



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 07:03 PM GMT

PDB ID : 4NXO
Title : Crystal Structure of Insulin Degrading Enzyme in complex with BDM44768
Authors : Liang, W.G.; Deprez, R.; Deprez, B.; Tang, W.
Deposited on : 2013-12-09
Resolution : 2.73 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
<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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-20026982

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	2H7	A	1102	-	-	-	X
3	2H7	B	1102	-	-	-	X
4	1PE	A	1103	-	-	-	X
4	1PE	B	1103	-	-	-	X
5	PEG	A	1105	-	-	-	X
5	PEG	B	1104	-	-	-	X
5	PEG	B	1106	-	-	-	X
6	EDO	B	1107	-	-	-	X
6	EDO	B	1108	-	-	-	X
8	DIO	B	1111	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 16088 atoms, of which 175 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
1	A	958	Total	C	N	O	S	0	0	0
			7789	5020	1310	1437	22			
1	B	956	Total	C	N	O	S	0	0	0
			7775	5010	1308	1435	22			

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

Continued on next page...

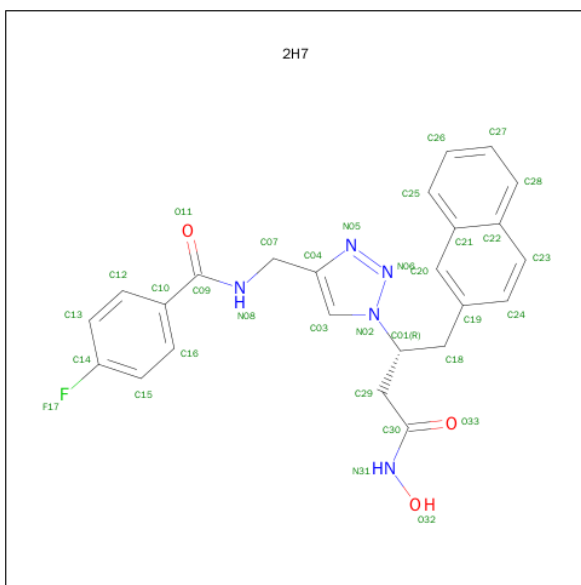
Continued from previous page...

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

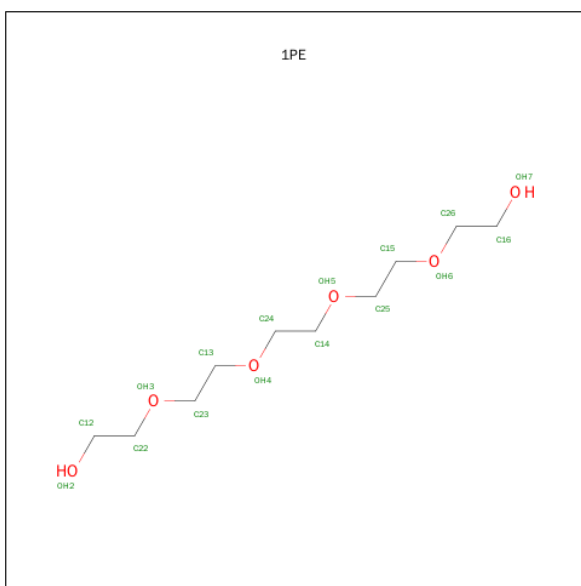
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0

- Molecule 3 is 4-FLUORO-N-({1-[(2R)-4-(HYDROXYAMINO)-1-(NAPHTHALEN-2-YL)-4-OXOBUTAN-2-YL]-1H-1,2,3-TRIAZOL-4-YL}METHYL)BENZAMIDE (three-letter code: 2H7) (formula: C₂₄H₂₂FN₅O₃).



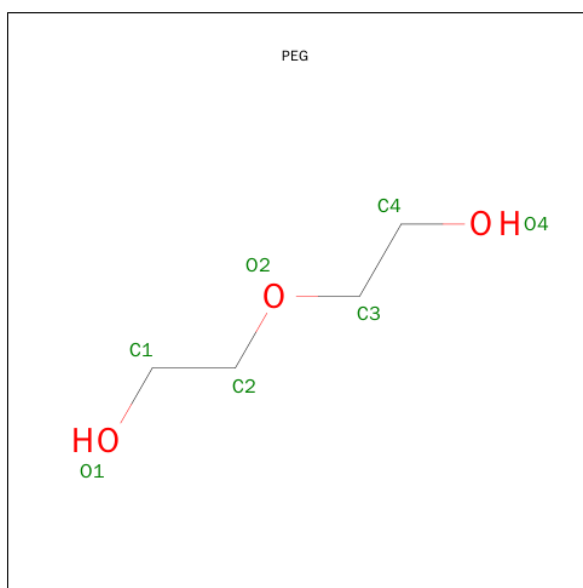
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			33	24	1	5	3		
3	B	1	Total	C	F	N	O	0	0
			33	24	1	5	3		

- Molecule 4 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



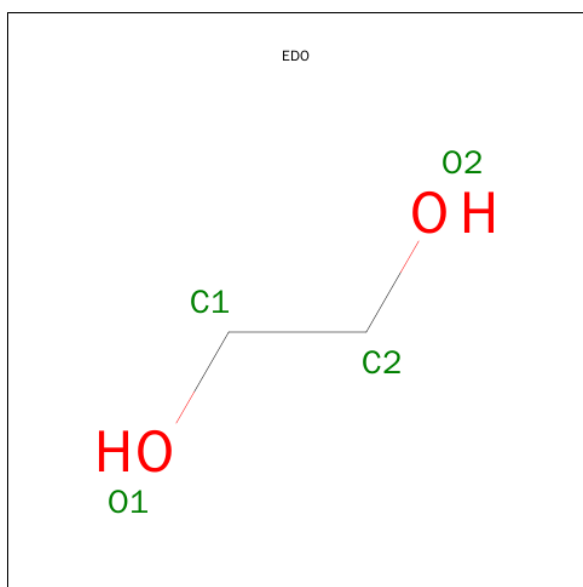
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			38	10	22	6		
4	B	1	Total	C	H	O	0	0
			30	8	17	5		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



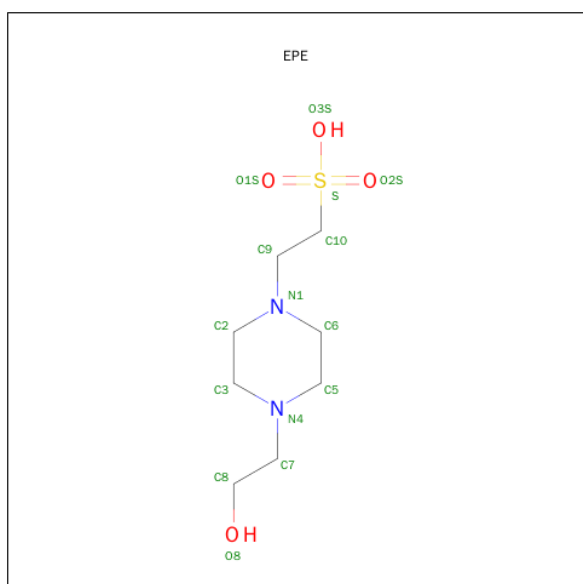
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



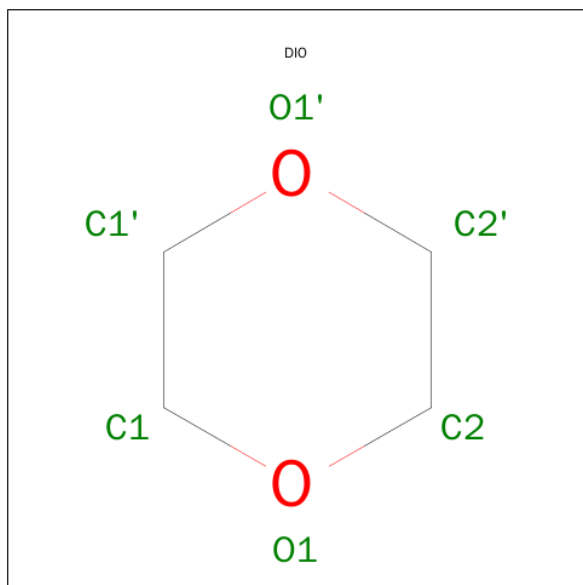
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 7 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	H	N	O	S	
			32	8	17	2	4	1	
7	B	1	Total	C	H	N	O	S	
			32	8	17	2	4	1	

- Molecule 8 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: C₄H₈O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	H	O		
			14	4	8	2	0	0

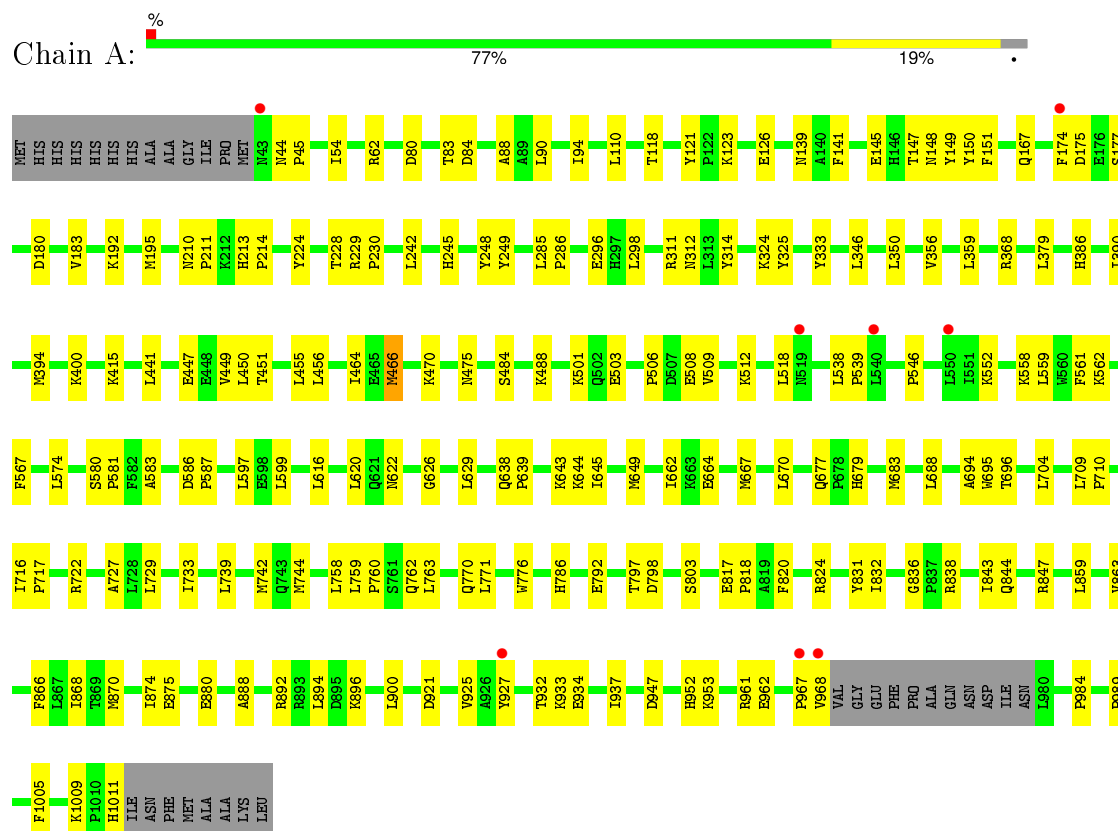
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	62	Total	O		
			62	62	0	0
9	B	89	Total	O		
			89	89	0	0

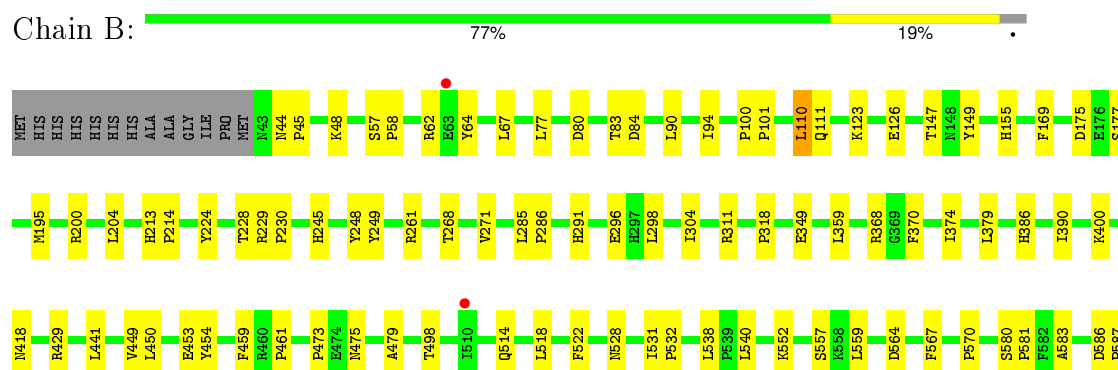
3 Residue-property plots [i](#)

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: Insulin-degrading enzyme



- Molecule 1: Insulin-degrading enzyme



K999	Y594	R722	Y863
R1000	E598	L723	I868
G1001	L599	G731	T869
L1002	L600	T734	K870
F1005	K601	I741	T874
H1011	L604	M742	A881
ILE	L616	Q743	K884
ASN	L620	V745	L894
PHE	E626	E746	D895
MET	L629	D747	K896
ALA	L634	L759	L900
ALA	Q638	Q762	Y925
LEU	P639	Y766	A926
	K643	Q770	Y927
	E647	L771	L931
	K648	P772	T932
	D655	M776	K933
	K658	R782	E934
	T662	H786	D935
	K663	I793	I936
	E664	D798	I937
	M667	M799	D947
	K674	Q800	H952
	H679	S803	K953
	M683	L810	R961
	L688	E817	E962
	L689	P818	H963
	Y693	M821	D964
	T696	R824	S965
	L704	T825	ASN
	L709	Y831	PRO
	P710	I843	VAL
	I716	Q844	VAL
	P717	R847	GLY
	S721	P855	PHE
		P856	PRO
		L859	ALA
			GLN
			ASN
			ASP
			ILE
			N979
			P984
			M995

4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	262.91Å 262.91Å 86.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.82 – 2.73 47.52 – 2.73	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.82-2.73) 94.5 (47.52-2.73)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.73Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.9_1692)	Depositor
R, R_{free}	0.170 , 0.219 0.185 , 0.232	Depositor DCC
R_{free} test set	2001 reflections (2.39%)	DCC
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	1.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 51.6	EDS
Estimated twinning fraction	0.025 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 90102 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16088	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, DIO, EDO, 2H7, 1PE, PEG, EPE

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	0.25	0/7985	0.43	0/10810
1	B	0.26	0/7970	0.43	0/10788
All	All	0.26	0/15955	0.43	0/21598

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	7789	0	7701	146	0
1	B	7775	0	7685	139	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	33	0	21	5	0
3	B	33	0	20	6	0
4	A	16	22	22	0	0
4	B	13	17	17	1	0
5	A	21	30	30	1	0
5	B	28	40	40	3	0
6	A	8	12	12	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	8	12	12	2	0
7	A	15	17	17	0	0
7	B	15	17	17	1	0
8	B	6	8	8	0	0
9	A	62	0	0	2	0
9	B	89	0	0	2	0
All	All	15913	175	15602	285	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 9.

The worst 5 of 285 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:559:LEU:HB2	1:A:742:MET:HE2	1.44	0.97
1:B:688:LEU:HD13	1:B:696:THR:HG22	1.48	0.95
3:A:1102:2H7:H8	3:A:1102:2H7:H4	1.49	0.94
3:B:1102:2H7:C03	3:B:1102:2H7:H4	1.97	0.93
1:A:599:LEU:HD23	1:A:662:ILE:HD12	1.52	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	954/990 (96%)	934 (98%)	19 (2%)	1 (0%)	56	83
1	B	952/990 (96%)	935 (98%)	17 (2%)	0	100	100
All	All	1906/1980 (96%)	1869 (98%)	36 (2%)	1 (0%)	56	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	967	PRO

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	842/879 (96%)	837 (99%)	5 (1%)	90	97
1	B	840/879 (96%)	836 (100%)	4 (0%)	92	97
All	All	1682/1758 (96%)	1673 (100%)	9 (0%)	92	97

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1011	HIS
1	B	1011	HIS
1	B	111	GLN
1	A	466	MET
1	B	110	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	788	ASN

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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	2H7	A	1102	2	34,36,36	2.40	7 (20%)	40,49,49	1.35	5 (12%)
4	1PE	A	1103	-	15,15,15	0.67	0	14,14,14	0.41	0
5	PEG	A	1104	-	6,6,6	0.68	0	5,5,5	0.23	0
5	PEG	A	1105	-	6,6,6	0.63	0	5,5,5	0.38	0
5	PEG	A	1106	-	6,6,6	0.68	0	5,5,5	0.36	0
6	EDO	A	1107	-	3,3,3	0.48	0	2,2,2	0.35	0
6	EDO	A	1108	-	3,3,3	0.48	0	2,2,2	0.32	0
7	EPE	A	1109	-	15,15,15	0.83	1 (6%)	19,20,20	2.29	6 (31%)
3	2H7	B	1102	2	34,36,36	2.35	12 (35%)	40,49,49	2.02	8 (20%)
4	1PE	B	1103	-	12,12,15	0.68	0	11,11,14	0.34	0
5	PEG	B	1104	-	6,6,6	0.67	0	5,5,5	0.27	0
5	PEG	B	1105	-	6,6,6	0.71	0	5,5,5	0.52	0
5	PEG	B	1106	-	6,6,6	0.66	0	5,5,5	0.37	0
6	EDO	B	1107	-	3,3,3	0.44	0	2,2,2	0.37	0
6	EDO	B	1108	-	3,3,3	0.50	0	2,2,2	0.27	0
5	PEG	B	1109	-	6,6,6	0.68	0	5,5,5	0.30	0
7	EPE	B	1110	-	15,15,15	0.75	1 (6%)	19,20,20	2.26	6 (31%)
8	DIO	B	1111	-	6,6,6	0.45	0	6,6,6	0.65	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	2H7	A	1102	2	-	0/17/23/23	0/4/4/4

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	1PE	A	1103	-	-	0/13/13/13	0/0/0/0
5	PEG	A	1104	-	-	0/4/4/4	0/0/0/0
5	PEG	A	1105	-	-	0/4/4/4	0/0/0/0
5	PEG	A	1106	-	-	0/4/4/4	0/0/0/0
6	EDO	A	1107	-	-	0/1/1/1	0/0/0/0
6	EDO	A	1108	-	-	0/1/1/1	0/0/0/0
7	EPE	A	1109	-	-	0/9/19/19	0/1/1/1
3	2H7	B	1102	2	-	0/17/23/23	0/4/4/4
4	1PE	B	1103	-	-	0/10/10/13	0/0/0/0
5	PEG	B	1104	-	-	0/4/4/4	0/0/0/0
5	PEG	B	1105	-	-	0/4/4/4	0/0/0/0
5	PEG	B	1106	-	-	0/4/4/4	0/0/0/0
6	EDO	B	1107	-	-	0/1/1/1	0/0/0/0
6	EDO	B	1108	-	-	0/1/1/1	0/0/0/0
5	PEG	B	1109	-	-	0/4/4/4	0/0/0/0
7	EPE	B	1110	-	-	0/9/19/19	0/1/1/1
8	DIO	B	1111	-	-	0/0/6/6	0/1/1/1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1102	2H7	O32-N31	-2.61	1.35	1.39
3	B	1102	2H7	N06-N02	-2.19	1.30	1.34
3	A	1102	2H7	C21-C22	-2.03	1.37	1.42
3	A	1102	2H7	C23-C24	2.01	1.40	1.36
3	A	1102	2H7	C26-C25	2.08	1.41	1.36

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1102	2H7	C19-C18-C01	-6.80	97.05	113.63
3	B	1102	2H7	O33-C30-N31	-4.98	117.93	123.60
3	B	1102	2H7	C03-N02-C01	-4.53	120.92	125.55
3	A	1102	2H7	O33-C30-N31	-3.59	119.52	123.60
3	A	1102	2H7	C03-C04-N05	-3.17	106.32	111.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1102	2H7	5	0
5	A	1105	PEG	1	0
6	A	1108	EDO	1	0
3	B	1102	2H7	6	0
4	B	1103	1PE	1	0
5	B	1104	PEG	2	0
5	B	1105	PEG	1	0
6	B	1108	EDO	2	0
7	B	1110	EPE	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	958/990 (96%)	-0.00	8 (0%) 87 88	45, 66, 90, 131	0
1	B	956/990 (96%)	-0.11	2 (0%) 95 96	41, 59, 82, 120	0
All	All	1914/1980 (96%)	-0.06	10 (0%) 91 93	41, 62, 88, 131	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	43	ASN	3.4
1	A	174	PHE	3.3
1	A	968	VAL	2.9
1	A	967	PRO	2.9
1	A	540	LEU	2.3

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	2H7	A	1102	33/33	0.88	0.33	9.55	51,83,103,116	7
6	EDO	B	1107	4/4	0.83	0.29	8.08	64,77,87,89	0
5	PEG	B	1106	7/7	0.71	0.37	7.77	74,101,127,127	0
5	PEG	A	1105	7/7	0.87	0.23	6.82	73,90,108,116	0
4	1PE	A	1103	16/16	0.73	0.34	6.78	61,99,112,119	0
6	EDO	B	1108	4/4	0.85	0.33	6.11	60,80,102,102	0
3	2H7	B	1102	33/33	0.85	0.30	5.67	57,85,99,104	8
4	1PE	B	1103	13/16	0.78	0.30	4.34	72,98,118,124	0
8	DIO	B	1111	6/6	0.85	0.29	3.93	78,95,126,126	0
5	PEG	B	1104	7/7	0.78	0.23	3.06	77,97,123,123	0
6	EDO	A	1108	4/4	0.60	0.26	1.86	82,99,109,123	0
5	PEG	B	1105	7/7	0.93	0.24	1.77	56,82,102,107	0
6	EDO	A	1107	4/4	0.81	0.22	1.67	70,94,113,113	0
7	EPE	B	1110	15/15	0.92	0.20	1.59	67,87,111,119	0
2	ZN	B	1101	1/1	0.96	0.19	0.58	55,55,55,55	0
7	EPE	A	1109	15/15	0.94	0.18	0.27	67,87,105,113	0
5	PEG	A	1106	7/7	0.91	0.13	-1.26	70,88,102,108	0
5	PEG	B	1109	7/7	0.91	0.22	-	56,77,104,104	0
5	PEG	A	1104	7/7	0.92	0.14	-	60,84,110,110	0
2	ZN	A	1101	1/1	0.99	0.14	-	58,58,58,58	0

6.5 Other polymers ⓘ

There are no such residues in this entry.