



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:13 PM GMT

PDB ID : 4HIZ
Title : Phage phi92 endosialidase
Authors : Schwarzer, D.; Browning, C.; Leiman, P.G.
Deposited on : 2012-10-12
Resolution : 1.60 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

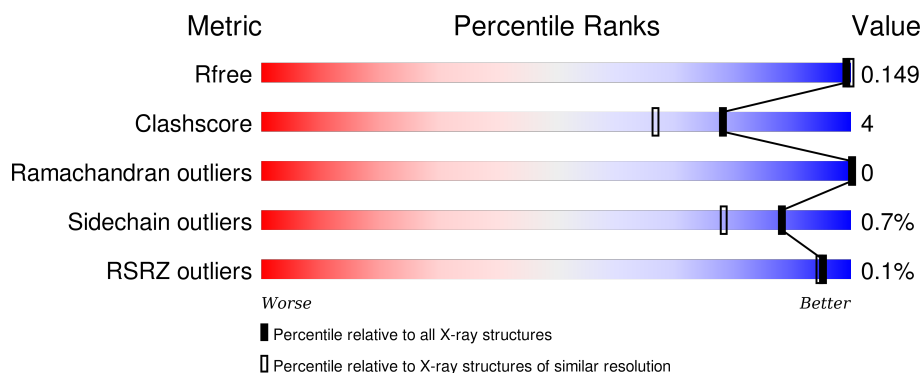
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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	683	<div> <div>91%</div> <div>6% .</div> </div>
1	B	683	<div> <div>88%</div> <div>7% 5%</div> </div>
1	C	683	<div> <div>87%</div> <div>8% .</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	SIA	A	802	-	-	-	X
2	SIA	B	802	-	-	-	X
2	SIA	C	802	-	-	-	X
3	SUC	A	803	-	-	-	X
3	SUC	B	803	-	-	-	X
3	SUC	C	803	-	-	-	X
4	EDO	A	804	-	-	-	X
4	EDO	A	806	-	-	-	X
4	EDO	A	807	-	-	-	X
4	EDO	A	808	-	-	-	X
4	EDO	A	810	-	-	-	X
4	EDO	A	811	-	-	-	X
4	EDO	A	812	-	-	-	X
4	EDO	A	815	-	-	-	X
4	EDO	A	817	-	-	-	X
4	EDO	A	818	-	-	-	X
4	EDO	A	819	-	-	-	X
4	EDO	B	804	-	-	-	X
4	EDO	B	808	-	-	-	X
4	EDO	B	810	-	-	-	X
4	EDO	B	811	-	-	-	X
4	EDO	B	813	-	-	-	X
4	EDO	B	815	-	-	-	X
4	EDO	B	816	-	-	-	X
4	EDO	C	804	-	-	-	X
4	EDO	C	807	-	-	-	X
4	EDO	C	808	-	-	-	X
4	EDO	C	809	-	-	-	X
4	EDO	C	810	-	-	-	X
4	EDO	C	811	-	-	-	X
4	EDO	C	814	-	-	-	X
4	EDO	C	816	-	-	-	X
7	CA	A	823	-	-	-	X
7	CA	B	819	-	-	-	X
7	CA	C	820	-	-	-	X
8	NA	A	828	-	-	-	X
8	NA	C	826	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 19802 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 Endosialidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	658	Total	C	N	O	S	0	22	0
			5321	3388	895	1017	21			
1	B	652	Total	C	N	O	S	0	17	0
			5249	3345	880	1003	21			
1	C	655	Total	C	N	O	S	0	28	0
			5345	3412	899	1012	22			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	GLY	-	EXPRESSION TAG	UNP I7HXG2
A	75	SER	-	EXPRESSION TAG	UNP I7HXG2
B	74	GLY	-	EXPRESSION TAG	UNP I7HXG2
B	75	SER	-	EXPRESSION TAG	UNP I7HXG2
C	74	GLY	-	EXPRESSION TAG	UNP I7HXG2
C	75	SER	-	EXPRESSION TAG	UNP I7HXG2

- Molecule 2 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			41	22	2	17		
2	B	2	Total	C	N	O	0	0
			41	22	2	17		
2	C	2	Total	C	N	O	0	0
			41	22	2	17		

- Molecule 3 is SUGAR (SUCROSE) (three-letter code: SUC) (formula: C₁₂H₂₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			23	12	11		
3	B	1	Total	C	O	0	0
			23	12	11		
3	C	1	Total	C	O	0	0
			23	12	11		

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



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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	Mg 1	0	0
5	A	1	Total 1	Mg 1	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total 2	Ca 2	0	0
7	A	2	Total 2	Ca 2	0	0
7	C	2	Total 2	Ca 2	0	0

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total 1	Na 1	0	0
8	A	5	Total 5	Na 5	0	0
8	C	6	Total 6	Na 6	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1215	Total 1215	O 1215	0	0

Continued on next page...

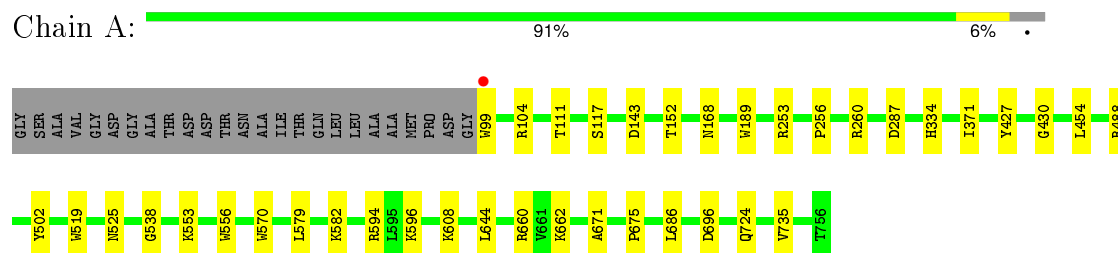
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1144	Total 1144	O 1144	0	0
9	C	1140	Total 1140	O 1140	0	0

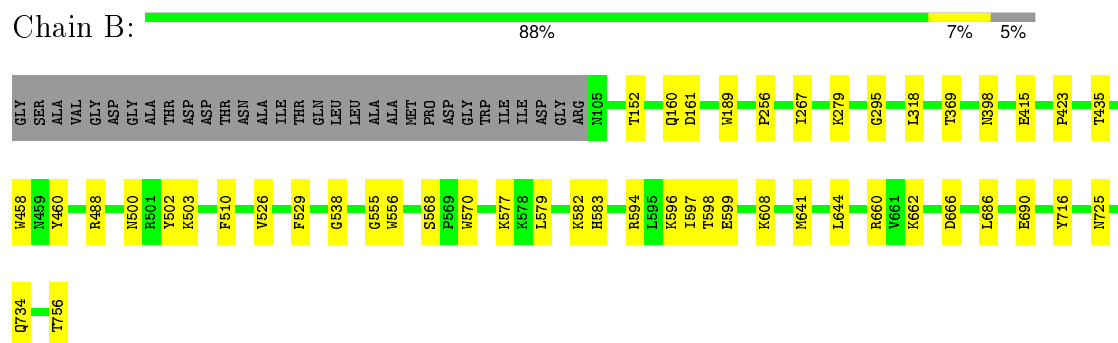
3 Residue-property plots

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.

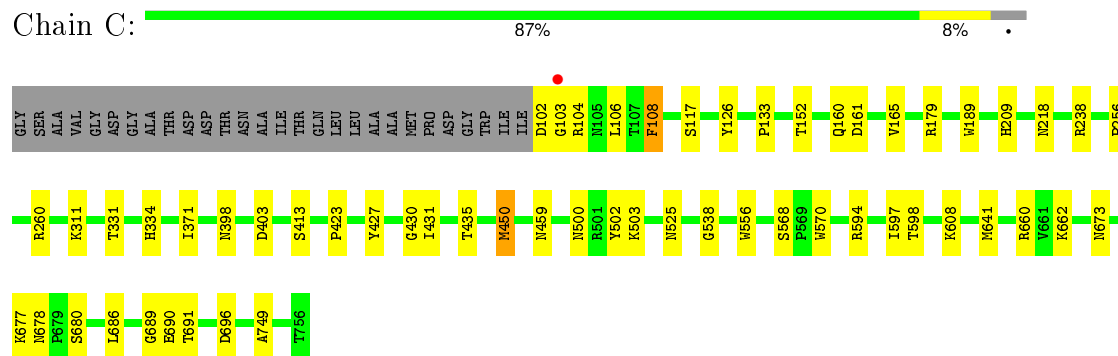
• Molecule 1: Endosialidase



• Molecule 1: Endosialidase



• Molecule 1: Endosialidase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.86Å 137.58Å 140.78Å 90.00° 94.64° 90.00°	Depositor
Resolution (Å)	19.97 – 1.60 19.97 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.97-1.60) 99.8 (19.97-1.60)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 1.60Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.107 , 0.147 0.110 , 0.149	Depositor DCC
R_{free} test set	3116 reflections (1.03%)	DCC
Wilson B-factor (Å ²)	12.7	Xtriage
Anisotropy	0.712	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 304592 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	19802	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SUC, CL, NA, CA, EDO, SIA, SLB

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	0.67	0/5521	0.72	1/7522 (0.0%)
1	B	0.67	0/5442	0.72	1/7413 (0.0%)
1	C	0.68	0/5557	0.75	3/7563 (0.0%)
All	All	0.67	0/16520	0.73	5/22498 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	108[A]	PHE	CB-CA-C	-8.31	93.78	110.40
1	C	108[B]	PHE	CB-CA-C	-8.31	93.78	110.40
1	A	488	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	C	238	ARG	NE-CZ-NH1	-5.64	117.48	120.30
1	B	488	ARG	NE-CZ-NH2	-5.39	117.60	120.30

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	5321	0	5121	36	0
1	B	5249	0	5052	37	0
1	C	5345	0	5180	52	2

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	41	0	34	0	0
2	B	41	0	34	0	0
2	C	41	0	34	2	0
3	A	23	0	22	1	0
3	B	23	0	22	0	0
3	C	23	0	22	0	0
4	A	64	0	96	6	1
4	B	52	0	78	7	0
4	C	56	0	84	5	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	2	0	0	1	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
7	A	2	0	0	0	0
7	B	2	0	0	0	0
7	C	2	0	0	0	0
8	A	5	0	0	0	0
8	B	1	0	0	0	0
8	C	6	0	0	0	0
9	A	1215	0	0	14	4
9	B	1144	0	0	15	4
9	C	1140	0	0	23	5
All	All	19802	0	15779	117	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 4.

The worst 5 of 117 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:C:660[B]:ARG:NH1	9:C:1808:HOH:O	1.97	0.96
6:A:822:CL:CL	9:C:1674:HOH:O	2.21	0.96
1:C:102:ASP:O	9:C:1804:HOH:O	1.89	0.91
1:C:450[A]:MET:SD	9:C:1757:HOH:O	2.32	0.88
1:A:660[B]:ARG:NH1	9:A:1883:HOH:O	2.05	0.85

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)
1:C:102:ASP:N	9:C:1554:HOH:O[2_555]	1.91	0.29
9:A:1820:HOH:O	9:B:1608:HOH:O[2_555]	2.01	0.19
9:A:1765:HOH:O	9:C:1450:HOH:O[2_555]	2.09	0.11
9:B:1630:HOH:O	9:C:1609:HOH:O[4_545]	2.10	0.10
9:B:1829:HOH:O	9:C:913:HOH:O[4_545]	2.12	0.08

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	678/683 (99%)	658 (97%)	20 (3%)	0	100	100
1	B	668/683 (98%)	649 (97%)	19 (3%)	0	100	100
1	C	681/683 (100%)	661 (97%)	20 (3%)	0	100	100
All	All	2027/2049 (99%)	1968 (97%)	59 (3%)	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	584/578 (101%)	580 (99%)	4 (1%)	88	78
1	B	575/578 (100%)	572 (100%)	3 (0%)	92	85
1	C	587/578 (102%)	582 (99%)	5 (1%)	84	71
All	All	1746/1734 (101%)	1734 (99%)	12 (1%)	88	78

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	189	TRP
1	B	597	ILE
1	C	450[A]	MET
1	B	152	THR
1	C	189	TRP

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

6 carbohydrates 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	$\# Z > 2$
2	SLB	A	801	2	17,21,21	3.00	6 (35%)	19,31,31	1.73	6 (31%)
2	SIA	A	802	2	16,20,21	0.50	0	18,28,31	0.87	0
2	SLB	B	801	2	17,21,21	2.94	5 (29%)	19,31,31	2.07	5 (26%)
2	SIA	B	802	2	16,20,21	0.59	0	18,28,31	1.27	2 (11%)
2	SLB	C	801	2	17,21,21	3.07	4 (23%)	19,31,31	1.47	2 (10%)
2	SIA	C	802	2	16,20,21	0.45	0	18,28,31	1.04	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	SLB	A	801	2	-	0/14/38/38	0/1/1/1
2	SIA	A	802	2	-	0/14/34/38	0/1/1/1
2	SLB	B	801	2	-	0/14/38/38	0/1/1/1
2	SIA	B	802	2	-	0/14/34/38	0/1/1/1
2	SLB	C	801	2	-	0/14/38/38	0/1/1/1
2	SIA	C	802	2	-	0/14/34/38	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	SLB	C3-C4	-4.53	1.45	1.53
2	A	801	SLB	C3-C4	-4.25	1.46	1.53
2	B	801	SLB	C3-C4	-3.53	1.47	1.53
2	A	801	SLB	C7-C6	-2.23	1.50	1.52
2	A	801	SLB	C8-C7	-2.16	1.49	1.53

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	SLB	C8-C7-C6	-5.56	101.83	113.01
2	A	801	SLB	C8-C7-C6	-4.23	104.51	113.01
2	C	801	SLB	C8-C7-C6	-3.27	106.44	113.01
2	A	801	SLB	C7-C6-C5	-3.01	109.76	114.32
2	B	801	SLB	O9-C9-C8	-2.90	104.80	111.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	802	SIA	2	0

5.6 Ligand geometry ⓘ

Of 70 ligands modelled in this entry, 24 are monoatomic - leaving 46 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	SUC	A	803	-	24,24,24	0.94	0	36,36,36	1.77	8 (22%)
4	EDO	A	804	-	3,3,3	0.59	0	2,2,2	0.21	0
4	EDO	A	805	-	3,3,3	0.54	0	2,2,2	0.17	0
4	EDO	A	806	-	3,3,3	0.46	0	2,2,2	0.31	0
4	EDO	A	807	-	3,3,3	0.51	0	2,2,2	0.35	0
4	EDO	A	808	-	3,3,3	0.58	0	2,2,2	0.09	0
4	EDO	A	809	-	3,3,3	0.34	0	2,2,2	0.72	0
4	EDO	A	810	-	3,3,3	0.41	0	2,2,2	0.86	0
4	EDO	A	811	-	3,3,3	0.47	0	2,2,2	0.45	0
4	EDO	A	812	-	3,3,3	0.39	0	2,2,2	0.46	0
4	EDO	A	813	-	3,3,3	0.44	0	2,2,2	0.68	0
4	EDO	A	814	-	3,3,3	0.48	0	2,2,2	0.40	0
4	EDO	A	815	-	3,3,3	0.52	0	2,2,2	0.25	0
4	EDO	A	816	-	3,3,3	0.44	0	2,2,2	0.66	0
4	EDO	A	817	-	3,3,3	0.45	0	2,2,2	0.70	0
4	EDO	A	818	-	3,3,3	0.50	0	2,2,2	0.30	0
4	EDO	A	819	-	3,3,3	0.45	0	2,2,2	0.43	0
3	SUC	B	803	-	24,24,24	0.92	0	36,36,36	1.80	7 (19%)
4	EDO	B	804	-	3,3,3	0.75	0	2,2,2	0.31	0
4	EDO	B	805	-	3,3,3	0.46	0	2,2,2	0.29	0
4	EDO	B	806	-	3,3,3	0.47	0	2,2,2	0.38	0
4	EDO	B	807	-	3,3,3	0.63	0	2,2,2	0.38	0
4	EDO	B	808	-	3,3,3	0.83	0	2,2,2	0.10	0
4	EDO	B	809	-	3,3,3	0.46	0	2,2,2	0.61	0
4	EDO	B	810	-	3,3,3	0.34	0	2,2,2	0.79	0
4	EDO	B	811	-	3,3,3	0.59	0	2,2,2	0.61	0
4	EDO	B	812	-	3,3,3	0.47	0	2,2,2	0.47	0
4	EDO	B	813	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	814	-	3,3,3	0.46	0	2,2,2	0.50	0
4	EDO	B	815	-	3,3,3	0.44	0	2,2,2	0.57	0
4	EDO	B	816	-	3,3,3	0.51	0	2,2,2	0.37	0
3	SUC	C	803	-	24,24,24	0.90	0	36,36,36	1.91	8 (22%)
4	EDO	C	804	-	3,3,3	0.67	0	2,2,2	0.14	0
4	EDO	C	805	-	3,3,3	0.50	0	2,2,2	0.44	0
4	EDO	C	806	-	3,3,3	0.62	0	2,2,2	0.21	0
4	EDO	C	807	-	3,3,3	0.58	0	2,2,2	0.68	0
4	EDO	C	808	-	3,3,3	0.65	0	2,2,2	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	C	809	8	3,3,3	0.48	0	2,2,2	0.23	0
4	EDO	C	810	-	3,3,3	0.78	0	2,2,2	0.47	0
4	EDO	C	811	-	3,3,3	0.74	0	2,2,2	0.14	0
4	EDO	C	812	-	3,3,3	0.48	0	2,2,2	0.37	0
4	EDO	C	813	-	3,3,3	0.52	0	2,2,2	0.46	0
4	EDO	C	814	-	3,3,3	0.46	0	2,2,2	0.38	0
4	EDO	C	815	-	3,3,3	0.57	0	2,2,2	0.31	0
4	EDO	C	816	-	3,3,3	0.44	0	2,2,2	0.40	0
4	EDO	C	817	-	3,3,3	0.49	0	2,2,2	0.38	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	SUC	A	803	-	-	0/12/51/51	0/2/2/2
4	EDO	A	804	-	-	0/1/1/1	0/0/0/0
4	EDO	A	805	-	-	0/1/1/1	0/0/0/0
4	EDO	A	806	-	-	0/1/1/1	0/0/0/0
4	EDO	A	807	-	-	0/1/1/1	0/0/0/0
4	EDO	A	808	-	-	0/1/1/1	0/0/0/0
4	EDO	A	809	-	-	0/1/1/1	0/0/0/0
4	EDO	A	810	-	-	0/1/1/1	0/0/0/0
4	EDO	A	811	-	-	0/1/1/1	0/0/0/0
4	EDO	A	812	-	-	0/1/1/1	0/0/0/0
4	EDO	A	813	-	-	0/1/1/1	0/0/0/0
4	EDO	A	814	-	-	0/1/1/1	0/0/0/0
4	EDO	A	815	-	-	0/1/1/1	0/0/0/0
4	EDO	A	816	-	-	0/1/1/1	0/0/0/0
4	EDO	A	817	-	-	0/1/1/1	0/0/0/0
4	EDO	A	818	-	-	0/1/1/1	0/0/0/0
4	EDO	A	819	-	-	0/1/1/1	0/0/0/0
3	SUC	B	803	-	-	0/12/51/51	0/2/2/2
4	EDO	B	804	-	-	0/1/1/1	0/0/0/0
4	EDO	B	805	-	-	0/1/1/1	0/0/0/0
4	EDO	B	806	-	-	0/1/1/1	0/0/0/0
4	EDO	B	807	-	-	0/1/1/1	0/0/0/0
4	EDO	B	808	-	-	0/1/1/1	0/0/0/0
4	EDO	B	809	-	-	0/1/1/1	0/0/0/0
4	EDO	B	810	-	-	0/1/1/1	0/0/0/0
4	EDO	B	811	-	-	0/1/1/1	0/0/0/0
4	EDO	B	812	-	-	0/1/1/1	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	813	-	-	0/1/1/1	0/0/0/0
4	EDO	B	814	-	-	0/1/1/1	0/0/0/0
4	EDO	B	815	-	-	0/1/1/1	0/0/0/0
4	EDO	B	816	-	-	0/1/1/1	0/0/0/0
3	SUC	C	803	-	-	0/12/51/51	0/2/2/2
4	EDO	C	804	-	-	0/1/1/1	0/0/0/0
4	EDO	C	805	-	-	0/1/1/1	0/0/0/0
4	EDO	C	806	-	-	0/1/1/1	0/0/0/0
4	EDO	C	807	-	-	0/1/1/1	0/0/0/0
4	EDO	C	808	-	-	0/1/1/1	0/0/0/0
4	EDO	C	809	8	-	0/1/1/1	0/0/0/0
4	EDO	C	810	-	-	0/1/1/1	0/0/0/0
4	EDO	C	811	-	-	0/1/1/1	0/0/0/0
4	EDO	C	812	-	-	0/1/1/1	0/0/0/0
4	EDO	C	813	-	-	0/1/1/1	0/0/0/0
4	EDO	C	814	-	-	0/1/1/1	0/0/0/0
4	EDO	C	815	-	-	0/1/1/1	0/0/0/0
4	EDO	C	816	-	-	0/1/1/1	0/0/0/0
4	EDO	C	817	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	803	SUC	O1-C2'-C1'	-4.45	95.43	109.69
3	C	803	SUC	O1-C2'-O2'	-4.29	96.91	110.52
3	C	803	SUC	O1'-C1'-C2'	-4.24	98.35	111.91
3	A	803	SUC	O1-C2'-C1'	-4.06	96.68	109.69
3	C	803	SUC	O1-C2'-C1'	-4.03	96.78	109.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

18 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	803	SUC	1	0
4	A	812	EDO	2	0
4	A	814	EDO	1	1
4	A	816	EDO	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	817	EDO	1	0
4	A	819	EDO	1	0
4	B	804	EDO	1	0
4	B	806	EDO	1	0
4	B	808	EDO	1	0
4	B	810	EDO	1	0
4	B	812	EDO	1	0
4	B	813	EDO	1	0
4	B	816	EDO	1	0
4	C	809	EDO	1	0
4	C	812	EDO	1	0
4	C	814	EDO	1	0
4	C	816	EDO	1	0
4	C	817	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	658/683 (96%)	-0.93	1 (0%) 95 94	9, 15, 26, 57	0
1	B	652/683 (95%)	-0.93	0 100 100	10, 15, 26, 50	0
1	C	655/683 (95%)	-0.87	1 (0%) 95 94	10, 16, 30, 72	0
All	All	1965/2049 (95%)	-0.91	2 (0%) 95 94	9, 15, 28, 72	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	99	TRP	2.8
1	C	103	GLY	2.7

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](#)

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
2	SIA	A	802	20/21	0.90	0.19	9.06	22,27,38,46	0
2	SIA	C	802	20/21	0.92	0.22	9.00	25,30,44,45	0
2	SIA	B	802	20/21	0.90	0.21	8.91	25,30,42,46	0
2	SLB	A	801	21/21	0.72	0.33	-	51,77,96,103	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	SLB	C	801	21/21	0.68	0.29	-	56,80,90,96	0
2	SLB	B	801	21/21	0.64	0.34	-	53,78,91,105	0

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(\AA^2)	Q<0.9
4	EDO	C	808	4/4	0.66	0.19	26.44	46,51,56,57	0
4	EDO	B	815	4/4	0.78	0.23	22.11	42,47,56,66	0
4	EDO	A	804	4/4	0.92	0.11	20.51	39,39,40,41	0
4	EDO	B	808	4/4	0.72	0.18	19.83	42,42,43,43	0
4	EDO	A	819	4/4	0.91	0.18	14.64	42,44,52,62	0
8	NA	C	826	1/1	0.98	0.11	13.10	49,49,49,49	0
4	EDO	B	816	4/4	0.89	0.18	12.54	55,59,59,59	0
8	NA	A	828	1/1	0.99	0.13	9.13	35,35,35,35	0
4	EDO	C	811	4/4	0.91	0.10	8.87	28,31,34,37	0
4	EDO	B	810	4/4	0.97	0.08	8.22	26,29,36,42	0
3	SUC	C	803	23/23	0.94	0.15	6.90	22,31,36,37	0
3	SUC	A	803	23/23	0.96	0.13	6.70	20,29,32,33	0
3	SUC	B	803	23/23	0.93	0.15	6.59	21,27,34,35	0
4	EDO	A	815	4/4	0.28	0.39	6.35	87,98,98,102	0
4	EDO	A	818	4/4	0.79	0.18	6.32	47,48,52,60	0
4	EDO	B	811	4/4	0.89	0.16	6.20	29,35,40,44	0
4	EDO	A	807	4/4	0.92	0.12	5.85	29,34,38,38	0
4	EDO	B	813	4/4	0.96	0.22	5.71	36,46,51,51	0
4	EDO	A	812	4/4	0.96	0.14	5.57	30,37,41,46	0
4	EDO	C	807	4/4	0.92	0.12	5.52	29,31,34,36	0
4	EDO	A	806	4/4	0.96	0.09	5.22	21,26,29,31	0
7	CA	B	819	1/1	1.00	0.07	5.17	16,16,16,16	0
7	CA	C	820	1/1	1.00	0.14	5.16	41,41,41,41	0
4	EDO	C	804	4/4	0.95	0.12	4.57	29,31,32,33	0
4	EDO	A	817	4/4	0.94	0.11	4.38	45,45,49,52	0
4	EDO	A	810	4/4	0.94	0.10	4.35	28,32,39,44	0
7	CA	A	823	1/1	1.00	0.06	4.22	16,16,16,16	0
4	EDO	A	808	4/4	0.88	0.15	4.07	43,43,49,56	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	EDO	C	809	4/4	0.96	0.09	3.76	21,26,27,29	0
4	EDO	C	814	4/4	0.91	0.15	3.47	46,48,53,56	0
4	EDO	C	816	4/4	0.95	0.20	3.45	35,43,53,61	0
4	EDO	B	804	4/4	0.92	0.09	3.41	27,29,29,30	0
4	EDO	C	810	4/4	0.90	0.12	3.24	24,30,34,40	0
4	EDO	A	811	4/4	0.97	0.10	3.12	33,36,41,46	0
8	NA	A	826	1/1	0.98	0.05	1.28	44,44,44,44	0
4	EDO	B	807	4/4	0.97	0.10	0.86	22,25,26,27	0
6	CL	A	821	1/1	1.00	0.05	0.46	25,25,25,25	0
4	EDO	B	806	4/4	0.93	0.07	0.43	51,52,56,59	0
4	EDO	A	805	4/4	0.97	0.07	0.05	18,20,22,23	0
8	NA	B	821	1/1	1.00	0.05	0.04	31,31,31,31	0
7	CA	C	819	1/1	1.00	0.04	-0.09	16,16,16,16	0
8	NA	A	829	1/1	0.99	0.04	-0.15	26,26,26,26	0
4	EDO	C	806	4/4	0.97	0.07	-0.31	22,25,26,28	0
8	NA	C	822	1/1	1.00	0.03	-0.97	23,23,23,23	0
6	CL	B	818	1/1	1.00	0.03	-1.00	24,24,24,24	0
4	EDO	A	814	4/4	0.90	0.09	-1.02	56,56,57,57	0
6	CL	C	818	1/1	1.00	0.03	-1.11	25,25,25,25	0
8	NA	C	821	1/1	1.00	0.01	-2.71	19,19,19,19	0
4	EDO	C	805	4/4	0.86	0.08	-	31,33,39,46	0
8	NA	A	825	1/1	0.89	0.09	-	76,76,76,76	0
4	EDO	C	812	4/4	0.74	0.20	-	59,60,64,69	0
4	EDO	C	815	4/4	0.67	0.20	-	53,53,54,60	0
8	NA	C	825	1/1	0.99	0.11	-	38,38,38,38	0
6	CL	A	822	1/1	0.97	0.04	-	59,59,59,59	0
8	NA	C	823	1/1	1.00	0.03	-	28,28,28,28	0
4	EDO	B	812	4/4	0.81	0.18	-	59,60,60,61	0
4	EDO	B	809	4/4	0.93	0.13	-	32,35,40,45	0
5	MG	A	820	1/1	1.00	0.05	-	32,32,32,32	0
4	EDO	C	813	4/4	0.48	0.29	-	52,54,54,54	0
4	EDO	A	813	4/4	0.76	0.22	-	88,88,90,92	0
7	CA	A	824	1/1	1.00	0.02	-	27,27,27,27	0
5	MG	B	817	1/1	0.96	0.05	-	51,51,51,51	0
4	EDO	A	809	4/4	0.95	0.07	-	29,32,36,40	0
8	NA	A	827	1/1	0.96	0.23	-	48,48,48,48	0
7	CA	B	820	1/1	1.00	0.01	-	22,22,22,22	0
4	EDO	C	817	4/4	0.79	0.28	-	62,64,74,83	0
8	NA	C	824	1/1	0.99	0.07	-	34,34,34,34	0
4	EDO	B	814	4/4	0.84	0.23	-	81,85,85,85	0
4	EDO	A	816	4/4	0.90	0.15	-	33,38,50,59	0
4	EDO	B	805	4/4	0.94	0.08	-	29,33,42,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.