



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:45 PM UTC

PDB ID : 8AY1 / pdb_00008ay1
Title : Crystal structure of the *C. elegans* POFUT2 (CePoFUT2) triple mutant (R298K-R299K-A418C) in complex with the *Rattus norvegicus* TSR4 single mutant (E10C) from F-spondin
Authors : Hurtado-Guerrero, R.; Merino, P.
Deposited on : 2022-09-01
Resolution : 2.13 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

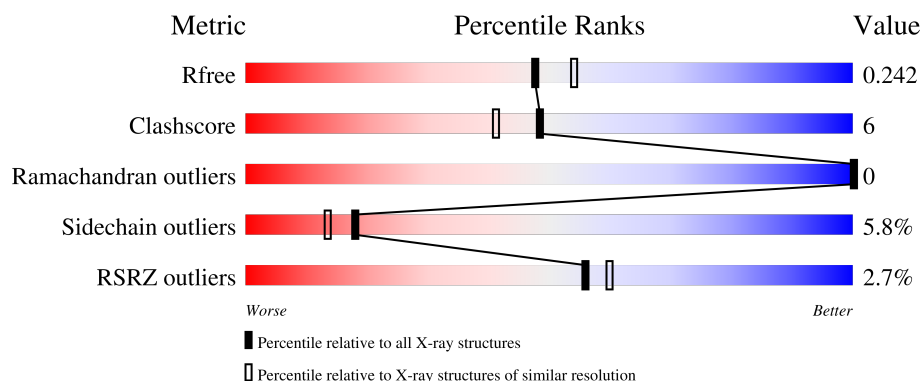
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

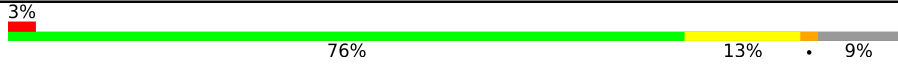
The reported resolution of this entry is 2.13 Å.

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}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 $\leq 5\%$. 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	462	
1	B	462	

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
3	EDO	A	1107	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7237 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 GDP-fucose protein O-fucosyltransferase 2,Spondin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	2	0
			3527	2254	607	647	19			
1	B	409	Total	C	N	O	S	0	1	0
			3417	2183	585	632	17			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	298	LYS	ARG	engineered mutation	UNP Q8WR51
A	299	LYS	ARG	engineered mutation	UNP Q8WR51
A	418	CYS	ALA	engineered mutation	UNP Q8WR51
A	979	SER	-	linker	UNP Q8WR51
A	980	SER	-	linker	UNP Q8WR51
A	981	GLY	-	linker	UNP Q8WR51
A	982	GLY	-	linker	UNP Q8WR51
A	983	GLY	-	linker	UNP Q8WR51
A	984	GLY	-	linker	UNP Q8WR51
A	985	SER	-	linker	UNP Q8WR51
A	986	GLY	-	linker	UNP Q8WR51
A	987	GLY	-	linker	UNP Q8WR51
A	988	GLY	-	linker	UNP Q8WR51
A	989	GLY	-	linker	UNP Q8WR51
A	990	SER	-	linker	UNP Q8WR51
A	991	GLY	-	linker	UNP Q8WR51
A	992	GLY	-	linker	UNP Q8WR51
A	993	GLY	-	linker	UNP Q8WR51
A	994	GLY	-	linker	UNP Q8WR51
A	995	GLY	-	linker	UNP Q8WR51
A	996	SER	-	linker	UNP Q8WR51
A	997	SER	-	linker	UNP Q8WR51
A	998	GLY	-	linker	UNP Q8WR51
A	999	SER	-	linker	UNP Q8WR51
A	1000	SER	-	linker	UNP Q8WR51

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1010	CYS	GLU	engineered mutation	UNP Q3B7D6
B	298	LYS	ARG	engineered mutation	UNP Q8WR51
B	299	LYS	ARG	engineered mutation	UNP Q8WR51
B	418	CYS	ALA	engineered mutation	UNP Q8WR51
B	979	SER	-	linker	UNP Q8WR51
B	980	SER	-	linker	UNP Q8WR51
B	981	GLY	-	linker	UNP Q8WR51
B	982	GLY	-	linker	UNP Q8WR51
B	983	GLY	-	linker	UNP Q8WR51
B	984	GLY	-	linker	UNP Q8WR51
B	985	SER	-	linker	UNP Q8WR51
B	986	GLY	-	linker	UNP Q8WR51
B	987	GLY	-	linker	UNP Q8WR51
B	988	GLY	-	linker	UNP Q8WR51
B	989	GLY	-	linker	UNP Q8WR51
B	990	SER	-	linker	UNP Q8WR51
B	991	GLY	-	linker	UNP Q8WR51
B	992	GLY	-	linker	UNP Q8WR51
B	993	GLY	-	linker	UNP Q8WR51
B	994	GLY	-	linker	UNP Q8WR51
B	995	GLY	-	linker	UNP Q8WR51
B	996	SER	-	linker	UNP Q8WR51
B	997	SER	-	linker	UNP Q8WR51
B	998	GLY	-	linker	UNP Q8WR51
B	999	SER	-	linker	UNP Q8WR51
B	1000	SER	-	linker	UNP Q8WR51
B	1010	CYS	GLU	engineered mutation	UNP Q3B7D6

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



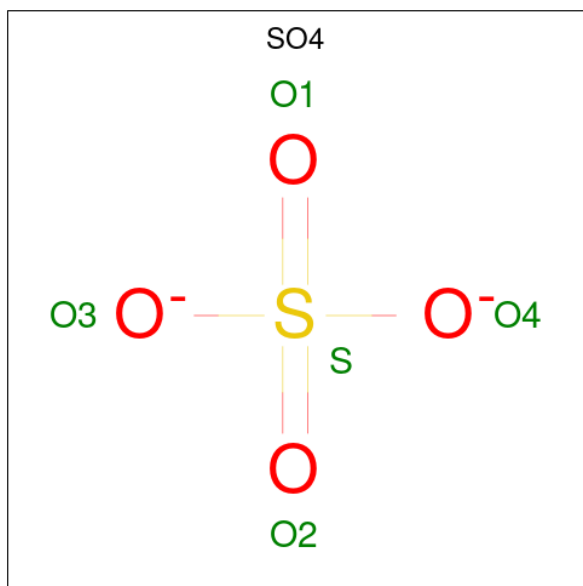
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



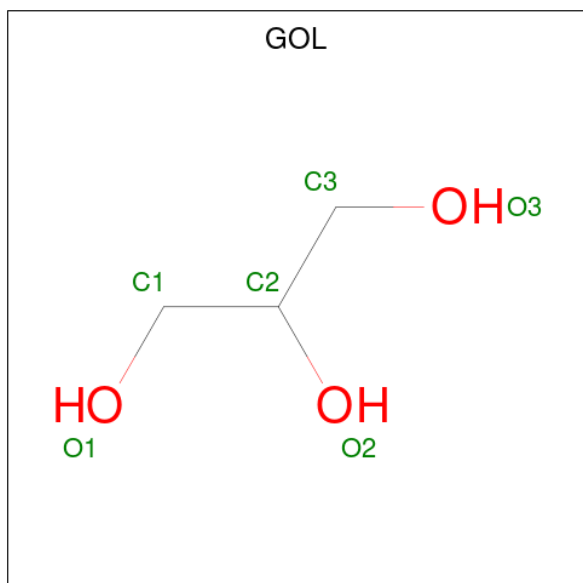
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		

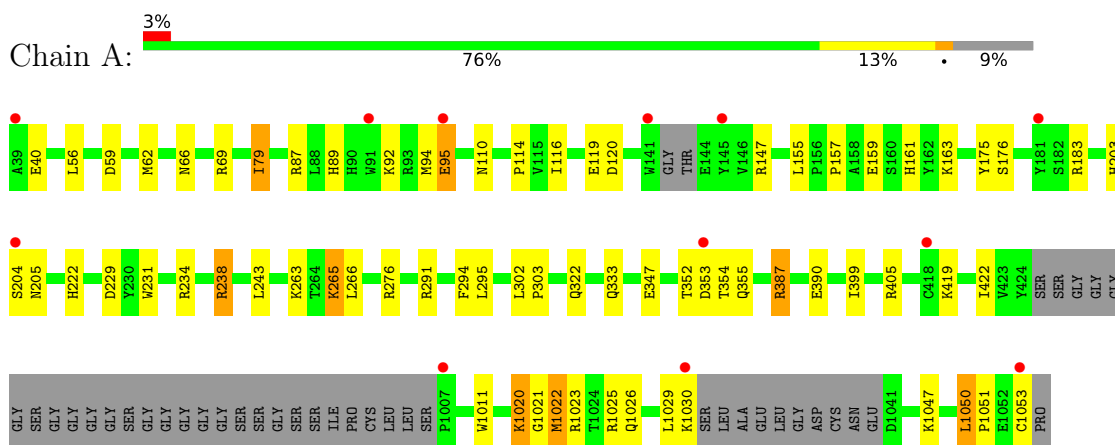
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	91	Total 91	O 91	0	0
6	B	64	Total 64	O 64	0	0

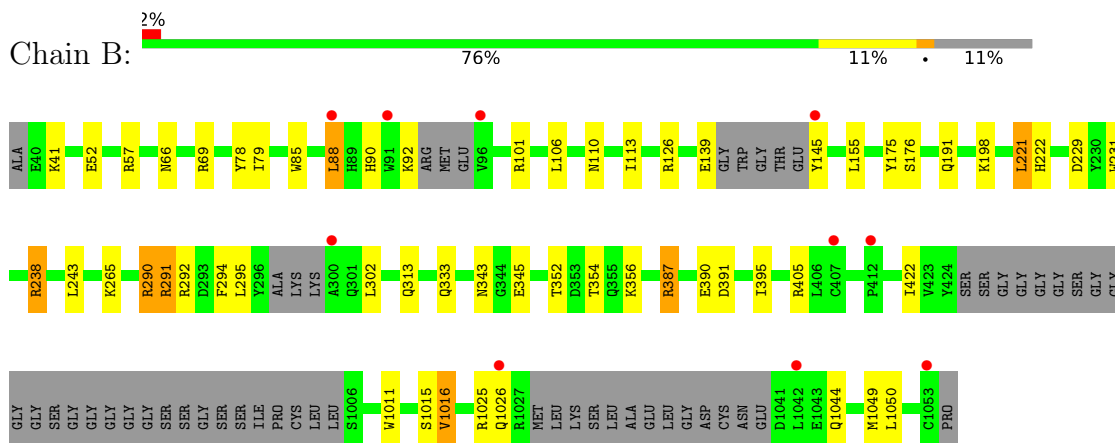
3 Residue-property plots [i](#)

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: GDP-fucose protein O-fucosyltransferase 2,Spondin-1



- Molecule 1: GDP-fucose protein O-fucosyltransferase 2,Spondin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	156.85Å 156.85Å 80.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.90 – 2.13 19.90 – 2.13	Depositor EDS
% Data completeness (in resolution range)	99.3 (19.90-2.13) 99.4 (19.90-2.13)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.13Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.194 , 0.240 0.201 , 0.242	Depositor DCC
R_{free} test set	2444 reflections (3.86%)	wwPDB-VP
Wilson B-factor (Å ²)	54.8	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7237	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: SO4, GOL, NAG, EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.53	0/3622	0.97	1/4889 (0.0%)
1	B	0.54	0/3505	0.95	1/4734 (0.0%)
All	All	0.54	0/7127	0.96	2/9623 (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	A	0	3
1	B	0	3
All	All	0	6

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1053	CYS	CA-C-O	-6.27	110.15	120.80
1	B	90	HIS	CB-CA-C	5.16	120.22	109.95

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1023	ARG	Sidechain
1	A	238	ARG	Sidechain
1	A	87	ARG	Sidechain
1	B	101	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	238	ARG	Sidechain

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	3527	0	3428	40	0
1	B	3417	0	3301	38	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
3	A	24	0	36	6	0
3	B	20	0	30	3	0
4	A	30	0	0	1	0
4	B	30	0	0	2	0
5	B	6	0	8	1	0
6	A	91	0	0	3	0
6	B	64	0	0	4	0
All	All	7237	0	6829	77	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 77 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:290:ARG:HG3	1:B:290:ARG:HH11	1.34	0.90
1:B:85:TRP:HA	3:B:1104:EDO:H12	1.65	0.77
1:A:234:ARG:HD3	3:A:1107:EDO:H22	1.71	0.71
1:B:291:ARG:HG2	1:B:291:ARG:HH11	1.57	0.69
1:A:222:HIS:HD2	6:A:1249:HOH:O	1.76	0.69

There are no symmetry-related clashes.

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	415/462 (90%)	407 (98%)	8 (2%)	0	100	100
1	B	398/462 (86%)	391 (98%)	7 (2%)	0	100	100
All	All	813/924 (88%)	798 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	383/405 (95%)	358 (94%)	25 (6%)	15	10
1	B	373/405 (92%)	354 (95%)	19 (5%)	21	17
All	All	756/810 (93%)	712 (94%)	44 (6%)	18	13

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	126	ARG
1	B	290	ARG
1	B	145	TYR
1	B	221	LEU
1	B	333	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	322	GLN
1	B	1044	GLN
1	A	355	GLN
1	A	372	HIS
1	B	66	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

26 ligands 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	NAG	B	1101	1	14,14,15	0.46	0	17,19,21	1.03	1 (5%)
4	SO4	A	1113	-	4,4,4	0.34	0	6,6,6	0.19	0
4	SO4	A	1110	-	4,4,4	0.25	0	6,6,6	0.17	0
3	EDO	B	1106	-	3,3,3	0.21	0	2,2,2	0.55	0
4	SO4	A	1109	-	4,4,4	0.33	0	6,6,6	0.12	0
3	EDO	B	1103	-	3,3,3	0.22	0	2,2,2	0.19	0
3	EDO	A	1105	-	3,3,3	0.13	0	2,2,2	0.26	0
4	SO4	B	1109	-	4,4,4	0.34	0	6,6,6	0.07	0
4	SO4	B	1112	-	4,4,4	0.30	0	6,6,6	0.17	0
4	SO4	B	1108	-	4,4,4	0.32	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	1107	-	3,3,3	0.41	0	2,2,2	0.77	0
2	NAG	A	1101	1	14,14,15	0.40	0	17,19,21	1.35	2 (11%)
3	EDO	A	1106	-	3,3,3	0.15	0	2,2,2	0.26	0
5	GOL	B	1102	-	5,5,5	0.14	0	5,5,5	0.39	0
4	SO4	B	1110	-	4,4,4	0.29	0	6,6,6	0.19	0
4	SO4	B	1113	-	4,4,4	0.31	0	6,6,6	0.08	0
3	EDO	A	1103	-	3,3,3	0.19	0	2,2,2	0.41	0
4	SO4	A	1111	-	4,4,4	0.37	0	6,6,6	0.16	0
3	EDO	B	1104	-	3,3,3	0.30	0	2,2,2	0.81	0
4	SO4	B	1111	-	4,4,4	0.38	0	6,6,6	0.08	0
3	EDO	A	1102	-	3,3,3	0.28	0	2,2,2	0.24	0
4	SO4	A	1112	-	4,4,4	0.33	0	6,6,6	0.14	0
3	EDO	A	1107	-	3,3,3	0.23	0	2,2,2	0.50	0
4	SO4	A	1108	-	4,4,4	0.36	0	6,6,6	0.19	0
3	EDO	B	1105	-	3,3,3	0.06	0	2,2,2	0.17	0
3	EDO	A	1104	-	3,3,3	0.37	0	2,2,2	0.17	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	EDO	B	1107	-	-	1/1/1/1	-
2	NAG	A	1101	1	-	4/6/23/26	0/1/1/1
3	EDO	B	1103	-	-	1/1/1/1	-
2	NAG	B	1101	1	-	0/6/23/26	0/1/1/1
3	EDO	A	1105	-	-	0/1/1/1	-
3	EDO	A	1102	-	-	1/1/1/1	-
3	EDO	A	1106	-	-	1/1/1/1	-
5	GOL	B	1102	-	-	4/4/4/4	-
3	EDO	A	1107	-	-	1/1/1/1	-
3	EDO	B	1106	-	-	1/1/1/1	-
3	EDO	A	1103	-	-	1/1/1/1	-
3	EDO	B	1104	-	-	0/1/1/1	-
3	EDO	B	1105	-	-	1/1/1/1	-
3	EDO	A	1104	-	-	1/1/1/1	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	NAG	C1-O5-C5	4.20	117.81	112.19
2	A	1101	NAG	C1-C2-N2	2.90	115.00	110.43
2	B	1101	NAG	C2-N2-C7	-2.42	119.66	122.90

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1102	GOL	C1-C2-C3-O3
5	B	1102	GOL	O2-C2-C3-O3
2	A	1101	NAG	C4-C5-C6-O6
2	A	1101	NAG	O5-C5-C6-O6
5	B	1102	GOL	O1-C1-C2-C3

There are no ring outliers.

7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1106	EDO	1	0
5	B	1102	GOL	1	0
4	B	1113	SO4	1	0
3	B	1104	EDO	3	0
4	B	1111	SO4	1	0
4	A	1112	SO4	1	0
3	A	1107	EDO	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	421/462 (91%)	0.05	12 (2%)	53 57	31, 58, 90, 127	2 (0%)
1	B	409/462 (88%)	0.12	10 (2%)	59 63	37, 61, 105, 127	1 (0%)
All	All	830/924 (89%)	0.09	22 (2%)	56 60	31, 59, 98, 127	3 (0%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	39	ALA	4.7
1	B	88	LEU	3.6
1	A	145	TYR	3.4
1	B	91	TRP	3.3
1	B	300	ALA	3.1

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	EDO	B	1104	4/4	0.63	0.23	74,82,91,94	0
4	SO4	A	1109	5/5	0.78	0.11	118,123,135,143	0
3	EDO	A	1106	4/4	0.79	0.14	75,92,92,97	0
4	SO4	B	1109	5/5	0.81	0.11	129,137,148,151	0
4	SO4	A	1113	5/5	0.82	0.10	93,103,120,123	0
4	SO4	B	1112	5/5	0.82	0.08	91,97,109,113	0
3	EDO	A	1105	4/4	0.84	0.28	57,75,77,83	0
3	EDO	A	1102	4/4	0.85	0.20	60,76,77,78	0
2	NAG	A	1101	14/15	0.85	0.10	63,78,86,91	0
3	EDO	A	1107	4/4	0.86	0.41	50,63,66,66	0
3	EDO	B	1103	4/4	0.87	0.10	79,79,87,100	0
3	EDO	B	1105	4/4	0.87	0.20	65,66,71,81	0
3	EDO	A	1104	4/4	0.88	0.20	62,68,71,75	0
4	SO4	B	1108	5/5	0.88	0.09	83,101,102,111	0
4	SO4	B	1110	5/5	0.89	0.09	79,85,98,103	0
3	EDO	B	1106	4/4	0.89	0.14	70,73,76,78	0
3	EDO	A	1103	4/4	0.90	0.13	73,75,75,76	0
3	EDO	B	1107	4/4	0.90	0.12	65,68,69,72	0
5	GOL	B	1102	6/6	0.90	0.09	64,75,82,87	0
4	SO4	A	1112	5/5	0.94	0.06	72,79,83,96	0
4	SO4	B	1111	5/5	0.94	0.06	73,85,97,101	0
2	NAG	B	1101	14/15	0.95	0.07	49,53,60,62	0
4	SO4	B	1113	5/5	0.95	0.04	80,85,97,101	0
4	SO4	A	1111	5/5	0.95	0.07	71,73,88,89	0
4	SO4	A	1108	5/5	0.96	0.11	67,69,75,92	0
4	SO4	A	1110	5/5	0.96	0.10	60,65,71,83	0

6.5 Other polymers [i](#)

There are no such residues in this entry.