wwPDB X-ray Structure Validation Summary Report (i)

Feb 6, 2024 – 04:23 PM EST

PDB ID	:	2GX8
Title	:	The Crystal Structure of Bacillus cereus protein related to NIF3
Authors	:	Minasov, G.; Brunzelle, J.S.; Shuvalova, L.; Vorontsov, I.I.; Collart, F.R.; Joachimiak, A.; Anderson, W.F.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2006-05-08
Resolution	:	2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

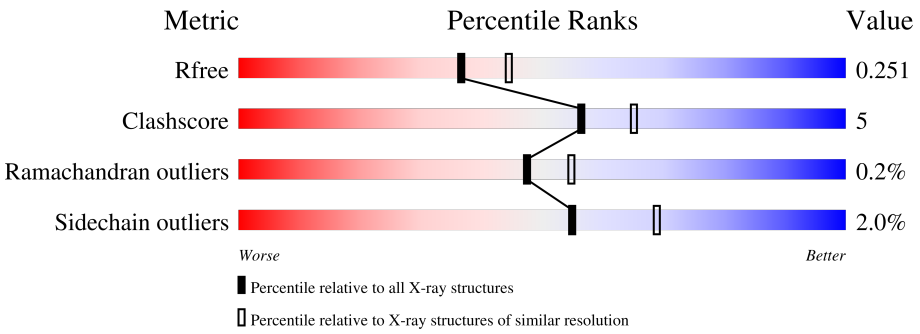
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	397	81% 8% • 10%
1	B	397	81% 10% • 9%
1	C	397	79% 12% • 8%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9083 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 NIF3-related protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	359	2785	1777	477	520	11	0	1	0
1	B	361	2788	1777	479	521	11	0	0	0
1	C	364	2805	1786	482	526	11	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	cloning artifact	GB 29897924
A	-22	HIS	-	expression tag	GB 29897924
A	-21	HIS	-	expression tag	GB 29897924
A	-20	HIS	-	expression tag	GB 29897924
A	-19	HIS	-	expression tag	GB 29897924
A	-18	HIS	-	expression tag	GB 29897924
A	-17	HIS	-	expression tag	GB 29897924
A	-16	SER	-	cloning artifact	GB 29897924
A	-15	SER	-	cloning artifact	GB 29897924
A	-14	GLY	-	cloning artifact	GB 29897924
A	-13	VAL	-	cloning artifact	GB 29897924
A	-12	ASP	-	cloning artifact	GB 29897924
A	-11	LEU	-	cloning artifact	GB 29897924
A	-10	GLY	-	cloning artifact	GB 29897924
A	-9	THR	-	cloning artifact	GB 29897924
A	-8	GLU	-	cloning artifact	GB 29897924
A	-7	ASN	-	cloning artifact	GB 29897924
A	-6	LEU	-	cloning artifact	GB 29897924
A	-5	TYR	-	cloning artifact	GB 29897924
A	-4	PHE	-	cloning artifact	GB 29897924
A	-3	GLN	-	cloning artifact	GB 29897924
A	-2	SER	-	cloning artifact	GB 29897924
A	-1	ASN	-	cloning artifact	GB 29897924

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	cloning artifact	GB 29897924
B	-23	MET	-	cloning artifact	GB 29897924
B	-22	HIS	-	expression tag	GB 29897924
B	-21	HIS	-	expression tag	GB 29897924
B	-20	HIS	-	expression tag	GB 29897924
B	-19	HIS	-	expression tag	GB 29897924
B	-18	HIS	-	expression tag	GB 29897924
B	-17	HIS	-	expression tag	GB 29897924
B	-16	SER	-	cloning artifact	GB 29897924
B	-15	SER	-	cloning artifact	GB 29897924
B	-14	GLY	-	cloning artifact	GB 29897924
B	-13	VAL	-	cloning artifact	GB 29897924
B	-12	ASP	-	cloning artifact	GB 29897924
B	-11	LEU	-	cloning artifact	GB 29897924
B	-10	GLY	-	cloning artifact	GB 29897924
B	-9	THR	-	cloning artifact	GB 29897924
B	-8	GLU	-	cloning artifact	GB 29897924
B	-7	ASN	-	cloning artifact	GB 29897924
B	-6	LEU	-	cloning artifact	GB 29897924
B	-5	TYR	-	cloning artifact	GB 29897924
B	-4	PHE	-	cloning artifact	GB 29897924
B	-3	GLN	-	cloning artifact	GB 29897924
B	-2	SER	-	cloning artifact	GB 29897924
B	-1	ASN	-	cloning artifact	GB 29897924
B	0	ALA	-	cloning artifact	GB 29897924
C	-23	MET	-	cloning artifact	GB 29897924
C	-22	HIS	-	expression tag	GB 29897924
C	-21	HIS	-	expression tag	GB 29897924
C	-20	HIS	-	expression tag	GB 29897924
C	-19	HIS	-	expression tag	GB 29897924
C	-18	HIS	-	expression tag	GB 29897924
C	-17	HIS	-	expression tag	GB 29897924
C	-16	SER	-	cloning artifact	GB 29897924
C	-15	SER	-	cloning artifact	GB 29897924
C	-14	GLY	-	cloning artifact	GB 29897924
C	-13	VAL	-	cloning artifact	GB 29897924
C	-12	ASP	-	cloning artifact	GB 29897924
C	-11	LEU	-	cloning artifact	GB 29897924
C	-10	GLY	-	cloning artifact	GB 29897924
C	-9	THR	-	cloning artifact	GB 29897924
C	-8	GLU	-	cloning artifact	GB 29897924
C	-7	ASN	-	cloning artifact	GB 29897924

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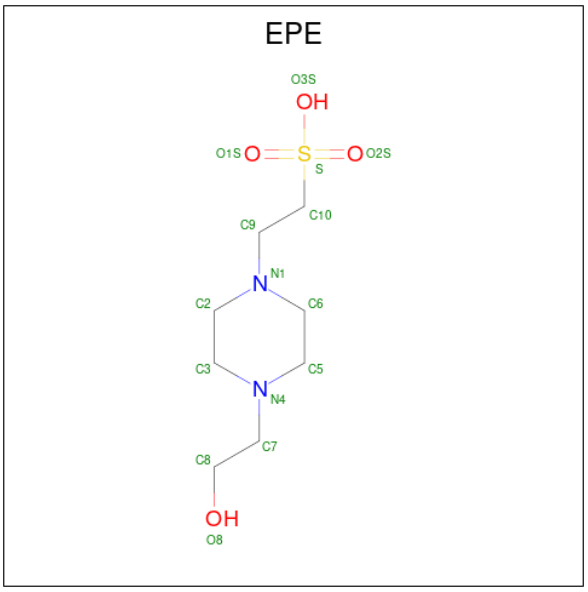
Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	LEU	-	cloning artifact	GB 29897924
C	-5	TYR	-	cloning artifact	GB 29897924
C	-4	PHE	-	cloning artifact	GB 29897924
C	-3	GLN	-	cloning artifact	GB 29897924
C	-2	SER	-	cloning artifact	GB 29897924
C	-1	ASN	-	cloning artifact	GB 29897924
C	0	ALA	-	cloning artifact	GB 29897924

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	15	8	2	4	1	0	0
			Total	C	N	O	S		
3	A	1	15	8	2	4	1	0	0

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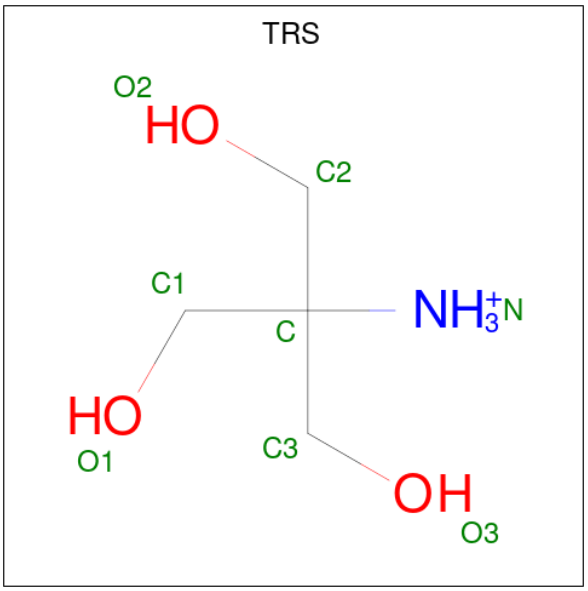
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	B	1	15	8	2	4	1	0	0
			Total	C	N	O	S		
3	C	1	15	8	2	4	1	0	0
			Total	C	N	O	S		
3	C	1	15	8	2	4	1	0	0

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



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

- Molecule 5 is water.

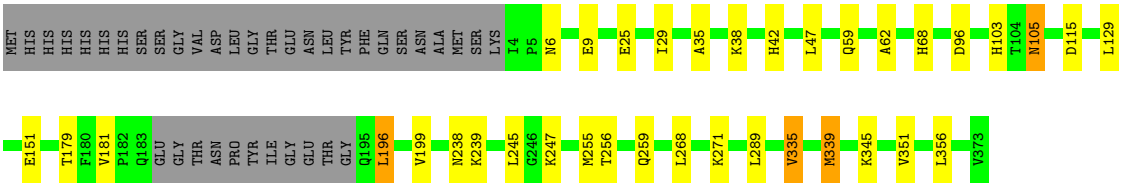
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	233	233	233	0	0
			Total	O		
5	B	220	220	220	0	0
			Total	O		
5	C	163	163	163	0	0

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. 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. 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.

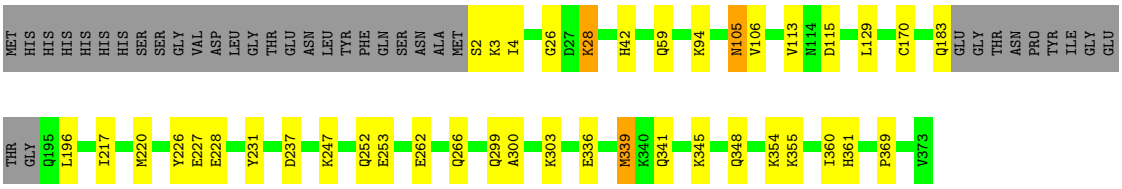
- Molecule 1: NIF3-related protein

Chain A:



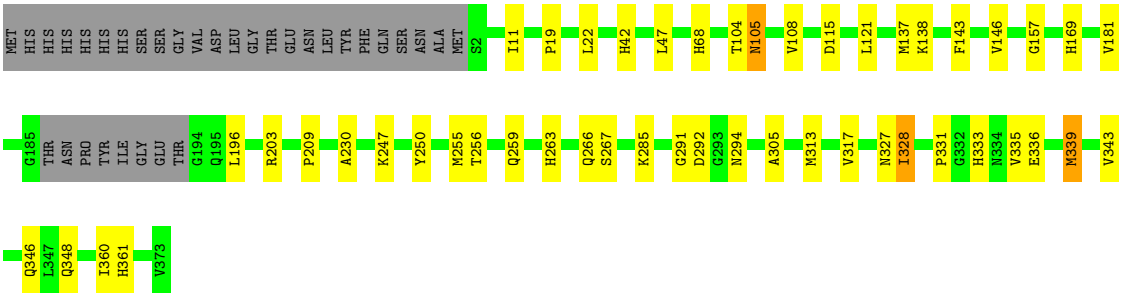
- Molecule 1: NIF3-related protein

Chain B:



- Molecule 1: NIF3-related protein

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	95.04Å 95.04Å 260.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.96 – 2.20 28.07 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.8 (28.96-2.20) 97.8 (28.07-2.20)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.89 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.196 , 0.261 0.191 , 0.251	Depositor DCC
R_{free} test set	3421 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	44.5	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9083	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, TRS, 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	0.66	0/2837	0.83	0/3838
1	B	0.75	1/2839 (0.0%)	0.84	1/3839 (0.0%)
1	C	0.65	0/2856	0.79	0/3861
All	All	0.68	1/8532 (0.0%)	0.82	1/11538 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	183	GLN	C-O	17.40	1.56	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	237	ASP	CB-CG-OD1	6.07	123.77	118.30

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	2785	0	2815	24	0
1	B	2788	0	2825	27	0
1	C	2805	0	2837	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	30	0	34	0	0
3	B	15	0	17	1	0
3	C	30	0	36	1	0
4	A	8	0	11	2	0
5	A	233	0	0	3	0
5	B	220	0	0	3	0
5	C	163	0	0	2	0
All	All	9083	0	8575	85	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 5.

The worst 5 of 85 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:105:ASN:H	1:B:105:ASN:HD22	1.08	0.99
1:A:105:ASN:H	1:A:105:ASN:HD22	1.06	0.98
1:A:105:ASN:HD22	1:A:105:ASN:N	1.81	0.77
1:C:105:ASN:HD22	1:C:105:ASN:H	1.30	0.76
1:B:348:GLN:HE22	1:B:360:ILE:H	1.33	0.74

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	356/397 (90%)	347 (98%)	8 (2%)	1 (0%)	41 46
1	B	357/397 (90%)	347 (97%)	9 (2%)	1 (0%)	41 46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	360/397 (91%)	349 (97%)	11 (3%)	0	100	100
All	All	1073/1191 (90%)	1043 (97%)	28 (3%)	2 (0%)	47	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	GLU
1	B	227	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	297/328 (90%)	289 (97%)	8 (3%)	44	57
1	B	298/328 (91%)	292 (98%)	6 (2%)	55	69
1	C	299/328 (91%)	295 (99%)	4 (1%)	69	81
All	All	894/984 (91%)	876 (98%)	18 (2%)	55	69

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	105	ASN
1	C	339	MET
1	C	328	ILE
1	B	28	LYS
1	B	369	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	263	HIS
1	C	266	GLN
1	C	348	GLN

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Mol	Chain	Res	Type
1	B	213	GLN
1	B	195	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	EPE	A	377	-	15,15,15	0.97	1 (6%)	18,20,20	2.04	5 (27%)
3	EPE	C	377	-	15,15,15	0.70	1 (6%)	18,20,20	1.99	5 (27%)
3	EPE	C	376	-	15,15,15	1.15	1 (6%)	18,20,20	1.94	6 (33%)
4	TRS	A	378	-	7,7,7	1.04	1 (14%)	9,9,9	1.27	1 (11%)
3	EPE	A	376	-	15,15,15	0.92	1 (6%)	18,20,20	1.74	5 (27%)
3	EPE	B	376	-	15,15,15	0.97	1 (6%)	18,20,20	1.94	4 (22%)

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	EPE	A	377	-	-	6/9/19/19	0/1/1/1
3	EPE	C	377	-	-	6/9/19/19	0/1/1/1
3	EPE	C	376	-	-	2/9/19/19	0/1/1/1
4	TRS	A	378	-	-	6/9/9/9	-
3	EPE	A	376	-	-	8/9/19/19	0/1/1/1
3	EPE	B	376	-	-	3/9/19/19	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	376	EPE	C10-S	4.04	1.83	1.77
3	B	376	EPE	C10-S	3.41	1.82	1.77
3	A	377	EPE	C10-S	3.40	1.82	1.77
3	A	376	EPE	C10-S	3.13	1.82	1.77
4	A	378	TRS	O2-C2	-2.43	1.34	1.42

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	377	EPE	C5-N4-C3	5.56	121.35	108.83
3	B	376	EPE	O3S-S-C10	4.62	113.23	105.77
3	A	377	EPE	C5-N4-C3	4.43	118.80	108.83
3	B	376	EPE	C7-N4-C5	4.20	121.98	111.23
3	C	376	EPE	C5-N4-C3	4.09	118.03	108.83

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	376	EPE	C9-C10-S-O2S
3	A	376	EPE	C9-C10-S-O3S
3	A	377	EPE	C8-C7-N4-C5
3	A	377	EPE	S-C10-C9-N1
3	A	377	EPE	C9-C10-S-O2S

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	377	EPE	1	0
4	A	378	TRS	2	0
3	B	376	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)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.