



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:08 PM GMT

PDB ID : 3WA3
Title : Crystal structure of copper amine oxidase from arthrobacter globiformis in N2 condition
Authors : Murakawa, T.; Hayashi, H.; Sunami, T.; Kurihara, K.; Tamada, T.; Kuroki, R.; Suzuki, M.; Tanizawa, K.; Okajima, T.
Deposited on : 2013-04-22
Resolution : 1.55 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

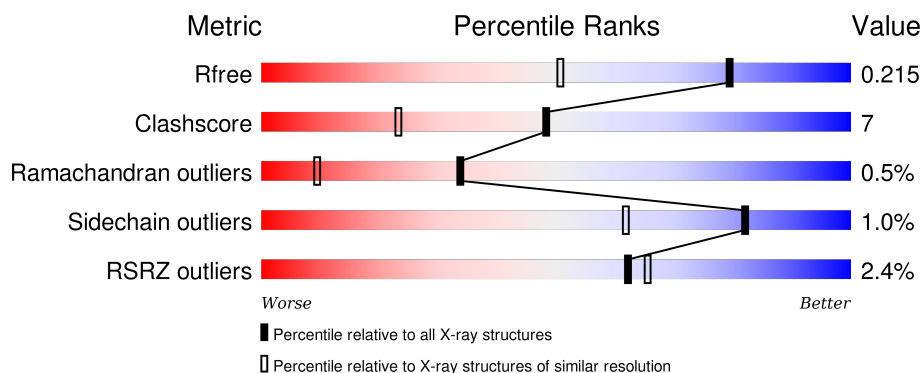
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	1665 (1.58-1.54)
Clashscore	102246	1014 (1.56-1.56)
Ramachandran outliers	100387	1704 (1.58-1.54)
Sidechain outliers	100360	1702 (1.58-1.54)
RSRZ outliers	91569	1668 (1.58-1.54)

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 ≥ 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	621	
1	B	621	

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	PGE	A	1005	-	-	-	X
4	PGE	B	1004	-	-	-	X
4	PGE	B	1005	-	-	-	X
5	PG4	A	1006	-	-	-	X
5	PG4	B	1006	-	-	-	X
5	PG4	B	1007	-	-	X	-
6	1PE	A	1008	-	-	-	X
7	EDO	A	1009	-	-	X	X
7	EDO	A	1013	-	-	-	X
7	EDO	A	1014	-	-	X	X
7	EDO	A	1015	-	-	-	X
7	EDO	B	1011	-	-	X	X
7	EDO	B	1014	-	-	X	X
7	EDO	B	1015	-	-	-	X
7	EDO	B	1017	-	-	-	X
8	PEG	A	1018	-	-	-	X
8	PEG	A	1019	-	-	X	-
8	PEG	A	1020	-	-	X	X
8	PEG	A	1021	-	-	X	X
8	PEG	B	1019	-	-	X	-
8	PEG	B	1020	-	-	-	X
8	PEG	B	1021	-	-	X	X
8	PEG	B	1022	-	-	-	X
8	PEG	B	1024	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 11978 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 Phenylethylamine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	621	Total	C	N	O	S	0	22	0
			5014	3168	885	952	9			
1	B	621	Total	C	N	O	S	0	10	0
			4947	3122	875	941	9			

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

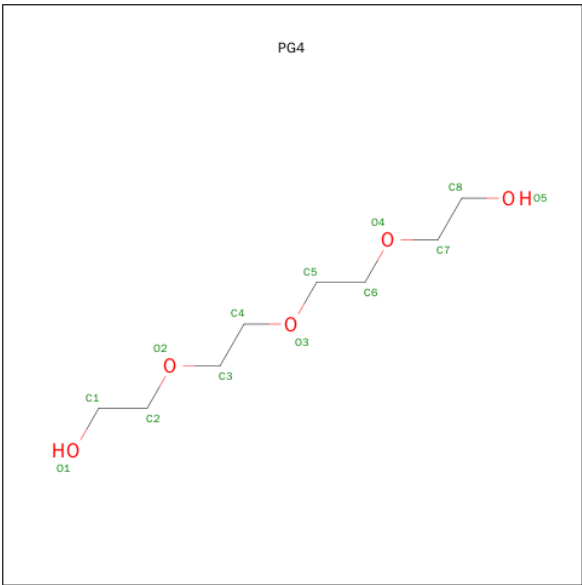
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Na	0	0
			1	1		
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



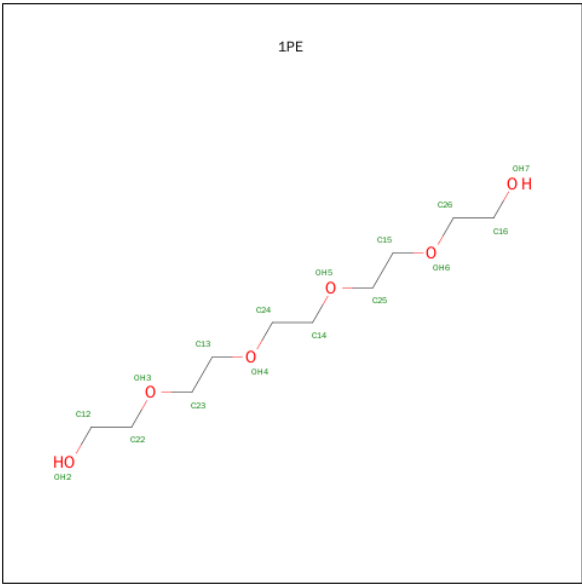
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



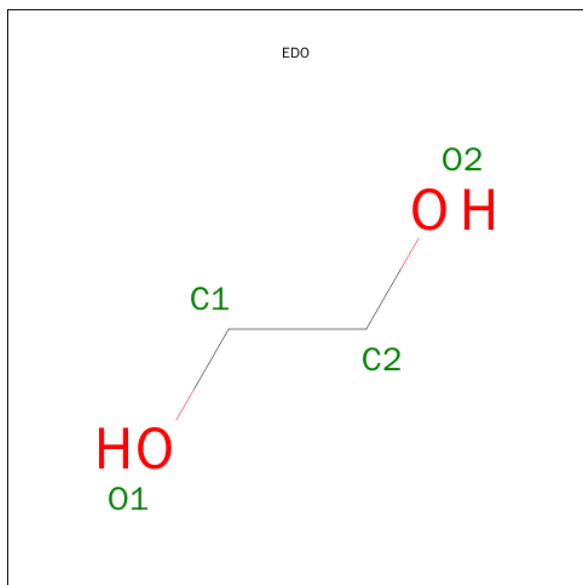
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	8	5		
5	A	1	Total	C	O	0	0
			13	8	5		
5	B	1	Total	C	O	0	0
			13	8	5		
5	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			16	10	6		
6	B	1	Total	C	O	0	0
			16	10	6		

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



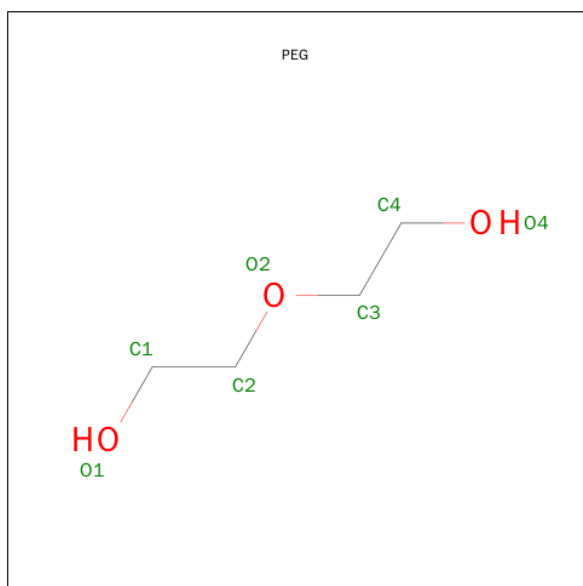
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total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

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

- Molecule 8 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



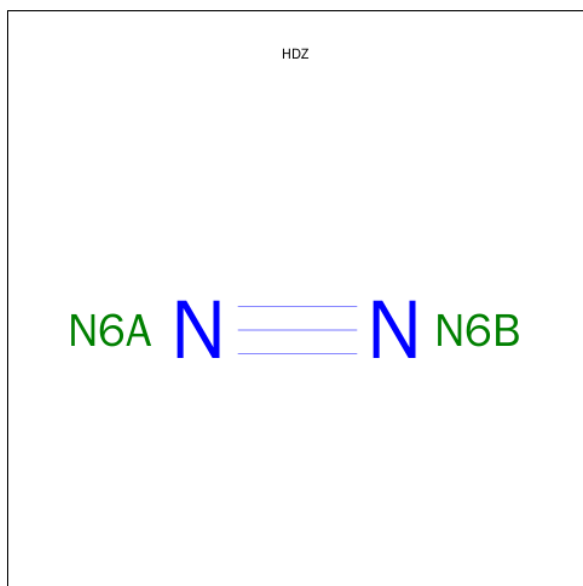
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			7	4	3		
8	A	1	Total	C	O	0	0
			7	4	3		
8	A	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 7 4 3	0	0
8	A	1	Total C O 7 4 3	0	0
8	A	1	Total C O 7 4 3	0	0
8	B	1	Total C O 7 4 3	0	0
8	B	1	Total C O 7 4 3	0	0
8	B	1	Total C O 7 4 3	0	0
8	B	1	Total C O 7 4 3	0	0
8	B	1	Total C O 7 4 3	0	0
8	B	1	Total C O 7 4 3	0	0

- Molecule 9 is NITROGEN MOLECULE (three-letter code: HDZ) (formula: N₂).



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

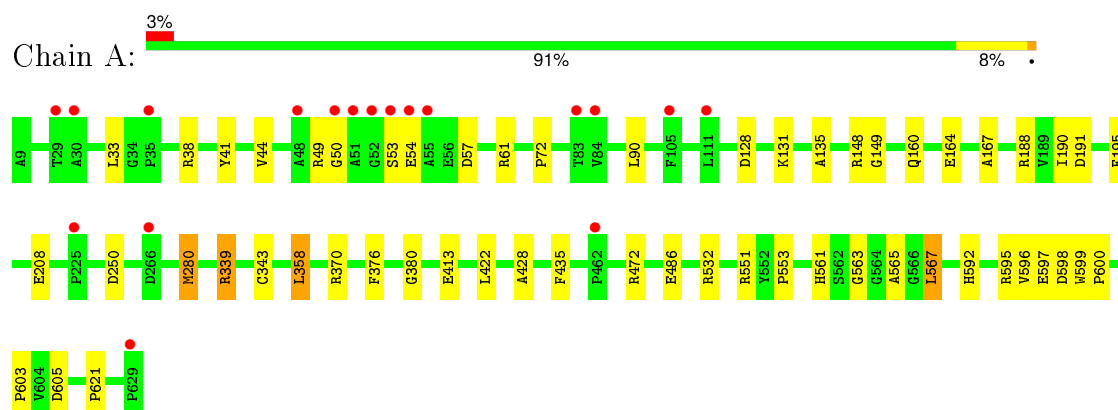
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	820	Total 820	O 820	0	0
10	B	889	Total 889	O 889	0	0

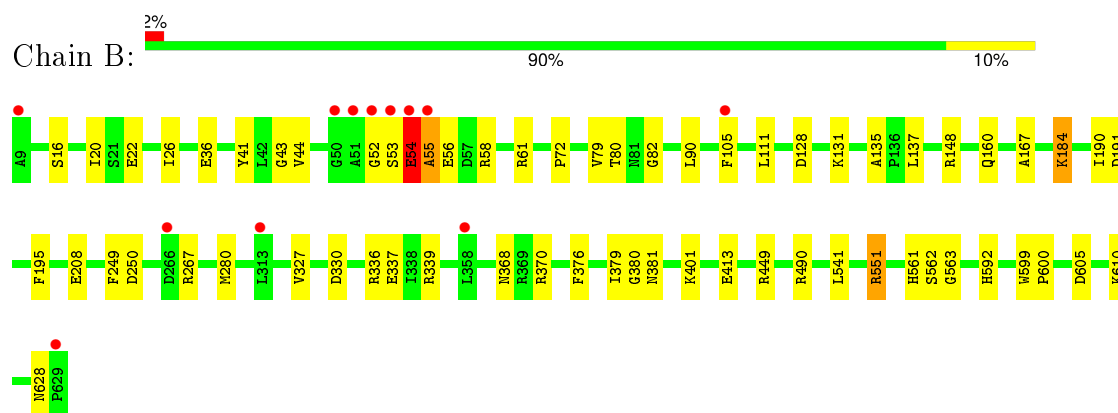
3 Residue-property plots [i](#)

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: Phenylethylamine oxidase



- Molecule 1: Phenylethylamine oxidase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	191.61Å 63.04Å 158.01Å 90.00° 117.44° 90.00°	Depositor
Resolution (Å)	29.93 – 1.55 29.93 – 1.55	Depositor EDS
% Data completeness (in resolution range)	94.7 (29.93-1.55) 94.8 (29.93-1.55)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 1.55Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.181 , 0.210 0.184 , 0.215	Depositor DCC
R_{free} test set	11525 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	16.2	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 230549 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11978	wwPDB-VP
Average B, all atoms (Å ²)	22.0	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 86.33 % 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 9.6872e-08. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, NA, HDZ, 1PE, PG4, TPQ, EDO, PEG, CU

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	0.65	1/5165 (0.0%)	0.76	1/7027 (0.0%)
1	B	0.68	0/5073	0.79	3/6903 (0.0%)
All	All	0.67	1/10238 (0.0%)	0.78	4/13930 (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	343	CYS	CB-SG	-5.15	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	280	MET	CG-SD-CE	-7.55	88.11	100.20
1	A	280	MET	CG-SD-CE	-7.07	88.89	100.20
1	B	551	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	B	541	LEU	CA-CB-CG	-5.02	103.76	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	56	GLU	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	5014	0	4871	63	1
1	B	4947	0	4782	67	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	30	0	42	4	0
4	B	30	0	42	6	0
5	A	26	0	35	8	0
5	B	26	0	36	13	0
6	A	16	0	22	5	0
6	B	16	0	22	3	0
7	A	32	0	48	9	0
7	B	40	0	60	17	0
8	A	42	0	60	23	0
8	B	42	0	60	16	2
9	A	2	0	0	0	0
9	B	2	0	0	0	0
10	A	820	0	0	19	6
10	B	889	0	0	18	3
All	All	11978	0	10080	149	9

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 7.

The worst 5 of 149 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:368:ASN:HD22	7:B:1015:EDO:H12	1.13	1.08
1:B:380:GLY:HA2	5:B:1007:PG4:H82	1.40	1.01
1:B:368:ASN:ND2	7:B:1015:EDO:H12	1.83	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:GLY:HA2	5:A:1007:PG4:H72	1.53	0.88
1:B:551:ARG:HD3	4:B:1005:PGE:H5	1.56	0.87

The worst 5 of 9 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)
10:A:1262:HOH:O	10:A:1262:HOH:O[2_756]	2.07	0.13
8:B:1022:PEG:O4	10:B:1566:HOH:O[2_755]	2.11	0.09
10:A:1815:HOH:O	10:A:1819:HOH:O[2_756]	2.12	0.08
8:B:1021:PEG:O4	10:B:1657:HOH:O[2_755]	2.13	0.07
1:A:532[B]:ARG:NH1	10:A:1648:HOH:O[2_756]	2.13	0.07

5.3 Torsion angles

5.3.1 Protein backbone

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	640/621 (103%)	612 (96%)	26 (4%)	2 (0%)	46	20
1	B	628/621 (101%)	607 (97%)	17 (3%)	4 (1%)	30	7
All	All	1268/1242 (102%)	1219 (96%)	43 (3%)	6 (0%)	34	9

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	53	SER
1	A	54	GLU
1	B	55	ALA
1	B	52	GLY
1	B	54	GLU

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	534/514 (104%)	528 (99%)	6 (1%)	80	58
1	B	523/514 (102%)	518 (99%)	5 (1%)	82	62
All	All	1057/1028 (103%)	1046 (99%)	11 (1%)	82	62

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	567[A]	LEU
1	A	567[B]	LEU
1	B	337	GLU
1	A	376	PHE
1	B	184	LYS

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	368	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](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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
1	TPQ	A	382	1	13,14,15	2.74	2 (15%)	15,19,21	2.44	3 (20%)
1	TPQ	B	382	1	13,14,15	2.71	2 (15%)	15,19,21	2.66	3 (20%)

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
1	TPQ	A	382	1	-	0/4/22/24	0/1/1/1
1	TPQ	B	382	1	-	0/4/22/24	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	382	TPQ	C6-C1	5.01	1.47	1.34
1	A	382	TPQ	C6-C1	5.70	1.49	1.34
1	A	382	TPQ	C3-C4	7.60	1.48	1.35
1	B	382	TPQ	C3-C4	7.94	1.48	1.35

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	382	TPQ	C1-C6-C5	-7.80	118.22	122.97
1	A	382	TPQ	C1-C6-C5	-7.33	118.51	122.97
1	B	382	TPQ	O-C-CA	-2.25	119.62	125.49
1	A	382	TPQ	C6-C1-C2	2.50	120.20	118.44
1	A	382	TPQ	C3-C2-C1	3.83	121.17	118.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 48 ligands modelled in this entry, 4 are monoatomic - leaving 44 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	PGE	A	1003	-	9,9,9	0.68	0	8,8,8	0.79	0
4	PGE	A	1004	-	9,9,9	0.61	0	8,8,8	0.77	0
4	PGE	A	1005	-	9,9,9	0.78	0	8,8,8	1.01	1 (12%)
5	PG4	A	1006	-	12,12,12	0.71	0	11,11,11	0.91	0
5	PG4	A	1007	-	12,12,12	0.65	0	11,11,11	0.76	0
6	1PE	A	1008	-	15,15,15	0.71	0	14,14,14	0.89	0
7	EDO	A	1009	-	3,3,3	0.44	0	2,2,2	0.10	0
7	EDO	A	1010	-	3,3,3	0.42	0	2,2,2	0.44	0
7	EDO	A	1011	-	3,3,3	0.56	0	2,2,2	0.30	0
7	EDO	A	1012	-	3,3,3	0.46	0	2,2,2	0.47	0
7	EDO	A	1013	-	3,3,3	0.42	0	2,2,2	0.44	0
7	EDO	A	1014	-	3,3,3	0.54	0	2,2,2	0.55	0
7	EDO	A	1015	-	3,3,3	0.72	0	2,2,2	0.07	0
7	EDO	A	1016	-	3,3,3	0.59	0	2,2,2	0.13	0
8	PEG	A	1017	-	6,6,6	0.51	0	5,5,5	0.76	0
8	PEG	A	1018	-	6,6,6	0.61	0	5,5,5	1.06	1 (20%)
8	PEG	A	1019	-	6,6,6	0.68	0	5,5,5	0.98	1 (20%)
8	PEG	A	1020	-	6,6,6	1.17	0	5,5,5	0.81	0
8	PEG	A	1021	-	6,6,6	0.71	0	5,5,5	0.86	0
8	PEG	A	1022	-	6,6,6	0.51	0	5,5,5	0.72	0
9	HDZ	A	1023	-	1,1,1	0.90	0	0,0,0	0.00	-
4	PGE	B	1003	-	9,9,9	0.67	0	8,8,8	0.72	0
4	PGE	B	1004	-	9,9,9	0.68	0	8,8,8	0.82	0
4	PGE	B	1005	-	9,9,9	0.63	0	8,8,8	0.82	0
5	PG4	B	1006	-	12,12,12	0.77	0	11,11,11	0.75	0
5	PG4	B	1007	-	12,12,12	0.54	0	11,11,11	1.03	2 (18%)
6	1PE	B	1008	-	15,15,15	0.66	0	14,14,14	1.05	2 (14%)
7	EDO	B	1009	-	3,3,3	0.54	0	2,2,2	0.57	0
7	EDO	B	1010	-	3,3,3	0.45	0	2,2,2	0.41	0
7	EDO	B	1011	-	3,3,3	0.50	0	2,2,2	0.69	0
7	EDO	B	1012	-	3,3,3	0.51	0	2,2,2	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	EDO	B	1013	-	3,3,3	0.45	0	2,2,2	0.33	0
7	EDO	B	1014	-	3,3,3	0.33	0	2,2,2	0.10	0
7	EDO	B	1015	-	3,3,3	0.65	0	2,2,2	1.07	0
7	EDO	B	1016	-	3,3,3	0.48	0	2,2,2	0.50	0
7	EDO	B	1017	-	3,3,3	0.48	0	2,2,2	0.14	0
7	EDO	B	1018	-	3,3,3	0.49	0	2,2,2	0.37	0
8	PEG	B	1019	-	6,6,6	0.60	0	5,5,5	0.86	0
8	PEG	B	1020	-	6,6,6	0.64	0	5,5,5	0.74	0
8	PEG	B	1021	-	6,6,6	0.89	0	5,5,5	0.74	0
8	PEG	B	1022	-	6,6,6	0.60	0	5,5,5	0.89	0
8	PEG	B	1023	-	6,6,6	0.57	0	5,5,5	0.78	0
8	PEG	B	1024	-	6,6,6	0.78	0	5,5,5	0.77	0
9	HDZ	B	1025	-	1,1,1	0.88	0	0,0,0	0.00	-

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	PGE	A	1003	-	-	0/7/7/7	0/0/0/0
4	PGE	A	1004	-	-	0/7/7/7	0/0/0/0
4	PGE	A	1005	-	-	0/7/7/7	0/0/0/0
5	PG4	A	1006	-	-	0/10/10/10	0/0/0/0
5	PG4	A	1007	-	-	0/10/10/10	0/0/0/0
6	1PE	A	1008	-	-	0/13/13/13	0/0/0/0
7	EDO	A	1009	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1010	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1011	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1012	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1013	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1014	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1015	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1016	-	-	0/1/1/1	0/0/0/0
8	PEG	A	1017	-	-	0/4/4/4	0/0/0/0
8	PEG	A	1018	-	-	0/4/4/4	0/0/0/0
8	PEG	A	1019	-	-	0/4/4/4	0/0/0/0
8	PEG	A	1020	-	-	0/4/4/4	0/0/0/0
8	PEG	A	1021	-	-	0/4/4/4	0/0/0/0
8	PEG	A	1022	-	-	0/4/4/4	0/0/0/0
9	HDZ	A	1023	-	-	0/0/0/0	0/0/0/0
4	PGE	B	1003	-	-	0/7/7/7	0/0/0/0
4	PGE	B	1004	-	-	0/7/7/7	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PGE	B	1005	-	-	0/7/7/7	0/0/0/0
5	PG4	B	1006	-	-	0/10/10/10	0/0/0/0
5	PG4	B	1007	-	-	0/10/10/10	0/0/0/0
6	1PE	B	1008	-	-	0/13/13/13	0/0/0/0
7	EDO	B	1009	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1010	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1011	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1012	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1013	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1014	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1015	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1016	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1017	-	-	0/1/1/1	0/0/0/0
7	EDO	B	1018	-	-	0/1/1/1	0/0/0/0
8	PEG	B	1019	-	-	0/4/4/4	0/0/0/0
8	PEG	B	1020	-	-	0/4/4/4	0/0/0/0
8	PEG	B	1021	-	-	0/4/4/4	0/0/0/0
8	PEG	B	1022	-	-	0/4/4/4	0/0/0/0
8	PEG	B	1023	-	-	0/4/4/4	0/0/0/0
8	PEG	B	1024	-	-	0/4/4/4	0/0/0/0
9	HDZ	B	1025	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1008	1PE	C23-OH3-C22	2.06	122.18	113.31
5	B	1007	PG4	C3-O2-C2	2.06	122.18	113.31
8	A	1019	PEG	C3-O2-C2	2.12	122.42	113.31
4	A	1005	PGE	C3-O2-C2	2.12	122.43	113.31
6	B	1008	1PE	C25-OH5-C14	2.19	122.70	113.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

28 monomers are involved in 103 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1003	PGE	1	0
4	A	1004	PGE	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1005	PGE	1	0
5	A	1006	PG4	4	0
5	A	1007	PG4	4	0
6	A	1008	1PE	5	0
7	A	1009	EDO	4	0
7	A	1014	EDO	4	0
7	A	1016	EDO	1	0
8	A	1019	PEG	7	0
8	A	1020	PEG	8	0
8	A	1021	PEG	7	0
8	A	1022	PEG	1	0
4	B	1003	PGE	1	0
4	B	1004	PGE	1	0
4	B	1005	PGE	4	0
5	B	1006	PG4	3	0
5	B	1007	PG4	10	0
6	B	1008	1PE	3	0
7	B	1011	EDO	7	0
7	B	1014	EDO	4	0
7	B	1015	EDO	3	0
7	B	1017	EDO	3	0
8	B	1019	PEG	4	0
8	B	1020	PEG	2	0
8	B	1021	PEG	5	1
8	B	1022	PEG	0	1
8	B	1024	PEG	5	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	620/621 (99%)	-0.24	18 (2%) 55 59	10, 19, 39, 110	0
1	B	620/621 (99%)	-0.39	12 (1%) 70 73	9, 17, 33, 96	1 (0%)
All	All	1240/1242 (99%)	-0.32	30 (2%) 62 65	9, 18, 36, 110	1 (0%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	52	GLY	12.1
1	A	53	SER	10.4
1	A	54	GLU	9.0
1	B	53	SER	8.9
1	A	51	ALA	8.7

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	TPQ	A	382	14/15	0.94	0.07	-	10,14,18,18	0
1	TPQ	B	382	14/15	0.96	0.06	-	9,14,17,18	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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(Å ²)	Q<0.9
7	EDO	B	1017	4/4	0.83	0.25	16.95	14,18,20,21	4
7	EDO	B	1014	4/4	0.86	0.24	13.60	22,23,27,29	4
8	PEG	B	1021	7/7	0.82	0.21	13.59	9,22,26,27	7
8	PEG	A	1021	7/7	0.88	0.18	8.87	15,26,33,35	7
7	EDO	B	1011	4/4	0.91	0.15	8.26	20,20,21,28	4
8	PEG	B	1020	7/7	0.79	0.17	7.83	27,29,31,35	7
7	EDO	A	1014	4/4	0.85	0.18	7.43	23,24,25,28	4
7	EDO	A	1009	4/4	0.90	0.17	6.15	23,26,27,34	4
5	PG4	A	1006	13/13	0.89	0.11	6.10	17,29,38,43	0
7	EDO	B	1015	4/4	0.89	0.17	6.06	8,11,14,17	4
7	EDO	A	1013	4/4	0.86	0.13	6.00	30,33,34,34	4
8	PEG	A	1018	7/7	0.65	0.29	5.98	38,38,42,44	7
8	PEG	B	1022	7/7	0.77	0.24	5.35	27,29,34,39	7
7	EDO	A	1015	4/4	0.68	0.13	5.10	34,35,36,37	0
6	1PE	A	1008	16/16	0.80	0.17	4.85	38,45,53,53	16
4	PGE	B	1004	10/10	0.74	0.21	4.63	55,60,64,66	0
4	PGE	B	1005	10/10	0.73	0.17	3.72	36,38,43,45	10
5	PG4	B	1006	13/13	0.91	0.09	3.31	15,23,39,39	0
8	PEG	A	1020	7/7	0.93	0.17	3.18	9,19,28,37	7
4	PGE	A	1005	10/10	0.81	0.12	3.13	23,30,36,36	0
8	PEG	A	1022	7/7	0.72	0.14	1.67	37,43,49,50	0
7	EDO	A	1016	4/4	0.77	0.12	1.51	38,45,46,48	0
8	PEG	B	1024	7/7	0.88	0.17	1.47	22,24,26,30	7
7	EDO	B	1012	4/4	0.93	0.09	1.29	27,32,35,39	0
8	PEG	A	1019	7/7	0.88	0.19	1.25	20,22,29,31	7
8	PEG	B	1019	7/7	0.77	0.14	1.22	28,38,40,43	0
7	EDO	B	1009	4/4	0.83	0.09	0.85	31,36,42,45	0
8	PEG	A	1017	7/7	0.86	0.11	0.82	26,33,37,41	7
7	EDO	B	1016	4/4	0.81	0.11	0.61	35,35,38,41	0
5	PG4	B	1007	13/13	0.90	0.11	0.60	9,23,31,36	0
3	NA	B	1002	1/1	0.99	0.08	0.59	11,11,11,11	0
5	PG4	A	1007	13/13	0.93	0.09	0.18	8,21,30,37	0
7	EDO	B	1018	4/4	0.88	0.12	-0.04	61,62,63,64	0
3	NA	A	1002	1/1	0.99	0.07	-0.17	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	PGE	A	1003	10/10	0.89	0.08	-0.17	31,40,46,48	0
7	EDO	A	1011	4/4	0.90	0.07	-0.28	28,31,34,37	0
4	PGE	A	1004	10/10	0.74	0.19	-	54,57,62,63	0
8	PEG	B	1023	7/7	0.94	0.07	-	27,32,33,35	0
7	EDO	A	1012	4/4	0.83	0.14	-	62,62,62,63	0
9	HDZ	B	1025	2/2	0.98	0.14	-	25,25,25,27	0
7	EDO	B	1013	4/4	0.87	0.21	-	27,32,35,37	4
7	EDO	A	1010	4/4	0.88	0.16	-	43,44,45,48	0
2	CU	B	1001	1/1	1.00	0.02	-	12,12,12,12	0
2	CU	A	1001	1/1	1.00	0.03	-	13,13,13,13	0
6	1PE	B	1008	16/16	0.76	0.16	-	36,42,45,46	16
9	HDZ	A	1023	2/2	0.97	0.18	-	26,26,26,28	0
4	PGE	B	1003	10/10	0.80	0.12	-	44,51,58,60	0
7	EDO	B	1010	4/4	0.88	0.14	-	37,39,42,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.