



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 11:07 AM EDT

PDB ID : 5DIM / pdb_00005dim
Title : Mutant toxin in 'native' space group
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Deposited on : 2015-09-01
Resolution : 3.32 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

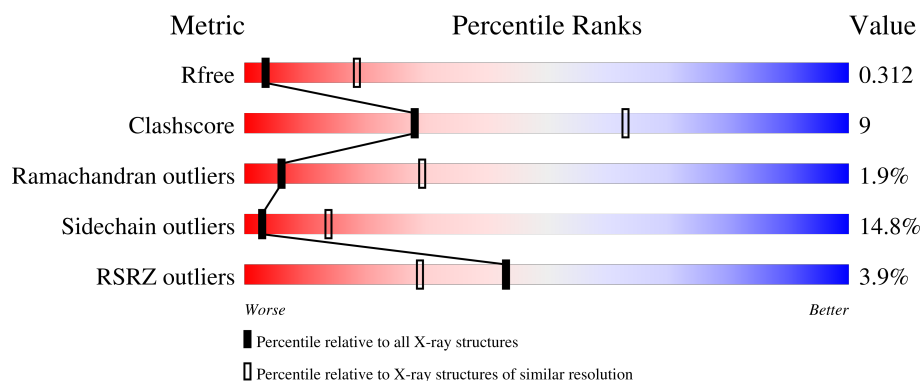
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.32 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	1153 (3.34-3.30)
Clashscore	190562	1193 (3.34-3.30)
Ramachandran outliers	187476	1172 (3.34-3.30)
Sidechain outliers	187428	1171 (3.34-3.30)
RSRZ outliers	180081	1153 (3.34-3.30)

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	472	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3692 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.

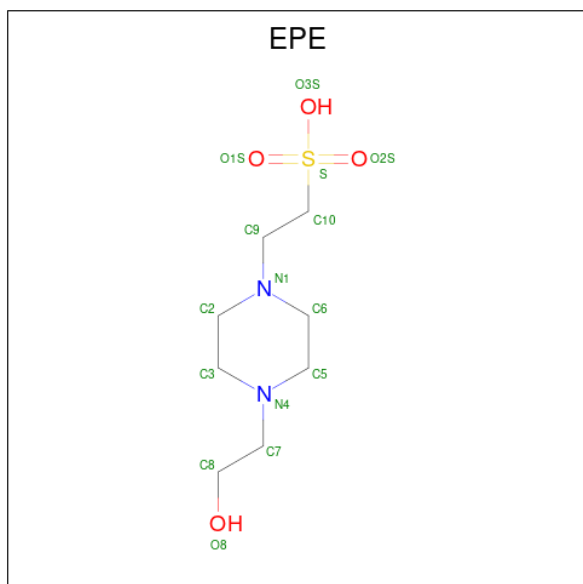
- Molecule 1 is a protein called Perfringolysin O.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	465	Total	C	N	O	S	0	1	0
			3675	2320	617	734	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	ALA	THR	cloning artifact	UNP P0C2E9
A	197	TRP	ASN	engineered mutation	UNP P0C2E9
A	459	ALA	CYS	cloning artifact	UNP P0C2E9

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



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

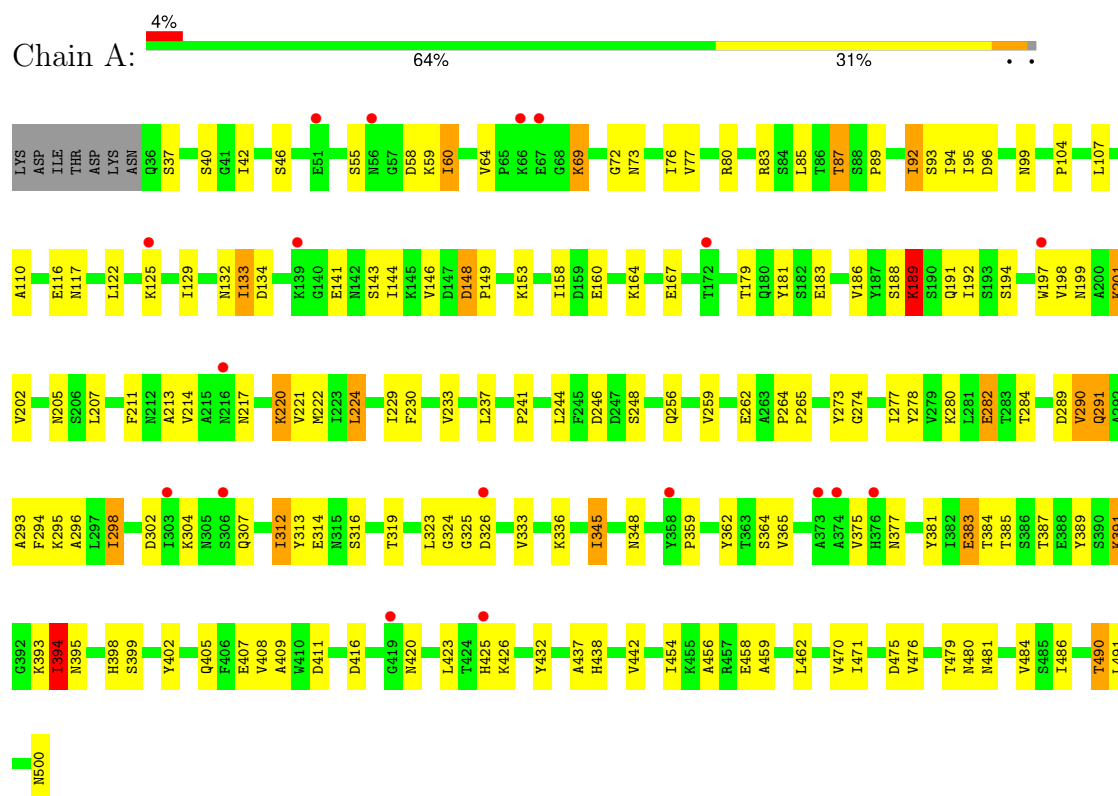
- Molecule 3 is water.

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

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: Perfringolysin O



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	46.95Å 207.33Å 212.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.27 – 3.32 47.27 – 3.32	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.27-3.32) 99.9 (47.27-3.32)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 3.33Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.236 , 0.297 0.252 , 0.312	Depositor DCC
R_{free} test set	827 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å ²)	62.6	Xtriage
Anisotropy	0.837	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 73.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	3692	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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: 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	0.88	0/3750	1.38	21/5093 (0.4%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	470	VAL	N-CA-C	-10.50	102.78	111.81
1	A	480	ASN	N-CA-C	-9.42	101.68	113.55
1	A	362	TYR	N-CA-C	6.57	119.20	108.55
1	A	189	LYS	N-CA-C	-6.43	104.35	111.36
1	A	59	LYS	CA-C-N	5.71	132.24	121.97
1	A	59	LYS	C-N-CA	5.71	132.24	121.97
1	A	213	ALA	CA-C-N	5.68	127.72	120.56
1	A	213	ALA	C-N-CA	5.68	127.72	120.56
1	A	416	ASP	CA-CB-CG	5.32	117.92	112.60
1	A	167	GLU	N-CA-C	-5.29	106.89	113.55
1	A	296	ALA	CA-C-N	5.20	127.20	120.44
1	A	296	ALA	C-N-CA	5.20	127.20	120.44
1	A	141	GLU	CA-C-N	5.18	128.98	120.63
1	A	141	GLU	C-N-CA	5.18	128.98	120.63
1	A	420	ASN	CA-C-N	5.13	128.13	120.95
1	A	420	ASN	C-N-CA	5.13	128.13	120.95
1	A	134	ASP	CA-CB-CG	5.09	117.69	112.60
1	A	394	ILE	N-CA-CB	5.08	116.26	110.72
1	A	96	ASP	CA-CB-CG	5.03	117.63	112.60
1	A	248	SER	CA-C-N	5.01	127.88	120.91
1	A	248	SER	C-N-CA	5.01	127.88	120.91

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3675	0	3619	65	0
2	A	15	0	17	0	0
3	A	2	0	0	0	0
All	All	3692	0	3636	65	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (65) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ILE:HD11	1:A:375:VAL:HG21	1.66	0.76
1:A:222:MET:HE1	1:A:298:ILE:HD11	1.70	0.74
1:A:402:TYR:HB3	1:A:490:THR:HG23	1.69	0.73
1:A:220:LYS:HG2	1:A:290:VAL:HG21	1.71	0.73
1:A:411:ASP:HB3	1:A:423:LEU:HD22	1.74	0.68
1:A:198:VAL:HG11	1:A:278:TYR:OH	1.96	0.66
1:A:222:MET:CE	1:A:298:ILE:HD11	2.26	0.65
1:A:481:ASN:HB2	1:A:500:ASN:HB2	1.84	0.59
1:A:188:SER:HB3	1:A:191:GLN:HB3	1.84	0.59
1:A:107:LEU:HB3	1:A:122:LEU:HB3	1.86	0.57
1:A:291:GLN:HE21	1:A:295:LYS:HD2	1.70	0.56
1:A:454:ILE:HG21	1:A:484:VAL:HG21	1.88	0.56
1:A:129:ILE:HD11	1:A:244:LEU:HA	1.88	0.55
1:A:201:LYS:HD3	1:A:205:ASN:HD21	1.72	0.54
1:A:37:SER:HB3	1:A:40:SER:HB3	1.90	0.53
1:A:69:LYS:HG3	1:A:76:ILE:HB	1.90	0.52
1:A:277:ILE:HD11	1:A:348:ASN:HB2	1.91	0.52
1:A:222:MET:HE2	1:A:294:PHE:HB3	1.92	0.52
1:A:454:ILE:HD12	1:A:476:VAL:HG21	1.93	0.51
1:A:222:MET:CE	1:A:294:PHE:HB3	2.40	0.51
1:A:319:THR:HA	1:A:333:VAL:O	2.09	0.51
1:A:290:VAL:HG23	1:A:291:GLN:H	1.75	0.50
1:A:83:ARG:HG3	1:A:383:GLU:HB2	1.93	0.50
1:A:407:GLU:HG3	1:A:432:TYR:OH	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:PRO:HB3	1:A:197:TRP:CE2	2.47	0.49
1:A:42:ILE:HD13	1:A:241:PRO:HB3	1.94	0.49
1:A:199:ASN:HB3	1:A:202:VAL:HG23	1.93	0.49
1:A:80:ARG:HG2	1:A:384:THR:HG22	1.95	0.49
1:A:393:LYS:HB2	1:A:442:VAL:HG13	1.95	0.49
1:A:409:ALA:HB1	1:A:425[A]:HIS:CE1	2.48	0.48
1:A:207:LEU:HD13	1:A:280:LYS:HB2	1.95	0.48
1:A:94:ILE:HD13	1:A:359:PRO:HB2	1.95	0.48
1:A:282:GLU:O	1:A:316:SER:HA	2.13	0.48
1:A:222:MET:HE3	1:A:224:LEU:HD21	1.95	0.48
1:A:456:ALA:HB3	1:A:471:ILE:HG22	1.95	0.48
1:A:230:PHE:CD2	1:A:274:GLY:HA2	2.49	0.47
1:A:85:LEU:HG	1:A:381:TYR:HE1	1.81	0.46
1:A:394:ILE:HD13	1:A:408:VAL:HG11	1.97	0.46
1:A:181:TYR:CZ	1:A:183:GLU:HB2	2.50	0.46
1:A:186:VAL:HG22	1:A:192:ILE:HD13	1.98	0.46
1:A:293:ALA:HB1	1:A:313:TYR:CE1	2.51	0.46
1:A:99:ASN:HB2	1:A:359:PRO:HG2	1.99	0.45
1:A:395:ASN:OD1	1:A:442:VAL:HG22	2.16	0.45
1:A:104:PRO:HD3	1:A:273:TYR:OH	2.17	0.45
1:A:437:ALA:HA	1:A:438:HIS:HA	1.79	0.45
1:A:188:SER:HB3	1:A:191:GLN:CB	2.46	0.45
1:A:407:GLU:HG3	1:A:432:TYR:CZ	2.52	0.44
1:A:110:ALA:HB3	1:A:264:PRO:HD2	1.99	0.44
1:A:259:VAL:HG13	1:A:265:PRO:HD3	1.99	0.44
1:A:189:LYS:HA	1:A:211:PHE:CE1	2.53	0.43
1:A:87:THR:HG21	1:A:197:TRP:HE1	1.84	0.43
1:A:230:PHE:CD1	1:A:230:PHE:N	2.84	0.43
1:A:95:ILE:HD12	1:A:117:ASN:HB2	2.02	0.42
1:A:290:VAL:HG12	1:A:312:ILE:HG21	2.02	0.42
1:A:148:ASP:O	1:A:153:LYS:HD3	2.20	0.42
1:A:77:VAL:HG23	1:A:389:TYR:HE2	1.83	0.41
1:A:158:ILE:HG12	1:A:233:VAL:HG21	2.02	0.41
1:A:295:LYS:HA	1:A:298:ILE:HD12	2.03	0.41
1:A:277:ILE:HD13	1:A:345:ILE:HA	2.01	0.41
1:A:133:ILE:HG12	1:A:233:VAL:HG22	2.03	0.41
1:A:221:VAL:HG22	1:A:282:GLU:HG2	2.03	0.41
1:A:73:ASN:HA	1:A:391:LYS:HE3	2.02	0.41
1:A:398:HIS:HA	1:A:486:ILE:HG13	2.03	0.40
1:A:181:TYR:OH	1:A:183:GLU:HB2	2.21	0.40
1:A:294:PHE:O	1:A:298:ILE:HG13	2.21	0.40

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	464/472 (98%)	417 (90%)	38 (8%)	9 (2%)	6 29

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	ASP
1	A	60	ILE
1	A	72	GLY
1	A	325	GLY
1	A	459	ALA
1	A	302	ASP
1	A	391	LYS
1	A	149	PRO
1	A	324	GLY

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	412/418 (99%)	351 (85%)	61 (15%)	3 14

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	SER
1	A	55	SER
1	A	60	ILE
1	A	64	VAL
1	A	69	LYS
1	A	87	THR
1	A	92	ILE
1	A	93	SER
1	A	116	GLU
1	A	125	LYS
1	A	132	ASN
1	A	133	ILE
1	A	143	SER
1	A	144	ILE
1	A	146	VAL
1	A	148	ASP
1	A	160	GLU
1	A	164	LYS
1	A	179	THR
1	A	189	LYS
1	A	194	SER
1	A	201	LYS
1	A	214	VAL
1	A	217	ASN
1	A	220	LYS
1	A	224	LEU
1	A	229	ILE
1	A	237	LEU
1	A	246	ASP
1	A	256	GLN
1	A	262	GLU
1	A	282	GLU
1	A	284	THR
1	A	289	ASP
1	A	290	VAL
1	A	291	GLN
1	A	298	ILE
1	A	304	LYS
1	A	307	GLN
1	A	312	ILE
1	A	314	GLU
1	A	323	LEU
1	A	326	ASP

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Mol	Chain	Res	Type
1	A	336	LYS
1	A	345	ILE
1	A	364	SER
1	A	365	VAL
1	A	377	ASN
1	A	383	GLU
1	A	385	THR
1	A	387	THR
1	A	394	ILE
1	A	399	SER
1	A	405	GLN
1	A	426	LYS
1	A	458	GLU
1	A	462	LEU
1	A	475	ASP
1	A	479	THR
1	A	490	THR
1	A	491	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	ASN
1	A	108	GLN
1	A	130	ASN
1	A	199	ASN
1	A	205	ASN
1	A	291	GLN
1	A	315	ASN
1	A	500	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	EPE	A	601	-	15,15,15	1.08	1 (6%)	19,20,20	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
2	EPE	A	601	-	-	6/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	EPE	C10-S	-4.06	1.71	1.77

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	EPE	C8-C7-N4-C3
2	A	601	EPE	C9-C10-S-O2S
2	A	601	EPE	C9-C10-S-O3S
2	A	601	EPE	N4-C7-C8-O8
2	A	601	EPE	C9-C10-S-O1S

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Mol	Chain	Res	Type	Atoms
2	A	601	EPE	C8-C7-N4-C5

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	465/472 (98%)	0.36	18 (3%)	43 29	26, 62, 100, 117	1 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	TRP	3.2
1	A	303	ILE	2.9
1	A	376	HIS	2.8
1	A	425[A]	HIS	2.8
1	A	419	GLY	2.7
1	A	51	GLU	2.6
1	A	306	SER	2.5
1	A	172	THR	2.5
1	A	67	GLU	2.4
1	A	373	ALA	2.3
1	A	66	LYS	2.2
1	A	125	LYS	2.2
1	A	56	ASN	2.1
1	A	139	LYS	2.1
1	A	358	TYR	2.0
1	A	374	ALA	2.0
1	A	216	ASN	2.0
1	A	326	ASP	2.0

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

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
2	EPE	A	601	15/15	0.78	0.24	76,83,106,107	0

6.5 Other polymers [i](#)

There are no such residues in this entry.