.08	27,27,27,27	0
2	CO	A	471	1/1	1.00	0.02	9,9,9,9	0

6.5 Other polymers (i)

There are no such residues in this entry.