wwPDB X-ray Structure Validation Summary Report (i)

Aug 30, 2023 – 09:09 AM EDT

PDB ID	:	3OFI
Title	:	Crystal structure of human insulin-degrading enzyme in complex with ubiquitin
Authors	:	Kalas, V.; Ralat, L.A.; Tang, W.-J.
Deposited on	:	2010-08-15
Resolution	:	2.35 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:

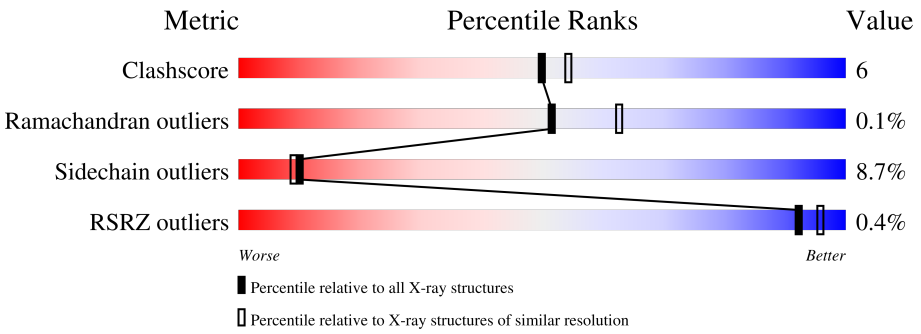
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.35 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))
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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	990	78% 14%
1	B	990	78% 15%
2	C	76	% 96%
2	D	76	96%

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
4	DIO	A	2013	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 16016 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 Insulin-degrading enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	954	7807	5029	1312	1444	22	0	0	0
1	B	954	7807	5029	1312	1444	22	0	0	0

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	expression tag	UNP P14735
A	31	HIS	-	expression tag	UNP P14735
A	32	HIS	-	expression tag	UNP P14735
A	33	HIS	-	expression tag	UNP P14735
A	34	HIS	-	expression tag	UNP P14735
A	35	HIS	-	expression tag	UNP P14735
A	36	HIS	-	expression tag	UNP P14735
A	37	ALA	-	expression tag	UNP P14735
A	38	ALA	-	expression tag	UNP P14735
A	39	GLY	-	expression tag	UNP P14735
A	40	ILE	-	expression tag	UNP P14735
A	41	PRO	-	expression tag	UNP P14735
A	110	LEU	CYS	engineered mutation	UNP P14735
A	111	GLN	GLU	engineered mutation	UNP P14735
A	171	SER	CYS	engineered mutation	UNP P14735
A	178	ALA	CYS	engineered mutation	UNP P14735
A	257	VAL	CYS	engineered mutation	UNP P14735
A	414	LEU	CYS	engineered mutation	UNP P14735
A	573	ASN	CYS	engineered mutation	UNP P14735
A	590	SER	CYS	engineered mutation	UNP P14735
A	789	SER	CYS	engineered mutation	UNP P14735
A	812	ALA	CYS	engineered mutation	UNP P14735
A	819	ALA	CYS	engineered mutation	UNP P14735
A	904	SER	CYS	engineered mutation	UNP P14735
A	966	ASN	CYS	engineered mutation	UNP P14735

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Chain	Residue	Modelled	Actual	Comment	Reference
A	974	ALA	CYS	engineered mutation	UNP P14735
B	30	MET	-	expression tag	UNP P14735
B	31	HIS	-	expression tag	UNP P14735
B	32	HIS	-	expression tag	UNP P14735
B	33	HIS	-	expression tag	UNP P14735
B	34	HIS	-	expression tag	UNP P14735
B	35	HIS	-	expression tag	UNP P14735
B	36	HIS	-	expression tag	UNP P14735
B	37	ALA	-	expression tag	UNP P14735
B	38	ALA	-	expression tag	UNP P14735
B	39	GLY	-	expression tag	UNP P14735
B	40	ILE	-	expression tag	UNP P14735
B	41	PRO	-	expression tag	UNP P14735
B	110	LEU	CYS	engineered mutation	UNP P14735
B	111	GLN	GLU	engineered mutation	UNP P14735
B	171	SER	CYS	engineered mutation	UNP P14735
B	178	ALA	CYS	engineered mutation	UNP P14735
B	257	VAL	CYS	engineered mutation	UNP P14735
B	414	LEU	CYS	engineered mutation	UNP P14735
B	573	ASN	CYS	engineered mutation	UNP P14735
B	590	SER	CYS	engineered mutation	UNP P14735
B	789	SER	CYS	engineered mutation	UNP P14735
B	812	ALA	CYS	engineered mutation	UNP P14735
B	819	ALA	CYS	engineered mutation	UNP P14735
B	904	SER	CYS	engineered mutation	UNP P14735
B	966	ASN	CYS	engineered mutation	UNP P14735
B	974	ALA	CYS	engineered mutation	UNP P14735

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	3	25	16	4	4	1	0	0	0
			Total	C	N	O	S			
2	D	3	25	16	4	4	1	0	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	1	1	1	0	0

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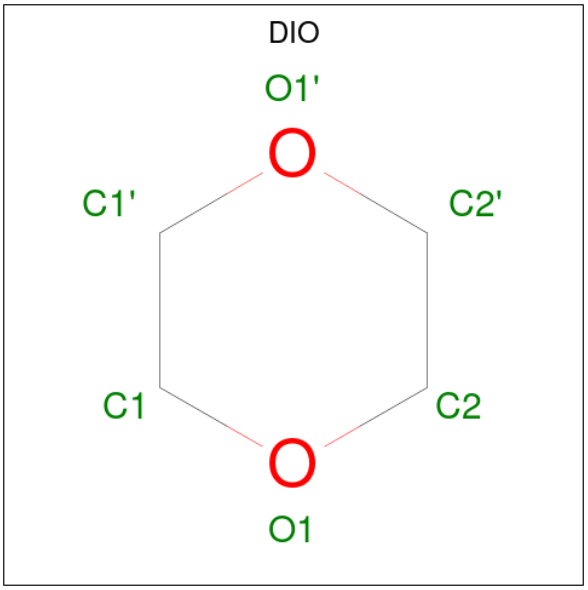
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	B	1	1	1	0	0

- Molecule 4 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: $C_4H_8O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	6	4	2	0	0
			Total	C	O		
4	B	1	6	4	2	0	0
			Total	C	O		
4	B	1	6	4	2	0	0

- Molecule 5 is water.

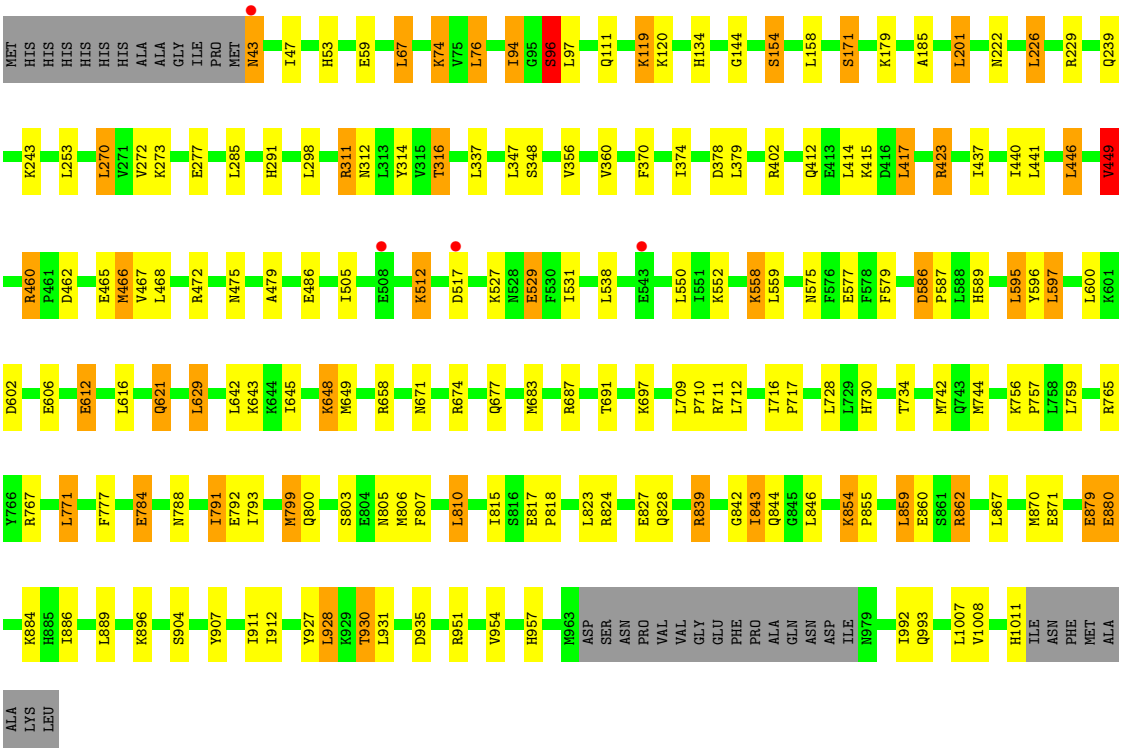
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	218	218	218	0	0
			Total	O		
5	B	113	113	113	0	0
			Total	O		
5	D	1	1	1	0	0

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.

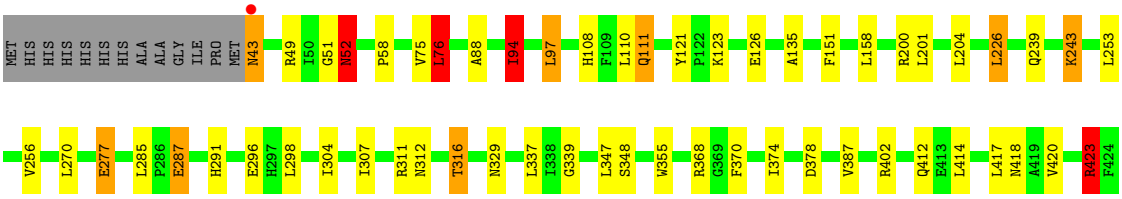
• Molecule 1: Insulin-degrading enzyme

Chain A: 78% 14%



• Molecule 1: Insulin-degrading enzyme

Chain B: 78% 15%



K425 I437 I440 L441 L446 V449 L450 Y454 E457 R460 I464 E465 M466 P473 E474 N475 V476 A479 I480 R491 E508 K511 K512 D517 L524 N528 I531 P532 K542 E543 M556 K566 E577 F578 D586 H589

L595 Y596 L597 L600 K601 D602 E606 Y607 A608 Y609 E612 L613 L616 I624 L629 K632 G633 Y634 L641 L642 K643 K644 I645 I646 E647 K648 M649 D655 E656 K657 R658 F659 E660 I661 N671 R674 T691 K697 T708 L709 P710 R711 L712 K713 I716

P717 I725 L728 L729 H730 I733 L758 L759 L771 E784 N788 D798 M799 S803 E804 N805 L810 E817 L823 E827 V833 G842 I843 Q844 G845 L846 I850 K854 L859 E860 S861 R862 L867 S873 E880 L889 R892

S904 W908 I912 Y927 L928 K929 T930 L931 E934 D935 I936 E942 V954 H957 M963 ASP SER ASN PRO VAL VAL GLY GLU PHE PRO ALA GLN ASN ASP ILE N979 Q993 K999 L1007 V1008 H1011 ILE ASN PHE MET ALA ALA LYS LEU

- Molecule 2: Ubiquitin

Chain C: % 96%

M1 Q2 I3 PHE VAL LYS THR LEU THR GLY LYS THR ILE THR LEU GLU VAL GLU PRO SER ASP THR ILE GLU ASN VAL LYS ALA LYS ILE GLN ASP LYS GLU GLY ILE PRO PRO ASP GLN GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS GLU SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY GLY

- Molecule 2: Ubiquitin

Chain D: 96%

M1 Q2 I3 PHE VAL LYS THR LEU THR GLY LYS THR ILE THR LEU GLU VAL GLU PRO SER ASP THR ILE GLU ASN VAL LYS ALA LYS ILE GLN ASP LYS GLU GLY ILE PRO PRO ASP GLN GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS GLU SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	262.94Å 262.94Å 90.97Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.35 49.69 – 2.35	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.35) 94.7 (49.69-2.35)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.35 (at 2.34Å)	Xtriage
Refinement program	REFMAC, CNS 1.1	Depositor
R, R_{free}	0.210 , 0.240 0.184 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	33.4	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 33.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.022 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	16016	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.66% 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 (i)

5.1 Standard geometry (i)

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

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	1.12	17/8002 (0.2%)	0.98	22/10824 (0.2%)
1	B	1.08	13/8002 (0.2%)	0.98	21/10824 (0.2%)
2	C	0.93	0/24	1.06	0/30
2	D	1.19	0/24	1.41	0/30
All	All	1.10	30/16052 (0.2%)	0.98	43/21708 (0.2%)

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	2

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	880	GLU	CG-CD	7.16	1.62	1.51
1	A	784	GLU	CG-CD	6.91	1.62	1.51
1	A	577	GLU	CG-CD	6.90	1.62	1.51
1	A	74	LYS	CE-NZ	6.39	1.65	1.49
1	A	612	GLU	CB-CG	-6.37	1.40	1.52

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	311	ARG	NE-CZ-NH2	-10.78	114.91	120.30
1	B	862	ARG	NE-CZ-NH2	-9.86	115.37	120.30
1	B	311	ARG	NE-CZ-NH2	-8.97	115.82	120.30
1	B	94	ILE	CG1-CB-CG2	-8.70	92.27	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	658	ARG	NE-CZ-NH2	-8.08	116.26	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	43	ASN	Peptide
1	B	51	GLY	Peptide

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	7807	0	7751	93	0
1	B	7807	0	7751	89	0
2	C	25	0	30	0	0
2	D	25	0	30	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	6	0	8	7	0
4	B	12	0	16	2	0
5	A	218	0	0	8	0
5	B	113	0	0	9	0
5	D	1	0	0	0	0
All	All	16016	0	15586	181	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 6.

The worst 5 of 181 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:800:GLN:HE22	4:A:2013:DIO:H12	1.19	1.03
1:A:94:ILE:HD11	1:A:253:LEU:CD1	1.89	1.02
1:B:243:LYS:HE2	1:B:243:LYS:HA	1.52	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:777:PHE:HB3	1:A:992:ILE:HD11	1.53	0.89
1:B:368:ARG:HD3	5:B:3057:HOH:O	1.73	0.89

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	950/990 (96%)	924 (97%)	25 (3%)	1 (0%)	51	63
1	B	950/990 (96%)	923 (97%)	27 (3%)	0	100	100
2	C	1/76 (1%)	1 (100%)	0	0	100	100
2	D	1/76 (1%)	1 (100%)	0	0	100	100
All	All	1902/2132 (89%)	1849 (97%)	52 (3%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	SER

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	850/879 (97%)	777 (91%)	73 (9%)	10	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	850/879 (97%)	779 (92%)	71 (8%)	11	10
2	C	3/68 (4%)	2 (67%)	1 (33%)	0	0
2	D	3/68 (4%)	0	3 (100%)	0	0
All	All	1706/1894 (90%)	1558 (91%)	148 (9%)	10	9

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	642	LEU
1	B	1007	LEU
1	B	711	ARG
1	B	823	LEU
1	A	691	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	730	HIS
1	B	957	HIS
1	B	770	GLN
1	B	841	ASN
1	B	993	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 5 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
4	DIO	B	2013	-	6,6,6	0.62	0	6,6,6	1.11	1 (16%)
4	DIO	A	2013	-	6,6,6	0.54	0	6,6,6	2.00	3 (50%)
4	DIO	B	2014	-	6,6,6	0.54	0	6,6,6	1.23	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	DIO	B	2013	-	-	-	0/1/1/1
4	DIO	A	2013	-	-	-	0/1/1/1
4	DIO	B	2014	-	-	-	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	2013	DIO	O1-C1-C1'	-2.98	96.36	110.95
4	A	2013	DIO	O1-C2-C2'	-2.63	98.06	110.95
4	A	2013	DIO	C2'-O1'-C1'	2.25	117.39	109.89
4	B	2013	DIO	C2'-O1'-C1'	2.12	116.95	109.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2013	DIO	1	0
4	A	2013	DIO	7	0
4	B	2014	DIO	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	954/990 (96%)	-0.41	4 (0%) 92 96	16, 29, 44, 64	0
1	B	954/990 (96%)	-0.39	3 (0%) 94 97	21, 32, 47, 72	0
2	C	3/76 (3%)	1.33	1 (33%) 0 0	45, 45, 45, 46	0
2	D	3/76 (3%)	0.95	0 100 100	43, 43, 43, 45	0
All	All	1914/2132 (89%)	-0.39	8 (0%) 92 96	16, 30, 46, 72	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	43	ASN	3.4
1	B	543	GLU	3.2
1	A	543	GLU	2.9
1	B	542	LYS	2.8
1	B	43	ASN	2.8

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
4	DIO	B	2014	6/6	0.91	0.23	49,55,59,60	0
4	DIO	A	2013	6/6	0.94	0.23	47,50,53,55	0
3	ZN	B	2012	1/1	0.96	0.11	36,36,36,36	0
4	DIO	B	2013	6/6	0.97	0.08	40,42,44,44	0
3	ZN	A	2012	1/1	0.99	0.11	34,34,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.